OCS Study
BOEM 2020-036

Ecological Drivers of Brown Pelican Movement Patterns, Health, and Reproductive Success in the Gulf of Mexico

US Department of the Interior
Bureau of Ocean Energy Management
New Orleans Office

BOEM
Bureau of Ocean Energy Management

OCS Study
BOEM 2020-036

Ecological Drivers of Brown Pelican Movement Patterns, Health, and Reproductive Success in the Gulf of Mexico

Authors

Juliet S. Lamb
Yvan G. Satgé
Rochelle A. Streker
Patrick G.R. Jodice

Prepared under BOEM Contract
M12PG00014
by
US Geological Survey
South Carolina Cooperative Fish and Wildlife Unit
260 Lehotsky Hall
Clemson University
Clemson, SC 29634

Published by

US Department of the Interior
Bureau of Ocean Energy Management
New Orleans Office

New Orleans, LA
June 2020

DISCLAIMER

This study was funded, in part, by the US Department of the Interior, Bureau of Ocean Energy Management (BOEM), Environmental Studies Program, Washington, DC, through Interagency Agreement Number M12PG00014 with the US Geological Survey South Carolina Cooperative Fish and Wildlife Research Unit. This report has been technically reviewed by BOEM, and it has been approved for publication. The views and conclusions contained in this document are those of the authors and should not be interpreted as representing the opinions or policies of BOEM. This report has been peer reviewed and approved for publication consistent with USGS Fundamental Science Practices (https://pubs.usgs.gov/circ/1367/).

REPORT AVAILABILITY

To download a PDF file of this report, go to the US Department of the Interior, Bureau of Ocean Energy Management Data and Information Systems webpage (http://www.boem.gov/Environmental-Studies-EnvData/), click on the link for the Environmental Studies Program Information System (ESPIS), and search on 2020-036. The report is also available at the National Technical Reports Library at https://ntrl.ntis.gov/NTRL/.

CITATION

Lamb JS, Satgé YG, Streker RA, Jodice PGR. 2020. Ecological drivers of brown pelican movement patterns, health, and reproductive success in the Gulf of Mexico. New Orleans (LA): US Department of the Interior, Bureau of Ocean Energy Management. 234 p. Report No.: BOEM 2020-036. Contract No.: M12PG00014.

ABOUT THE COVER

An Eastern brown pelican (*Pelecanus occidentalis carolinensis*) returns to its nest on Raccoon Island, Louisiana. Photo credit: S. Desaivre 2014.

Contents

List of Figures

List of Tables

List of Abbreviations and Acronyms

Short Form	Long Form
A:G	albumin-to-globulin ratio
A1G	Alpha 1 globulin
A2G	Alpha 2 globulin
AIC	Akaike's information criterion
ALT	alanine aminotransferase
ANOVA	analysis of variance
ASE	accelerated solvent extraction
AST	aspartate aminotransferase
BCI	body condition index
BOEM	Bureau of Ocean Energy Management
BPR	biomass provisioning rate
BUN	blood urea nitrogen
CBC	complete blood count
CI	confidence interval
CORT	corticosterone
CPK	creatine phosphokinase
CV	coefficient of variation
DDT	Dichlorodiphenyltrichloroethane
DOI	US Department of the Interior
DSR	daily survival rate
EPR	energy provisioning rate
GGT	Gamma glutamyl transferase
GLM	generalized linear model
GMT	Greenwich Mean Time
GOM	Gulf of Mexico
GoMAMN	Gulf of Mexico Avian Monitoring Network
GoMMAPPS	Gulf of Mexico Marine Assessment Program for Protected Species
HDLc	high density lipoprotein cholesterol
HMM	hidden Markov model
HSD	honestly significant difference
JFH	junk-food hypothesis
MRPP	multi-response permutation procedure
NOAA	National Oceanic and Atmospheric Administration
OMI	outlying mean index
PAH	polycyclic aromatic hydrocarbons
PC1	first principal component axis
PCA	principal component analysis

Short Form	Long Form
PCR	polymerase chain reaction
PCV	packed cell volume
PTT	platform transmitter terminal
SD	standard deviation
SE	standard error
sumALK	sum of alkylated PAHs
sumPAH	sum of all PAHs
sumPAR	sum of parent PAHs
UD	utilization distribution
UPLC	ultra-performance liquid chromatograph
VLDLc	very low density lipoprotein cholesterol
WBC	white blood cells

ACKNOWLEDGMENTS

This work was supported by the US Department of the Interior, Bureau of Ocean Energy Management (BOEM), Environmental Studies Program, Washington, DC, through Inter-Agency Agreement Number M12PG00014 with the US Geological Survey and the South Carolina Cooperative Fish and Wildlife Research Unit. Special thanks to Jeff Gleason for his efforts conceptualizing and initiating this research. Dave Moran (BOEM) provided administrative and contract support. Additional funding and/or in-kind support was provided by a Sigma Xi Grant-in-Aid of Research awarded to Juliet Lamb, by the Oiled Wildlife Care Network for GPS tracking used in the assessment of effects of satellite tags on bird behavior, and by Clemson University. Field research was conducted with permission from the Clemson University Animal Care and Use Committee (2013-026). Permitting for field data collection was provided by the US Geological Survey Bird Banding Laboratory (22408), Texas Parks and Wildlife (SPR-0113-005), Audubon Texas, The Nature Conservancy in Texas, Louisiana Department of Wildlife and Fisheries (LNHP-13-058 and LNHP-14-045), and the Florida Fish and Wildlife Conservation Commission (LSSC-13-00005). All laboratory work for analysis of corticosterone took place at University of Portland, in collaboration with Kathleen O'Reilly, and Clemson University facilities. Genetic sexing of pelicans was conducted in collaboration with Amy MacMillan (Buffalo State University) and Ludovic Besaury (Clemson University). Plasma chemistry and hematology samples were analyzed at the Avian & Wildlife Laboratory, University of Miami, Miami, Florida. Samples for polycyclic aromatic hydrocarbons were analyzed at the University of Connecticut Center for Environmental Sciences and Engineering by Christopher Perkins and Anthony Provatas. Michael Hooper and John Rodgers provided advice and insight on collection and interpretation of polycyclic aromatic hydrocarbon (PAH) data. Christine Fiorello advised on interpretation of data from blood panels. Videos of pelican behaviour were recorded by Justin Cox of the One Health Institute, University of California, Davis.

For assistance and logistical support with field research and laboratory activities, we thank Elizabeth Ford, Steve Desaivre, Tim and Peggy Wilkinson, Mark Dumesnil, Beau Hardegree, Amanda Hackney, Scott Walter, John Dindo, Caroline Poli, Ludovic Besaury, Tommy King, and technicians from Texas Audubon Society and The Nature Conservancy. The Dauphin Island Sea Lab and the Buccaneer Yacht Club provided assistance and support for research in Mobile Bay. Christine Fiorello, Michael Ziccardi, Kyra Mills-Parker, Robert McMorran, Richard Golightly, Laird Henkel, and the International Bird Rescue staff at the Los Angeles Oiled Bird Care and Education facilities assisted with research conducted in California associated with the assessment of tags on pelican behavior. Carolyn Wakefield and Brenna Byler provided administrative support, and Brenna Byler assisted with editing and layout of the final report. Katherine McFadden (now deceased) was originally a Co-PI on the project and developed the initial research plan for health and contaminants. We also acknowledge Lisa Ferguson, Robert Baldwin, Robert Suryan, Yoichiro Kanno, Pablo Yorio, Emily Weiser, Beth Ross, Anthony Diamond, John Dindo, Troy Farmer, Robert Ronconi, Don Lyons, Pete Tuttle, Brian Spears, Mary Ann Ottinger, Dave Moran, Maureen DeZeeuw, and Jeri Wisman for input at various stages of the project.

The South Carolina Cooperative Fish and Wildlife Research Unit is jointly supported by the US Geological Survey, South Carolina DNR, and Clemson University. Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the US Government.

1 Introduction

The number of marine wind and tidal energy (Pelc and Fujita 2002) developments and proposals (Pelc and Fujita 2002), as well as petroleum extractions (Freudenburg and Gramling 1994), is increasing to meet the growing global demand for energy. However, the rapid progress of energy extraction and development often outpaces the understanding of these actions' effects on marine systems and their organisms (Ward et al. 1979, Burke et al. 2012). Assessments of post-installation offshore energy projects document that effects on marine species, whether positive or negative, can be more significant than anticipated (Boesch and Rabalais 1987, Daan and Mulder 1996, Sammarco et al. 2004). Energy extraction can impact marine species directly (e.g., adult mortality) and indirectly through various pathways, including: compromised condition from contaminants exposure, altered availability or distribution of prey, altered behavior, or reduced reproductive output (Alonso-Alvarez et al. 2007, Dean et al. 2017, Haney et al. 2014).

Marine birds are valuable and commonly used models for studying the impacts of threats on their environment, such as offshore development influences on the broader marine ecosystem (Furness and Greenwood 1993). Seabirds are relatively accessible compared to other marine vertebrates, are wide-ranging migrators, and their foraging behaviors increase the likelihood for interactions with energy installation (Wiese and Jones 2001). Seabirds also rely on a variety of above- and below-water habitats, including both terrestrial breeding colonies and pelagic foraging grounds (Hunt 1990, Pinaud and Weimerskirch 2005). As top-level marine predators they are particularly vulnerable to bioaccumulation of contaminants (Walker 1990, Pérez et al. 2008) and may provide indications of perturbations at lower trophic levels (Thompson et al. 1998, Wiese and Jones 2001). Understanding the effects of existing development and predicting the impacts of future development on seabirds requires a thorough understanding of seabird population dynamics, behavior, physiology, and habitat use under baseline conditions (Ballance 2007, Soanes et al. 2013, Jodice et al. 2019). However, such information is often not collected until after development or contamination has altered baseline processes. Also, the direct influence of anthropogenic stressors on demographic parameters in the marine environment varies widely and can be difficult to estimate (Burger 1993, Uhlmann et al. 2005).

The Gulf of Mexico (GOM) contains a high density of oil and gas infrastructure and coastal development. It also has a rich assemblage of nearshore seabirds, pelagic seabirds, wading birds, migratory waterfowl, and shorebirds (Duncan and Havard 1980). The region is of year-round importance to seabirds, including local breeding populations and breeders from distant locations that winter along the Gulf Coast (Mikuska et al. 1998, Montevecchi et al. 2012, Haney et al. 2014, Jodice et al. 2019). Many terrestrial areas of known importance to breeding, migrating, and wintering waterbirds have been designated for protection at state and federal levels. However, few marine protected areas have been designated in the GOM, and much of the marine environment there, including offshore foraging and migratory habitat of seabirds, is open to oil development, ship traffic, fishing, and contaminants release (Coleman et al. 2004, Davis et al. 2000).

Because of its distribution patterns, behavior, and known sensitivity to chemical and oil contaminants exposure (Blus 1982, King et al. 1985, Shields 2014), the brown pelican (*Pelecanus occidentalis*) is potentially a good indicator of species-level impacts from interactions with coastal and marine development (Wilkinson et al. 1994, Jodice et al. 2019). The species is widespread throughout the Northern GOM and common during all phases of the annual cycle. Brown pelicans nest along the Gulf coast from Corpus Christi Bay, Texas through southwestern Florida. During the non-breeding season, the species can be found throughout the Northern GOM as well as along the Yucatan Peninsula, Cuba, and as far south as Guatemala. Because of the spatial extent of this annual range, the species is exposed to a

substantial array of environmental and anthropogenic stressors that may influence its health, habitat use, and survival. The species is generally regarded by managers and stakeholders in the region as a good indicator of ecosystem health for estuarine and nearshore habitats. For example, brown pelicans were recently included as a priority species for monitoring in the Seabird Monitoring Plan for the Gulf of Mexico Avian Monitoring Network (GoMAMN) (Jodice et al. 2019). Despite the species' long history as a focus for conservation and restoration efforts, much of the information required to understand pelican population dynamics and habitat requirements (i.e., adult and fledgling mortality, dispersal, site fidelity, diet composition, foraging behavior, migration patterns, and nonbreeding habitat use) remains unknown or is poorly understood (Briggs et al. 1981 for habitat use, Schreiber and Mock 1988 for survival rates, Wood et al. 1995 for Florida colony site fidelity, and Shields 2014, Jodice et al. 2019 for addressing multiple data gaps).

In this study, we used several unique research avenues to address questions regarding movement, habitat use, physiology, and reproductive ecology of brown pelicans. Our research encompassed six principal objectives: (1) assessing reproductive ecology; (2) assessing baseline habitat use by the species in this region, particularly individual and regional variability; (3) assessing baseline health and exposure to contaminants in this region, particularly individual and regional variability; (4) predicting overlap of pelicans with anthropogenic risk factors; (5) understanding pathways by which changes to adult movement patterns might influence reproductive ecology and how to best measure such effects in wild populations; and (6) assessing movement ecology in the context of interactions with key prey resources. The remainder of the report is organized with a common introduction (Chapter 1), common methods (Chapter 2), and overall summary (Chapter 8). Chapter 3 through Chapter 7 are focused on specific data streams and objectives. Within chapters 3 through 7, the structure includes a brief introduction to the topic, followed directly by a combination of individual results and interpretation. Figures and tables appear at the end of each chapter.

1.1 Baseline Habitat Use

Animals use various habitats for different needs, including: foraging, sheltering from predators, thermoregulating, raising young, moving among patches, and migrating stopovers (Börger et al. 2008, Morrison et al. 2012). Each need requires specific habitat characteristics and features; thus an animal's interaction with its environment varies depending on its location on the landscape and its fine-scale movement and behavioral patterns (Garthe and Hüppop 2004). Seabirds are unique among many avian species in that they regularly require terrestrial and aquatic habitats, although the extent to which each is used varies between nearshore and pelagic seabirds. For example, in wide-ranging pelagic and semi-pelagic seabirds, habitat use typically changes between the breeding season, when birds are central-place foragers based in terrestrial colonies, and the nonbreeding season, when birds rely primarily on marine habitats (Weimerskirch and Wilson 2000). Within each stage of the breeding cycle, habitat use also depends on individual characteristics (Bearhop et al. 2006), phenology (Catry et al. 2009), colony size and location (Lewis et al. 2001), and environmental features (Tew Kai et al. 2009). These factors all contribute to variation in individual energy requirements, resulting in differences in foraging strategies and habitat preferences (Daunt et al. 2006, Phillips et al. 2009).

Compared to pelagic species, nearshore seabirds, such as brown pelicans, generally occupy smaller foraging ranges that extensively overlap human-dominated marine and coastal areas year-round (Thaxter et al. 2012). These smaller areas contain a higher diversity of habitat features and prey species assemblages (Becker and Bessinger 2003) and respond to different oceanographic processes than do large marine ecosystems (Gray 1997). Despite these habitat differences, many of the same individual, colonial, and environmental factors that influence habitat choice in pelagic species also operate within nearshore seabird populations (e.g., Erwin 1977, Suryan et al. 2000). However, the role of density-dependent prey depletion in determining movement patterns has been well-established in pelagic seabirds (e.g., Ainley et

al. 2004, Ford et al. 2007, Ballance et al. 2009), but has received little study in nearshore seabirds. Additionally, partial migration (Lack 1944) influences individual differences in year-round seabird movements but has received little study in nearshore systems.

A principal goal of our work was to establish a framework for understanding pelican movement patterns under baseline conditions (i.e., not immediately associated with a recent disturbance event), including preferred habitat characteristics, sources of individual variation in movement, and dispersal and habitat selection throughout the year (breeding and the lesser studied non-breeding periods). This work provides an important comparison point for studying the effects of any future changes to the GOM marine environment on brown pelican movements and energetic expenditure, as well as addressing key ecological questions in relation to the spatial ecology of nearshore seabirds.

1.2 Risk Exposure

Evaluating the effects of environmentally heterogeneous stressors on mobile wildlife requires understanding of the spatial and temporal overlap between individuals and threats as well as the extent of risk individuals encounter in relation to adverse effects based upon their habitat use and behavior (Desholm and Kahlert 2005, Jaeger et al. 2005, Beaudry et al. 2010). Increases in the spatial and temporal resolution of individual tracking technologies have resulted in a shift toward individual-based analysis of habitat requirements (Hebblewhite and Haydon 2010); however, habitat assessments derived from individual tracking data often incorporate only presence or absence across landscapes and do not account for behavior (Tremblay et al. 2009). Nearshore seabirds experience higher levels of human disturbance and habitat modification of breeding, resting, and foraging grounds than pelagic species (Croxall et al. 2012). Habitat features that concentrate nearshore seabirds and their prey may also concentrate risk factors such as pollutants, bycatch, and anthropogenic disturbance. Temporal variation in habitat needs and movement patterns can significantly contribute to the likelihood of risk exposure and the degree to which risk factors impact individuals and populations (Beaudry et al. 2010). The effects of environmental perturbations on seabirds depend on temporal factors (e.g., breeding stage) that influence their behavior and use of affected areas (Eppley and Rubega 1990, Montevecchi et al. 2012).

Due to its large size and persistence along human-dominated coastlines, the brown pelican represents one of the most high-profile nearshore seabirds for much of the GOM and southeastern US. The species was reduced to near-extinction by exposure to dichlorodiphenyltrichloroethane (DDT) during the mid-twentieth century (McNease et al. 1992) and continues to experience high mortality rates during oil spills (USFWS 2011, DWH NRDAT 2016). Despite these factors, baseline assessments of health and exposure to petroleum-based contaminants are minimal for the species in the region (Jodice et al. 2019). Furthermore, within the GOM, the source of data on brown pelican movements are from observations of a small number of marked and banded birds across limited geographic areas (Schreiber and Mock 1988, Stefan 2008, King et al. 2013, Walter et al. 2014), despite their prevalence throughout the region.

The discrete nature of existing data makes it difficult to reliably predict how, or at what spatial and temporal scales, individuals may interact with current or future acute and chronic contamination from oil spills or other pollution sources. For example, until recently, home range size for the species was based on limited data from VHF telemetry or inferred from observations of individuals foraging in relation to the nearest colony, neither of which provide the spatial or temporal resolution needed to assess risk exposure. Therefore, if significant winter and migratory ranges of pelicans from different breeding colonies overlap with each other, and if these areas also overlap with contaminants (i.e., spilled oil) then relatively localized oiling events in certain GOM areas during the non-breeding season could affect birds from multiple colonies and result in population-level impacts. Moreover, though efforts to restore injured populations following stressor events, such as oil spills, generally target colony sites, most threats associated with marine energy development (e.g., acute or chronic spills) also affect offshore foraging

grounds and therefore the risk to individuals and populations extends across multiple ecosystems (Campagna et al. 2011). Developing reference ranges for various health metrics (e.g., hematology and serum chemistry) will improve management, conservation, and response activities (e.g., responses to oil spoils, hurricanes) for the species. Understanding the year-round overlap of brown pelicans with risk factors and contaminants (e.g., polycyclic aromatic hydrocarbons, PAHs) throughout the region could improve targeted mitigation efforts. Affected at-sea habitats could be linked to individual breeding colonies and improvements can be made in predicting which portions of the GOM-wide metapopulation are likely to be affected by contamination events.

1.3 Ecology and Physiology of Reproduction

Brown pelicans have been a species of high conservation concern in the GOM for decades (Schreiber 1980, Nelson 2005). Following the 2010 *Deepwater Horizon* (DWH) oil spill, which caused widespread mortality of pelicans and other coastal birds (Haney et al. 2014), restoration activities for seabirds increased across the Northern GOM. However, to be successful, continued restoration efforts will require data beyond levels currently available. For example, detailed data are required on the relationship between environmental conditions at the nest site and reproductive success, which can be affected by numerous characteristics (e.g., density of breeders, exposure to inclement weather, vegetation characteristics, landscape features, and weather) (Robinson and Dindo 2011, Walter et al. 2013, Lamb 2016). Reproductive output may also be limited by environmental variables beyond the nest site or even the nesting island. For example, weather and stochastic events, such as storms and flooding, can decrease egg and chick survival either directly (e.g., through overwash) or indirectly (e.g., through exposure) (Ramos et al. 2002, Frederiksen et al. 2006, Sherley et al. 2012, Bonter et al. 2014). Understanding which site-specific factors contribute to the success of nests will inform restoration efforts and better allow projects to maximize population-level impacts for the focal species.

Impacts of acute or chronic environmental stressors on wildlife are typically quantified directly using mortality rates derived from carcass counts (Piatt et al. 1990, Burger 1993) or multi-year census data (Wiens et al. 1996, Yaukey 2012). Data are subsequently incorporated into demographic models to estimate the population-level effects of stressors (Haney et al. 2014). In addition to causing immediate mortality, stressors can impact seabirds sublethally through secondary pathways, including: reduced habitat quality (Cheng et al. 2009, Williams et al. 2010), compromised physical condition (Romero and Wikelski 2001), physiological and genetic modifications (Møller and Mousseau 2011), and/or increased susceptibility to existing threats (e.g., disease or environmental fluctuation) (Balseiro et al. 2005, Whitehead 2013). Many indirect and sublethal stressors subsequently impact demographic processes by reducing reproductive fitness in surviving individuals (Krebs and Burns 1977, Peterson 2001), but are often not explicitly or adequately addressed in demographic calculations and projections. Moreover, the breeding process itself is likely to compound impacts of environmental stress as reductions in the adult condition and habitat suitability make it less likely for breeders to meet the energetic demands of territory defense, gestation, and provisioning young (Butler et al. 1988, Gannon and Willig 1994). Demographic models that do not accurately incorporate secondary effects of environmental stressors on breeding success and recruitment cannot accurately predict or quantify the complex population-level impacts of environmental perturbations (Peterson et al. 2003, Haney et al. 2014).

Despite widespread understanding of the capacity of sublethal environmental stress to negatively affect reproduction and recruitment, it can be difficult to determine the most appropriate endpoints for measuring these effects (Smits and Fernie 2013). There must be a pre-existing understanding of the level of variation in reproductive parameters expected under baseline conditions for post-disturbance measurements to be informative (Teal and Howarth 1984, Velando et al. 2005). Such data are not always available for species of interest before catastrophic events (Eppley 1992). Moreover, the collection of reproductive data can be time- and labor-intensive and can involve researcher disturbance, which may make it difficult to implement rapidly in the wake of an unexpected external change (Wiens et al. 1984). Snapshot measures of reproductive health (Jakob et al. 1996, Benson et al. 2003), which can be collected during a single visit with minimal disturbance, allow for rapid data collection across large areas after disturbance events; however, the relationship of such snapshot measurements to demographic parameters of interest (e.g., reproductive success) must be evaluated to select appropriate metrics.

Stress hormone production offers a broadly applicable metric for assessing the impacts of environmental stressors on free-living wildlife populations (Romero and Wikelski 2001). Corticosterone (CORT) is the principal glucocorticosteroid stress hormone in birds, rodents, reptiles, and amphibians, and is frequently used as a measure of individual stress responses to environmental conditions and disturbance (Marra and Holberton 1998, Kitaysky et al. 2001, Blas et al. 2005, Bonier et al. 2006, Almasi et al. 2009). Stress hormones are upregulated in response to perceived stressors, prompting short-term behavioral and physiological modifications (McEwen et al. 1997). Over time, however, chronic elevation in CORT levels in response to chronic stress may negatively affect organism health by compromising immunosuppression, growth rates, body condition, and behavior (Sapolsky et al. 2000). CORT levels can be complicated by individual physiology (Angelier et al. 2007) and may change over life stages (Williams et al. 2008, Bonier et al. 2009). Within avian taxa, measuring CORT in altricial young controls for some of these influences because their exposure to stress is localized and their range of behavioral responses is restricted (Kitaysky et al. 2003, Eggert et al. 2010). Elevated stress in early life can result in severe developmental consequences (Kitaysky et al. 2003, Müller et al. 2009, Spencer et al. 2008, Butler et al. 2009). Therefore, the CORT stress response can be used to test whether chick development, condition, growth, and/or survival are affected by acute and/or chronic environmental stress during nestling development. CORT stress response can also explore mechanisms underlying survival, reproductive performance, and population dynamics (Kitaysky et al. 2010).

Though CORT levels in blood plasma can be elevated by short-term factors (e.g., stress resulting from capture; Love et al. 2003, Romero and Reed 2005), CORT in avian feathers provides a more sustained record of stress levels over days or weeks (Bortolotti et al. 2008, Harms et al. 2010). Feather CORT measurements allow for a direct comparison of nestling condition between different breeding habitats, where variations in nutrition, contamination, predation, and parental attendance may affect chronic chick stress even if no physiological differences are apparent (Bortolotti et al. 2008, Harms et al. 2010). Recent laboratory and field studies have demonstrated that chronic nutritional stress elevates feather CORT levels in both captive and free-living seabirds (Will et al. 2015). We undertook a direct comparison of body condition index (BCI) with feather CORT as a predictor of fledging success and post-fledging survival. This information will help to create rapid evaluation metrics for brown pelicans and other seabirds following environmental perturbations and is already being considered as a monitoring tool by the Gulf of Mexico Avian Monitoring Network (Jodice et al. 2019).

1.4 Foraging Ecology

The ability of apex marine predators to survive and reproduce depends primarily on the production and availability of sufficient food resources at lower trophic levels to meet the energetic requirements of both adults and young (Frederiksen et al. 2006). Both the quantity and quality of available prey can influence survival, reproduction, and population dynamics in apex predators, and reductions in either prey availability or quality can affect demographic parameters (Trites and Donnelly 2003, Jodice et al. 2006, Hjernquist and Hjernquist 2010). A switch to nutrient-poor prey may cause reduced fitness even if abundant prey is available (Rosen and Trites 2000, Österblom et al. 2008). Both experimental (Rosen and Trites 2004, Romano et al. 2006) and field (Golet et al. 2000, Kadin et al. 2012, Cohen et al. 2014) studies have found that switching high-lipid prey for lower-energy alternatives can result in measurable reductions in breeding parameters, even when the amount and rate of delivery are unchanged. Most of these data come from cold-water systems, where prey species are likely to have higher lipid reserves on average than warm-water species (Stickney and Torres 1989). Few data are available from tropical systems (waters $\geq$ 23°C average temperature: Ballance and Pitman 1999), in which the relatively low variation in lipid levels among fish species may reduce the range of energetic values in prey species available to top predators.

Even in a prey community with limited interspecific variation in energy density, differences in prey quality may still exist. For example, the junk-food hypothesis posits that energy density, particularly as represented by lipid density, is positively related to productivity. Optimal foraging theory (MacArthur and Pianka 1966) takes into account the energy a predator obtains from prey and the energy it expends in finding, capturing, handling, and digesting prey. An optimal forager is expected to maximize the net energy gain, calculated as the difference between energy obtained from prey and energy expended in foraging. Thus, differences in both predator foraging strategies and prey behavior could result in variation in the amount of energy predators obtain from different prey types, even among prey species with similar energy content. Marine predators employ a wide variety of foraging strategies, which allow them to exploit different prey types and forage in different sections of the water column (Ashmole 1971, Spear and Ainley 1998). Tropical seabirds, most of which forage near the water's surface, compete for limited prey resources using a variety of capture techniques including skimming, surface-plunging, surface-seizing, plunge-diving, and, occasionally, pursuit-diving (Ballance and Pitman 1999). Though the various modifications of surface-feeding techniques allow some partitioning of prey, species at tropical latitudes do not partition prey species as extensively as high-latitude species that forage at a wider variety of depths and often specialize on different prey items. Thus, the definition of junk food should include not only the energy density of prey but also how readily prey can be captured given the foraging techniques used by the species of interest. Differences in availability between prey species reflect both abundance, which is an absolute measure, and accessibility, which can differ from predator to predator both within and among species.

Studies of brown pelicans in the tropical waters of the GOM have suggested reliance on a single prey species, Gulf menhaden (*Brevoortia patronus*), which can constitute over 95% of biomass in diet samples in the central Northern GOM (Arthur 1919). The Gulf menhaden is one of the most abundant forage fish species in the region and supports the second-largest fishery in the United States (Vaughan et al. 2007). Samples collected from eastern portions of the species' GOM range, where menhaden are naturally less abundant than in the central and western portions of the GOM, show a decreasing trend in the predominance of menhaden in pelican diets (Fogarty 1981). Although this suggests that relative availability plays a role in the frequency of menhaden in pelican diets, it is unclear how or whether this underlying variation in diet composition affects demographic parameters, or how menhaden compares energetically to other available alternatives. Furthermore, pelicans may benefit from land- and ship-based supplemental feeding at fishing piers or trawlers (Wickliffe and Jodice 2010), although the extent of this behavior and its effect on nutritional status remains unclear. Because of the role of brown pelicans as an indicator species for assessing the effects of contamination and oil pollution in the region (Shields 2014), understanding underlying dietary and demographic variation provides a crucial reference point for quantifying the effects of environmental stressors.

2 Methods

2.1 Study Area

2.1.1 Colony Selection

Research was conducted at pelican colonies within each of the BOEM planning areas (east, central, and west) within the Gulf of Mexico (GOM) (Figures 2.1 and 2.2). Study sites extended from the Florida panhandle in the east to the central coast of Texas in the west. We selected colonies within each of the three BOEM planning areas to sample among different levels of oil and gas development (central = most developed, east = least developed, and western = intermediate development between east and central). We did not extend our research onto colonies in peninsular Florida due primarily to logistical constraints and to avoid adding additional ecological variability into the data (e.g., the addition of mangrove ecosystems).

Individual tracking was conducted from seven colonies in the GOM. We selected 2–3 colonies each in the western (Texas), central (Louisiana, Mississippi, and Alabama), and eastern (Florida) planning areas of the GOM and selected 2–3 colonies each in the western (Texas), central (Louisiana, Mississippi, and Alabama), and eastern (Florida) planning areas of the GOM between 83° and 98° W and 27° and 31° N (Figure 2.1; hereafter, with respect to colonies and the coastal zone in general, the term "Northern GOM" refers to this area). Within planning areas, colonies were 50–150 km (31–93 miles) apart, and colony groups in separate planning areas were 500–600 km (311–373 miles) apart. The number of breeding pairs at each study site was obtained from the most recent (i.e., 2013) colonial waterbird censuses for each planning area (Colibri Ecological Consulting and R. G. Ford Consulting, 2015, Texas Colonial Waterbird Survey[1]). We also sampled and observed nestlings between 2013 and 2015. Colony locations varied between years but included nine colonies throughout the study area (Figure 2.2).

We extracted environmental variables, including two fixed parameters (bathymetry and bottom substrate) and three seasonally-averaged parameters (salinity, sea surface temperature, and chlorophyll a) to compare underlying environmental conditions between colonies. Salinity, sea surface temperature, and chlorophyll a were measured at distances of 10, 20, 50, and 150 km from the colony, bounded by the coastline and up to 50 km offshore, sea surface temperature, and chlorophyll a were measured at distances of 10, 20, 50, and 150 km from the colony, bounded by the coastline and up to 50 km offshore. These distances were chosen post-hoc to GPS tracking to represent the range of movements we observed among individuals. We used a multivariate hierarchical clustering approach (K-means clustering; MacQueen 1967) to compare environmental characteristics between sites, and tested the resultant clusters using multi-response permutation procedure (MRPP) on a Euclidean distance matrix (McCune and Grace 2002). All statistical analyses were conducted in R (R Core Team 2014).

[1] See the survey here: https://tpwd.texas.gov/huntwild/wild/wildlife_diversity/tcws/data.phtml

2.1.2 Data Collection Schedule

Between 26 April and 3 July 2013, we captured 60 adult pelicans that were breeding on colonies throughout the study area and equipped them with GPS transmitters. During the same period, we collected physical measurements and feather samples from 3–4 week-old chicks at the six colonies used for adult tracking.

Between 26 April and 29 May 2014, we captured 25 additional adult pelicans that were breeding on colonies throughout the study area and equipped them with GPS transmitters. We also conducted chick sampling and monitored nest productivity at four colonies along the central and northern Texas coast from 8 May to 31 July 2014.

Between 5 May and 31 July 2015, we conducted chick sampling and monitored nest productivity at three colonies in the Florida panhandle and one in Alabama. We did not capture or GPS tag any additional adults in 2015.

On 26 June 2016, we captured and attached GPS transmitters to five additional adult pelicans on Gaillard Island, Alabama.

Between 20 April and 15 August 2017, we monitored nests and chicks on Gaillard Island and Cat Island, Alabama.

Between 20 April and 15 August 2018, we monitored nests and chicks on Gaillard Island, Alabama. Cat Island did not support nesting pelicans in 2018.

2.2 Individual Tracking

2.2.1 Capture Technique

We captured and attached GPS transmitters to 90 breeding adult Eastern brown pelicans, with a maximum of one adult captured per nest. Capture and handling techniques were approved by the Clemson University Institutional Animal Care and Use Committee, in consultation with a veterinarian. All adults were captured on nests using leg nooses during the late incubation and early chick-rearing stages. If eggs were present in the nest, they were replaced with porcelain eggs during capture to prevent damage. If chicks were present, they were moved to the nest edge to avoid injury. Following successful captures, a plastic laundry basket was placed over the nest to protect nest contents from weather and predation during the adult's absence. The basket was used to eliminate the possibility of predation and we did not observe chicks behaving abnormally during or following this procedure. Median handling time was 17.5 minutes (range = 11–35 mins) from capture to release. After release, we observed individuals for several minutes to ensure that they displayed normal flight, swimming, and balance capabilities. Observation methods and results are described below.

2.2.2 Measurements and Sampling

We collected physiological measurements from all individuals while captured. Immediately following capture, we measured body mass using a 5000 g Pesola spring scale (Pesola, Switzerland) to ensure that the transmitter weight represented less than 3% of total body mass. The minimum body mass necessary to attach a 65 g GPS unit was 2167 g, therefore pelicans falling below this threshold were released without a transmitter. Immediately after weighing, we collected 5 mL of metatarsal blood in a heparinized vacutainer for later analysis of contaminants and blood chemsitry. We also collected 0.1µL of metatarsal blood on filter paper, which was later used to determine the sex of all captured adults through PCR (Itoh et al. 2001). Then, we obtained three contour feathers for contaminant analysis. Finally, we measured

three indices of skeletal size: wing chord length (last wing joint to tip of longest primary feather) and culmen length (forehead to bill tip) using a 600 mm wing rule, and tarsus length (intertarsal to metatarsal joint) using a 150 mm caliper.

2.2.3 Tracking Devices

2.2.3.1 Transmitter Specifications and Duty Cycle

We tracked adults using GPS-PTTs (65 g, GeoTrak, Inc., Apex, North Carolina: 65 units) and GPS-GSM (65 g, NorthStar Science and Technology, Oakton, Virginia: 20 units), which records GPS locations and uploads data to Argos satellites and cellular towers, respectively, for remote download. Transmitters were programmed to collect 12 locations day $^{-1}$ during breeding (April–August; every 90 minutes from 1030 to 0130 GMT), 10 locations day^{-1} during pre- and post-breeding (September–October and February–March; every 90 minutes from 0700–0100 GMT), and 8 locations day^{-1} during winter (November–January; every 120 minutes from 0700–0100 GMT). We obtained an average error estimate for GPS points from transmitters at known locations (N = 220) of 4.03 ± 2.79 m (13.22 ± 9.15 ft).

2.2.3.2 Transmitter Attachment

Transmitters were attached dorsally between the wings using a backpack-style Teflon ribbon harness (Dunstan 1972; Figure 2.3). Transmitters were constructed with sloped fronts, to minimize resistance while diving. Transmitters ranged from 1.5–2.9% of individual body mass (μ = 1.9%), below the generally accepted 3% threshold for seabirds (Phillips et al. 2003). To elevate the transmitters and prevent feathers from covering the solar panels and antenna, we mounted each device on a 6 mm thick neoprene pad that also extended 6 mm beyond the perimeter of the transmitter in all directions.

2.2.3.3 Transmitter Effects

2.2.3.3.1 Captive Trial

Because captured birds often leave the colony area after release to forage or loaf off-site (i.e., short-term absence), we chose to assess the immediate behavioral responses of pelicans to transmitter attachment in a captive setting. Five adult California brown pelicans were fitted with transmitters at the Los Angeles Oiled Bird Care and Education Center rehabilitation facility in San Pedro, California on 11 June 2015. All GPS-tagged pelicans were released into a 6 × 13 × 5 m outdoor net enclosure containing a large pool and several perches 4 m in elevation, and filmed for 142 minutes pre- and 167 minutes post-transmitter attachment, for a total of approximately five hours (309 minutes) per individual and 25 total observation hours. Four additional adult pelicans that did not receive transmitters were housed in the same enclosure and filmed during the same time period to serve as behavioral controls. We used EthoLog 2.2 software (Ottoni 2000) to record behaviors of all pelicans during the pre- and post-attachment phases. Behaviors included six mutually exclusive state events: resting (standing or crouching with neck folded and head down), loafing (standing or crouching with head up), perching (standing or crouching in a location accessible only by flight), preening (using beak or feet to rearrange feathers), swimming (floating or paddling on water), and flying and nine instant events: walking, flapping (extension and rapid movement of wings while standing), stretching (brief extension of neck, leg or wing), scratching, eating, shaking (brief, rapid movement while stationary), bathing (splashing in water), diving (completely underwater) and interacting (behaviors directed at or responding to other individuals). To minimize observer bias, all coding was done by the same observer (JSL).

2.2.3.3.2 Field Trial

1–3 days after capture, we conducted 3 h behavioral observations on all adults present at their respective nests during return visits to the colony (N = 35 individuals; 105 observation hours). The remaining individuals were not present during return visits, either due to nest abandonment or because their mates were attending the nest at the time. Before beginning the observation, we selected a nearby (≤ 2 m; ≤ 6.6 ft distance) nest at the same phenological stage as each focal nest (i.e., incubation, small chick-rearing, or large chick-rearing) to act as a control for comparison of behaviors.

During the observation, we recorded the behavior of the tagged and control adults at 5 min intervals, classifying behaviors as resting, preening, alert (moving nest material, interacting with chicks or neighboring birds; comparable to loafing behavior in the captive trials), or agitated (alert and exhibiting signs of stress). For each individual observed, we calculated the percent of time spent in each behavior. We then separated the data by behavior and used paired t-tests to compare frequency of each individual behavior between GPS-tagged and untagged individuals.

Using transmitter data, we recorded the duration in days of subsequent nest attendance by all GPS-tagged individuals. Nests were considered active for as long as adults continued to visit the nesting colony at least once a day. We inferred approximate hatching dates from nest stage at date of capture, and considered breeding successful if adult attendance continued for at least 60 days after hatch. This represents the minimum age at which nestlings are likely to fledge (Shields 2014). For pelicans that re-nested following capture, we interpreted the start of attendance at the new site as the beginning of incubation and used a 90-day cutoff for successful breeding, incorporating 30 days of incubation time (Shields 2014) in addition to the 60-day fledging period.

2.2.3.3.3 Statistical Analyses

To assess post-capture nest survival and breeding success, we used a generalized linear modeling (GLM) framework to model the probability that parents would attend the nest for at least 60 days after hatch, which we interpreted as likely brood success (binomial function, Bernoulli with logit link). To test which factors most influenced post-capture nest persistence and reproductive success, we included handling time, nest stage, sex, body condition index (BCI; residual of the linear relationship between mass and culmen length), capture date, and capture location (i.e., breeding colony) as predictor variables. We used a Hosmer-Lemeshow Goodness of Fit test to assess the fit of the global model and compared models using Akaike's Information Criterion (AIC) values. Models were preferred if they resulted in a decrease in AIC of ≤ 2 relative to the best-fitting model, while models with Δ AIC of 4–7 were considered weakly supported (Burnham and Anderson 2004). We estimated means-parameterized model-averaged coefficients over the suite of preferred models, weighted by AIC weights.

2.3 Annual Habitat Use by Adults

Unless otherwise specified, all statistical manipulation of spatial data was conducted using the adehabitat family of packages (Calenge 2006) in R 3.2.3 (R Core Team 2014).

2.3.1 Data Screening and Interpolation

Of the 90 transmitters deployed in 2013 and 2014, 74 recorded at least one full breeding season of GPS data (87% of tagged individuals). Only these were included in subsequent analyses of reproductive success. We manually identified and removed outlying data points using a speed cutoff of 65 km hour^{-1} between successive points, which is the maximum travel speed recorded for brown pelicans (Schnell and Hellack 1978). Cleaned locations for each individual were then interpolated to regular 90-minute intervals. Because location data were not collected overnight, we chose not to interpolate tracks between

successive days, and we differentiated each day as a separate trajectory by cutting tracks between each set of two successive points separated by a gap of greater than 6 h. Subsequent analyses focused on off-colony locations (i.e., habitat use at the nest site was not analyzed here).

2.3.2 Habitat Variables

Because the scale of movement that we observed was relatively small (on the order of tens of kilometers per day, rather than hundreds of kilometers as is commonly observed in pelagic seabirds), we selected environmental variables likely to relate to the distribution of prey rather than those that might facilitate long-distance movement (e.g., prevailing winds) or visual identification of foraging areas (e.g., ocean color). We measured environmental characteristics of brown pelican habitat using seven habitat variables. Four habitat variables were constant year-round for any given point (distance to coastline, distance to river outflow, bathymetry, and bottom substrate) and three habitat variables varied by month (net primary production, sea surface salinity, and sea surface temperature) (Table 2.1). We selected these variables to represent a suite of likely drivers of nearshore habitat variation, particularly the distribution of pelican prey populations (e.g., Deegan 1990). Because limited data are available on fine-scale variations in oceanographic features (e.g., currents and eddies), and because these features have a high degree of short-term variability in coastal areas (Kaltenberg et al. 2010), we used the distance to physical features that influence the movement of water (coastline, river outflow) as proxies for these processes. Depth and bottom substrate can influence both prey distributions and oceanographic characteristics. Net primary production, which integrates chlorophyll concentrations over a range of depths (Behrenfeld and Falkowski 1997), provides an index of oceanographic productivity that influences the distribution of consumers at higher trophic levels. Salinity and temperature also influence the distribution of aquatic prey species, depending on their osmotic and thermal tolerances. Because some data were reported at finer spatial resolutions than others (Table 2.1), we standardized all variables to a resolution of 0.1 degree (approximately 10 km) grid squares. Distance values were calculated as the distance from the grid square centroid to the feature of interest. For all other variables, we resampled the data using the mean value for each 0.1 degree grid square.

2.3.3 Habitat Selection

We mapped preferred habitat characteristics in ecological space using a multivariate ordination of all habitat variables using a Hill-Smith principal components analysis (PCA; Hill and Smith 1976), which allows the inclusion of both categorical and continuous variables. For each grid square, we calculated habitat suitability as the squared Mahalanobis distance of that point from optimal location of the species in the multivariate ordination (i.e., higher distances indicate less suitable habitat) (Clark et al. 1993, Calenge et al. 2008). We projected habitat suitability as the probability of obtaining a higher squared Mahalanobis distance for that cell than the calculated value. Thus, in the final suitability scores, values closer to one indicate lower distance from the multivariate optimum location and higher habitat suitability.

To characterize individual responses to the measured habitat variables, we used an Outlying Mean Index (OMI) analysis (Dolédec et al. 2000). OMI is an ordination technique that characterizes available sites based on a set of environmental variables. It sets the mean of all conditions at zero in n-dimensional space and determines the axis that describes the maximum amount of marginality (difference from the mean) of individual animals or species in ecological space. Thus, the first axis of the OMI is the combination of environmental characteristics that best explains the position of animals across available resources. Similarly, the position of each habitat characteristic on the first axis of the OMI represents that variable's contribution to animal distributions; that is, the strength of selection on that characteristic. OMI does not assume specific resource selection functions, and allows differences in individual niche selection to be taken into account when describing the distribution of a group of animals. We conducted OMIs for each month on all individuals and habitat variables for each behavioral state. We then averaged the scores of

individuals on the first OMI axis to calculate niche location and breadth for groups within the population. We also examined the spatial distribution of breeders from different planning areas. We determined 50% and 95% kernel density estimates (utilization distributions, UD) for all individuals from each planning area using the "ks" package (Duong 2015) with a plugin bandwidth estimator (Wand and Jones 1994, Gitzen et al. 2006). We then used an Albers Conic Equal-area Projection to calculate the areas included within each planning area's 95% kernel contour, and to estimate the intersection areas between kernels from different planning areas.

2.3.4 Movement States

We fit a two-state Hidden Markov Model (HMM; Patterson et al. 2009) to the regularized movement trajectories using the moveHMM R package (Michelot et al. 2015) to distinguish resident behavior from commuting behavior. HMMs are a particularly flexible and efficient way of characterizing behavioral states from precise and regularized tracking data (Langrock et al. 2012), and thus are a good fit for GPS tracked locations. Briefly, the model assumes a priori that observed movement data are driven by underlying movement "states," characterized by a distribution of step lengths (distance between successive points) and turning angles. A Markov chain is used to describe the state parameters and classify data according to its most probable state membership.

Because we intended to characterize patterns of movement between days rather than within, we fit the model to a reduced data set of one location per day (i.e., the centroid of all locations for that day). We assumed that local (i.e., resident) movement would be characterized by short step lengths and sharp turning angles, and commuting movement by long step lengths and wide turning angles. Therefore, initial step lengths were set at 5 ± 5 km (3.1 ± 3.1 miles) for State 1 and 10 ±10 km (6.2 ± 6.2 miles) for State 2. Initial turn angles were set at π radians for State 1 and 0 radians for State 2. Angle concentration for each state was initially set at one. In subsequent analyses, all points along the trajectory for a given day were assigned to the movement state associated with that day.

2.3.5 Statistical Analyses

We modeled individual adult home ranges (50% UD, 95% UD) and migratory parameters (migration strategy, migration distance) using full-factorial generalized linear models as a function of colony size, environmental characteristics (principal component 1 and/or 2), and individual characteristics (body size (culmen length), sex, and BCI). In all cases, the global model including all five predictor variables fit the data well (Hosmer–Lemeshow goodness-of- fit tests, $p > .1$ for all). We selected the best candidate models using Akaike's information criterion (AICc) values. Models that increased AICc by $\leq$2 relative to the top model were substantially supported, while models with ΔAICc of 4–7 received weak support (Burnham and Anderson, 2004). We calculated means-parameterized model-averaged Coefficients and importance values for each predictor based on the full 95% confidence set of tested models. We conducted model selection using the "AICcmodavg" package in R (Mazerolle 2016). To assess relationships between individual predictor and response variables, we used univariate linear models.

2.4 Risk Exposure

2.4.1 Surface Pollutant Data Layer

We created a combined index of potential pollutant sources to calculate surface pollutant concentrations for each grid square (Table 2.2). These potential sources included: an ocean pollution data layer generated from shipping traffic and port locations (Halpern et al. 2008), locations of oil drilling rigs and platforms, and locations of oil and gas pipelines (Bureau of Ocean Energy Management; State of Alabama Oil and Gas Board; Louisiana: Strategic Online Natural Resources Information System; Texas General Land Office). Together, these potential pollutant sources (i.e., non-plastic pollutants) account for the majority

of acute and chronic pollution in this region (NOAA Incident news c2016). After restricting the dataset to active platforms and pipelines, we calculated oil infrastructure concentrations using values of platform counts and total lengths of pipeline per grid square. We assumed each layer contributed equally to pollution risk; therefore, we summed evenly across the three pollutant layers and normalized the resulting values to create a combined surface pollutant and oil infrastructure data layer.

2.4.2 Individual Risk Exposure

We calculated overall surface pollution overlap with potential brown pelican habitat by multiplying monthly habitat suitability values (Mahalanobis distance probabilities) by surface pollution scores for each grid square. For each interpolated individual location, we extracted the value of the surface pollution score at the corresponding grid cell. We then averaged the values of all points obtained from each individual by month to obtain a mean monthly pollution overlap index for that individual. To compare risk exposure between groups of individuals, we calculated the mean and standard deviations of individual overlap scores and tested for between-group differences using one-way analyses of variance (ANOVA). To assess the influence of behavioral states on exposure risk, we assigned resident points a weight of one and transient points weights of either one (equal exposure probability between states), 0.5 (exposure during rapid linear movement is half as likely as during slow movement), 0.1 (exposure probability is proportional to travel speed), or zero (no exposure during rapid linear movement). We then multiplied the scores of transient squares by the range of potential weights and averaged across all locations for each individual.

2.5 Ecology and Physiology of Reproduction

2.5.1 Nest Monitoring

During 2013–2015 we visited nesting colonies close to the end of the incubation period and selected 3–4 groups of focal nests per colony, each group containing 20–30 nests. In colonies containing both elevated (shrub) and ground nests, we selected closely spaced groups (i.e., with nests <2 m from each other within the group) such that nests of both types were represented to allow for comparison. During our initial visit, we photographed the nest group from marked observation points that could be accessed without disturbance to focal nests, assigned an identifying number to each nest, and recorded nest contents. During return visits, we identified nests using the numbered photograph and checked the contents of each nest from the observation point. Once nestlings reached 3–4 weeks of age, based on either hatch dates (when known) or plumage development (fully developed scapular contour feathers, remiges and rectrices in pin), we captured all monitored nestlings for sampling. Nestlings were readily captured by hand at or near nest sites. We collected physical measurements (culmen length, tarsus length, wing chord, and mass), checked for the presence of ectoparasites, and counted all ticks found on the underside of the left wing. We banded nestlings on the left tarsus with a permanent plastic band (Haggie Engraving, Crumpton, Maryland: 2014–Green; 2015–Blue) engraved with a unique three-digit white alphanumeric code. We also banded nestlings on the right tarsus with a metal engraved U.S. Geological Survey Bird Banding Lab band, with a unique nine-digit identifying code for later recovery outside the study area. Once nestlings began to disperse away from nest locations, we searched the surrounding areas of the colony with binoculars for banded chicks and recorded all bands observed. We continued observations until chicks reached at least 60 d of age.

During 2017 and 2018 we established productivity plots within brown pelican colonies on Cat Island (2017: n = 2 plots) and Gaillard Island (2017: n = 4 plots; 2018: n = 7 plots), Alabama, during early incubation. Each plot contained 10–30 nests, depending on nest configuration and proximity. All plots were spaced based on natural contours and aspects of the islands, resulting in distance between plots ranging from 60–260 m (197–840 ft). Plots were visited as often as possible given weather conditions and

logistics (range: 2–11 d) although cameras were also used to record activity and status daily. During each visit, we enumerated and recorded nest contents. We subsequently banded all nestlings of approximately 21 d of age with a permanent plastic band on the left tarsus (Haggie Engraving, Crumpton, Maryland; 2017: n = 145; 2018: n = 156) engraved with a unique three-digit white alphanumeric code. We also banded nestlings on the right tarsus with a metal engraved US Geological Survey Bird Banding Lab band, with a unique nine-digit identifying code for later recovery outside the study area.

2.5.2 Nestling Health

During 2013–2015, we compared two different assessments of nestling health: BCI (a measurement of the ratio of mass to skeletal size) and feather CORT (a measurement of stress hormone levels in nestling feathers).

2.5.2.1 Body Condition

We ran a PCA on the three measures of skeletal size (tarsus length, culmen length, and wing chord) to calculate BCI (Benson et al. 2003). Using each individual's score on the first principal components axis (PC1) as an index of overall skeletal size, we calculated the best-fitting regression equation for the relationship between mass and PC1 score. We chose a second-order polynomial to accurately represent the asymptotic nestling growth process, which is initially linear but reaches a peak and descends slightly before fledging. Finally, we calculated BCI as the standardized residual of actual body mass from the value predicted by the regression equation.

2.5.2.2 Stress Hormone Levels

At capture, we collected 3–4 scapular contour feathers from each nestling. Feathers were bagged and stored at room temperature until processing. We used a random number generator to select 150 samples per year for CORT analysis, divided equally among study colonies. Following the recommendations of Lattin et al. (2011), we restricted the range of sample sizes analyzed by excluding samples that were extremely small (< 20 mg), and dividing samples larger than 160 mg into separate units for analysis.

We closely followed the methods for feather CORT extraction and analysis originally described by Bortolotti et al. (2008). Briefly, we removed the calamus from each feather, weighed and measured feathers individually, and prepared the sample for analysis by snipping feathers into small (< 0.5 mm) pieces with scissors and transferring the entire sample into a 16 mL test tube. Each sample received 7 mL of methanol and was placed in a sonicating water bath overnight at 30 °C. Then we pipetted the methanol into a separate 13 mL tube and conducted two additional washes, each with 2.5 mL methanol. The cumulative methanol sample, totaling 12 mL, was dried down under N2, reconstituted in 200 µL buffer, and centrifuged to ensure that all accumulated CORT was dissolved in buffer. We conducted a radioimmunoassay (MP Biomedicals, LLC, Solon, Ohio: ImmuniChem™ Double Antibody CORT 125I RIA Kit) on diluted samples. Simultaneous parallelism tests indicated that the assay accurately detected CORT, and we used a standard sample with known CORT to measure intra-assay variation (1.7–1.9%) and subsampled a single feather sample to measure inter-assay variation (11%). We assessed feather CORT in a total of 365 chicks (2013: N = 126; 2014: N = 144; 2015: N = 95).

Because CORT concentrations may reflect feather quality as well as quantity (Patterson et al. 2014), we divided the total amount of CORT detected in each sample by the total mass of all feathers in the sample (pg mg^{-1}), log-transformed values to meet assumptions of normality, and calculated feather mass per unit length (mg mm^{-1}) as an index of feather quality. Because feather mass and feather length were significantly negatively correlated ($p < 0.001$, slope = -1.14 ± 0.15), we calculated the residual of the best-fitting regression line between log-transformed CORT mg-1 and feather mass per unit length, de-trended the data by subtracting the regression line, and used the adjusted values in all analyses.

2.5.3 Nest and Fledging Success

During 2013–2015, beginning approximately 8 w after hatching, we conducted regular searches of the colony for dead banded chicks and recovered all bands found. Nestlings that were observed alive at least 60 d after hatching and disappeared from the colony, but were not found dead, were presumed to have successfully fledged (Shields 2014). We used this information to determine apparent fledging success (fledglings $nest^{-1}$). We calculated plot- and colony-wide fledge success as the number of chicks fledged from observation nests, divided by the total number of nests observed. Because detectability of fledglings is high in this species and habitat, we considered this method to accurately represent overall fledging success.

During 2017–2018 (i.e., Gaillard and Cat islands, Alabama), we enumerated and recorded nest contents during each visit. During subsequent visits, we searched for banded chicks at the colony site and by observations from a small power boat within 70 m of the shore until all banded chicks were located and identified. We continued re-sighting efforts until ≥ 80% of the banded chicks were > 70 (2017) or 65 (2018) days post hatch, which we defined as "fledged" (Schreiber 1980). All monitored nests were assigned a final fate of either successful (≥ 1 egg hatched) or failed (0 eggs hatched) and all broods were assigned a final fate of either successful (≥ 1 chick fledged) or failed (0 chicks fledged). We refer to these fates as nest success and brood success, respectively.

At Gaillard and Cat islands, we measured ten environmental variables to assess in relation to daily survival rate (DSR) of nests and broods (Table 2.3). Nest-based variables that remained fixed throughout the breeding season (n = 3) included substrate beneath nest (rock from rip rap or bare ground), nest elevation above sea level (low = 0 - 0.59 m / 1.94 ft, medium = 0.60 - 0.75 m / 1.97–2.46 ft, high = 0.76–1.0 m / 2.49–3.28 ft, and berm > 1.0 m / 3.28 ft; except brood stage of 2017, when low = 0–0.75 m / 0–2.46 ft, high > 0.75 m / 2.45 ft due to restricted sample sizes within categories), and distance from nest to Mobile Bay waters (range = 1.5–127.7 m). These are hereafter referred to as fixed variables and we recorded these once at the start of the nesting season. Nest-based variables that could change during the breeding season (n= 2) included nest height above ground and vegetation cover directly above the nest. These are hereafter referred to as dynamic variables and we measured these approximately every 3 weeks (range 2–4 weeks) beginning with the establishment of the plots. We used the average value of the dynamic variables in subsequent analyses. Nest height above ground level (range = 0–156 cm) was measured by placing a level across the nest, then measuring the distance from the ground to the edge of the level (i.e. the rim of the nest). Vegetation cover (range = 0–100%) was measured using photographs taken from the center of the nest, with the lens facing the sky. These photographs were analyzed in Adobe® Photoshop® by overlaying a grid of 100 squares on each photo and enumerating the grids that contained vegetation to establish percent cover.

We also measured nest-specific temperature using HOBO temperature dataloggers (Onset Computer Corporation, Bourne, Massachusetts). Not all nests received loggers as we stratified placement of loggers (2017: n = 28 nests; 2018: n = 31 nests) by nest height (approximate even sample of nest heights within 10 cm/ 4 in intervals available from 0 cm to 140 cm/ 55 in). Dataloggers recorded the temperature of nests hourly throughout each 24 h period during incubation and chick-rearing, or until failure, and we subsequently calculated the average and maximum temperatures between each nest visit. We also measured regional weather by collecting hourly measures of barometric pressure and humidity from local climatological data and from the Mobile Downtown Airport weather station[2], which is located on the western side of Mobile Bay, 14 km to the northeast of Gaillard Island. We then calculated average and

[2] See https://www.ncdc.noaa.gov/cdo-web/datasets/GHCND/stations/GHCND:USW00013838

maximum values for each of these parameters for the time interval between each nest check from nest initiation until failure or the day the last chicks were classified as fledged.

2.5.4 Post-fledging Survival

We relied on opportunistic re-sighting of banded chicks by colony monitors and birders along the coast of the GOM to determine survival post-fledging of birds banded in 2013–2015. We received band re-sightings and recoveries reported to the US Geological Survey Bird Banding Lab, as well as directly through a dedicated web portal. Sightings and recoveries were obtained throughout the US Gulf Coast and from Mexico through January 2016. To calculate colony-wide survival rates, we used a joint live recapture–dead recovery model (Burnham 1993). We assessed survival rates at two time steps: survival to fledge (3 months after hatch) and post-dispersal survival (6 months after hatch). Dead individuals were recovered in the intervals between time steps, and individuals were considered to have survived to a new time step if they were re-sighted alive after that period ended. Because re-sightings and recoveries occurred across the entire range of the population, we fixed dispersal parameters (F) at a value of one (i.e., 100% probability that banded individuals remained in the sampling area). We derived parameter estimates for survival (S), recovery (r), and re-sighting (p) during each time interval using Markov chain Monte Carlo estimators with a burn-in of 1000 samples, followed by 4000 tuning samples and 10000 runs.

2.5.5 Statistical Analysis

For data collected in 2013–2015, we conducted a logistic regression with a binary outcome (fledged/ died) on each metric and assessed the fit of the resulting models to evaluate health metrics as predictors of individual survival to fledge. We ran independent GLMs, each with a binary outcome (fledged/ died; re-sighted alive/ recovered dead) and logit link, with health parameters (CORT, BCI) and individual covariates (nest elevation, nesting colony, date, hatch order, and number of siblings) as fixed factors to assess the utility of measured covariates as predictors of individual nestling survival. We used a GLM framework (Gamma, log link) with fledge success as the response variable and health metrics as predictor variables to compare the relative value of different metrics for predicting aggregate nest productivity and survival rates at the colony level. We computed AICc values to account for the small sample sizes that resulted from using colony as the sampling unit and used these values for model comparison. Models were considered to receive strong support if they resulted in a Δ AICc ≤ 2 (Burnham and Anderson 2004).

For data collected from 2017–2018 in Alabama, we assessed reproductive success by calculating the DSR of nests (incubation stage, laying to hatch) and broods (chick-rearing stage, hatch to fledge) using package RMark (Laake and Rexstad 2014). The nest survival module models the survival probability (i.e., DSR) over the course of each breeding stage as a function of user-specified covariates using generalized linear models with a logit-link function and binomial errors. Before analyses, we compared the DSR of nests and broods between Gaillard and Cat islands and, finding no difference ($P > 0.10$ for each), pooled data from both islands in subsequent analyses. We report DSR and apparent survival to allow for comparisons to previous studies.

We modeled the relationships of the independent variables with DSR separately for incubation and brood rearing. We also included the following independent variables: Julian date, nest age (nest success models), and age of first chick hatched (brood success models) (calculated in RMark using AgeFound and AgeDay1). We tested both linear and quadratic terms for the age and time covariates and used the best performing term for each variable (quadratic for age covariates in all breeding stages except for 2017 brood rearing; linear for all time covariates in all models) in subsequent models (Streker 2019). We developed a suite of hypotheses to assess the relationship between the independent variables and daily survival rates (Table 2.4). Variables that were highly correlated ($|r| \geq 0.5$) were not included in the same model and therefore multiple global models were developed to separate correlated values. For each year

for incubation data we re-ran the top performing models (see below on identification of top-performing models) on the subset of nests within which temperature was recorded to assess whether the addition of nest-specific temperature variables substantially improved model fit. Temperature variables were not tested during chick-rearing due to the small sample size of broods that failed that also had temperature loggers (2017: n = 1 nest with temperature logger + brood failure; 2018: n = 7 nests with temperature logger + brood failures).

We used Akaike's information criterion (AIC) to rank the models and evaluated the strength of the models using normalized weights (Burnham and Anderson 2002). We ran models separately by year (2017, 2018) and breeding stage (incubation, brood-rearing). We report models that were within $\Delta AIC \leq 2$ of the lowest-scoring model. We report coefficient estimates and confidence intervals from top-performing models. Daily survival rates were calculated from top performing models for each year and breeding stage. We reported apparent success as the total number of observed nests and broods divided by the number of nests and brood successful at the end of their respective breeding stage.

2.6 Nestling Diet

2.6.1 Diet Sampling

In Year 1 (2013), we collected meals opportunistically from chicks captured for banding and sampling. In years 2–3 (2014–2015), we visited each study colony regularly (every 5–7 days). We selected recently-fed nestlings, based on either having seen a feeding occur or observing that the nestling had a visible bolus or engorged throat, to obtain meals from nestlings. We approached the nest from the colony edge and waited for the nestling to voluntarily regurgitate the meal. If the target nestling did not regurgitate, we selected a different nestling and repeated the process until we had obtained approximately ten complete meals. We targeted different areas of the colony on subsequent visits to limit disturbance to individual nests; we also varied the time of day at which samples were collected. We collected meals throughout the chick-rearing period, from hatch (late April) through fledging (early August). We targeted nestlings at the same stage of feather development to limit chick age variation within each sample, indicating similar hatch dates, and recorded overall nestling age for the sample as estimated from feather growth (*sensu* Walter et al. 2013). We did not collect samples from recently hatched nestlings (one week old or less), both to limit disturbance and because pelican nestlings do not consume whole fish until several days after hatch (Sachs and Jodice 2009). Additionally, because nestlings regurgitated food less readily as they reached adult size, we were not able to sample chicks older than approximately ten weeks of age. Samples were stored on ice in the field and then moved to a freezer within ~6 hours of collection.

2.6.2 Diet Composition

During processing, we thawed each sample in a warm-water bath, removed it from plastic, dried off surface water using paper towels, then weighed, measured, and identified the species of each individual fish. We based species identifications on descriptions in McEachran and Fechhelm (2010), relying on soft tissue and external characterists. We also classified each fish as whole (no visible damage), partial-whole (total or standard length obtained, but some soft tissues missing), and partial (length could not be obtained). For samples containing large numbers (50–1000) of small fish of the same species (26% of samples), we counted the total number of individuals of the species, weighed and measured a subsample of ten individual fish, and obtained a total weight and overall classification (whole, partial-whole, partial) for each species group. For samples containing extremely large numbers (> 1000) of small fish (<1% of samples), we weighed and measured a subsample of ten fish per species, weighed the overall sample, and used the average weight per fish to approximate the total number of fish in the sample. For samples in which individual fish were no longer intact, we counted the number of heads and tails present in the

sample and used the larger of the two numbers as an approximate count. We did not analyze samples for which the digestive process was too advanced to identify fish to species (< 1% of all samples collected).

Where needed, we corrected standard lengths of fish to total lengths using the best-fitting regression equation between standard and total length for that species calculated from whole samples. We calculated the length-weight relationship as the best-fitting regression equation between log total length and log mass of whole fish for each species by year to estimate the mass of partial-whole and partial fish. For partial-whole fish (i.e., degraded fish for which we were able to measure total length), we used the regression line to estimate the corrected mass of the whole fish from its length. For partial fish (i.e., degraded fish for which total length was not measurable), we used the mean total length of whole and partial-whole individuals collected from the same breeding colony on the same day to estimate a corrected mass from the regression equation. Finally, we totaled the corrected masses of individual fish within each meal to obtain a total corrected meal mass.

2.6.3 Provisioning Rates

To assess meal delivery rates, we conducted 3 h nest observations during each colony visit throughout the chick-rearing period (i.e., every 5–7 d from hatch through fledging, late April to early August). We selected groups of 15–20 nests, varying both the location within the colony and the time of day of observations. During each 3 h period, we recorded all direct feedings in which a nestling's head entered an adult's throat and the nestling's throat was subsequently engorged. Indirect feedings in which parents regurgitate prey onto the floor of the nest as opposed to the chick directly (Sachs and Jodice 2009) appeared to take place only within the first few days after hatch. Because chicks are brooded by adults during this time and are hidden from view, the frequency of such feedings was difficult to quantify; thus, we excluded recently hatched nests from observation.

We calculated meal delivery rates on a per-nest basis. This measure reflects the rate of provisioning by adults, but not necessarily the rate at which each individual nestling consumes food. Pelicans can raise up to three young, hence meals delivered to a nest may be shared among as many as three nestlings. However, each nestling may not receive an equal share, because nestlings that hatch earlier can often consume a larger share of feedings based on superior competitive ability (larger body size, more advanced muscle development and mobility) or preferential feeding by adults. Because we were not able to consistently distinguish first, second, and third-hatched chicks in the field throughout the extended chick-rearing period and subsequently allocate feedings to individual chicks, we chose to assess delivery rates by nest with number of chicks as a covariate. We standardized delivery rates to a 15 h day, representing the average day length (civil twilight) during the study period. Pelicans are visual foragers and are considered not to forage at night (Shields 2014), and our observations suggest that adult activity diminishes shortly after sunset.

2.6.4 Proximate Composition and Energy Density

We measured proximate composition and energy density of common prey species using methods described by Anthony et al. (2000). Briefly, we dried fish to a stable mass in a 60 °C oven and homogenized samples using a mortar and pestle. We then extracted lipids from the sample using a Soxhlet apparatus with a 7:2 (v:v) hexane: isopropyl alcohol solvent. Following the 10 h extraction, the sample was left to dry for 24 h and re-weighed to determine lean mass. We then extracted proteins from the sample by ashing at 600 °C for 12 h. The mass of the remaining skeletal ash was subtracted from the pre-ashing mass to determine the ash-free lean dry mass, which is composed primarily of proteins (94%: Anthony et al. 2000). We then multiplied the lipid and protein contents by standard energetic values based on their relative assimilation efficiencies (lipids: 39.5 kJ g^{-1}; proteins: 17.8 kJ g^{-1}: Schmidt-Nielsen 1997) to obtain the overall energy density of the sample.

We measured energy densities in both regurgitated fish that we identified as whole during processing and bait fish purchased live or freshly caught from fishing suppliers close to study colonies. For the three most common prey species (Gulf menhaden; Atlantic croaker, *Micropogonius undulatus*; and pinfish, *Lagodon rhomboides*), we ran ANOVAs to determine whether energy content differed among planning areas or sample types (bait fish compared to regurgitated fish). Because energy values for one of the three species, Atlantic croaker, differed significantly between the eastern and western planning areas, we calculated energy densities separately for the two planning areas where possible. However, we did not find differences in energy content between bait and regurgitated samples, and therefore combined all samples within each planning area during further analysis. Gulf menhaden had an apparent difference in energy content between bait samples and regurgitated fish ($p = 0.056$). In this case, regurgitated fish were higher in energy than bait samples, so we chose to use only regurgitated samples to determine energy content for this species. We also tested for differences in energy density between locations within planning areas, and found over time that the energetic content in Atlantic croaker and Gulf menhaden did not differ within planning areas and did not change as the season progressed. Therefore, we considered energy density of prey to be consistent throughout the breeding season and within each planning area. Because Gulf menhaden were the only prey species to show a bimodal size distribution, we measured energy content of juveniles (< 110 mm total length: Ahrenholz 1991) and adults (> 110 mm) separately.

We multiplied the total mass of each prey species in the meal by the mean energetic value of that species to determine meal-specific energy density. For species without directly measured energy density, we obtained energetic values for the same or closely related species from published literature. Species with directly measured energy content accounted for 93% of the total biomass, while species with inferred values from closely related species measured directly (4%) and those with values obtained from scientific literature (3%) constituted the remaining 7%. We then summed the energy derived from each individual species and divided the sum by the total meal mass to obtain an energetic value (kJ g^{-1}) for the full meal. We calculated meal-specific lipid content using the same process.

2.6.5 Energy Provisioning Rates

We compared values of meal mass (g $meal^{-1}$), nest-specific provisioning rate (meals $nest^{-1}$ $hour^{-1}$), and energy density of meals (kJ g^{-1}) for each colony using ANOVAs with post-hoc Tukey's Honestly Significant Difference (HSD) tests to assess nutritional stress by colony. The product of these three components is the energy-provisioning rate (EPR: g $nest^{-1}$ $hour^{-1}$, Jodice et al. 2006). We modeled energy-days for each colony, similarly to Jodice et al. (2006), by randomly selecting (with replacement) 100 values for provisioning rate (meals day^{-1}) from the set of measured values to obtain a combined measure of EPR by colony. The model then randomly selected (with replacement) a mass and an energetic value for each meal, multiplied the meal mass by energy density to obtain the total energy content per meal, and summed the total energy across all meals for each modeled day to obtain a set of EPRs (kJ day^{-1}). We calculated the mean and standard deviation of EPR for each colony by averaging values obtained from 1000 runs of the model. We calculated EPR on a per-nest basis rather than a per-chick basis, to avoid the confounding relationship between higher provisioning rates and increased longevity of second- and third-hatched chicks (Jodice et al. 2006). Then we evaluated the relationships of individual provisioning metrics to EPR using ANOVAs on nested sequential linear models. Finally, we conducted non-metric multidimensional scaling on proportional composition of meals by species to assess the relationship between species composition and rate of energy delivery to nestlings, and overlaid provisioning metrics on the resulting ordination.

2.7 Health and Physiological Parameters

2.7.1 Blood Analytes

2.7.1.1 Sample Collection

Adult brown pelicans were sampled from active nests during the breeding seasons of 2013–2015 from six different colonies in the Northern GOM. We collected samples from Audubon and Smith islands, Florida; Gaillard Island, Alabama; Felicity and Raccoon islands, Louisiana; and Chester and Shamrock islands, Texas. We collected blood smears from 90 adults and blood samples from 81 of the 90 adults for complete blood counts (CBCs). Not all samples, however, were suitable for complete analyses and so sample size varies among analytes and blood smears. We measured body mass (± 50 g/ 1.76 oz), culmen length (± 1mm/ 0.04 in), tarsus length (± 1mm/ 0.04 in), and wing length (± 5mm/ 0.20 in). These variables were not assessed individually; instead they were used to create a new variable, BCI (n = 64), which provides an index for the mass of the bird in relation to its size (see 2.5.2.1). The more positive the BCI, the better the condition of the individual. In brown pelicans, sex cannot be easily determined in situ. Therefore, the distribution of samples between sexes is opportunistic. Sex was later determined from collected blood samples through PCR (Itoh et al. 2001).

Brown pelican chicks were sampled from active nests during the breeding seasons of 2014–2015 from seven colonies in the Northern GOM. We sampled from Audubon and Ten Palms islands, Florida; Gaillard Island, Alabama; Marker 52 and North Deer (regrouped as Galveston Bay colonies), Chester, and Shamrock islands, Texas. We collected blood smears and blood samples for CBCs from 35 individuals. As in adults, we measured body mass, culmen length, tarsus length, and wing length, and used these variables to assess BCI (n = 35). Sex was not determined for chicks.

For both adults and chicks, blood samples were collected within two minutes of capture from the tarsometatarsal vein. After sterilizing the collection site, we collected a 5 mL blood sample using a 23-gauge needle and VacuTainer tube (Becton Dickinson, Franklin Lakes, New Jersey) with lithium heparin anticoagulant. Samples were stored over cold packs until returning from the field (~5–10 h).

2.7.1.2 Sample Processing

In the lab, we created blood smears from stored samples, filled three capillary tubes for hematocrit analysis, and spun down both samples and capillary tubes using a centrifuge (Becton Dickinson, Franklin Lakes, New Jersey). We recorded hematocrit percent volume from each of the three capillary tubes. We separated plasma from red blood cells in centrifuged samples by pipetting. All plasma and red blood cell samples were then stored frozen until analysis.

Biochemical, protein electrophoresis, and serological tests were conducted at the University of Miami (Department of Pathology, Miami, Florida). A full biochemical analysis was conducted on plasma samples on a dry-slide chemistry analyzer (Ortho Vitros 250 XR, Ortho Clinical Diagnostics, Rochester, New York) controlled daily for quality and ran per manufacturer's instructions. Evaluated analytes (Table 2.5) included alanine aminotransferase (ALT), aspartate aminotransferase (AST), creatinine phosphokinase (CPK), gamma glutamyl transferase (GGT), lactate dehydrogenase, amylase, bile acids, blood urea nitrogen (BUN), calcium, cholesterol, CO_2, creatinine, glucose, lipase, phosphorus, potassium, sodium, total protein, triglycerides, and uric acid. Lipoprotein analysis included high-density (HDLc) and very low-density (VLDLc) lipoprotein cholesterol. Plasma samples were analyzed following procedures provided in the Helena SPIFE 3000 system with the use of Split Beta gels (Helena Laboratories, Inc. Beaumont, Texas). Protein electrophoresis were scanned and analyzed by Helena software for pre-albumin, albumin, and Alpha 1 (A1G), Alpha 2 (A2G), Beta and Gamma globulins. Percentages for each fraction were determined by this software, and absolute concentrations (g dL^{-1}) for each fraction were

obtained by multiplying the percentage by the total protein concentration. The albumin to globulins ratio (A:G) was calculated by dividing albumin by the sum of the globulin fractions. Concentrations of CORT were measured by radioimmunoassay (MP Biomedicals Double Antibody Corticosterone radioimmunoassay, Santa Ana, California). We classified each analyte as a blood gas, electrolyte/mineral, enzyme, lipid, metabolite, plasma protein, or stress hormone (Table 2.5). We also noted typical indications from each analyte (e.g., nutrition, hepatic damage).

Blood smears were stained with Diff-Quik (Siemens Healthcare Ltd., Ontario, Canada) and reviewed at 1000x to determine differential counts of white blood cells (WBC). We also measured the concentration (*10^3 mu L^{-1}) of all WBC and the concentration of heterophils, lymphocytes, monocytes, eosinophils, and basophils (Table 2.5).

2.7.1.3 Statistical Analysis

Among the 30 blood analytes, we identified any with a binomial distribution and separated the data into "high" and "low" categories, then treated those as two separate analytes (i.e., analysed each category separately). We tested for differences in the independent variables between the low and high categories using t-tests, χ^2 tests, and Wilcoxon rank tests. Sodium as measured in samples from adults was the only analyte for which this bimodal treatment was necessary. Measures of sodium classified as "low" ranged from 111–156 mEq L^{-1} and measures of sodium classified as "high" included only the maximum measured value for sodium of 250 mEq L^{-1}.

We assessed outliers for all data that did not have a binomial distribution (i.e., all analytes other than adult sodium) using the Dixon outlier range statistic. Following guidance in Geffré et al. (2011), we retained rather than deleted an outlier unless it seemed likely to be an aberrant observation. We examined the distance between points identified as potential outliers and non-outlying points to make this decision. We also compared points identified as potential outliers to published values for species within the same order. Once aberrant outliers were removed, we checked normality of the data using the Anderson-Darling test. We then calculated reference values using Reference Value Advisor (Geffré et al. 2011). When sample sizes were sufficient, we computed a nonparametric reference interval, calculated the lower and upper confidence intervals on the reference intervals using a bootstrap approach, and provided descriptions of alternate approaches when appropriate (Geffré et al. 2011). We reported reference values from raw data for all analytes. For analytes that did not meet assumptions of normality, we followed guidance from Geffré et al. (2011) and conducted a Box-Cox transformation for subsequent statistical analyses. The Box-Cox transformation is commonly used for data such as concentrations of blood analytes that are often heteroscedastic (i.e., non-constant variance).

We assessed the relationship between each blood analyte and a suite of independent variables using GLMs. Independent variables for analyses of blood analytes and smears included: sex (adults; categorical), BCI (adults and chicks; continuous), planning area (adults and chicks; categorical), and home range size (adults; continuous). Planning area was classified using the planning areas for BOEM in the GOM. Oil and gas development are highest in the central planning area (coasts of Louisiana, Mississippi, and Alabama), least in the eastern planning area (Florida Panhandle), and moderate in the western planning area (Texas coast). Home range was reported as the 50% core area for any individual that was equipped with a satellite transmitter (n = 64). We selected the 50% core area as opposed to the 95% use area for analysis with blood analytes to assess the overall individual condition. We suggest the 50% core area better represents the conditions encountered regularly by an individual compare to the 95% use area and therefore the core area is most likely to affect an individual's overall condition. Deployment methods for satellite tags and calculation of home range size are detailed in Chapter 2 and Chapter 3. Note, the sample of animals with home range data is a subsample of those reported in Chapter 3 and therefore reported measures of home range size are not identical between Chapter 3 and Chapter 8. Continuous variables were scaled before running logistic models. Therefore, coefficient estimates were on

a standardized scale with respect to independent variables and on either a raw or Box-Cox scale with respect to dependent variables. However, all figures used a raw scale for both dependent and independent variables. Correction procedures for repeated tests were not conducted (Moran 2003, García 2004, Nakagawa 2004).

We built eight models (Table 2.6) to assess the relationships among blood analytes and independent variables and compared them using AIC. We reported coefficient estimates from the top-ranked model when coefficient estimates ± SE did not overlap 0. Transformed data were used for analyses when appropriate, but raw data were presented for ease of interpretation.

When box plots were used to display data, the median and quartiles defined the boxes, the whiskers defined the 10^{th} and 90^{th} percentiles, and data beyond the 10^{th} and 90^{th} percentiles were shown as circles.

2.7.2 Polycyclic Aromatic Hydrocarbons

2.7.2.1 Sample Collection

Adult brown pelicans were sampled from active nests during the breeding seasons of 2013–2015 from seven different colonies in the Northern GOM. We sampled from Audubon and Smith islands, Florida; Gaillard Island, Alabama; Felicity and Raccoon islands, Louisiana; and Chester and Shamrock islands, Texas. We collected feathers from 92 individuals and randomly selected blood from a subset of 33 individuals (from the pool of sample available described in 2.8.1.1) for PAH analysis. We measured body mass (± 50 g/ 1.76 oz), culmen length (± 1 mm/ 0.04 in), tarsus length (± 1 mm/ 0.04 in), and wing length (± 5mm/ 0.2 in) of every individual. These variables were not assessed individually; instead they were used to create a new variable, BCI (n = 79), which provides an index for the mass of the bird in relation to its size. The more positive the BCI, the better the condition of the individual. In brown pelicans, sex cannot be easily determined in situ. Therefore, the distribution of samples between sexes is opportunistic. Sex was determined from collected blood PCR (Itoh et al. 2001).

Brown pelican chicks were sampled from active nests during the breeding seasons of 2014–2015 from seven colonies in the Northern GOM. We sampled from Audubon and Ten Palms islands, Florida; Gaillard Island, Alabama; Marker 52 and North Deer (regrouped as Galveston Bay colonies), Chester, and Shamrock islands, Texas. We collected feathers from 606 individuals and randomly selected 35 of these samples for PAH analysis. We did not collect blood from chicks for PAH analysis. As with adults, we used measurements of body mass, culmen length, tarsus length, and wing length to calculate body condition index. Sex was not determined for chicks.

We collected blood samples within two minutes of capture from the tarsometatarsal vein. After sterilizing the collection site, we collected a 5 mL blood sample using a 23-gauge needle and VacuTainer tube (Becton Dickinson, Franklin Lakes, New Jersey) with lithium heparin anticoagulant. We then stored samples over cold packs until returning from the field (~5–10 hours). We collected 3–4 scapular feathers from each adult and chick. Feathers were stored at room temperature until processing.

2.7.2.2 Sample Processing

PAH analyses were conducted at the University of Connecticut Center for Environmental Sciences and Engineering (Storrs, Connecticut). In the lab, we weighed 0.2 g (0.007 oz) of blood sample into a 1.5 mL plastic centrifuge tube. Samples were spiked with quality control standard solutions and vortexed for 1 min at 2500 rounds per minute. Methanol or acetonitrile (500 µL) were added to each tube along with MgSO4. Samples were then vortexed for 5 min at 2500 rounds per minute, then centrifuged for 10 min at 14,000 rounds per minute. Next, 190 µL of the supernatant were transferred to a 300 µL liquid-chromatography vial. These samples were then spiked with an internal standard and vortexed.

Following extraction, the samples were analyzed for alkylated PAHs using an Agilent 6890 gas chromatograph (Agilent Technologies, Inc., Santa Clara, California) equipped with a Restek Rxi-5Sil MS column (Restek, Bellefonte, Pennsylvania; 30 m) using splitless injection coupled to a Waters QuattroMicro triple quadrupole mass spectrometer (Waters Corporation, Milford, Massachusetts). Parent PAHs were quantified using a Waters Acquity ultra-performance liquid chromatograph (UPLC; Waters Corporation, Milford, Massachusetts) with fluorescence and photo diode array detection, which was equipped with an Acquity UPLC BEH C18 column (Waters Corporation, Milford, Massachusetts; 1.7 µm, 2.1 × 100 mm). All peaks were quantified against the internal standard, and the extraction efficiency was evaluated using a surrogate standard of naphthalene-d8. Standard quality assurance procedures were employed, including analysis of duplicate samples, method blanks, post-digestion spiked samples, and laboratory control samples.

Feathers were washed three times in acetone, three times in high performance liquid chromatography water, and one additional time in acetone before allowing them to dry overnight (ca. 10 h). Feathers were weighed (± 0.2 g/ 0.007 oz) on folded weighing paper and transferred directly into the accelerated solvent extraction (ASE) cell using forceps when needed. Hydromatrix powder was added to pack the 11 mL ASE cells. Using gelatin as the matrix for the blank and laboratory control samples, a 0.2 g (0.007 oz) sample was weighed out and transferred to ASE cells. Samples were then spiked with quality control standards. ASE extracts were subsequently run and collected utilizing acetonitrile solvent, and the solution was transferred into the pre-marked conical evaporation vials and evaporated to just below 0.5 mL under a gentle nitrogen stream (set flowrate on N-Evap unit to 180 mL/min). Samples were spiked again with internal standard. The volume was then brought up to 500uL with acetonitrile and vortexed for a few seconds to mix. Filtered samples were injected into liquid-chromatography vials using 1 mL plastic syringes and 4 mm, 0.2 µm syringe filter.

The detection limit was 5 ng g^{-1} (i.e., part per billion) and values for PAHs were reported as wet weight for blood and dry weight for feathers.

2.7.2.3 Statistical Analysis

For subsequent PAHs analyses, we considered three dependent variables: the sum of all PAHs detected (sumPAH), the sum of Parent PAHs detected (sumPAR), and the sum of Alkylated PAHs detected (sumALK). We assessed the relationship between each and a suite of independent variables, including: BCI (adults and chicks; continuous), planning area (adults and chicks; categorical), sex (adults; categorical), migration class (adults; categorical) and home range size (adults; continuous). Planning area was classified using the planning areas for the BOEM as defined above. Home range was reported as the 95% use area for any individual that was equipped with a satellite transmitter. We selected the 95% use area for PAHs analysis rather than the core (50%) use area because we were interested in assessing the overall exposure of the individuals and suggest that this is best represented by the full extent of the area used. Methods for deployment of satellite tags and calculation of home range size are detailed in Chapters 2 and 3. Note, the sample of animals with home range data is a subsample of those reported in Chapter 3; therefore, reported measures of home range size are not identical between Chapters 3 and 8. Migration distance was calculated as the distance between the center of breeding home range and the center of winter home range, and classified as short (i.e., resident: < 200 km/ 124 mi), medium (200–800 km/ 124–497 mi), and long (> 800 km/ 497 mi).

We used a hurdle modeling approach to assess relationships between PAHs and independent variables. Step one of the hurdle model used a binomial logistic regression with a log link function, using the presence or absence of each of the three PAH variables as the response variable. Step two of the hurdle model used a GLM with a gamma distribution and a log link function, using the sum of the concentration of each of the three PAH variables as the response variable. The gamma model included individuals where sumPAH, sumPAR, or sumALK were superior to detectable limit of PAHs (i.e., sum $\neq$ 0).

We built 12 models for adult blood samples, 16 models for adult feather samples, and 3 models for chick feather samples and compared them using AIC (Table 2.7) to assess the relationships among PAHs and independent variables. We reported coefficient estimates from all models within delta AIC ≤ 2.0 and average coefficient estimates if they appeared in > 1 of the top models. We reported coefficient estimates when estimate ± SE did not overlap 0. We provided odds ratios for coefficient estimates from binomial logistic models (the odds of a PAH being detected for a change in categorical levels, or for a one unit increase in a continuous variable) and from gamma models (the odds of the concentration of a PAH increasing by 1 ng g^{-1} for a change in categorical levels, or for a one unit increase in a continuous variable).

Table 2.1. Environmental Data Layers and Data Sources Used for Analysis of Annual Habitat Use by Adult Brown Pelicans

Variable name	Layer name	Data source	Resolution
Distance to coast	World Vector Shoreline, Intermediate Resolution	Global Self-consistent Hierarchical High-Resolution Geography Database, NOAA (Wessel et al. 1996)	1:25000
Distance to river outflow	North American Rivers and Lakes	North American Data Atlas, US Geological Survey	1:100000
Bathymetry	2-minute Gridded Global Relief Data, (ETOPO2) v2	NOAA (National Geophysical Data Center 2006)	0.033
Bottom substrate	Dominant Bottom Types and Habitats	Gulf of Mexico Data Atlas, NOAA	
Net primary production	Vertically Generated Production Model	Ocean Productivity, Oregon State University (O'Malley 2012)	0.083
Sea surface temperature	Sea Surface Temperature, Climatological Mean, 10 m depth	NOAA National Centers for Environmental Information (Boyer et al. 2011)	0.1
Sea surface salinity	Sea Surface Salinity, Climatological Mean, 10 m depth	NOAA National Centers for Environmental Information (Boyer et al. 2011)	0.1

Table 2.2. Surface Pollutant Data Layers and Data Sources Used for Risk Analysis

Variable name	Layer name	Data source	Resolution
Surface pollution	Ocean Pollution (Ship Traffic and Ports)	Global Map of Human Impact Project, National Center for Ecological Analysis and Synthesis (Halpern et al. 2008)	0.01
Platforms	Drilling Platforms–federal waters	Bureau of Safety and Environmental Enforcement Gulf of Mexico OCS Region	NA
	Drilling Platforms–state waters	Texas General Land Office; Louisiana Strategic Online Natural Resources Information System; Alabama Oil and Gas Board	NA
Pipelines	Oil and Gas Pipelines–Gulf of Mexico	Bureau of Safety and Environmental Enforcement Gulf of Mexico OCS Region	NA

Table 2.3. Environmental andNest-based Variables Collected at Brown Pelican Nests on Gaillard and Cat islands, Alabama, 2017 and 2018

Variable	Description	Data	Range and/or Category
Nest height	Height of nest above ground	Continuous	0–156 cm (61 in)
Location	Location of the nest, either by island (2017) or by location on Gaillard (2018)	Discrete	2017: Gaillard or Cat 2018: Interior or Exterior
Substrate	Material under and supporting the nest	Discrete	Rock or Ground
Elevation	Elevation of nest location (m above sea level) stratified using elevational range of nests	Discrete	Low, Medium, High, or Berm
Distance to water	Distance from the nest to the closest water's edge	Continuous	1.5–127.7 m (4.9–419.0 ft)
Vegetation Cover	Amount of vegetation covering the nest	Continuous	0–100%
Humidity Average	Average humidity between nest visits (% water vapor) from the nearest NOAA weather station	Continuous	70.31–90.22%
Barometric pressure average	Average barometric pressure between nest visits from the nearest NOAA weather station	Continuous	100.772–102.225 kPa
Average temperature	Average temperature within selected nests between nest visits	Continuous	24.09–32.29 °C
Maximum temperature	Maximum temperature within selected nests between nest visits	Continuous	31.03–41.07 °C

Table 2.4. Models Assessed in Relation to Daily Survival Rates of Eggs and Broods of Brown Pelicans Breeding on Gaillard and Cat islands, Alabama, 2017 and 2018

Model name	Hypothesis	Variables included
Time	Survival has a linear relationship with time	Julian date
Age	Survival has a nonlinear relationship with age	Nest age*
Weather^	Survival has a positive relationship with mild weather	Average humidity + Average barometric pressure
Storm	Survival has a negative relationship with increasing storm activity	Average humidity + Average barometric pressure + Distance to water
Location	Survival has a nonlinear relationship with location	Distance to water + Elevation + Location+ Julian date + Nest age*
Habitat^	Survival as a positive relationship with habitat variables	Nest height + Vegetation cover +Substrate + Julian date + Nest age*
Null	Survival is constant	~1
Global	Survival has a linear relationship with all variables	All variables
Temperature^	Survival has a linear relationship with temperature within the nest	Average temperature + Maximum temperature + Julian date + Nest age*

*Quadratic age term for all years and breeding stages except for 2017 chick-rearing, when a linear term was used

^ Ran both the models listed and additional models that included average daily temperature and maximum daily temperature as recorded by loggers placed in a subset of nests.

Table 2.5. Blood Analytes from Samples Collected from Adult and Chick Brown Pelicans from Colonies throughout the Northern Gulf of Mexico, 2013–2015

Analyte	Abbrev	Units	Primary indicator of:	Category
Carbon dioxide	CO_2	mEq L^{-1}	Respiratory function	Blood gas
Calcium	Ca	mg dL^{-1}	Nutrition, hepatic damage	Electrolytes & minerals
Potassium	K	mEq L^{-1}	Nutrition	Electrolytes & minerals
Phosphorous	P	mg dL^{-1}	Nutrition, hepatic damage	Electrolytes & minerals
Sodium	Na	mEq L^{-1}	Nutrition	Electrolytes & minerals
Alanine aminotransferase	ALT	Units L^{-1}	Hepatic damage	Enzyme
Amylase	AML	Units L^{-1}	Pancreatic function	Enzyme
Aspartate aminotransferase	AST	Units L^{-1}	Hepatic damage	Enzyme
Creatine phosphokinase	CPK	Units L^{-1}	Tissue damage	Enzyme
Gamma-glutamyl transferase	GGT	Units L^{-1}	Hepatic damage	Enzyme
Lactate dehydrogenase	LDH	Units L^{-1}	Tissue damage	Enzyme
Lipase	LIP	Units L^{-1}	Pancreatic function	Enzyme
High density lipoprotein cholesterol	HDLc	mg dL^{-1}	Cardiovascular function	Lipids
Triglycerides	TRI	mg dL^{-1}	Nutrition	Lipids
Very low density lipoprotein cholesterol	VLDLc	mg dL^{-1}	Cardiovascular function	Lipids
Blood urea nitrogen	BUN	mg dL^{-1}	Hepatic damage	Metabolite
Cholesterol	CHL	mg dL^{-1}	Nutrition	Metabolite
Creatinine	CRE	mg dL^{-1}	Nutrition, hepatic damage	Metabolite
Glucose	GLU	mg dL^{-1}	Nutrition	Metabolite
Ratio BUN/CRE	BUN:CRE	Unitless	Nutrition	Metabolite-Ratio
Total protein	TPR	g dL^{-1}	Nutrition, hepatic damage	Metabolite
Uric acid	UA	mg dL^{-1}	Nutrition, hepatic damage	Metabolite
Albumin	ALB	mg dL^{-1}	Nutrition, hepatic damage, immune response	Plasma protein
Alpha 1 globulin	A1G	mg dL^{-1}	Hepatic damage, respiratory function	Plasma protein
Alpha 2 globulin	A2G	mg dL^{-1}	Immune response	Plasma protein
Beta globulin	BEG	mg dL^{-1}	Immune response	Plasma protein
Gamma globulin	GAG	mg dL^{-1}	Immune response	Plasma protein
Pre-albumin	PRA	mg dL^{-1}	Nutrition, immune response	Plasma protein
Ratio ALB/Globulin	A:G	Unitless	Nutrition, immune response	Plasma protein
Corticosterone	CORT	mg dL^{-1}	Stress response	Stress hormone
White blood cell count	WBC	*10^3 µL	Immune response, condition	White Blood Cell
Heterophils	HET	*10^3 µL	Immune response, stress	White Blood Cell
Lymphocytes	LYM	*10^3 µL	Bacterial infection, hepatic disease	White Blood Cell
Monocytes	MON	*10^3 µL	Immune response, parasite infection	White Blood Cell

Analyte	Abbrev	Units	Primary indicator of:	Category
Eosinophils	EOS	*10^3 µL	Allergies, vascular disease	White Blood Cell
Basophils	BAS	*10^3 µL	Allergies, vascular disease	White Blood Cell
Hematocrit (average of 3 readings)	HEM	% blood volume	Hydration, O2 storage	Red Blood Cell

Table 2.6. Models Used in an Information Theoretic Approach to Assess Relationships among Blood Analytes and Independent Variables for Brown Pelican Adults and Chicks Sampled from Breeding Colonies in the Northern Gulf of Mexico, 2013–2015

	Variables included	Adults	Chicks	Comments
Model 1	sex	Yes	No	Sex not available for chicks
Model 2	BCI	Yes	Yes	
Model 3	planning area	Yes	Yes	
Model 4	home range size	Yes	No	Home range irrelevant for chicks
Model 5	home range size + sex	Yes	No	Neither variable available for chicks
Model 6	BCI + planning area	Yes	No	Two terms are related so not modeled together
Model 7	BCI + home range size	Yes	No	Home range irrelevant for chicks
Model 8	null model	Yes	Yes	

Models were compared using Akaike's Information Criteria. BCI = body condition index (see methods for definition).

Table 2.7. Models Used in an Information Theoretic Approach to Assess Relationships among PAHs and Independent Variables for Brown Pelican Adults and Chicks Sampled from Breeding Colonies in the Northern Gulf of Mexico, 2013–2015

	Variables included	Adult blood	Adult feathers	Chick feathers	Comments
Model 1	sex	Yes	Yes	No	Sex not available for chicks
Model 2	BCI	Yes	Yes	Yes	
Model 3	planning area	Yes	Yes	Yes	
Model 4	home range size	Yes	Yes	No	Home range irrelevant for chicks
Model 5	sex + BCI	Yes	Yes	No	Sex not available for chicks
Model 6	sex + planning area	Yes	Yes	No	Two terms are related so not modeled together
Model 7	sex + home range size	Yes	Yes	No	Home range irrelevant for chicks
Model 8	BCI + planning area	Yes	Yes	No	Two terms are related so not modeled together
Model 9	BCI + home range size	Yes	Yes	No	Home range irrelevant for chicks
Model 10	planning area + home range size	Yes	Yes	No	Home range irrelevant for chicks
Model 11	sex + BCI + planning area + home range size	Yes	Yes	No	See above
Model 12	migration class	No	Yes	No	Temporal mismatch w/ adult blood; not relevant for chicks
Model 13	migration class + BCI	No	Yes	No	Temporal mismatch w/ adult blood; not relevant for chicks
Model 14	migration class + sex	No	Yes	No	Temporal mismatch w/ adult blood; not relevant for chicks
Model 15	migration class + planning area	No	Yes	No	Temporal mismatch w/ adult blood; not relevant for chicks
Model 16	null model	Yes	Yes	Yes	Temporal mismatch w/ adult blood; not relevant for chicks

Models were compared using Akaike's Information Criteria. BCI = body condition index (see methods for definition).

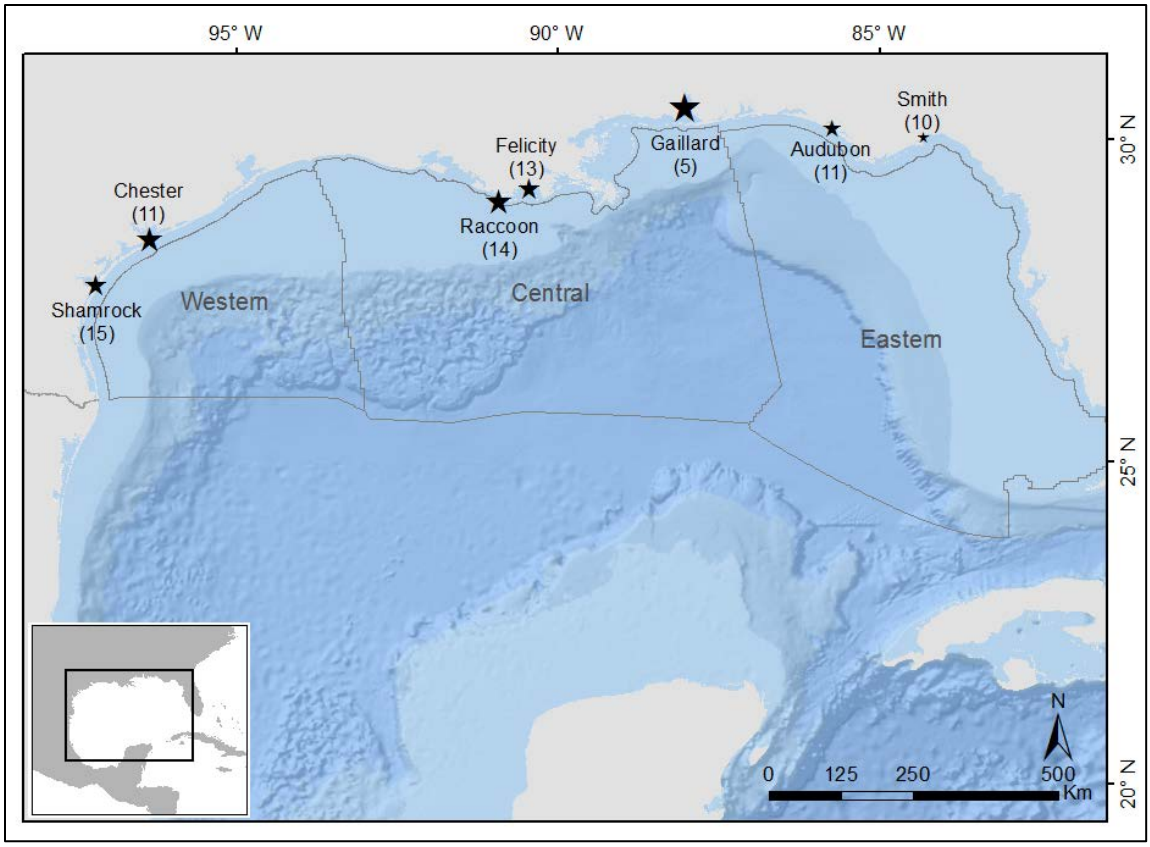


Figure 2.1. Map of colony locations of brown pelicans fitted with GPS transmitters, Gulf of Mexico, 2013–2015.
Number of adult pelicans tracked through the end of the breeding season from each colony is indicated in parentheses. Marker sizes represent relative colony size (75–5000 nesting pairs). Planning areas are delineated by dashed lines (Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors).

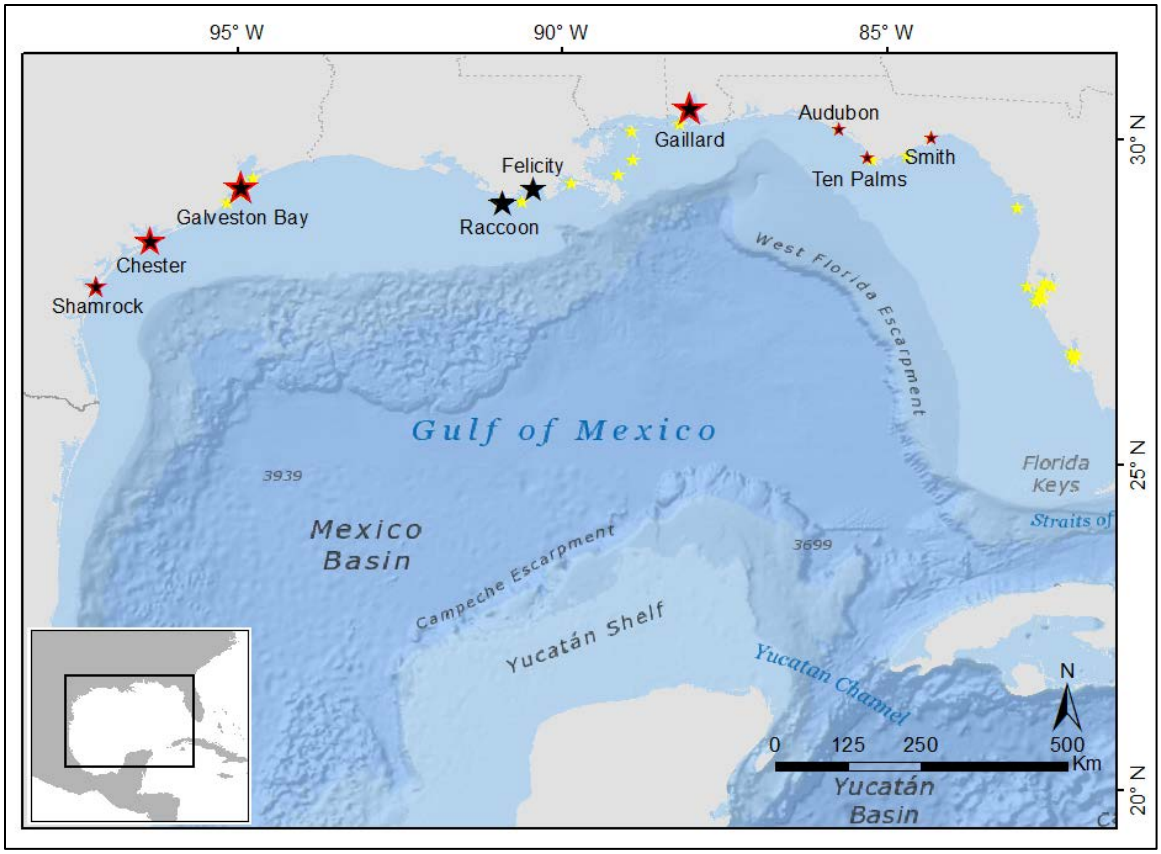


Figure 2.2. Location of brown pelican colonies sampled, Gulf of Mexico, 2013–2015.
Marker sizes represent relative colony size (75–5000 nesting pairs). Nestling health samples were collected from all colonies, and nutrition and productivity data were also collected from colonies outlined in red. Locations of other brown pelican nesting colonies in the Northern GOM are indicated in yellow. (Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors).

Figure 2.3. Positioning of GPS transmitter and harness.
(Left) Dorsal location of GPS transmitter and (right) ventral location of harness. Los Angeles Oiled Bird Care and Education Center, San Pedro, California, 11 June 2015 (J. Lamb). Green arrows point to the locations of the dorsal and ventral attachments.

3 Individual Tracking

Between 2013 and 2015 we deployed 86 transmitters on breeding pelicans throughout the Northern Gulf of Mexico (GOM) (Table 3.1; Figure 2.1). Transmitters were evenly distributed between the eastern (Smith, Audubon, and Gaillard Islands, Florida-Alabama), central (Felicity and Raccoon Islands; Louisiana), and western (Shamrock and Chester Islands, Texas) planning areas, with colony sizes ranging from 40 to 4500 breeding pairs. Transmitters typically collected data for between six months and three years, with most transmitting for 1–2 years before tag failure or mortality occurred (Figure 3.1). Transmitters collected data for breeding and non-breeding movements, including staging and migration. Brown pelicans used local habitat during the breeding season but showed substantial movement during the non-breeding season (Figure 3.2). Individuals breeding in the eastern GOM wintered as far west as southern Louisiana and as far south as central Cuba. Individuals breeding in the central GOM wintered along the entire GOM coastline, travelling as far south as Chiapas, Mexico and Belize. Individuals breeding in the western GOM staged as far east as southeastern Louisiana and wintered as far south as Chiapas, Mexico.

3.1 Tag Effects

3.1.1 Behavioral Effects

Before treatment, captive pelicans spent the majority of time loafing (18–47%), preening (11–32%), or resting (20–49%). Swimming, perching, and flying each occupied less than 10% of individual time budgets. In the first 1–2 h after receiving transmitters, GPS-tagged individuals spent an increased percentage of time preening (mean = + 16.4%, $F_{(1,7)} = 6.41$, $p = 0.038$) and decreased time resting (mean = -29.1%, $p = 0.047$, $F_{(1,7)} = 5.62$) relative to individuals that had not been tagged or handled (Figure 3.3a). Changes in time spent swimming, flying, loafing, and perching did not differ from zero (Figure 3.3a). We did not find significant differences in frequency (events hour^{-1}) after tagging for any of the instant events we quantified (Figure 3.3b; also see Lamb et al. 2017). In free-ranging pelicans 1–3 days post-capture, we did not observe differences between tagged individuals and untagged neighbors in the proportion of observation time spent in preening ($t_{31} = -0.59$, $p = 0.56$), resting ($t_{31} = -0.88$, $p = 0.38$), alert/loafing ($t_{31} = 1.60$, $p = 0.12$), or agitated ($t_{31} = -1.42$, $p = 0.17$) behavioral states (Figure 3.4).

3.1.2 Effects on Nesting Success

Overall, GPS-tagged pelicans (N = 74) continued attending nests for an average of 50 d (SD ± 34; Range 0–113) after capture, with a 51% apparent success rate for breeding (N = 38 successful nests). Apparent success rates of tagged breeders were slightly lower than but not significantly different from success rates of untagged adults measured in the same colonies in 2014–2015 (62%; N = 482; $X^2_1 = 3.46$; p = 0.06). The majority (88%; N = 65) continued breeding at their original nest sites following capture. The remaining adults either abandoned the breeding colony within one day of capture and did not re-nest that season (N = 3), re-nested at a different nest site in the same breeding colony (N = 3), or re-nested at different breeding colonies between 30 and 65 km (18.64–40.40 mi) from the original nesting colony (N = 3) (Table 3.2). Successful breeders attended colony sites for an average of 83 d after hatch (SD ± 13 d), while unsuccessful breeders attended on average 18 d (SD ± 14.7 d). We observed successful breeding in pelicans that re-nested elsewhere as well as pelicans that remained at their original nest sites (Table 3.2). Breeding success was similar in the eastern (76%) and central (67%) planning areas and lower in the western (15%) planning area (Figure 3.5a). In the eastern planning area, breeding success of tagged pelicans in 2013–2014 was similar to that of untagged pelicans at the same study colonies in 2015 (72%: $X^2_1 = 0.23$; p = 0.63). In the western planning area, breeding success was lower in tagged pelicans in

2013–2014 than in untagged pelicans in 2014 (45%; $X^2_1 = 9.91$; p = 0.002). We did not measure breeding success of untagged pelicans at the central colonies during any of the three study years.

The global model predicting breeding success of tagged birds was a good fit for the observed data, indicating that the full suite of parameters effectively explained variation in breeding success ($X^2_8 = 1.85$, $p = 0.99$). The four best-performing models for breeding success included capture location (Table 3.3), an index of underlying variability among planning areas. The model-averaged coefficient estimates (± SE) for location, with the eastern planning area set as the reference location, were -0.43 ± 0.66 for the central planning area and -2.83 ± 0.75 for the western planning area. Two of the top models also included handling time (-0.64 ± 0.54), and two included sex (0.67 ± 0.56). Phenological variables (capture date and nest stage), year of capture, physical condition (BCI), and percent body mass of transmitters were not included in the best-performing models for breeding success.

Handling time at capture was significantly longer in unsuccessful than successful breeders ($t_{55} = 1.7$, one-tailed $p = 0.047$), with a significant decrease in breeding success among birds that were handled for more than 20 min (Figure 3.5b: Fisher's Exact Test, one-tailed $p = 0.045$). Sex did not differ significantly between successful and unsuccessful breeders (Figure 3.5c: Fisher's Exact Test, one-tailed $p = 0.33$); however, females were more likely than males to abandon or re-nest within one day of capture (Fisher's Exact Test, one-tailed $p = 0.045$).

We observed short-term behavioral effects of handling and transmitter attachment in a captive setting 1–2 h post-release, but not in a field setting 1–3 d post-release. Captive and free-ranging groups were observed under different conditions and had different histories. Because of these differences, the behavioral patterns we observed in captive birds may differ from those of free-ranging individuals. However, both captive and free-ranging pelicans were observed relative to control individuals under the same conditions that were not captured or GPS-tagged. Because we observed behavioral changes immediately after transmitter attachment but not within several days of capture, we suggest that behaviors indicative of stress or discomfort in our study (due to either the attached device, the harness, the capture process, or any combination of the above) diminished rapidly. Although we did not separate handling from device effects (i.e., include procedural controls), the process of fitting an individual with a transmitter inevitably involved both handling and device effects. A meta-analysis by Barron et al. (2010) found that behavioral effects of transmitter attachment are generally indistinguishable between studies with and without procedural controls, indicating that most effects can be attributed to the device alone.

Immediately after transmitter attachment, we observed differences in tagged captive birds' time spent preening and resting relative to the controls. Because both handling and harness attachment may disrupt plumage and reduce waterproofing, increased preening behavior suggests an attempt to restore feather structure and represents a potential short-term increase in energy expenditure following handling and transmitter attachment. Other behaviors (e.g., swimming, perching, flying, loafing, and instantaneous events) did not increase or decrease following transmitter attachment. As swimming and flight are particularly critical to foraging, migrating, provisioning chicks, and escaping predators, these behaviors are often tested for adverse effects of transmitter attachment (Pennycuick et al. 2012; Matyjasiak et al. 2016). Our results suggest that individuals fitted with external transmitters continued to engage in swimming and flight at similar rates to control individuals immediately post-capture. However, our observations are limited to captive birds in a small enclosure, and we did not measure foraging movements or flight and swimming behavior in the field. Further, we did not assess the speed or efficiency of either swimming or flight, which can be altered by the presence of an external transmitter (Barron et al. 2010; Vandenabeele et al. 2011).

All supported models for breeding success included capture location as a predictor variable, which may result from underlying differences in breeding success among planning areas rather than from capture and tracking. Currently, there are limited data on factors affecting productivity in brown pelicans throughout their range. However, Walter et al. (2014) also reported regional differences within the state of Louisiana in failure rates of brown pelican nests following capture and GPS-tagging, thus suggesting that nesting success may vary spatially depending on underlying conditions (e.g., prey distribution, habitat availability, and environmental conditions). In 2015 in the eastern planning area, we recorded similar rates of apparent brood success of untagged brown pelicans compared to those of tagged pelicans in 2013–2014 (i.e., suggesting no effect of tagging on reproductive success). In comparison we did observe apparently higher rates of brood success among untagged (45%) compared to tagged (15%) pelicans at the two Texas colonies included in this study, although this comparison was confounded among years. Our data are not, therefore, conclusive as to whether lower rates or brood success in the Texas colonies were due to tagging or other underlying factors (e.g., prey availability, see 5.1). It is important to note that measured rates of nest success for brown pelicans in previous studies have ranged widely between years and locations (Shields 2014). Direct comparisons are limited by likely inter-annual variation and the small sample size of tagged pelicans relative to untagged individuals. Further assessment of the environmental factors underlying regional variation in nest productivity could help to elucidate the conditions under which tagging may depress nesting success.

Handling time appeared in two of the top models for breeding success. Longer handling periods resulted in a decrease in breeding success, with sharply reduced breeding success among birds that were handled for more than 20 minutes. Adults handled for longer time periods spent more time away from the nest during handling, which resulted in longer exposure of eggs to ambient temperature and may have affected egg viability. Longer periods of high stress resulting from handling may also have affected adult condition and likelihood of returning to the nest site. Effects of increased handling time on behavior have also been observed by Jodice et al. (2003) for black-legged kittiwakes (*Rissa tridactyla*). Handling time decreased during the course of our study, suggesting that researcher experience is an important factor in minimizing the effects of capture and tagging.

Sex also appeared as a predictor in two of the four top models. Although we did not observe a significant difference in breeding success between tagged male and female pelicans, our results indicate that females may be more likely than males to abandon immediately after being captured and fitted with GPS transmitters. As pelicans are sexually dimorphic, the percentage of body weight represented by a transmitter is higher for females ($\mu = 2.2 \pm 0.2\%$) than for males ($\mu = 1.7 \pm 0.1\%$). However, sex alone remained the strongest individual-level predictor of breeding success and transmitter mass, and neither body condition nor transmitter payload improved model fit. Transmitter weight represented < 3% of body mass for all individuals included in this study, which is generally considered an acceptable payload for seabirds (Phillips et al. 2003, although see Vandenabeele et al. 2012 for discussion of the limitations of this rule). There is limited evidence that females of some seabird species may take longer than males to recover from disturbance (Weimerskirch et al. 2002) and may be more sensitive to environmental conditions (Jodice et al. 2003). Female seabirds can also exhibit higher baseline CORT levels than males following the physiologically intensive egg-laying process (Lormée et al. 2003; Goutte et al. 2010), which may exacerbate the effects of stressors (e.g., capture and handling).

We did not observe the high rates of nest failure previously reported in GPS-tagged brown pelicans in the Northern GOM following transmitter attachment (Walter et al. 2014). Our study included pelicans from a much broader geographic range, but among birds breeding in the central planning area (comparable to the Louisiana study area in Walter et al. 2014) we observed a lower rate of relocation and nest failure (48% in our study, vs. 94% in Walter et al. 2014), a lower rate of abandonment within 48 h of tagging (19% compared to 44%), and a longer duration of nesting among breeders that remained on their original nest sites but eventually failed (40 ± 9 d vs. 7 ± 10 d). Both studies used the same capture method, transmitter

weight and profile, attachment location, and harness shape. However, average handling times were significantly shorter in our study (18.8 ± 6.5 min) compared to the aforementioned study (approximately 45 minutes). This was likely due to differences in harness attachment methods. Though the previous study used metal clamps and sutures to fasten harnesses, our study used knots covered in cyanoacrylate, which could be secured more rapidly. Additionally, following observations by the authors of the previous study that neighboring pelicans would often destroy unattended nests, we used a plastic mesh basket to protect nest contents while captured adults were absent from the nest. These differences may have contributed to lower rates of abandonment and egg loss in our study. Future tracking studies of nesting brown pelicans might include such precautions to ensure that nest contents are protected during the tagging process and to improve the likelihood of successful breeding by tracked adults.

Our study suggests that capture and GPS-tagging in brown pelicans results in short-term behavioral effects, but that these effects are minimal and do not persist into the days following transmitter attachment. According to our data, behavioral changes resulting from the transmitter attachment process could be accounted for by excluding locations obtained during the first 24 h after transmitter attachment to avoid biased inference in the GPS data analysis. Our study also indicates that tagged individuals can continue breeding and successfully raise young following capture, and that efforts to minimize handling time and protect nest contents during capture may contribute to improved nesting success. However, female breeders and individuals in relatively poor breeding locations may be more likely to abandon after capture and transmitter attachment. Because our study included only the breeding season following capture, we did not assess long-term effects of transmitter attachment on adult overwinter or inter-annual survival, or on lifetime fitness. Though reproductive and survival values are key to understanding the demographic effects of such perturbations, baseline data on these parameters are lacking in brown pelicans and many other seabird species. Future studies are needed on long-term impacts of carrying a GPS transmitter on site fidelity, survival, and reproductive success in the years following transmitter attachment in pelicans and other seabirds.

3.2 Foraging Movements and Home Range during the Breeding Period

During the breeding period, brown pelicans utilized coastal areas in the vicinity of their nesting site (Figure 3.6.a). We found some degree of overlap between neighbouring colonies in both 50% UD and 95% UD home ranges (Figure 3.7). This suggests that individuals from neighbouring colony sites were not partitioning foraging habitat. During the breeding season, colony size alone was the top predictor of individual 50% UD and 95% UD areas (Table 3.4). Overall, the linear relationship between colony size and breeding season home range size was significantly positive for both 50% UD ($t_{65} = 3.65$, $p = 0.005$) and 95% UD home ranges ($t_{65} = 3.56$, $p = 0.007$) (Table 3.5). For each increase of 100 breeding pairs at a colony, mean core home range size of individual breeders increased by approximately 3 km^2 (1.86 mi^2; Figure 3.8a) and mean full home range size increased by approximately 19 km^2 (11.81 mi^2; Figure 3.8b). A model including both colony size and body condition also received substantial support as a predictor of 95% UD areas (Table 3.5). The relationship between body condition and 95% UD area was positive, indicating an increase in 95% UD area with increasing body condition. However, condition was not a significant predictor of 95% UD area ($t_{65} = 1.20$, $p > 0.2$).

Density-dependent competition for prey resources is one of several factors potentially influencing foraging distances, and migratory movements of colonial seabirds. We tested for effects of density-dependent resource competition on several parameters related to movement patterns in brown pelicans and related these effects between-individual variation. We found a strong positive linear relationship between the size of both core (50% UD) and full (95% UD) home ranges of individual breeders, and the size of the breeding colony. Individuals at larger colonies consistently foraged over larger areas than individuals at smaller colonies. Body condition was included as a predictor in one of our top models of full home range area (95% UD), but only in combination with colony size, and breeders that foraged over

greater distances were generally in better physical condition. Other individual characteristics (e.g., sex, body size) and regional environmental conditions were not included as predictors in any highly supported models of either core or full home range areas during the breeding season. This adds to a growing body of evidence that colonial birds consistently increase their foraging radius in response to localized density-dependent prey depletion (e.g., Brown and Brown 1996; Lewis et al. 2001; Ainley et al. 2003; Ford et al. 2007; Bonal and Aparicio 2008). The fact that we did not observe a decline in adult body condition with increased foraging area further suggests that pelicans in this system were able to increase their foraging effort without experiencing compromised physical condition.

Most research to date has concentrated on pelagic seabirds breeding at temperate latitudes. Our study adds a new perspective to the understanding of the relationship between colony size and foraging distance in seabirds. For instance, in contrast to previous studies (e.g., Grémillet et al. 2004; Wakefield et al. 2013), we did not observe strong spatial segregation in foraging ranges between closely neighbouring colonies. For example, adults from two Florida colonies (Audubon and Smith Islands) frequently travelled over 100 km (62.14 mi) to a common foraging area at the mouth of the Apalachicola River. Prey concentrations in nearshore environments may occur predictably in and around stationary coastal features, including: headlands, river mouths, and upwelling zones (Becker and Beissinger 2003). Thus, the overlap we observed between neighbouring colonies may represent common exploitation of prey-concentrating features that are spatially predictable.

We did not find a significant relationship between colony size and either of the nestling condition metrics we tested (body condition or feather CORT). We previously determined that both feather CORT and body condition are effective predictors of chick survival in this system (Lamb et al. 2016), so we can extrapolate from our results that the reproductive rates of pelicans do not decline with colony size. This result contradicts several previous studies suggesting a relationship between chick condition and colony size (e.g., Gaston et al. 1983, Hunt et al. 1986, Cairns 1992); however, several other studies have failed to find a correlation (Brown and Brown 1996; Ainley et al. 2004; Gaston et al. 2007). The identified relationship between colony size and adult foraging ranges, but not chick condition, indicates that, within the range of colony sizes included in this study, adults can adjust their foraging ranges in response to density-dependent prey depletion without sacrificing reproductive output. Brown pelicans in this system may be operating well below metabolic limitations on their energetic expenditure (Drent and Daan 1980), allowing for plasticity in foraging effort.

This study also differs from previous studies on the effects of colony size on seabird breeding success by focusing on nearshore seabirds in subtropical waters. Previous studies have suggested a negative effect of colony size on chick condition, but have been conducted in high-latitude, pelagic systems. Both the life-history strategies of nearshore compared to pelagic seabirds and the relative complexity of nearshore compared to pelagic habitats may affect the relationship between colony size and chick condition (Suryan et al. 2006). For example, nearshore seabirds tend to have a more variable clutch and brood size compared to pelagic seabirds, allowing for adjustments in reproductive output in response to changes in local prey availability. Similarly, higher concentrations of resources within nearshore environments compared to pelagic habitats may allow nearshore seabirds to remain well below their energetic thresholds during chick-rearing (Ballance et al. 2009); thus, increases in foraging effort due to density-dependent competition might be less likely to result in measurable declines in chick condition than in pelagic environments.

3.3 Non-breeding Movements and Migratory Strategy

3.3.1 Influence of Individual Characteristics and Colony Size on Migratory Movements

We obtained data on migratory movements of 63 individuals. Proportion of migrants per colony was similar among colony sites.

Colony size was included as a predictor in 11 of 13 substantially supported models of migratory movements (Table 3.6), and had the highest importance value among all parameters for predicting migration distance. Colony size had a significant positive correlation with both migratory strategy (t_{62} = 2.16, p = 0.03) and migration distance (t_{62} = 2.85, p = 0.006). For each increase of 100 pairs at the breeding colony, individuals were 1% more likely to migrate (Figure 3.9a), and wintered approximately 16 km (10 mi) further from their breeding sites (Figure 3.9b).

Twelve of 13 top models for migratory movements included individual covariates. Body size was included in ten supported models, including all models of migratory strategy, and had the highest importance value among all parameters for predicting migratory strategy (Table 3.7). Body size had a negative correlation with migratory strategy (i.e., smaller individuals were more likely to migrate) (t_{62} = -3.15, p = 0.001; Figure 3.10a) but not with migration distance (t_{62} = -1.19, p > 0.2).

Sex was included in four of the top models. Males (47% migrants; N = 36) were less likely to migrate than females (78% migrants; N = 32) t_{62} = -2.50, p = 0.01), although migration distances did not differ significantly between sexes (t_{62} = -1.03, p > 0.2). Since males were larger-bodied than females, we also tested for within-sex differences in body size. Resident males were significantly larger than migrant males ($F_{1,34}$ = 4.65, p = 0.04), but resident and migrant females did not differ significantly in body size ($F_{1,30}$ = 2.18, p = 0.14) (Figure 3.10b).

Body condition was included in three of the top models, and environmental parameters appeared in one model, but neither was a significant predictor of either migratory strategy or migration distance (p > 0.2 in all cases).

Interaction terms were included in three of the 13 supported models (Table 3.6). A model including colony size, body size, and their interaction was the best-supported model of migration distance and was among the top models of migration strategy. A model including colony size, body size, sex, and their interactions was included among the top models of migration distance.

We chose study colonies within a single ecoregion to limit environmental variation, but we were unable to control all factors that could contribute to local variation in foraging conditions. Underlying resource availability, which is difficult to measure directly in marine systems, may also vary between colonies and can confound an assessment of the influence of colony size on seabird behaviour. Gulf menhaden, which comprise a large portion of pelican diets in the Northern GOM (Shields 2014), are concentrated in the central portion of the Gulf, meaning that colonies at the margins of our study area may have experienced lower availability of this prey item. We incorporated remotely-sensed environmental variables associated with menhaden availability (Ahrenholz 1991) into our models of adult movement patterns and chick condition to help account for this underlying prey variation. However, such variables are only a proxy for underlying prey variation, and the most effective way to account for prey availability would be to measure prey concentrations directly.

We found a positive correlation between breeding colony size and the proportion of individuals that migrated away from the colony during nonbreeding, as well as the distance travelled by migrants. Partial migration in seabirds has been little-studied and, to the best of our knowledge, a relationship between migratory strategies of individual breeders and breeding colony size has not previously been observed in either nearshore or pelagic seabirds. Density dependent competition for resources may present a significant obstacle to remaining residents in the Northern GOM. During winter months, prey populations in the region migrate offshore, , further reducing prey availability. By reducing predation pressure during periods of resource scarcity, partial migration provides a potential mechanism for increasing overwinter survival in the face of density-dependent competition.

Previous research on density-dependent population regulation in seabirds has focused almost exclusively on foraging movements and nesting health during the breeding season. The study of migratory behaviour in relation to conspecific prey depletion due to density-dependence has been less common, and has primarily been limited to species-level patterns (Diamond 1978). In contrast, investigations of relationships between colony size and migratory behaviour within a single species have been rare. Previous evidence has indicated a complex migration strategy in brown pelicans (King et al. 2013), but has not explored how migratory behaviour varies throughout the population or what drives individual migration patterns.

In addition to suggesting a relationship between colony size and migration propensity, our results also highlight the importance of individual physical characteristics in driving migration patterns. Whether individuals were migratory or resident was highly dependent on body size, as well as the interaction between body size and colony size. Five of the seven top models of migratory strategy included both body size and colony size, including one model with an interaction between the two covariates. The best-supported model of migration distance included a body size–colony size interaction. Partial migration patterns have previously been associated with individual differences in social status (e.g., Terril 1987; Cristol et al. 1999), variation in thermal tolerance with body size (e.g., Belthoff and Gathreaux 1991; Chapman et al. 2011, Macdonald et al. 2016), and/or differential fitness benefits to males of early arrival at the breeding site (e.g., Myers 1981; Pérez et al. 2013). The majority of our top models for migratory behaviour contained colony size in combination or interaction with one or more individual characteristics (e.g., sex, body size, and/or condition), indicating that the influence of individual characteristics on migration propensity and distance is mediated by density-dependent competition. Smaller individuals and females were more likely to migrate overall and were increasingly likely to migrate as colony size increased, lending support to the importance of social status as a driver of migration decisions. Local intraspecific competition may place subdominant individuals at a competitive disadvantage during periods of reduced prey availability, thus forcing them to move further from colony sites during the winter.

Our results offer insight into the ecological underpinnings of migratory decisions, suggesting that local intraspecific competition may be a driver of partial migration, and that changes to brown pelican breeding densities could result in corresponding migratory behaviour and nonbreeding location shifts that differentially affect individuals within the population. The relationship between colony size and migration includes a complex combination of factors, including competition, survival, and site selection. By establishing a link between intraspecific competition and migration, our results may elucidate a demographic mechanism underlying the differences observed in migration strategies among individuals.

3.3.2 Overlap of Populations During Staging

We examined specific habitat use by brown pelicans captured while breeding in colonies in three sections of the Northern Gulf: the eastern (Florida panhandle), central (Alabama, Mississippi, and Louisiana coasts), and western planning areas. We observed a distinct separation between birds from eastern Gulf colonies and those in the central and western planning areas. Year-round habitat overlap between breeders from colonies in the central and western planning areas totaled 30–40%; eastern breeders shared only 15% of their total habitat area. Moreover, while central and western Gulf breeders extensively used the same set of nonbreeding areas in the southern Gulf along the east coast of Mexico and throughout the Yucatan Peninsula, eastern Gulf breeders typically migrated southward to the Florida Keys and Cuba. We did not observe overlap between the eastern breeding population and the central or western groups in southern Gulf wintering habitat. The only area in which breeders from all three planning areas overlapped was in the Mississippi Delta, located in the central Gulf (Figure 3.11). The apparent separation between the eastern breeding colonies and the rest of the Northern Gulf population is unexpected as translocations from eastern colonies were used to re-establish the central Gulf breeding population following DDT-related extirpation (McNease et al. 1992).

To date, studies of brown pelican nonbreeding movements have been limited to information on band recoveries, typically from birds banded as juveniles (Schreiber and Mock 1988, Stefan 2008) and tracking data from individuals captured during non-breeding (King et al. 2013). This has limited the possibility of linking non-breeding birds to breeding colonies outside the breeding season. Ours is the first study to incorporate individual data on year-round movements of brown pelicans from known breeding locations. Understanding the likelihood of overlap between different breeding populations in different planning areas of the Gulf helps to refine current understanding of the distribution of environmental risk among breeding populations, and to better identify which segments of the overall breeding population are affected by spatially explicit threats in the marine environment.

3.3.3 Migration through the Tehuantepec Isthmus

Two of the 34 (6%) brown pelicans tracked from the western and central GOM through a full migratory cycle wintered along the Pacific coast of the Tehuantepec Isthmus (Figure 3.12), including one breeder from Louisiana tracked through a single annual cycle, and another from Texas tracked through two annual cycles.

Migratory routes for both pelicans crossed the isthmus within a longitudinal span of 250 km (155 mi) from its narrowest point, and each individual crossed wind energy installations on at least one route. Distance to the nearest wind energy installation from the estimated migratory path ranged from 0 to 59 km ($\bar{x}$ = 27 ± 30 km) (0 to 37 km, $\bar{x}$ = 17 ± 19 mi). Fall migrations occurred between late October and late November; spring migrations occurred from March through May, with average dates falling between late March and early April. Brown pelicans traveled only during daylight hours. Fall migrations occurred within a single day, while spring migrations spanned 2–3 days of daylight travel and overnight stops. Brown pelicans that passed through wind energy installations did so either at the end (fall) or beginning (spring) of their migration (Figure 3.12). Brown pelicans conducted fall migrations through the isthmus under lower-than average wind speeds (-58%), while spring migrations occurred within 10% of average wind speeds.

Although the Tehuantepec Isthmus has previously been identified as a potential migration route through which marine bird species breeding on the East coast of North America might cross to the Pacific (Binford 1989), regular inter-oceanic migrations of marine birds across Central America have not previously been described, with the exception of a single red-necked phalarope (*Phalaropus lobatus*) tracked from Scotland (Smith et al. 2014). Molecular data suggest that Central America is a significant barrier to gene flow for marine birds (Steeves et al. 2005, Friesen et al. 2007); however, the use of this migratory route by brown pelicans suggests that Atlantic and Pacific populations may overlap in non-breeding areas.

Our data suggest that the proportion of brown pelicans involved in inter-oceanic migration is low relative to overall population size. However, anomalous migratory routes can serve important roles in population health and persistence by facilitating genetic mixing (Liedvogel et al. 2011). Dispersive migration may also help to distribute risk across the population (Johnson and Gaines 1990), and individuals in remote wintering areas may serve as a source of re-colonization following environmental catastrophe (King et al. 1985). A full understanding of complex migration pathways is also critical to estimating how risks (e.g., disease transmission and spatially heterogeneous anthropogenic stressors) are distributed across populations (Martin et al. 2007), as well as to develop conservation strategies for preserving species with complex migratory movements in the face of global change (Martin et al. 2007).

Our study also establishes that brown pelican migratory paths overlap spatially with terrestrial wind energy installations in the Tehuantepec Isthmus. Our analysis is focused on coastal marine bird species that breed or stage in the GOM; however, recent data from Arctic-breeding semipalmated sandpipers (*Calidris pusilla*) suggest that other species typically associated with coastal migration routes may be using the Tehuantepec Isthmus to move between Atlantic and Pacific coastal flyways (Brown et al. 2017). It is important to note that, though tracking data can suggest the potential for individuals to interact with terrestrial features along their movement paths, it does not prove that interaction is taking place (Drewitt and Langston 2006, Furness et al. 2013). Because our data do not include flight altitudes, we are able to establish only macro-scale overlap between migrating birds and wind turbines. Establishing macro-scale interaction represents only an initial step in identifying locations and extent of potential conflict, with further targeted research needed to determine whether micro-scale interaction is likely. Furthermore, migratory birds in the Tehuantepec region may adjust their routes to avoid turbines (Villegas-Patraca et al. 2014, Cabrera-Cruz et al. 2017), incurring energetic costs even in the absence of direct interaction (Masden et al. 2010).

Mitigation strategies to reduce impacts of wind turbines on birds, including changing operations schedules, reducing rotor speeds, and improving turbine visibility (Drewitt and Langston 2006), require knowledge of both distribution and biology of at-risk species in the region of the installation. Wind turbine mitigation efforts in the Tehuantepec Isthmus have previously targeted Swainson's hawks (*Buteo swainsoni*) (Kochert et al. 2011) and Franklin's gulls (*Larus pipixcan*) (Villegas-Patraca and Herrera-Alsina 2015). However, brown pelicans differ from these target species in their migration patterns, flight behavior, and residence times. Moreover, risk factors of wind turbines are highly variable among avian taxa and depend on flight behavior, body size, and wing loading (Herrera-Alsina et al. 2013). Further information is needed on micro-scale flight altitude and behavior throughout the residence period to accurately evaluate collision risk for the species included in this study.

Table 3.1. Colony Characteristics and Measurements of Tracked Adults Captured at Six Brown Pelican Breeding Colonies, GOM, 2013–2014

	Smith		Audubon		Gaillard		Felicity		Raccoon		Shamrock		Chester	
Colony size (breeding pairs)	40[a]		100[a]		4500[b]		1800[c]		4300[c]		1400[d]		3200[d]	
# of adults tracked	9		11		5		12		14		11		10	
% male	78		64		40		50		57		55		30	
Mass (g)	3414	± 432	3414	± 558	3190	± 329	3448	± 36	3546	± 353	3459	± 562	3070	± 508
Culmen length (mm)	322	± 22	315	± 21	312	± 20	313	± 23	316	± 23	321	± 25	309	± 19
BCI[e]	-141	± 273	-241	± 205	-131	± 343	77	± 195	121	± 263	-19	± 306	-147	± 281

Data Sources:
[a] Florida Fish and Wildlife Conservation Commission (https://public.myfwc.com/crossdoi/shorebirds/)
[b] Dauphin Island Sea Labs
[c] Walter et al. (2014)
[d] Texas Colonial Waterbird Census (https://tpwd.texas.gov/huntwild/wild/wildlife_diversity/tcws/data.phtml)
[e] Body Condition Index (BCI) is a derived parameter representing the relationship between mass and skeletal size. Positive values indicate higher mass than predicted by the regression between mass and skeletal size, while negative values indicate lower mass than predicted.

Table 3.2. Nest Persistence and Apparent Breeding Success of GPS-tagged and Untagged Brown Pelicans, GOM, 2013–2014

	N	Mean days attending nest after hatch (SD)	% successful
GPS-Tagged	74	50 (34)	51
Remained at original site	65	49 (33)	52
Re-nested (same colony)	3	57 (22)	67
Re-nested (different colony)	3	47 (24)	67
Abandoned	3	0	0

Breeding success is defined as adults attending nests for at least 60 days post-hatching for the purposes of this study.

Table 3.3. Candidate Models for Breeding Success of Brown Pelicans, GOM, 2013–2014

Model ID	Terms	AIC	Δ_i (AIC)	w_i (AIC)	Σw	L_i (AIC)
10	Location	85.75	0	0.30	0.30	1
13	Sex + Location (2 + 10)	86.3	0.55	0.23	0.53	0.76
16	Handling + Location (9 + 10)	86.97	1.22	0.16	0.69	0.54
19	Sex + Handling + Location (2 + 9 + 10)	87.56	1.81	0.12	0.81	0.40
15	Phenology + Location (8 + 10)	88.81	3.06	0.07	0.88	0.22
18	Sex + Phenology + Location (2 + 8 + 10)	89.46	3.71	0.05	0.93	0.16
20	Phenology + Handling + Location (8 + 9 + 10)	90.15	4.4	0.03	0.96	0.11
21	Global (2 + 8 + 9 + 10)	90.91	5.16	0.02	0.98	0.08
11	Sex + Phenology (2 + 8)	95.29	9.54	< 0.01		< 0.01
8	Phenology (5 + 6)	95.45	9.7	< 0.01		< 0.01
15	Sex + Phenology + Handling (2 + 8 + 9)	96.72	10.97	< 0.01		< 0.01
14	Phenology + Handling (8 + 9)	96.75	11.0	< 0.01		< 0.01
5	Nest stage	97.8	12.05	< 0.01		< 0.01
2	Sex	103.9	18.15	< 0.01		< 0.01
12	Sex + Handling (2 + 9)	104.3	18.55	< 0.01		< 0.01
6	Capture date (Julian)	104.5	18.75	< 0.01		< 0.01
22	Null model	104.5	18.75	< 0.01		< 0.01
9	Handling time	104.6	18.85	< 0.01		< 0.01
1	BCI	105.1	19.35	< 0.01		< 0.01
3	Payload (% body mass of transmitter)	106.5	20.75	< 0.01		< 0.01
7	Capture year	106.5	20.75	< 0.01		< 0.01
4	Individual (BCI + sex + payload)	107.5	21.75	< 0.01		< 0.01

Models are ranked in order of increasing AIC values with model weights (wi), cumulative weights (Σw) and relative likelihoods (Li). Models above the dashed line were considered strongly preferred (Δ AIC < 2). Terms used in models are defined in Methods. Numbers in parentheses represent model IDs.

Table 3.4. Generalized Linear Models, Model Weights and Top Model Evidence Ratios for Breeding Movements of Adult Brown Pelicans in the Northern GOM, 2013–2016

	K	AIC_c	Δ_i (AIC_c)	w_i (AIC_c)	Σw	E
Breeding (*N* = 73)						
Core home range (gamma)						
Colony size	3	835.44	0	0.31	0.31	3.0
Full home range (gamma)						
Colony size	3	1094.34	0	0.27	0.27	2.12
Colony size + Condition	4	1095.84	1.50	0.13	0.40	

Substantially supported (Δ_i $AIC_c \leq 2$) generalized linear models are shown. w_i= model weights; E= evidence ratios. Link functions are given in parentheses.

Table 3.5. Model-averaged Coefficients and Importance Values for Individual Covariates across the 95% Confidence Set of Models for Each Breeding Movement Parameter

Variable	50% UD		95% UD	
	Coefficient	Importance	Coefficient	Importance
Colony size	0.03 ± 0.01	**0.96**	0.19 ± 0.07	**0.92**
Body size (culmen)	0.7 ± 1.0	0.25	3.6 ± 6.5	0.25
Condition	9.3 ± 79.7	0.24	548 ± 544	0.31
SexMale	-10.8 ± 46.3	0.25	-43.4 ± 307	0.24
Environment	2.3 ± 17.7	0.27	75.5 ± 120	0.29

SE are shown. Bold values indicate the highest importance value for each outcome.

Table 3.6. Generalized Linear Models, Model Weights and Top Model Evidence Ratios for Non-breeding Movements of Adult Brown Pelicans in the GOM, 2013–2016

	K	AIC_c	Δ_i (AIC_c)	w_i (AIC_c)	Σw	E
Migratory strategy (binomial)						
Colony size + Body size	4	80.82	0	0 .18	0.18	1.63
Colony size + Body size + Sex	5	81.80	0.97	0.11	0.29	
Colony size + Body size + Condition	5	81.87	1.05	0.11	0.40	
Body size + Environment	4	82.51	1.68	0.08	0.48	
Colony size * Body size	5	82.54	1.71	0.07	0.55	
Body size	3	82.72	1.90	0.07	0.62	
Colony size + Body size + Sex + Condition	6	82.74	1.91	0.07	0.69	
Migration distance (gamma)						
Colony size * Body size	5	1075.11	0	0.15	0.15	1.03
Colony size	3	1075.17	0.06	0.14	0.29	
Colony size * Body size * Sex	9	1075.59	0.47	0.12	0.41	
Colony size + Body size	4	1076.51	1.34	0.10	0.51	
Colony size + Condition	4	1077.04	1.87	0.08	0.59	
Colony size + Sex	4	1077.06	1.89	0.08	0.67	

Substantially supported (Δi AICc ≤ 2) generalized linear models are shown. wi= model weights; E= evidence ratios. Link functions are given in parentheses.

Table 3.7. Model-averaged Coefficients and Importance Values for Individual Covariates across the 95% Confidence Set of Models for Each Non-breeding Movement Parameter

Variable	Migratory strategy		Distance	
	Coefficient	Importance	Coefficient	Importance
Colony size	0.01 ± 0.005	0.63	0.12 ± 0.05	**0.78**
Body size (culmen)	-0.06 ± 0.03	**0.95**	-4.5 ± 5.5	0.34
Condition	-1.6 ± 2.0	0.37	-283 ± 448	0.28
Sex–Male	1.3 ± 1.5	0.39	-3.3 ± 278	0.28
Environment	0.2 ± 0.3	0.36	76.9 ± 86.2	0.38

SE are shown. Bold values indicate the highest importance value for each outcome.

Figure 3.1. Deployment duration and behavioral states of GPS-tagged brown pelicans, GOM, 2013–2016. Total numbers of GPS locations after cleaning and interpolation are listed to the right of each bar. Bar colors indicate behavioral states derived from HMM (red: resident; green: transient).

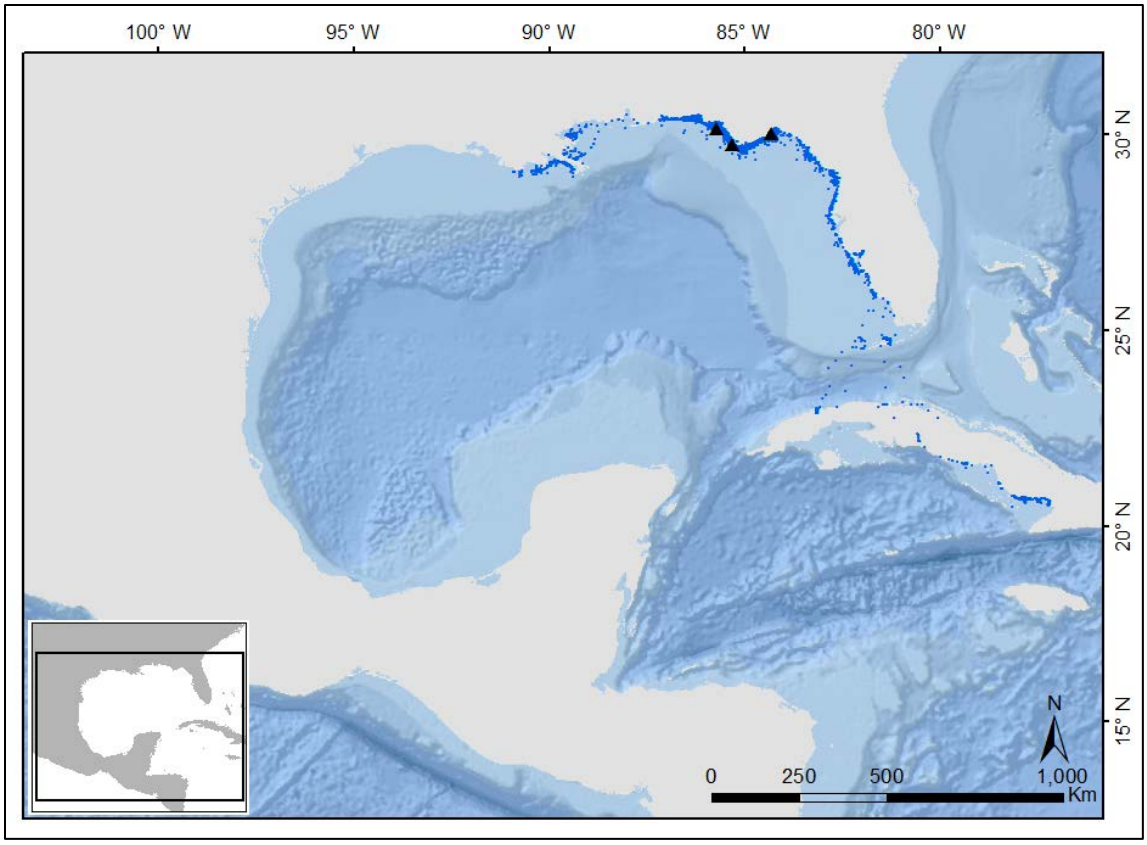


Figure 3.2.a. GPS locations of brown pelican originally captured at breeding colonies in the eastern, central, and western planning areas of the Northern GOM, 2013–2016, eastern planning area.
Black triangles indicate capture locations. Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

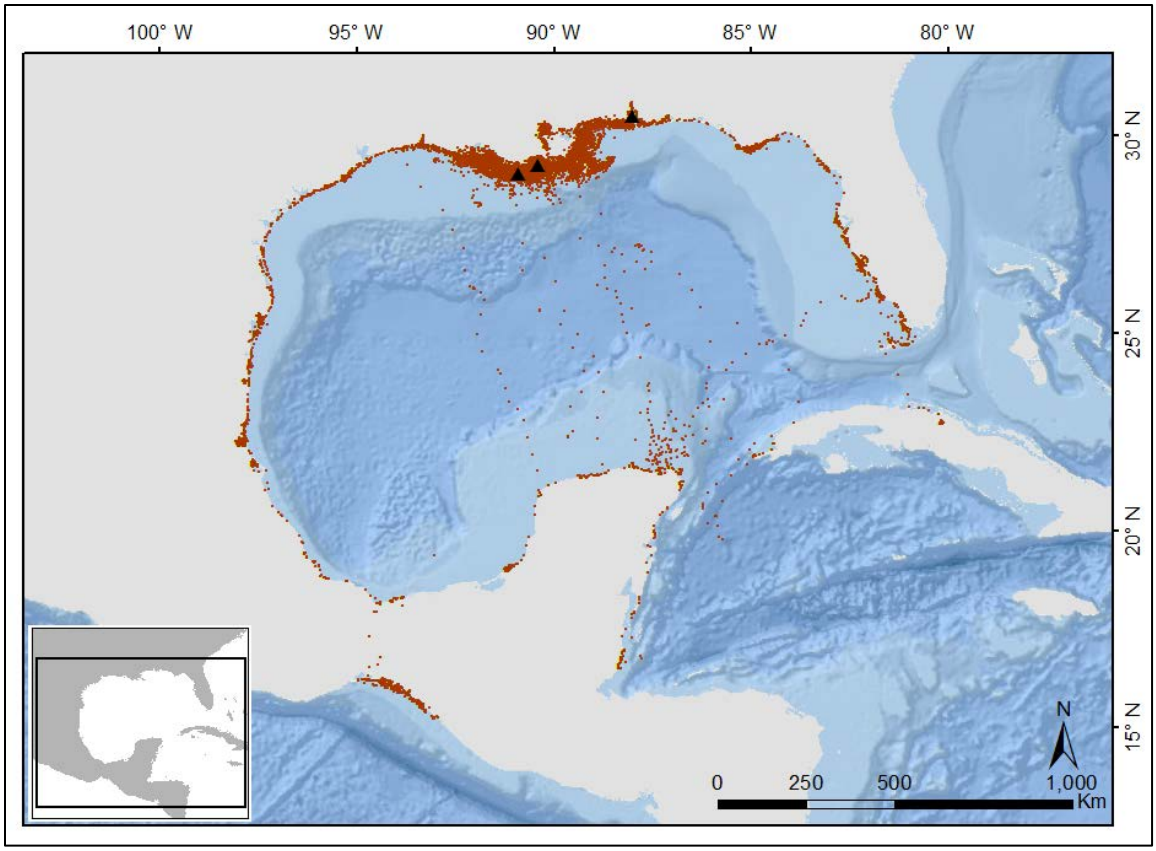


Figure 3.3.b. GPS locations of brown pelican originally captured at breeding colonies in the eastern, central, and western planning areas of the Northern GOM, 2013–2016, central planning area.
Black triangles indicate capture locations. Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

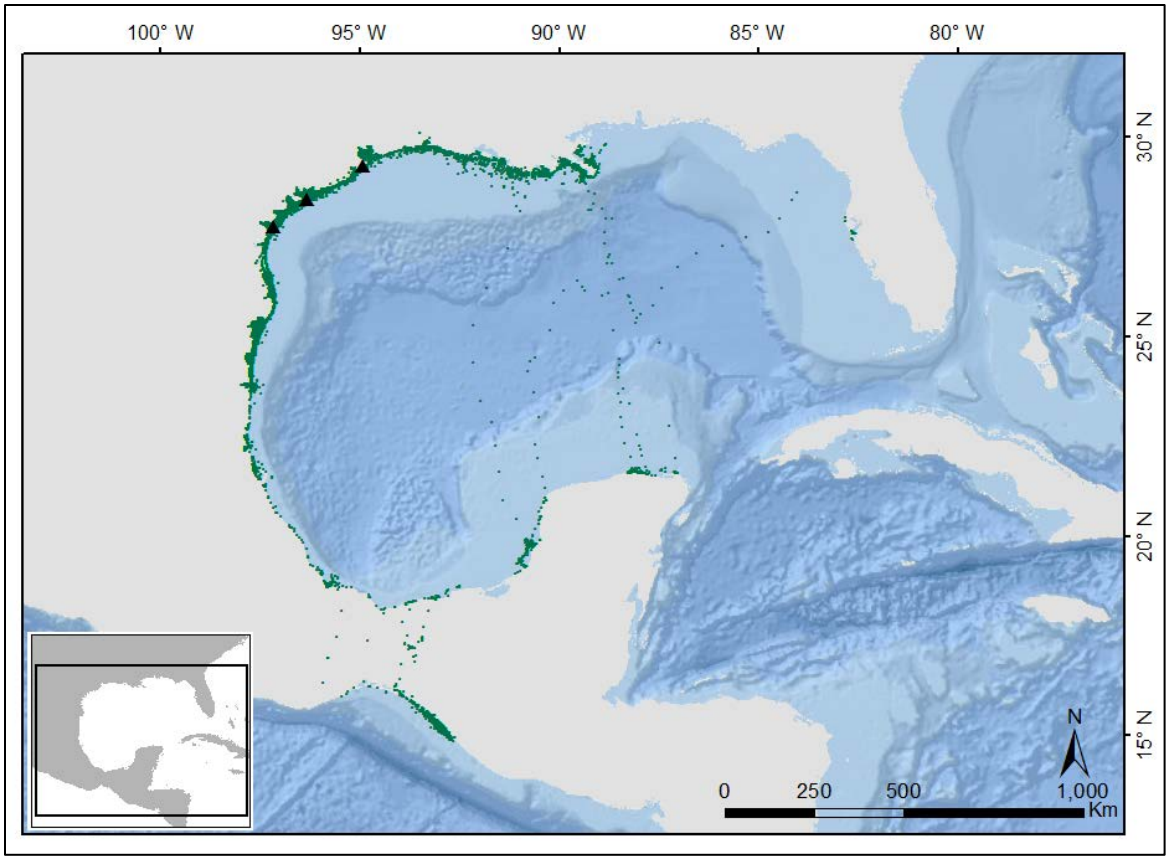


Figure 3.4.c. GPS locations of brown pelican originally captured at breeding colonies in the eastern, central, and western planning areas of the Northern GOM, 2013–2016, western planning area.
Black triangles indicate capture locations. Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

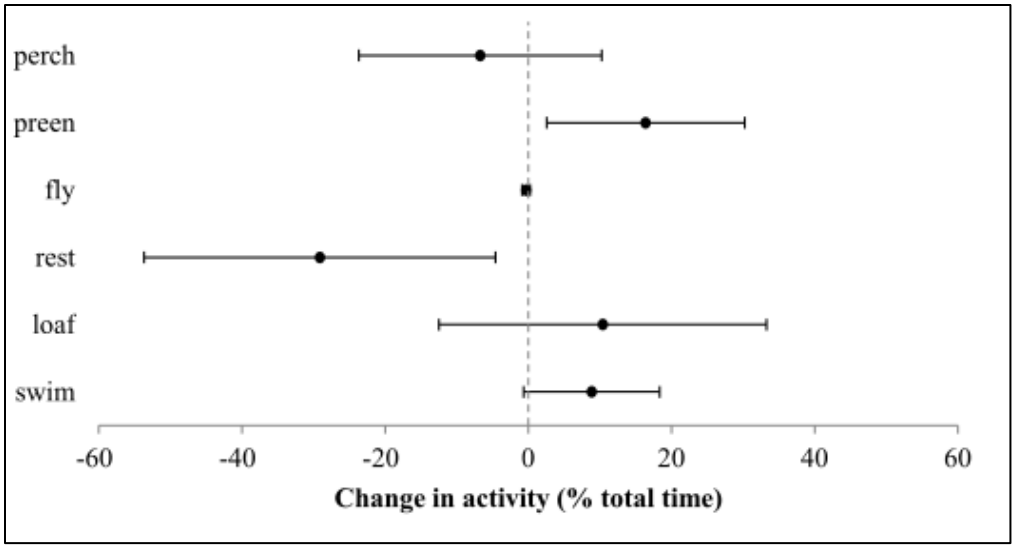


Figure 3.5.a. Change in activity pre- and post-tagging for brown pelicans in a captive holding facility, San Pedro, California, 2015, state behaviors (percent time).
Error bars represent 95% confidence intervals.

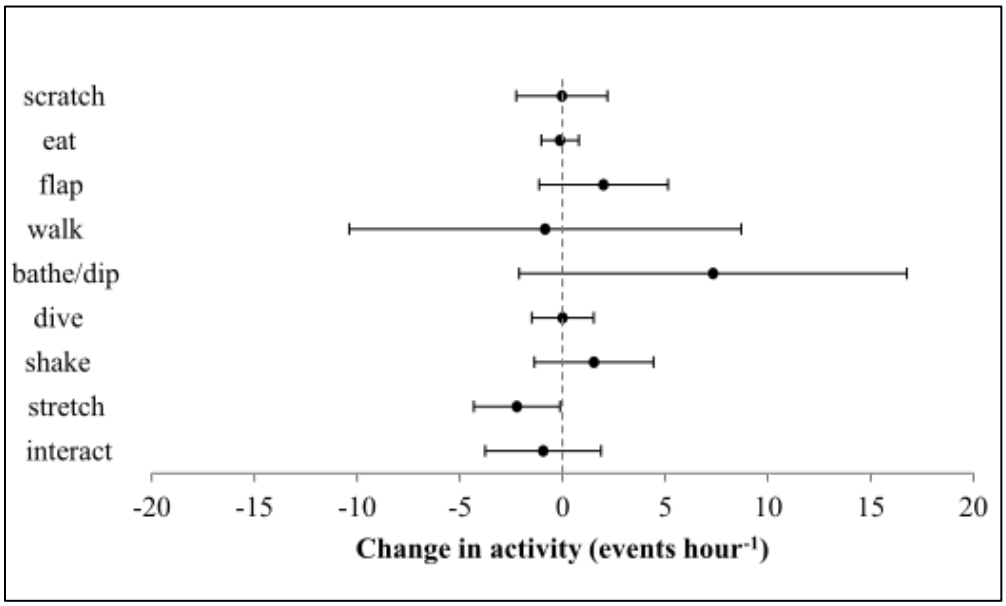


Figure 3.6.b. Change in activity pre- and post-tagging for brown pelicans in a captive holding facility, San Pedro, California, 2015, instant events (frequency).
Error bars represent 95% confidence intervals.

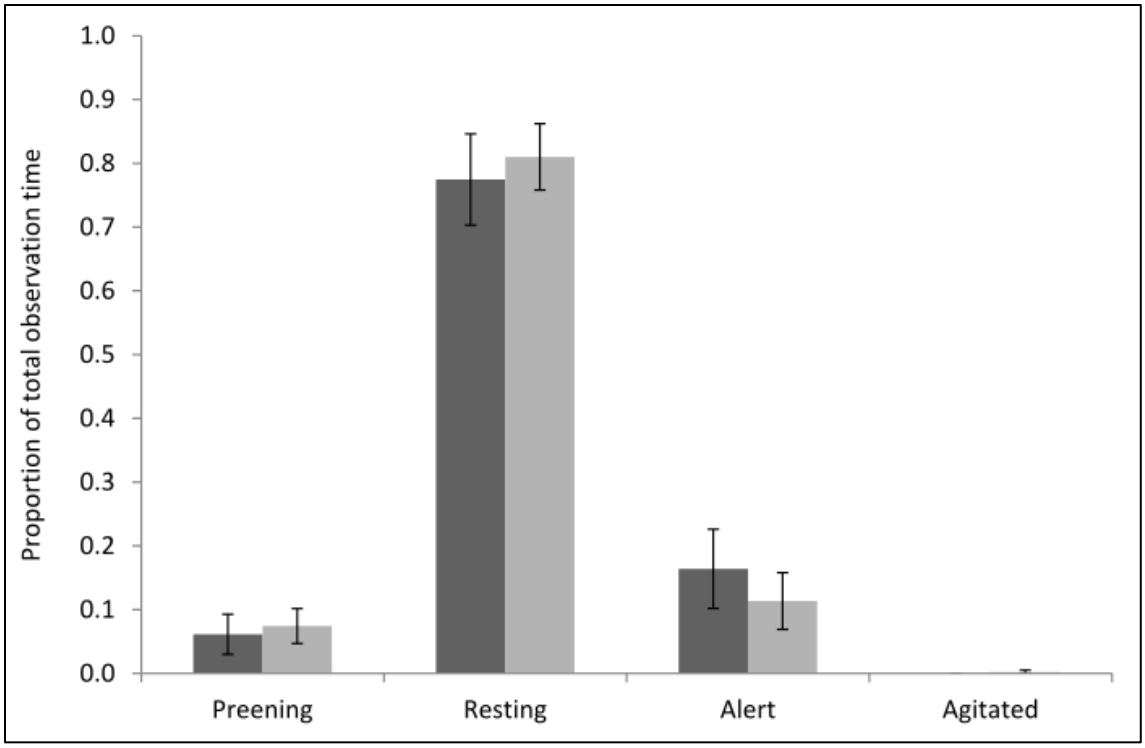


Figure 3.7. Percentage time spent by brown pelicans in different behavioral states 1–3 days after capture in field trials, GOM, 2013–2014.
Tagged individuals are shown in dark grey, and untagged neighbors in light grey. Error bars represent 95% confidence intervals. All differences between tagged and untagged individuals were non-significant ($p > 0.05$).

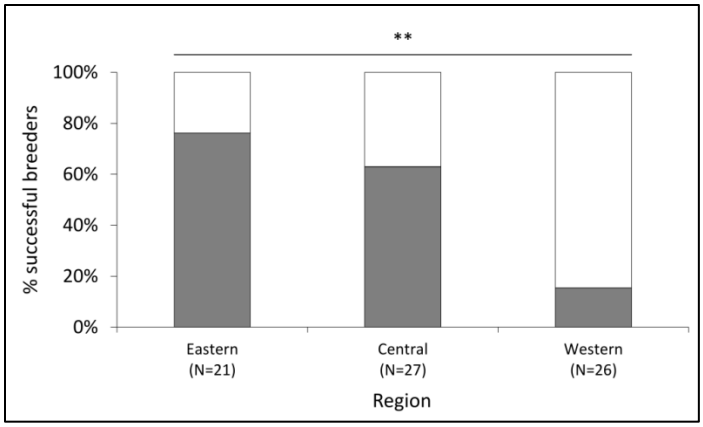


Figure 3.8.a. Influence of capture location, handling time, and sex on probability of successful breeding in GPS-tagged adult pelicans, GOM, 2013–2014, capture location.
Shaded bars represent successful breeders. N = number of tagged individuals. ** = $p < 0.001$; * = $p < 0.05$

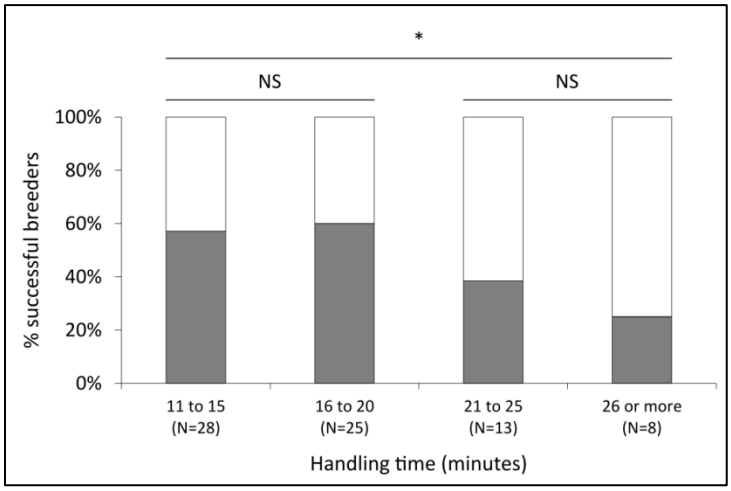


Figure 3.9.b. Influence of capture location, handling time, and sex on probability of successful breeding in GPS-tagged adult pelicans, GOM, 2013–2014, handling time.
Shaded bars represent successful breeders. N = number of tagged individuals. ** = $p < 0.001$; * = $p < 0.05$.

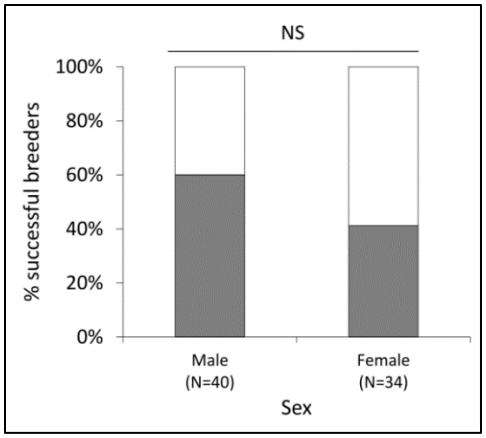


Figure 3.10.c. Influence of capture location, handling time, and sex on probability of successful breeding in GPS-tagged adult pelicans, GOM, 2013–2014, sex.
Shaded bars represent successful breeders. N = number of tagged individuals. ** = $p < 0.001$; * = $p < 0.05$.

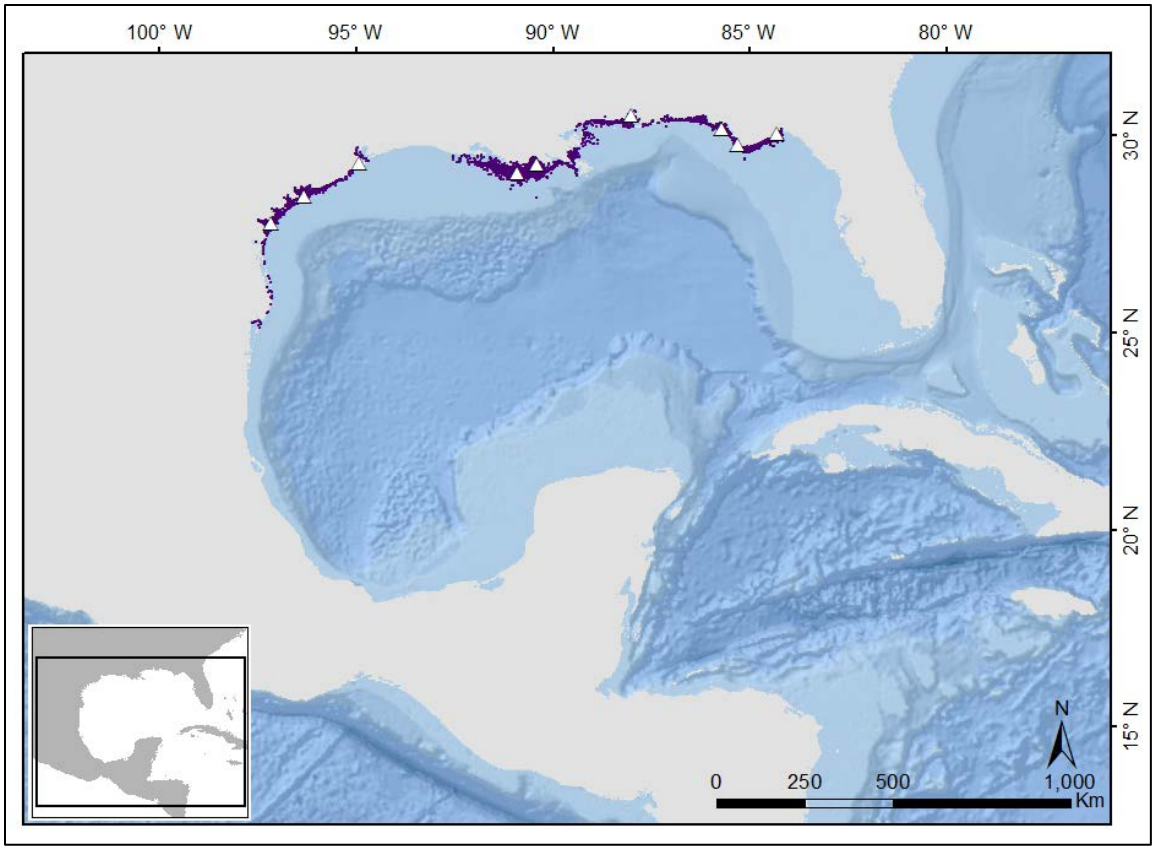


Figure 3.11.a. Seasonal GPS locations of brown pelican originally captured at breeding colonies in the Northern GOM, 2013–2016, during the breeding season.
White triangles indicate capture locations. Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

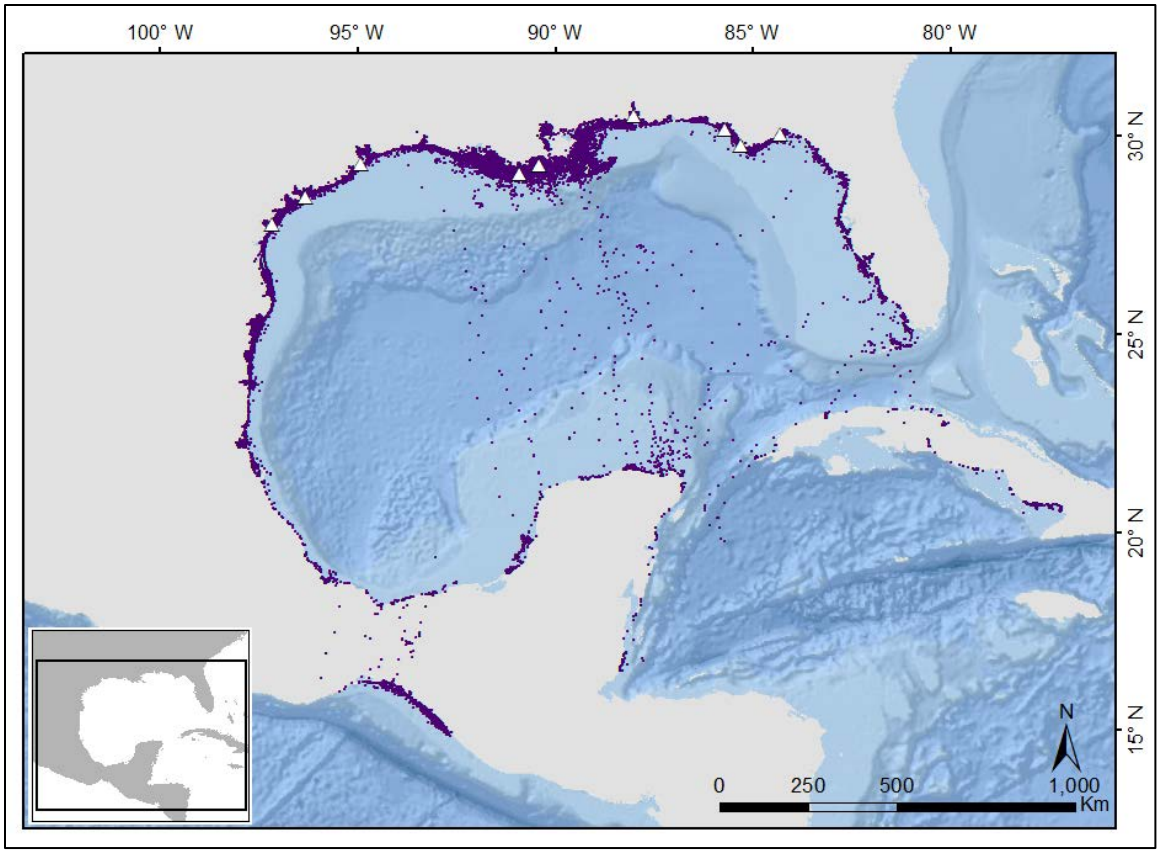


Figure 3.12.b. Seasonal GPS locations of brown pelican originally captured at breeding colonies in the Northern GOM, 2013–2016, during the non-breeding season.
White triangles indicate capture locations. Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

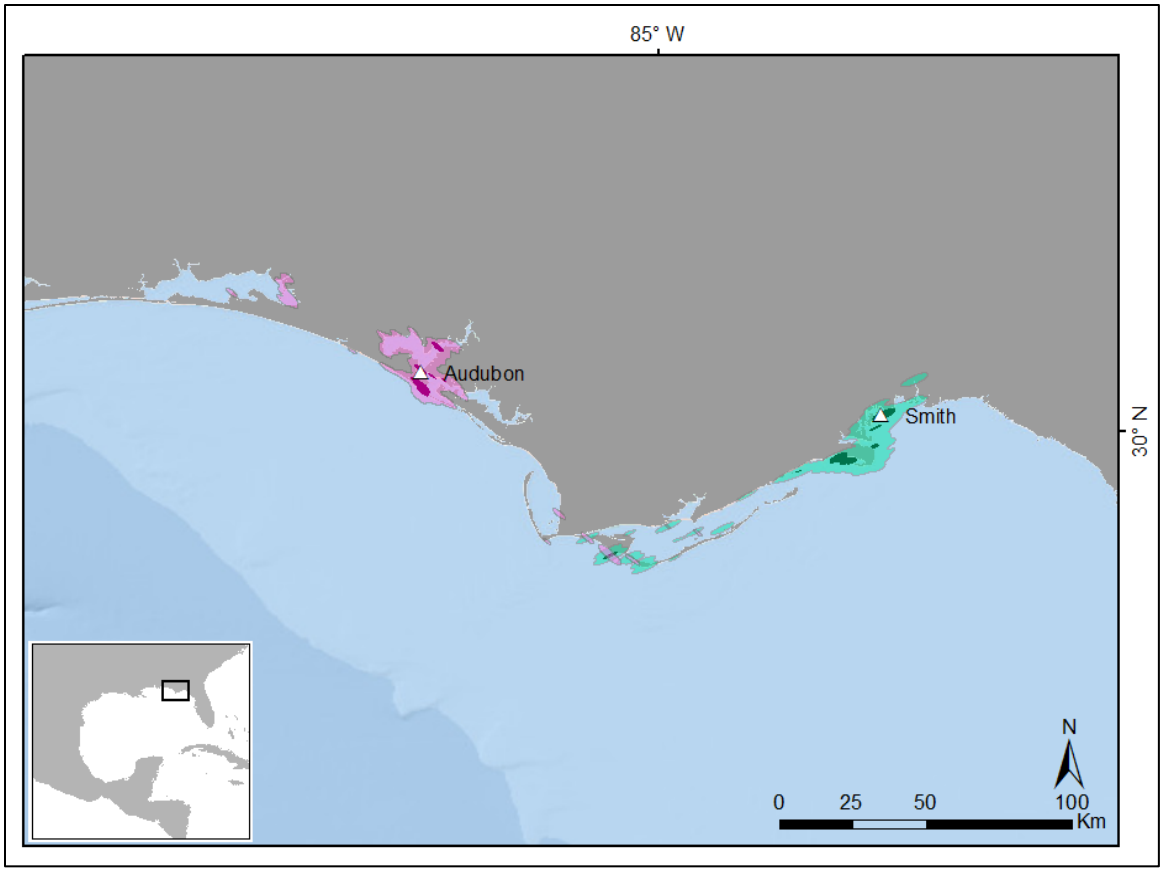


Figure 3.13.a. Brown pelican breeding home ranges by colony for the eastern, central, and western breeding planning areas of the Northern GOM, 2013–2016, captured in the eastern planning area. Breeding home ranges of brown pelicans captured in the eastern planning area. Darker contours represent 50% UD estimates, and lighter contours represent 95% UD estimates. Base layer: ESRI, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

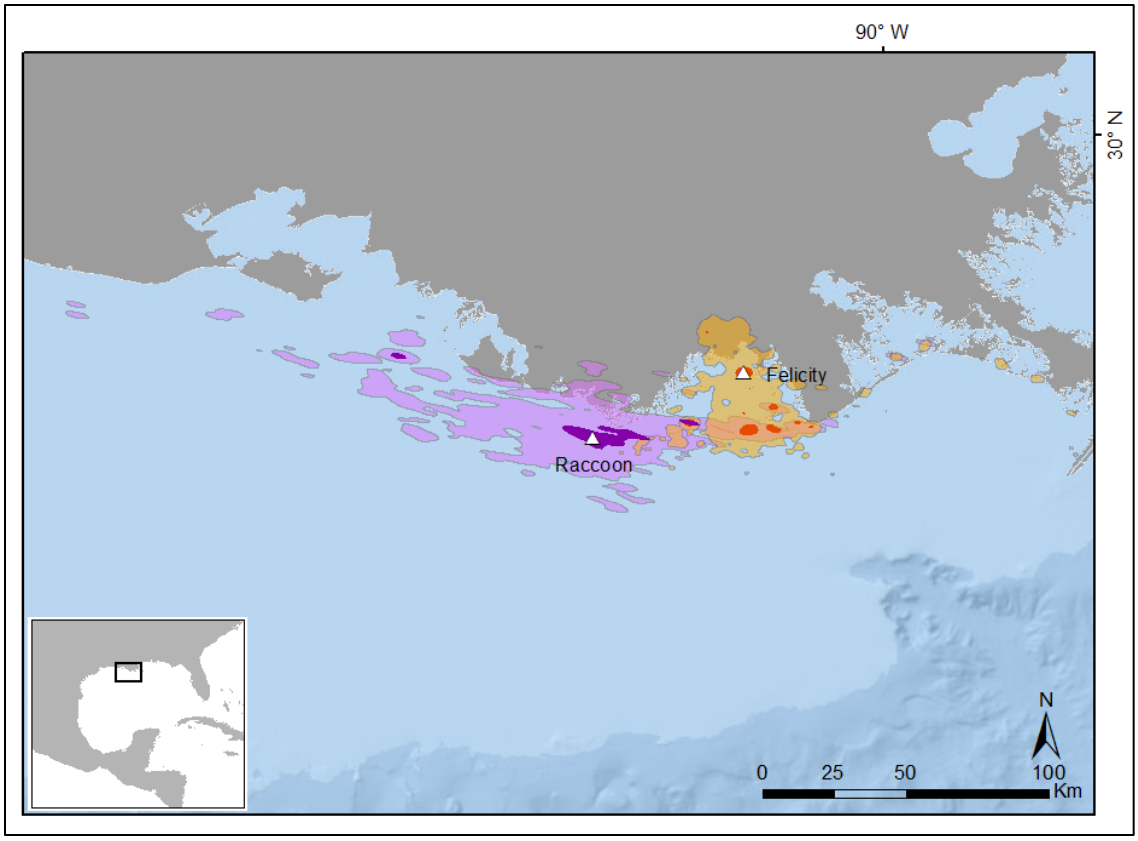


Figure 3.14.b. Brown pelican breeding home ranges by colony for the eastern, central, and western breeding planning areas of the Northern GOM, 2013–2016, captured in the central planning area. Breeding home ranges of brown pelicans captured in the central planning area. Darker contours represent 50% UD estimates, and lighter contours represent 95% UD estimates. Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

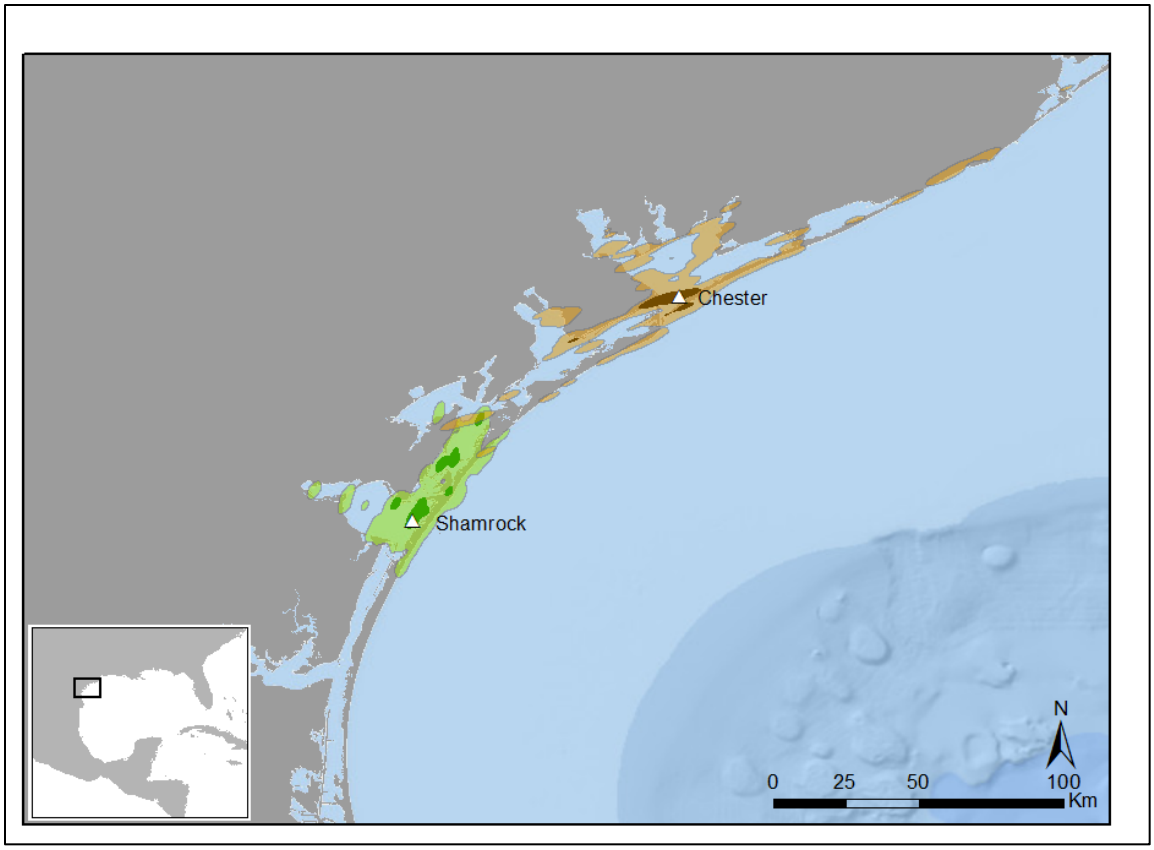


Figure 3.15.c. Brown pelican breeding home ranges by colony for the eastern, central, and western breeding planning areas of the Northern GOM, 2013–2016, captured in the western planning area. Breeding home ranges of brown pelicans captured in the western planning area. Darker contours represent 50% UD estimates, and lighter contours represent 95% UD estimates. Base layer: Esri, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

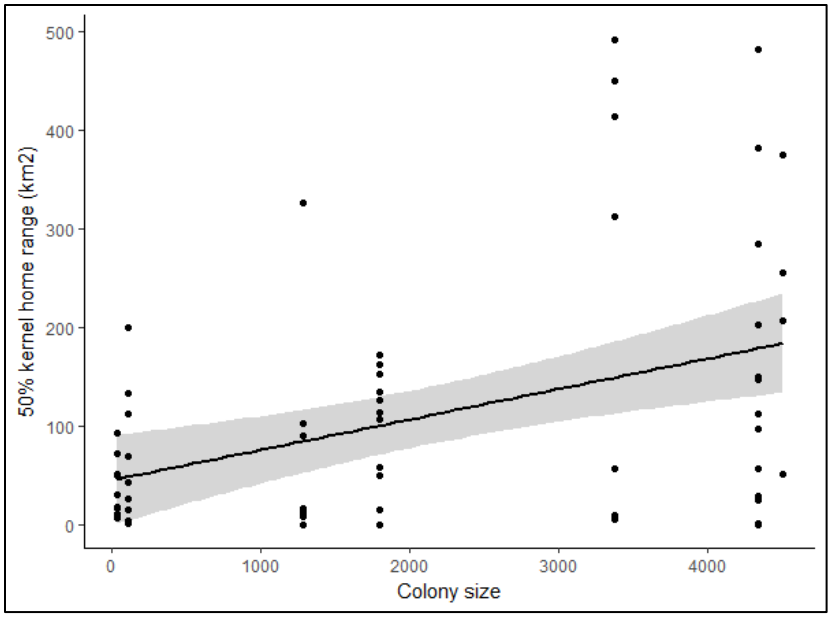


Figure 3.16.a. Mean home range areas of breeding adult brown pelicans at each study colony, Northern GOM, 2013–2016, 50% kernel.
Regression lines are shown with 95% confidence estimates (shaded).

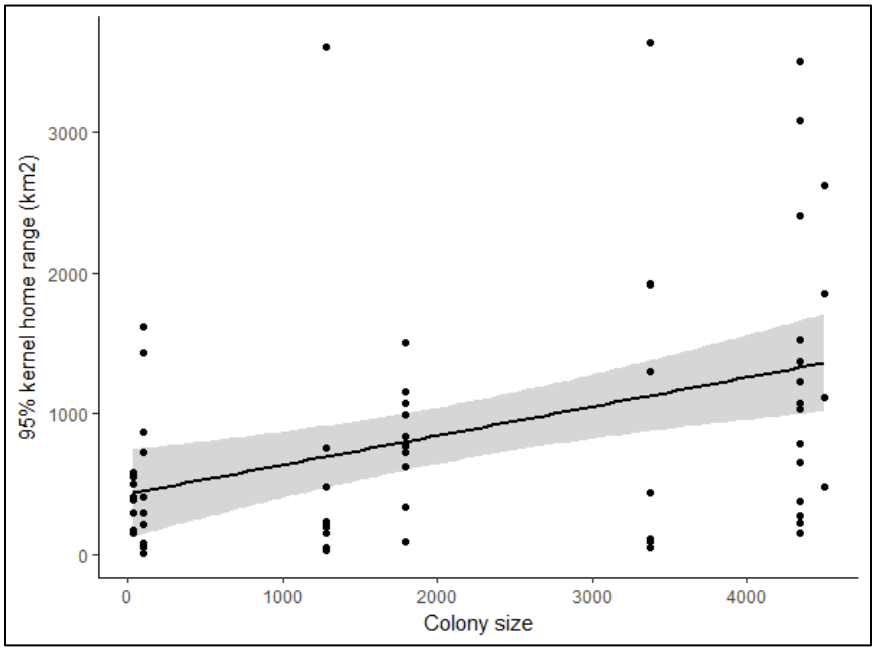


Figure 3.17.b. Mean home range areas of breeding adult brown pelicans at each study colony, Northern GOM, 2013–2016, 95% kernel.
Regression lines are shown with 95% confidence estimates (shaded).

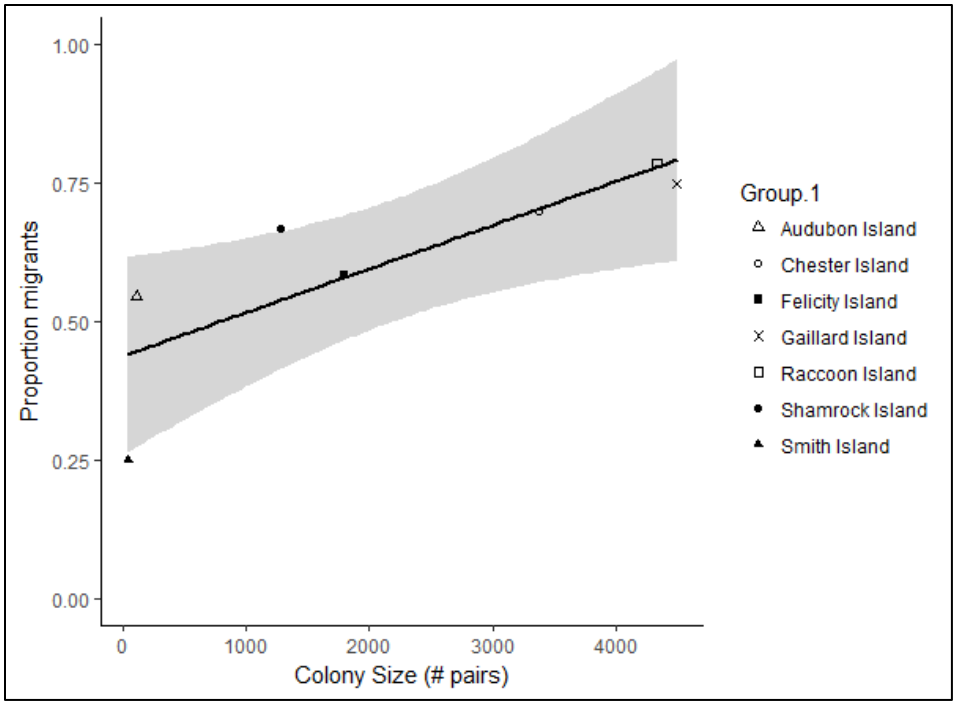


Figure 3.18.a. Relationships of brown pelican migratory characteristics between summer and winter home ranges to colony size, Northern GOM 2013–2016, proportion of migrants.
95% confidence estimates of regression lines are shaded.

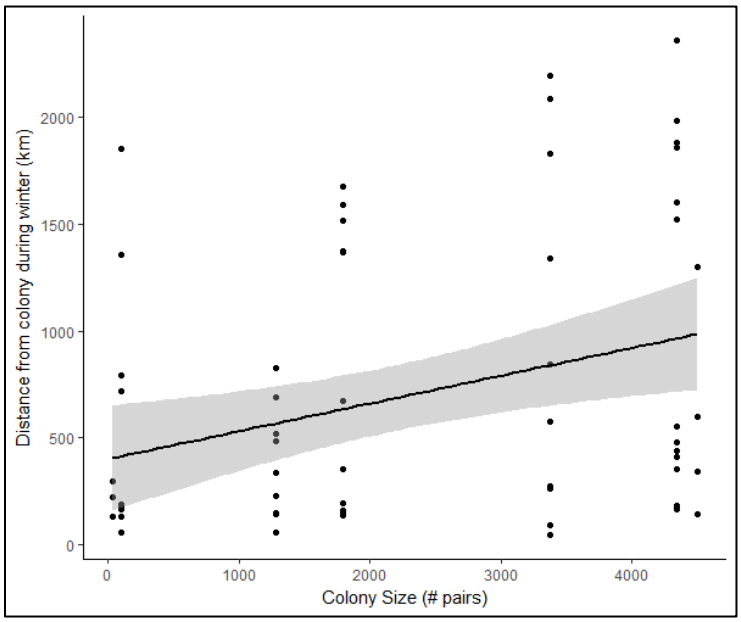


Figure 3.19.b. Relationships of brown pelican migratory characteristics between summer and winter home ranges to colony size, Northern GOM 2013–2016, average distance from colony during winter.
95% confidence estimates of regression lines are shaded.

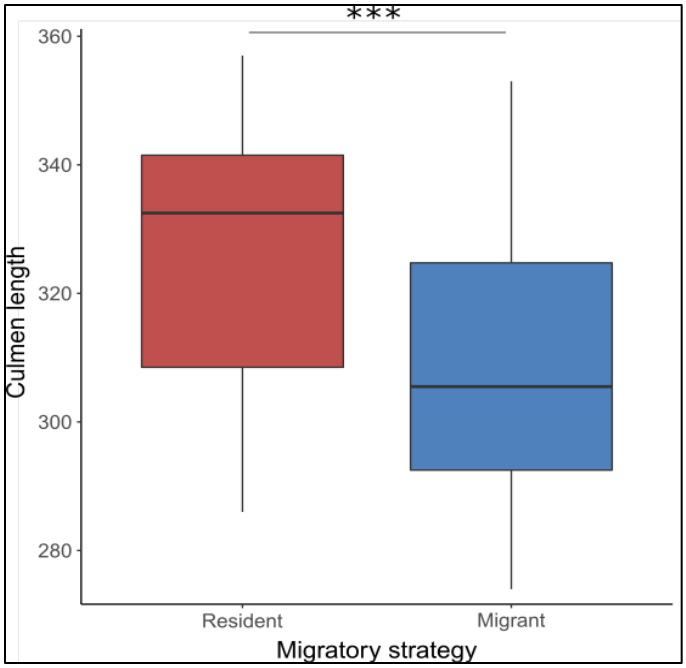


Figure 3.20.a. Differences in body size between migratory behavior of brown pelicans birds, and within sexes, Northern GOM 2013–2016, all tracked birds.
Residents are shown in red and migrants in blue. Asterisks denote significance levels of between-group comparisons (***: $p < 0.001$; *: $0.1 < p < 0.05$; NS: $p > 0.05$).

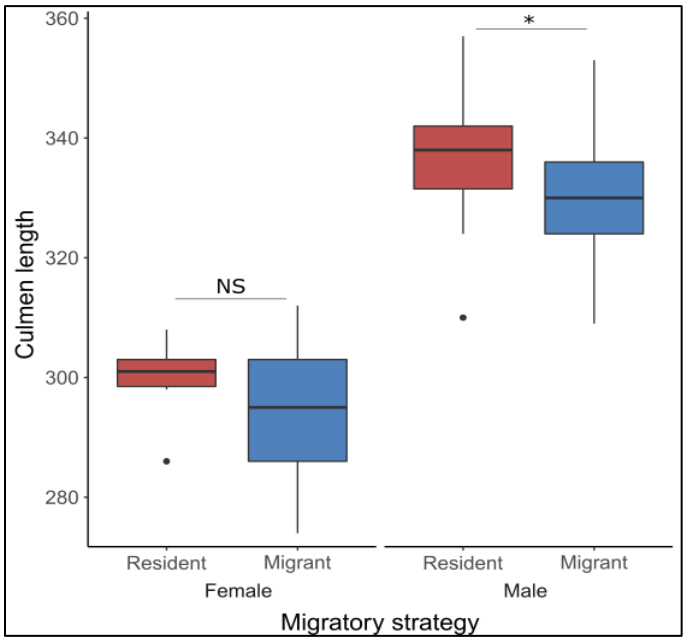


Figure 3.21.b. Differences in body size between migratory behavior of brown pelicans birds, and within sexes, Northern GOM 2013–2016, within sexes.
Residents are shown in red and migrants in blue. Asterisks denote significance levels of between-group comparisons (***: $p < 0.001$; *: $0.1 < p < 0.05$; NS: $p > 0.05$).

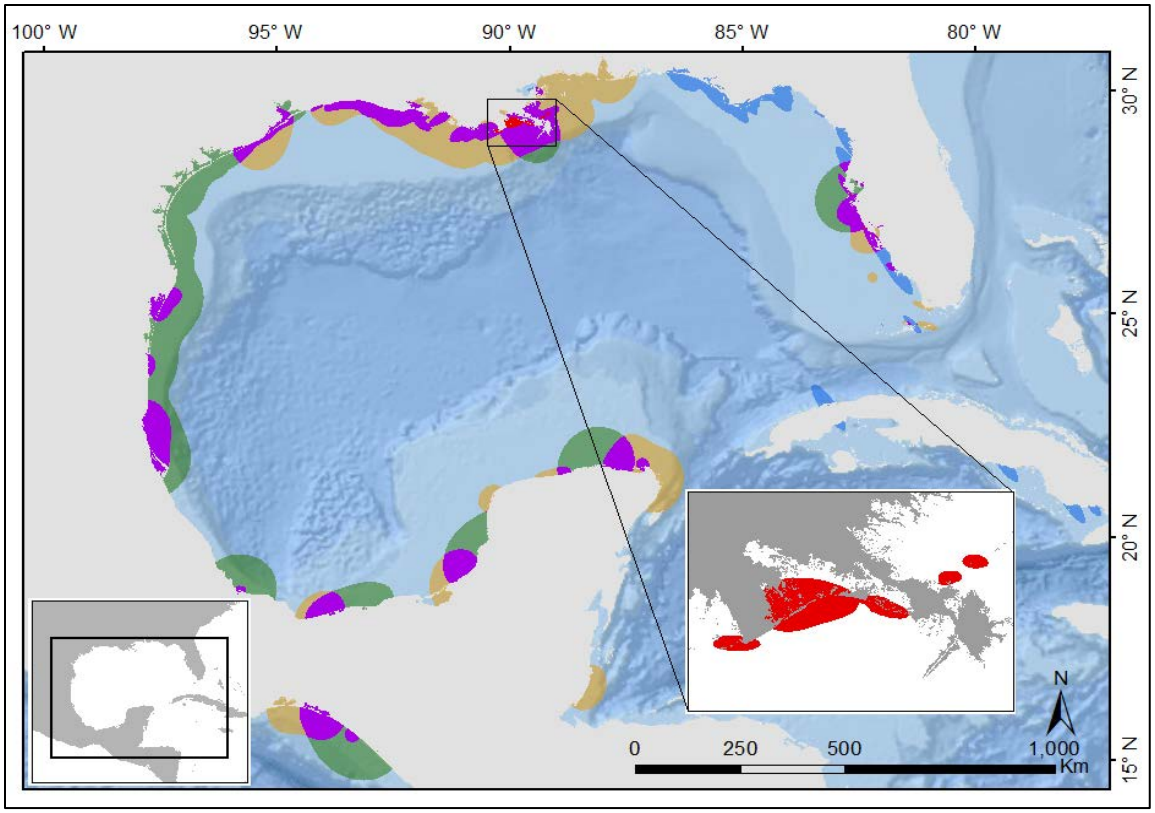


Figure 3.22. Annual 95% kernel density estimates for locations of brown pelicans originally captured at breeding colonies in the Northern GOM, 2013–2016.
Polygons show utilization distributions of brown pelicans nesting in the eastern (blue), central (orange), and western (green) planning areas. Areas shared by two or more planning areas are shaded in purple, and areas shared by all planning areas are shaded in red (detail in inset). Base layer: ESRI, DeLorme, GEBCO, NOAA, NGDC, and other contributors.

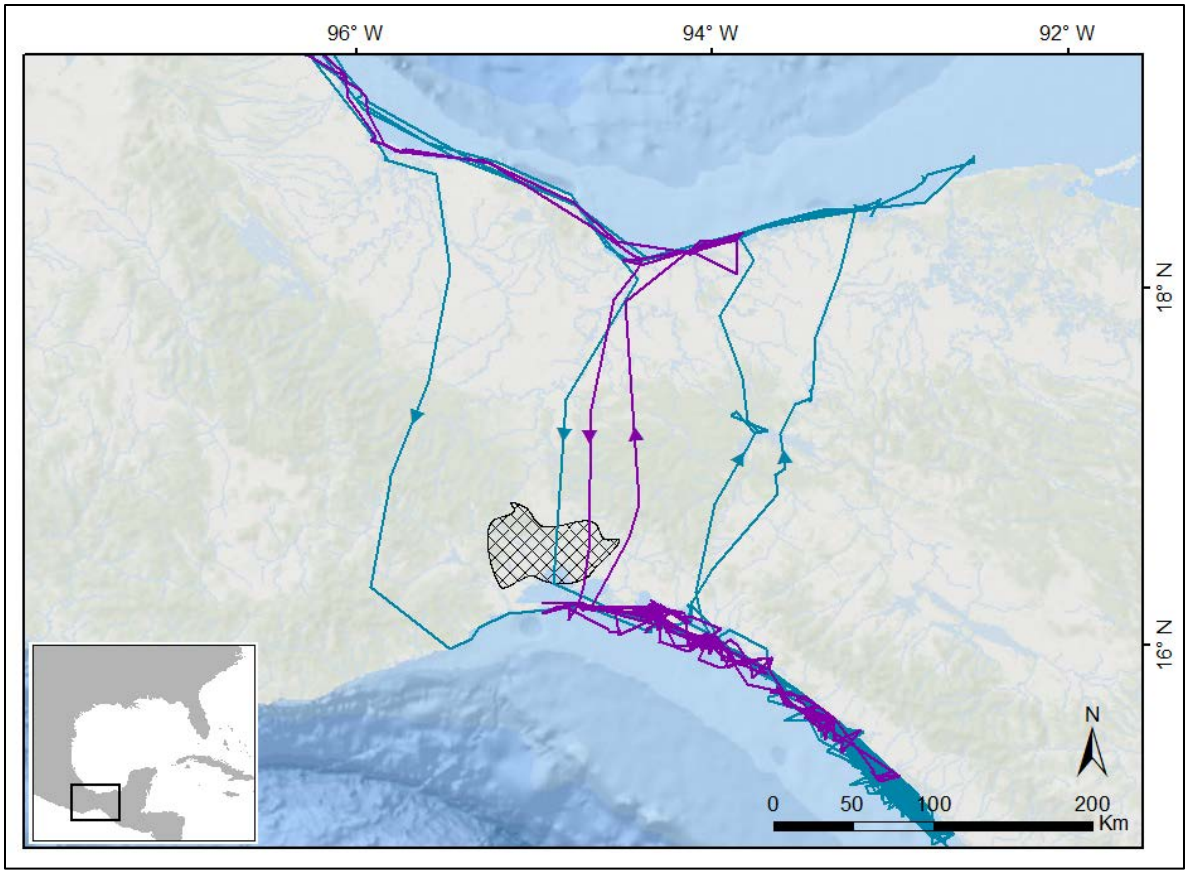


Figure 3.23. Migration routes of brown pelicans in the Tehuantepec Isthmus, Mexico, 2013–2015. N = 2. Arrows indicate direction of fall and spring migration; hatched area represents wind energy installations. Base layer: ESRI, DeLorme, GEBCO, NOAA, NGDC, and other contributors. Revised from Lamb et al. 2018.

4 Habitat Use and Risk Exposure

4.1 Annual Habitat Use of Breeding Adults

Overall, 61.5% of bird-days were classified as resident and 38.5% as transient (Figure 3.1). The proportion of time individuals spent in each state did not differ significantly by sex (ANOVA, $F_{1,76} = 2.12$, $p = 0.15$). Between planning areas, individuals tagged in the eastern planning area spent relatively more time in the resident state ($\mu = 0.73 \pm 0.04$) than did individuals tagged in the central ($\mu = 0.53 \pm 0.03$) or western ($\mu = 0.65 \pm 0.05$) planning areas (ANOVA, $F_{2,74} = 6.61$, $p = 0.002$). Both states were observed year-round; however, resident behavior was relatively more common between December and March and between May and August. Transient behavior was more frequently observed during the remaining months. Niche position and breadth on measured habitat variables did not change depending on behavioral state (Figure 4.1).

The habitat variables most strongly associated with brown pelican residency year-round were net primary production (positive) and sea surface salinity (negative) (Figure 4.2). Sea surface temperature was negatively associated with residency during non-breeding, but the association diminished to near zero during the breeding season. Compared to seasonally dependent variables, fixed factors were less associated and less variable in their relationship to pelican habitat use, and did not vary during the year. Bathymetry had a positive relationship with residency (i.e., pelicans were more likely to occupy shallower waters), while distance to coastline and distance to river outflow were both negatively associated with use by brown pelicans.

Patterns of association with seasonally dependent habitat variables varied between planning areas (Figure 4.3). Pelicans breeding in the central planning area of the GOM exhibited the highest degree of variation in environmental characteristics of selected habitat. Pelicans were more associated with waters characterized by high productivity and low salinity during summer (breeding) than during winter (non-breeding). Pelicans from the central and eastern planning areas selected habitat with a lower degree of seasonal variation in environmental characteristics, although pelicans from all planning areas associated more with sea surface temperature during breeding than during non-breeding.

Overall, areas of highest habitat suitability year-round were located in the Northern GOM, particularly the central and western planning areas (Figure 4.4). The total area of preferred habitat was narrowly restricted to coastal areas of the Northern Gulf during the summer; however, suitable habitat characteristics also occurred from the nearshore region out to approximately 600 km (372.8 mi) offshore during the fall and winter. Breeders from central GOM colonies shared 41% of their total habitat with breeders from other locations, western GOM breeders shared 36%, and eastern GOM breeders shared 15%. Habitats shared by central and western breeders accounted for 94% of total shared habitat.

Although extensive work has described the environmental factors driving seabird at-sea habitat usage in pelagic waters (e.g., Haney 1985, Pinaud and Weimerskirch 2005, Tew-Kai et al. 2009), relatively little is known about the factors driving marine habitat use in nearshore seabirds, particularly in the North Atlantic. For the most part, previous studies of habitat preferences in nearshore-foraging species have been conducted in northern temperate waters (e.g., Becker and Beissinger 2003, Yen et al. 2006, McLeay et al. 2010). We found that, similar to results from these systems, marine productivity was the most significant driver of brown pelican habitat selection in nearshore GOM environments. Also, in concordance with previous results (Day et al. 2000, Becker and Beissinger 2003), we found that the influence of sea surface temperature on at-sea distribution was significant but highly variable over time. In a departure from previous assessments of habitat use of nearshore seabirds, which generally found little

effect of salinity on habitat use (Zamon et al. 2014), we found that salinity strongly influenced brown pelicans' habitat use. Although the effects of salinity have not been extensively documented for this species or other coastal seabirds, recent studies (e.g., Zamon et al. 2014) have suggested that river plumes can be important nearshore foraging habitat for seabirds as prey are concentrated in a manner analogous to pelagic system oceanic fronts. Though distance to river outflow only weakly related to pelican habitat suitability in this study, pelicans were often located in relatively large estuarine complexes. Therefore, brown pelicans may ultimately be responding to salinity gradients that exist even at a greater distance from river mouths.

Because the scale of movement that we observed was relatively small (on the order of tens of kilometers per day, rather than hundreds of kilometers as is commonly observed in pelagic seabirds), we selected environmental variables likely to relate to the distribution of prey rather than those that might facilitate long-distance movement (e.g., prevailing winds) or visual identification of foraging areas (e.g., ocean color). The influence of salinity, in particular, is correlated to the abundance and distribution of prey items. Brown pelicans in the GOM forage primarily on Gulf menhaden, which concentrate during the spring and summer in low-salinity estuarine environments (Deegan 1990). Both summer and winter distribution of preferred brown pelican habitat corresponded closely with Gulf menhaden distributions, indicating that pelicans select habitat principally as a function of prey concentrations. We did not find that the tested spatially fixed metrics had a strong influence on habitat suitability (e.g., distance to coastline, distance to river outflow, bathymetry, or bottom substrate). Previous studies (e.g., Suryan et al. 2012) have suggested that such metrics tend to provide a more consistent predictor of seabird distributions than seasonally varying environmental characteristics. The lack of a strong relationship of pelican distributions to static marine features may result from the short timescale of this study. They may also be a feature of the GOM, which is dominated by silt and sand and has a highly dynamic coastal geography and bathymetry relative to rocky shores in more northern regions where most other studies have occurred (Britton and Norton 2014).

Another possible explanation for the lack of a strong relationship of pelican habitat suitability to static features may relate to the scale of our analysis. The spatial scale of the environmental data available (10 km^2/ 6.21 mi^2) and the temporal resolution of the GPS data we collected (90 min intervals) did not allow us to distinguish fine-scale foraging areas from commuting or resting habitat. We confined observations to mesoscale movement patterns and habitat selection on a monthly timescale. The fact that seasonally varying parameters were more related to habitat selection than physical oceanographic features is consistent with previous observations that mesoscale habitat use is likely to be driven by primary productivity, and physical features become more important at the micro (<10 km/ 6.21 mi) scale (Becker and Bessinger 2003). Habitat selection likely also occurs at finer scales than those described by this study (Kristan 2006), and may vary with daily or weekly changes in estuarine dynamics that alter distribution and concentrations of prey.

4.2 Risk Exposure

4.2.1 Spatial and Temporal Aspects of Risk Exposure

Hot spots of overlap between preferred brown pelican habitat and surface pollutants (i.e., areas of high overlap) were consistent throughout the year and included most of the central and western planning areas of the Northern Gulf, particularly the Mississippi Delta and Galveston Bay (Texas) areas (Figure 4.5). Other hot spots varied seasonally in intensity and included Corpus Christi Bay (Texas), Tampa Bay (Florida), the Florida Keys, the mouth of the Apalachicola River (Florida), and locations along the Yucatan Peninsula (Mexico) and in the Caribbean.

Pollutant exposure through the annual cycle varied by breeding location and sex among individuals (Table 4.1). Average overlap between individuals and pollution sources was lowest during non-breeding, increased at the start of the breeding season, and reached a maximum during post-breeding (Figure 4.6a). Overlap rates differed significantly by planning areas (ANOVA: $F_{2,74} = 11.97$, $p < 0.001$). Breeders from the eastern planning area experienced lower year-round exposure to potential surface pollutants, while central and western breeders had similar year-round exposure rates (Table 4.1). Exposure varied seasonally in both central and western breeders, but individuals breeding in the eastern planning area experienced lower overall exposure and seasonal variation (Figure 4.6b). Between sexes, males averaged higher exposure than females (ANOVA, $F_{1,75} = 4.48$, $p = 0.037$), which was driven by higher levels of overlap with surface pollutants during the non-breeding season (Figure 4.6c).

Down-weighting transient locations that were classified as transient generally reduced or removed the localized peak in pollutant exposure that occurred during the late fall (October–November) in most groups. This also emphasized the downward trend in exposure risk from a peak at early breeding to a low during winter (Figure 4.6 a-c). Between planning areas differences in individual exposure probability were still significant after down-weighting transient points by 0.5 (ANOVA: $F_{2,74} = 5.93$, $p = 0.004$); however, between sex differences were not (ANOVA: $F_{1,75} = 2.53$, $p = 0.11$).

We found the highest levels of overlap between preferred brown pelican habitat and potential surface pollution in the Northern GOM. Other overlap hotspots were concentrated around large river outflows, which experienced high pollution pressure from ports and shipping as well as favorable pelican habitat characteristics (e.g., low salinity, high productivity). Overall exposure risk increased sharply at the start of the breeding season, when pelicans returned to the higher pollution levels of the Northern GOM to breed and environmental factors restricted suitable habitat to a very narrow range in the nearshore environment. Risk levels either remained constant or declined during the breeding season, then peaked again during autumn (September–November), which coincides with the annual molt in brown pelicans. The post-breeding, molt phase of the annual cycle represents a period of constrained resident behavior, since molting limits flight capabilities. Our model indicated that breeders from the western GOM, which supports less oil infrastructure than the central planning area, experienced statistically similar levels of risk to pollutant exposure year-round compared to those from the highly developed central planning area. The similarity in risk despite the difference in exposure (i.e., infrastructure and development) may be due to the high level of spatial overlap between breeders from these two planning areas, or that major pelican breeding colonies in the western planning area are located near major shipping lanes (another significant source of pollutants). Our model suggested that female brown pelicans experienced a lower year-round probability of pollution exposure. Female pelicans were more likely to migrate to the less-developed southern GOM, which had generally lower concentrations of surface pollutants during the non-breeding season, and usually departed the breeding colony immediately following breeding completion or failure.

4.2.2 Individual Behavior and Model Structure

Spatial distribution and habitat use of seabirds are often used in combination with threat distributions to assess exposure to risk (e.g., Le Corre et al. 2012, Tranquilla et al. 2013, Renner and Kuletz 2015); however, overlap models have generally accounted for exposure only in terms of co-occurrence of birds and threats. The likelihood of threat exposure also varies depending on how birds interact with their environments, which can differ from species to species (Garthe and Hüppop 2004) or between phenological states within a species (Eppley and Rubega 1990). We used a HMM to distinguish resident behavior (individuals were restricted to limited habitat areas) from transient behavior (more frequent and longer-distance movements). This technique can improve predictive risk models by incorporating *a priori* biological understanding of expected behavioral states (Patterson et al. 2009) to better predict the likelihood that co-occurrence of individual locations with threats will result in exposure.

The parameters used to model risk could easily be modified to reflect future improvements in our understanding of pelican behavior or the spatiotemporal aspects of marine pollution risk. We assessed the effects of down-weighting transient points by 50%, by 90%, and 100% (complete removal from analysis), reflecting different levels of inferred interaction with surface pollutants during long-distance movement. Although the same general patterns in temporal pollution risk were not altered by lowering the assumed risk of pollutant exposure during long-distance movement, down-weighting transient points had the effect of reducing estimated peaks in exposure risk during the late-autumn migration and dispersal period. Further direct observations of pelicans outside the breeding season, especially during staging and molting, would help refine understanding of how behavior affects surface pollution exposure risk during periods of frequent long-distance movement. We chose to equally weight contributions of oil platforms and drilling rigs, oil pipelines, and ship- and port-based pollution to overall pollution risk; however, there are important differences between these factors. Pollution at ports and along shipping lanes is likely chronic and low-level, while pollution from oil infrastructure is more likely short-term and acute. Both sources can be acute or chronic pollution. This approach could be refined by monitoring the frequency, size, and location of pollutant spills and incorporating frequency and intensity of spills into analysis of pollution probability. Evaluating pollutant concentrations in brown pelican tissue from different planning areas would also provide a useful test of the model's exposure risk predictions.

Table 4.1. Mean Pollutants Overlap for Observed Brown Pelican Locations in the Northern GOM, 2013–2016

		Mean	Standard deviation	Number of individuals
Planning area				
	Eastern	0.082	0.023	23
	Central	0.133	0.034	26
	Western	0.122	0.049	28
Sex				
	Female	0.102	0.043	33
	Male	0.123	0.041	44
Month				
	January	0.050	0.059	44
	February	0.041	0.056	31
	March	0.057	0.054	28
	April	0.119	0.068	27
	May	0.136	0.051	56
	June	0.127	0.048	63
	July	0.125	0.058	69
	August	0.115	0.053	64
	September	0.109	0.060	63
	October	0.119	0.063	60
	November	0.103	0.075	63
	December	0.074	0.076	51

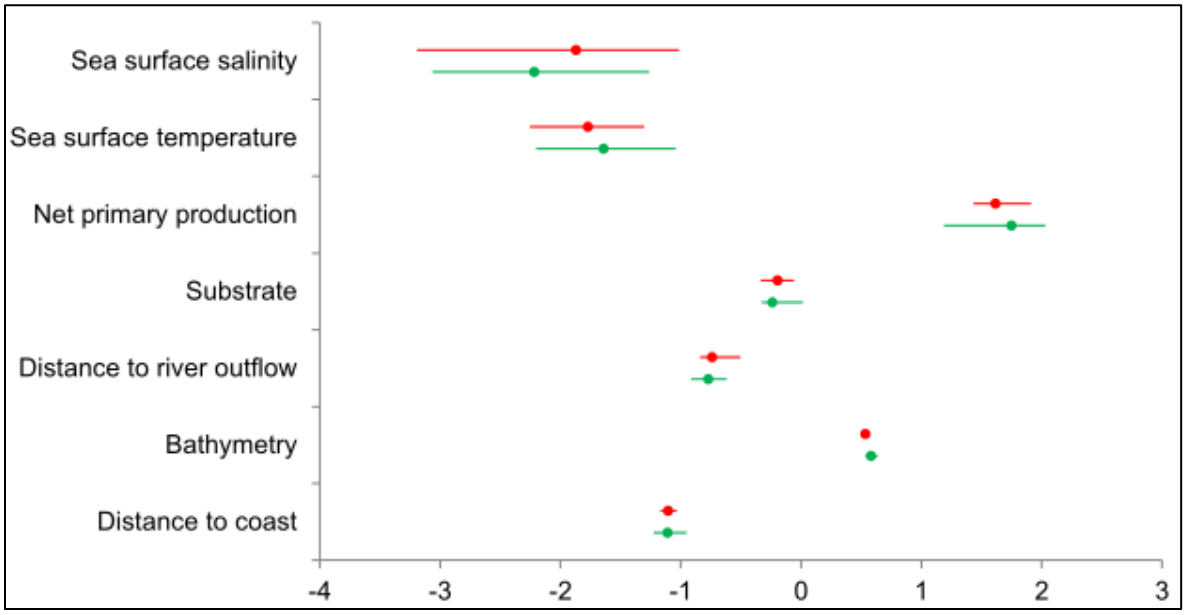


Figure 4.1. Niche center and breadth of resident and transient behavioral states of brown pelicans on measured habitat variables in the GOM, 2013–2016.
Resident behavioral state is shown in red, and transient behavioral state is shown in green.

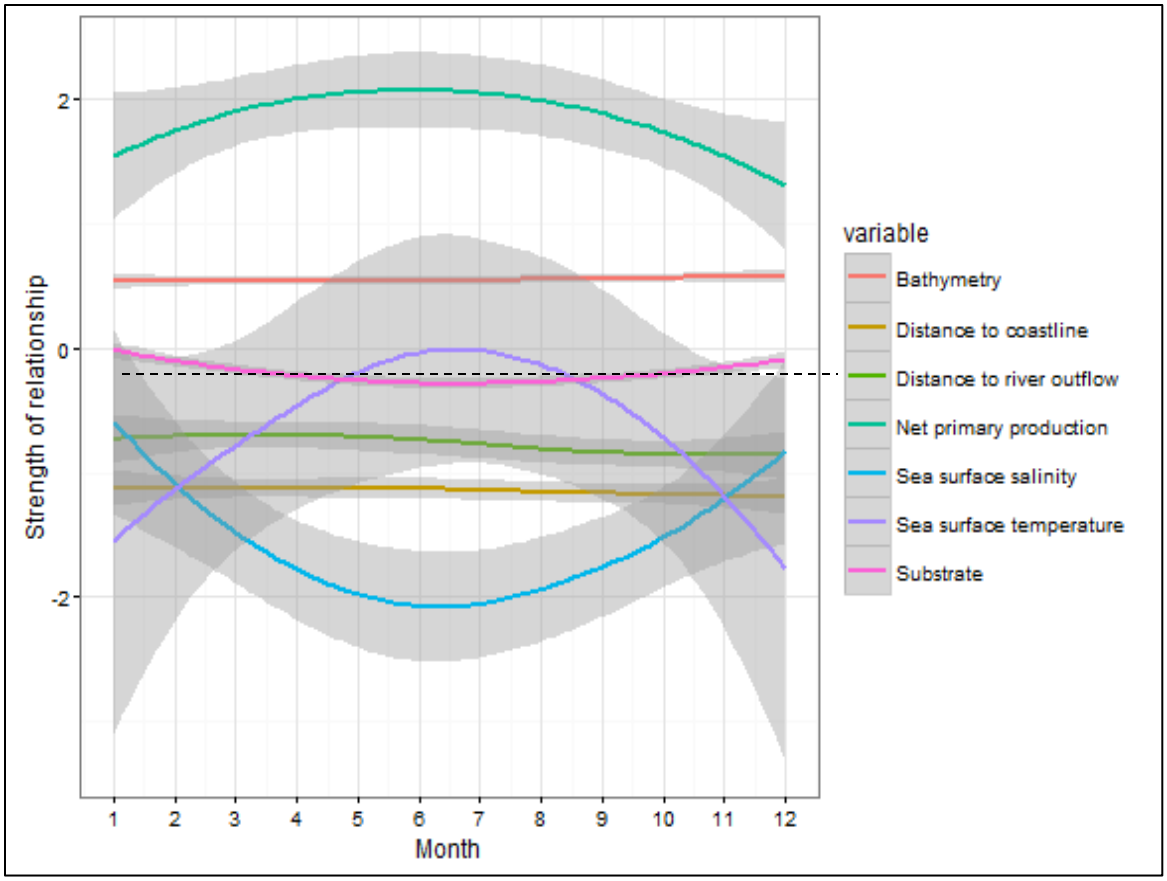


Figure 4.2. Annual patterns of strength and direction of selection by brown pelicans on measured habitat variables, GOM, 2013–2016.
Strength of selection (positive or negative) is generated from OMI and increases with distance from zero. Lines represent generalized additive model regressions (smoothing parameter = 1.3) of monthly averages for each variable, and grey bars are 95% confidence intervals of regression lines.

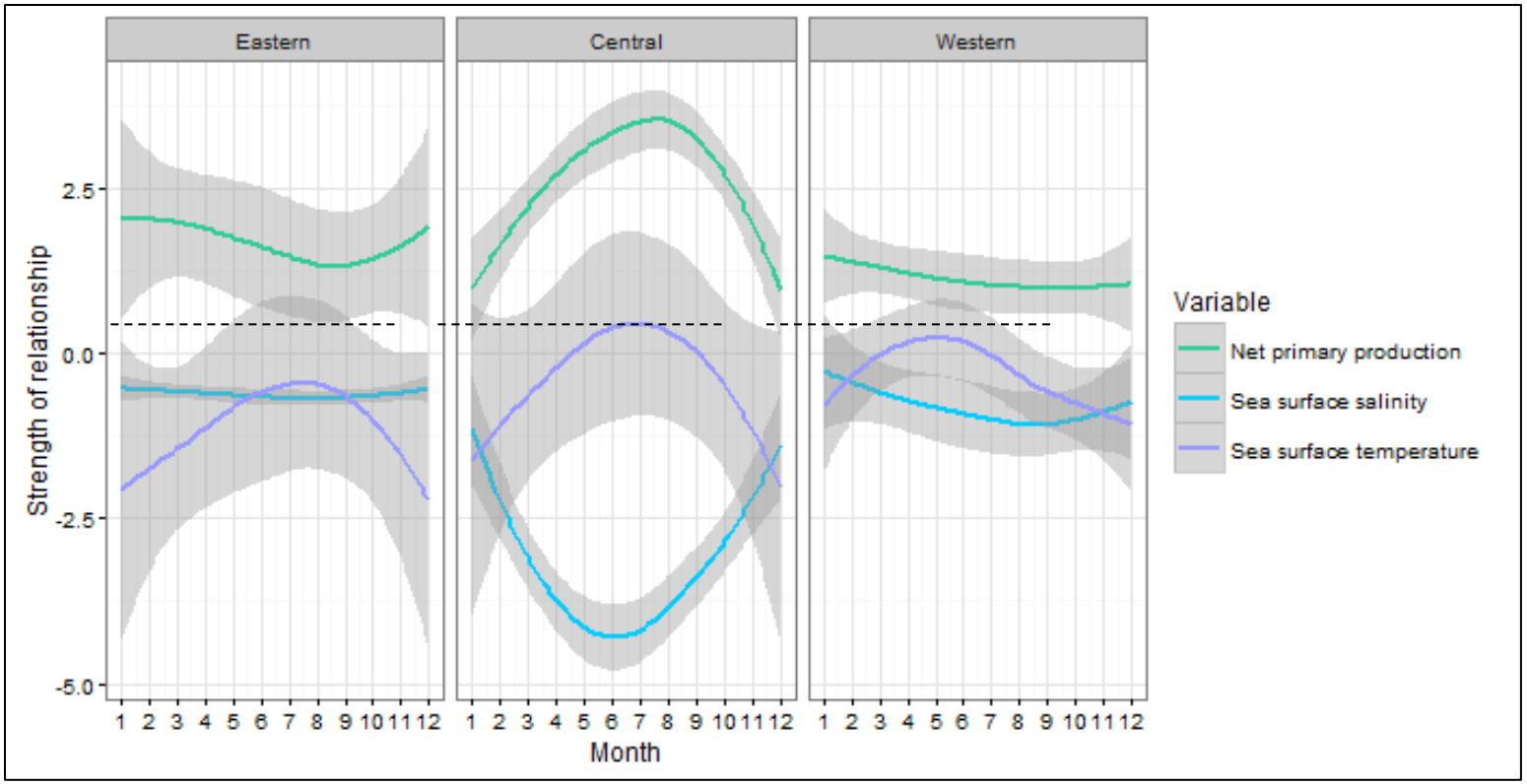


Figure 4.3. Annual patterns of strength and direction of selection by brown pelicans on seasonally varying habitat variables by planning area, GOM, 2013–2016.
Strength of selection (positive or negative) is generated from OMI and increases with distance from zero. Lines represent generalized additive model regressions (smoothing parameter = 1.3) of monthly averages for each variable, and grey bars are 95% confidence intervals of regression lines.

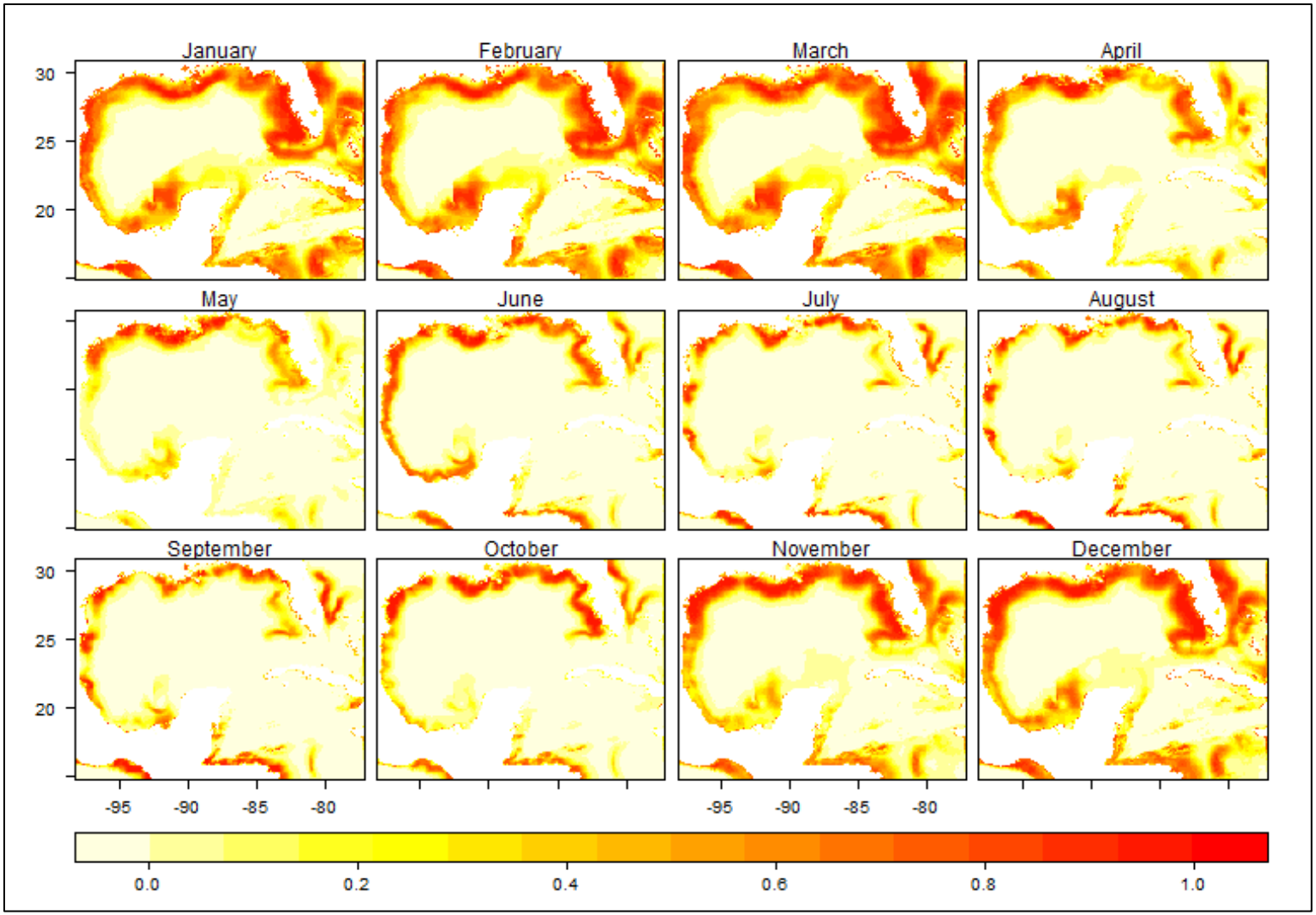


Figure 4.4. Suitability scores of available brown pelican habitats in the GOM, based on Mahalanobis distances.
Darker colors indicate higher suitability.

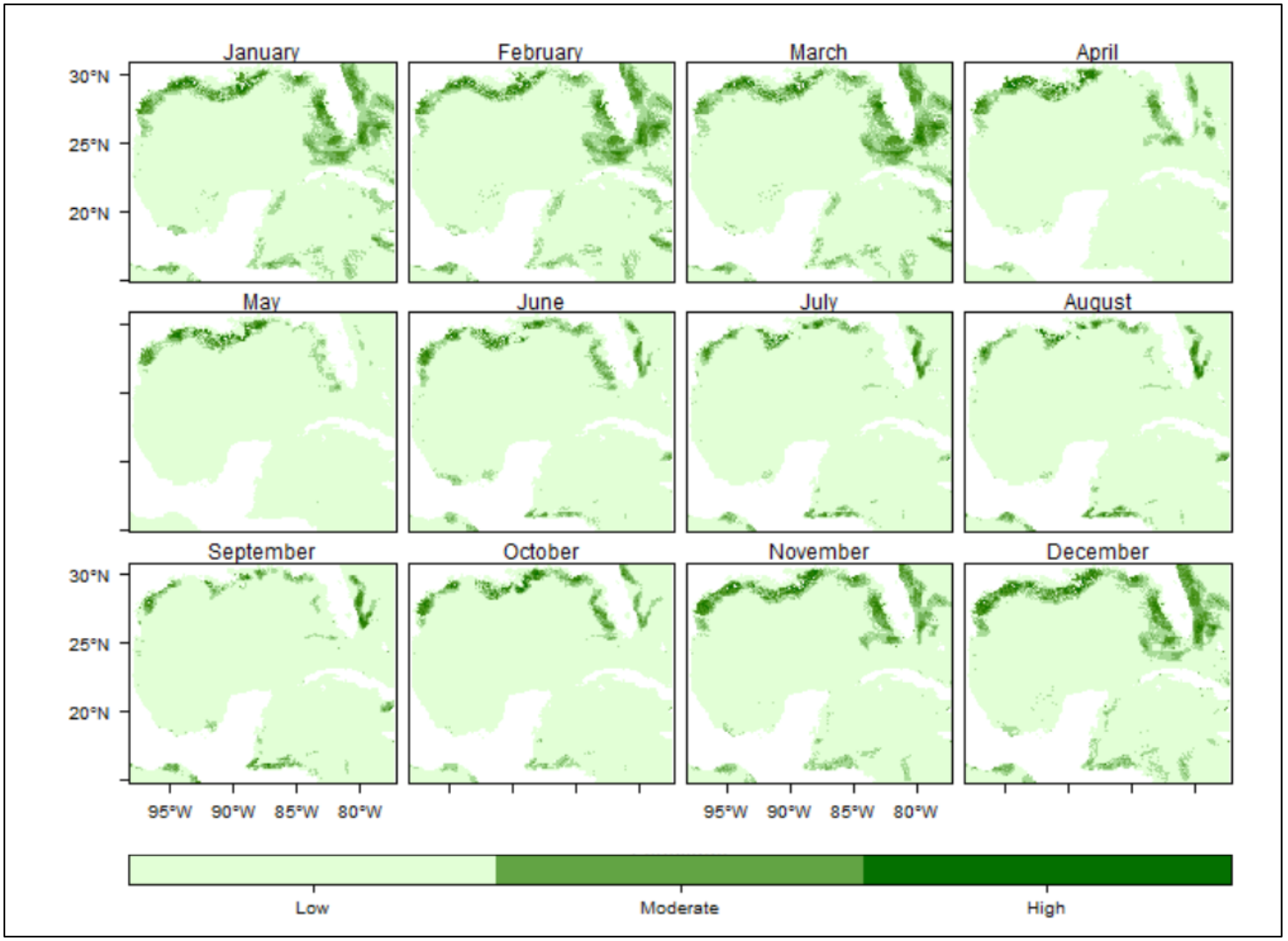


Figure 4.5. Levels of monthly overlap between preferred brown pelican habitat and surface pollution concentrations, GOM. Darker colors indicate higher surface pollution concentration.

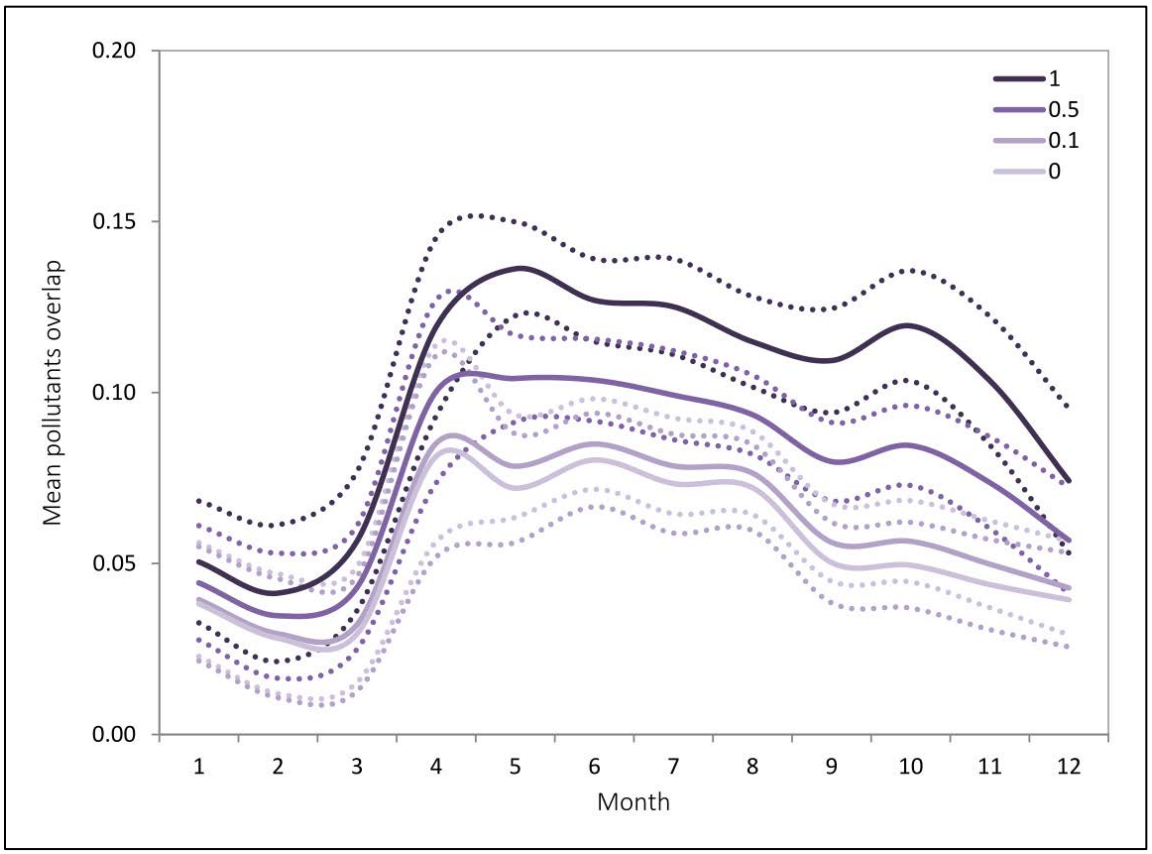


Figure 4.6.a. Overlap between year-round brown pelican locations (weighted by movement state) and surface pollutant concentrations, GOM, 2013–2016: all individuals and all weights.
Dotted lines represent 95% confidence intervals of monthly mean values.

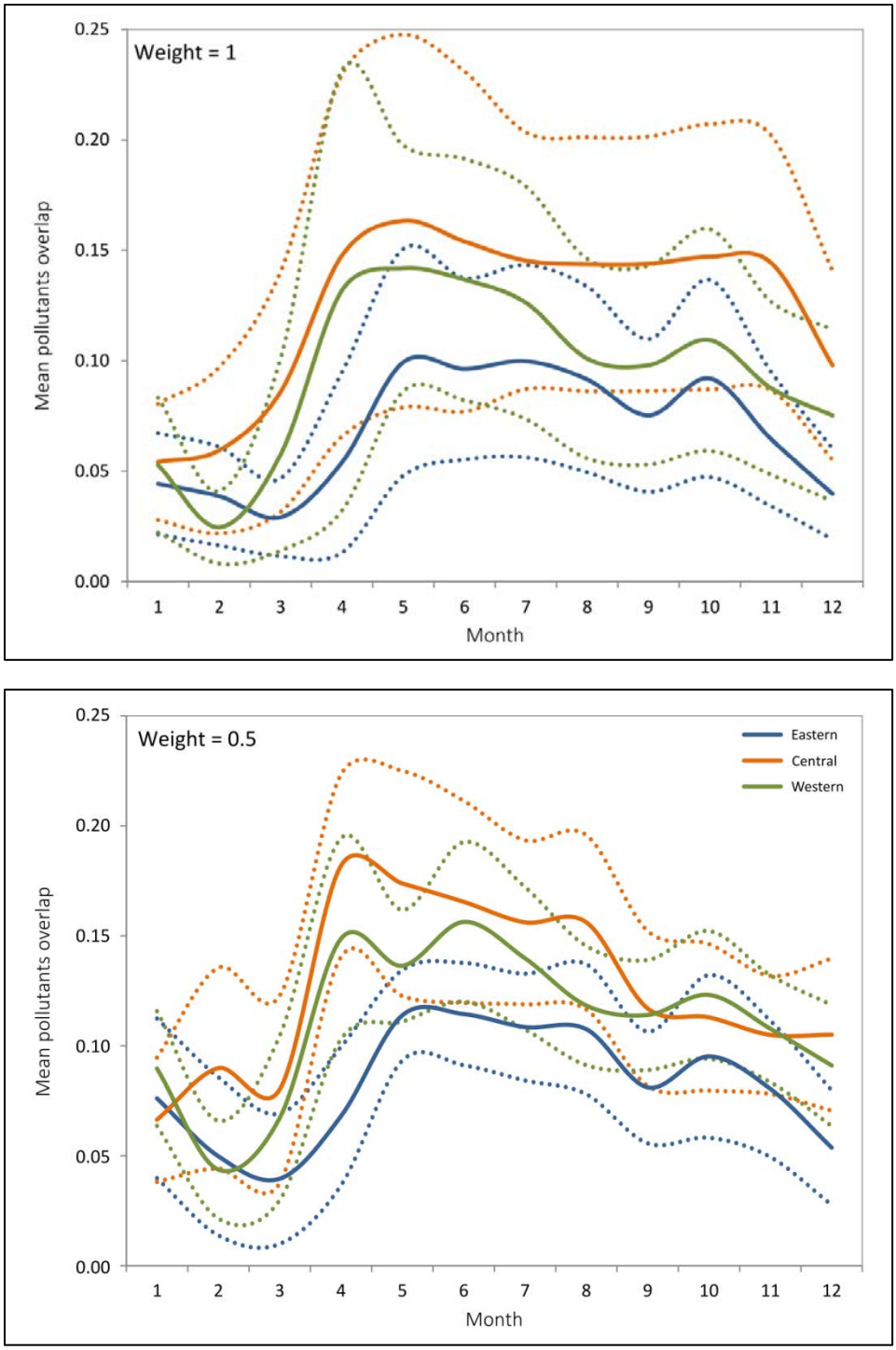


Figure 4.7.b. Overlap between year-round brown pelican locations (weighted by movement state) and surface pollutant concentrations, GOM, 2013–2016: individuals separated by planning area and weighted by 1 and 0.5.
Dotted lines represent 95% confidence intervals of monthly mean values.

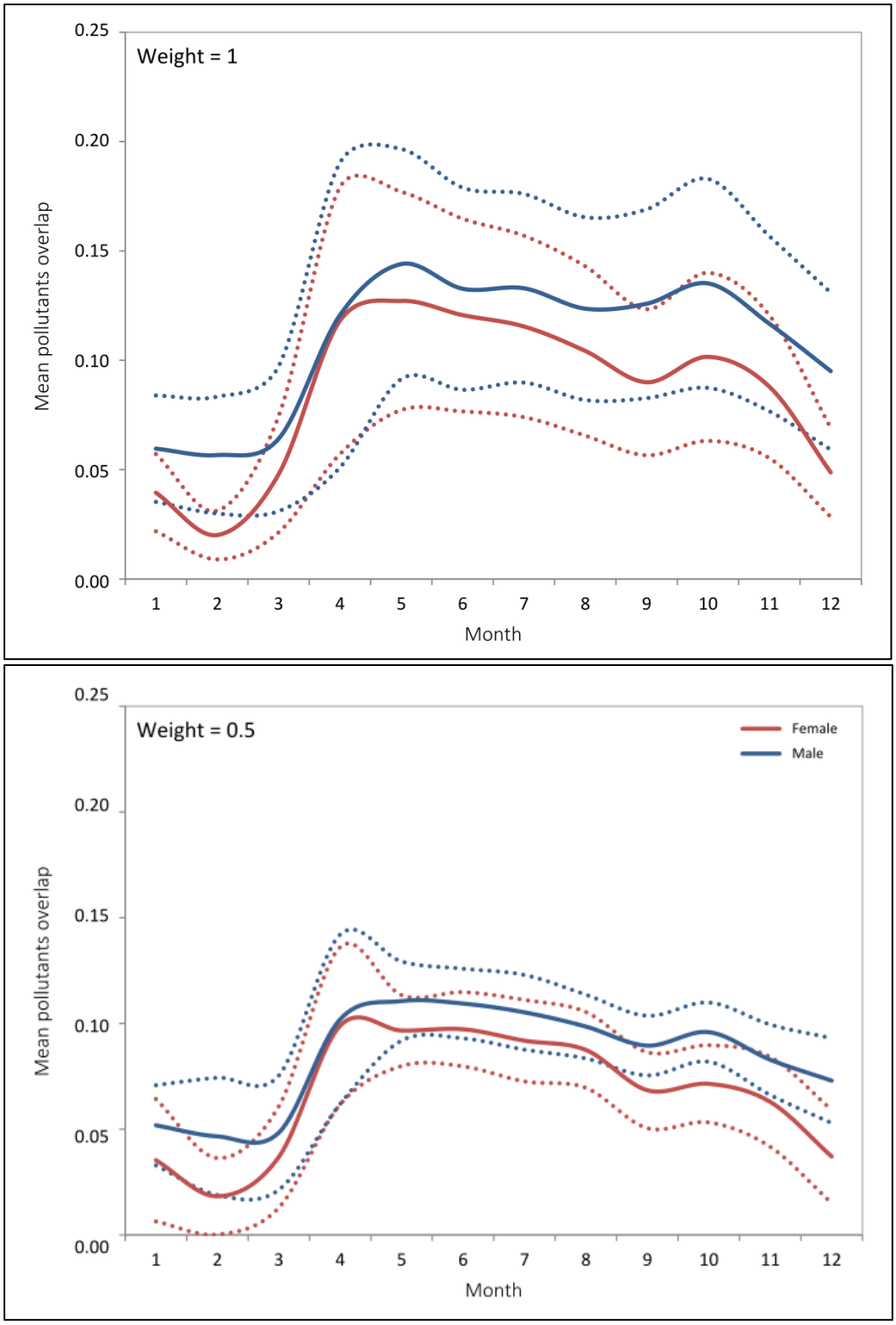


Figure 4.8.c. Overlap between year-round brown pelican locations (weighted by movement state) and surface pollutant concentrations, GOM, 2013–2016: individuals separated by sex and weighted by 1 and 0.5.
Dotted lines represent 95% confidence intervals of monthly mean values.

5 Ecology and Physiology of Reproduction

5.1 Individual Nestling Survival

CORT concentrations from feathers of nestlings were significantly negatively correlated to BCI (linear model: coefficient = -194 ± 31.6, $F_{1,364} = 37.7$, $p < 0.001$, $R^2 = 0.09$). Chicks that died before fledging had lower BCI ($F_{1, 239} = 6.1$, $p = 0.01$) and higher CORT deposited in feathers ($F_{1, 239} = 24.7$, $p < 0.001$) at 3–4 w of age than chicks that were presumed fledged (i.e., survived until at least 60 d after hatching) (Figure 5.1). Of the other covariates we tested, only nest height (linear model, ground relative to elevated: coefficient = -2.79 ± 0.80, $z_{109} = -3.76$, $p < 0.001$) and body size (linear model: coefficient = 1.25 ± 0.43, $z_{109} = 2.88$, $p = 0.004$) were significantly correlated with individual fledging success. Nestlings from ground nests had significantly lower BCI (ground: $\mu_{74} = -97.2 \pm 479$; elevated: $\mu_{117} = 72.0 \pm 363$; $F_{1,191} = 7.74$, $p = 0.006$) and higher feather CORT (ground: $\mu_{74} = 2.08 \pm 0.71$; elevated: $\mu_{117} = 1.72 \pm 0.64$, $F_{1,191} = 17.8$, $p < 0.001$) than nestlings from elevated nests. We did not find a significant effect of colony, planning area, year, sampling date, hatch order, number of siblings, or their interactions on fledging probability (linear models: $p > 0.10$ for each).

Survival probabilities of individual nestlings > 60 d post-hatch were positively related to BCI and negatively related to CORT (Figure 5.1). Chicks found dead at the colony post-fledging had significantly lower BCI (ANOVA: $F_{1,40} = 11.4$, $p = 0.002$) and significantly higher CORT (ANOVA: $F_{1,40} = 18.4$, $p < 0.001$) at 3–4 w after hatching than did chicks that were re-sighted alive after fledge.

5.1.1 Colony-specific Nest Productivity and Chick Survival

CORT levels were correlated with nest productivity at individual observation plots within breeding colonies. Nest productivity (Figure 5.2a) and nestling feather CORT (Figure 5.2c), but not nestling BCI (Figure 5.2b), differed significantly between ground and elevated subplots at two of the four colonies with both ground and elevated nests. Two of the three remaining colonies contained only shrub nests; the third contained too few ground nests to assess differences in productivity relative to shrub nests.

Overall, colony-wide productivity rates were positively correlated with average BCI (Figure 5.3a) and negatively correlated with average CORT (Figure 5.3b) of sampled chicks.

The strongest model predicting colony-specific nest productivity as a function of chick health parameters contained CORT alone (Table 5.1). This was also the only model supported by comparison to AIC_c values. The top model explained 84% of the observed deviance (null = 1.91; residual = 0.31).

Modeled chick survival to fledge (3 m after hatch) at individual colony sites was negatively correlated with average CORT (Figure 5.4a). The strongest model predicting chick survival to fledge as a function of chick health parameters, which was also the only model supported by comparison of AIC_c values, contained CORT alone (Table 5.1). The top model explained 91% of the observed deviance (null = 0.144; residual = 0.013). The relationship between BCI and survival to fledge showed a non-significant positive trend, and BCI was not supported as a predictor of average colony-wide survival rates (Table 5.1).

Average CORT values at individual colony sites were negatively correlated with modeled chick survival post-dispersal (to 6 m after hatch) (Figure 5.4b). Both the CORT-only model and the null model were supported as predictors of post-dispersal survival, although the former was 1.7 times as likely as the latter to be the best model (Table 5.1). The top model explained 48% of the observed deviance (null = 0.026; residual = 0.012). BCI was not included in any supported models of post-dispersal survival.

We found a weak negative correlation between colony size and nestling CORT levels (t_{253} = -2.00, p = 0.05) (Figure 5.5a). Colony size and nestling BCI were not significantly correlated (t_{253} = -1.04, p > 0.20) (Figure 5.5b). We did not find a significant relationship between environmental conditions or environment-colony size interactions and either of the chick health parameters (p > 0.20 for all variables).

We found that CORT in nestling feathers, which represents an integrated measure of developmental stress during feather growth, was highly correlated with traditional measures of reproductive success (i.e., fledglings per nest) and nestling health (BCI) at individual, sub-colony, and colony-wide scales. Moreover, our results indicate that information gathered from measuring feather CORT in young, altricial chicks can explain differences in chick health, fledging success, and post-fledging survival that are not captured by body condition alone.

Our first objective was to assess the relationship between feather CORT and a more traditional measure of nestling health, BCI (Benson et al. 2003), as predictors of nestling survival. In accordance with recent work on other avian taxa, we found that nestling feather CORT was negatively correlated to both body condition (Fairhurst et al. 2013; López-Jiménez et al. 2016) and fledging probability (Fairhurst et al. 2013; Lodjack et al. 2015) at the individual level. Although both feather CORT and BCI were significantly correlated with chick survival to fledge, feather CORT predicted the fate of individual nestlings slightly better than BCI. At the colony level, models containing only feather CORT were favored over models containing BCI with and without feather CORT as predictors of nest productivity, survival to fledge, and post-dispersal survival. Additionally, feather CORT predicted within-colony differences in fledging success by habitat type that were not apparent in comparisons of BCI. The enhanced explanatory power of CORT compared to BCI may be due to both the longer time frame over which CORT integrates physiological condition and the sensitivity that BCI has to short-term variation in nutritional stress. For example, at the Shamrock Island colony the average mass of chicks was 2,660 g (93.8 oz) and average meal mass was 181 g (6.4 oz), or about 7% of body weight. This relatively high ratio of meal mass to body mass, combined with the daily variation we observed in mass of meals (range = 5.6–1039.8 g (0.2–36.7 oz), CV = 0.76), makes BCI highly sensitive to feeding frequency and time since feeding. Meal delivery rates and the size of meals in relation to chick mass can vary by more than one order of magnitude both among and within avian species (Ricklefs et al. 1985; Anderson and Ricklefs, 1992). Therefore, the use of BCI as a measure of nestling condition requires consideration of how these short-term factors may influence its usefulness in describing long-term patterns of chick condition. Feather CORT integrates a longer time series of conditions (Bortolotti et al. 2008) and thus may be less susceptible than BCI to short-term variation. The fact that we measured feather CORT early in development (about 20–30 d into a 60–90 d nesting period) and found a strong relationship to fledging probability further indicates that feather CORT levels during early development can accurately predict survival through the breeding season.

We also assessed the relationship between feather CORT and variation in local (site-and nest-specific) conditions. Although nestling feather CORT is strongly correlated to environmental conditions during development (e.g., Harms et al. 2010; Will et al. 2015; Lodjack et al. 2015), site and nest-specific factors can still confound the environment-stress relationship (Fairhurst et al. 2012; Lodjack et al. 2015). We did not find a significant influence of either hatch order or number of siblings on feather CORT. A previous study of plasma CORT in brown pelican nestlings (Eggert et al. 2010) also found no effect of brood size or hatch order on stress levels; however, sibling dynamics have been found to affect feather CORT levels in nestling raptors (Yosef et al. 2013; López-Jiménez et al. 2016). We did find an influence of microhabitat characteristics (elevated compared to ground nest location) on feather CORT. Nestlings at elevated nests may benefit from improved passive thermoregulation, reduced energy expended in movement, and reduced aggressive interactions with neighboring adults and nestlings that subsequently act to maintain lower levels of feather CORT. Our study concurs with data on brown pelican nest productivity in Louisiana (Walter et al. 2013), suggesting that nestlings from elevated nests tend to

survive longer than nestlings from ground nests, contributing to increased nest productivity at elevated sites. If elevated nest sites offer improved fledging success, positive reinforcement may occur at these sites if experienced or dominant breeders preferentially select and defend elevated nesting sites.

5.1.2 Nutritional Stress

Energy provisioning rate showed a non-significant positive trend in relation to BCI (linear model, coefficient = 1.04 ± 0.52, $t_5 = 2.02$, $p = 0.10$; Figure 5.6a) and a significant negative relationship to feather CORT (linear model, coefficient = -613 ± 155, $t_5 = 3.97$, $p = 0.01$; Figure 5.6b). The two biomass components of EPR, feeding frequency (meals chick^{-1} day^{-1}, $\mu = 2.51$, $N = 142$) and meal mass (g meal^{-1}, $\mu = 157.6$, $N = 583$), had similarly high levels of overall variation (CV frequency = 0.64; CV mass = 0.76), while energy density of meals (kJ g^{-1}, $\mu = 4.34$, N = 583) was less variable (CV = 0.10). EPR explained 76% of observed variance in colony-wide average feather CORT and 45% of observed variance in colony-wide average BCI (Figure 5.6). Of the separate components of EPR, meal delivery rate explained the largest portion of variance in each of the two chick health metrics (CORT: 30.5%; BCI: 33.0%), followed by meal mass (CORT: 22.1%; BCI: 3.7%) and energy density (CORT: 3.2%; BCI: 0.1%). EPR was positively correlated to nest productivity (coefficient = 739 ± 258, $t_5 = 2.85$, $p < 0.04$, $R^2 = 0.62$) and nestling survival to fledge (coefficient = 3365 ± 580, $t_4 = 5.80$, $p = 0.002$, $R^2 = 0.87$), and the relationship between EPR and post-fledging survival rates showed a positive but non-significant trend (coefficient = 6482 ± 3042, $t_4 = 2.13$, $p = 0.09$).

Finally, we tested the relationship between nestling health metrics, nutritional stress (energy provisioning rate), and breeding success. Brown pelicans in our study area rarely experience nest predation, human disturbance, or extreme weather events during breeding, and hence few factors are likely to confound the relationship between developmental stress and chick mortality. Our results indicated that both nestling feather CORT and nestling BCI were highly correlated to EPR, and that EPR explained 87% of the variation in chick survival between the colonies we studied. Of the components of EPR, meal delivery rate explained a larger portion of the variance in survival metrics and nestling health than did meal mass or energy density of prey. Meal mass also explained a high proportion of variance in nestling feather CORT, although not BCI or survival, while energy density had no significant linear relationships with nestling health or survival metrics. The low correlation between nestling health and energy density in this system is in contrast to previous studies of seabirds (reviewed in Österblom et al. 2008) that have suggested prey quality as a key driver of nestling survival. We posit that the weaker relationship we observed may be due, in part, to a narrower range of energy content of prey in the GOM, particularly a lack of prey with the high levels of energy density and lipid content that occur in high latitude systems (Stickney and Torres 1989, Anthony et al. 2000). Once nestlings fledged, EPR at the natal colony was no longer a strong predictor of survival probability, indicating that differences in the quantity of food during development are not a dominant driver of survival after dispersal. However, both feather CORT and BCI were correlated to post-fledging survival, which suggests that nutritional stress during development may continue to influence the probability that individuals will survive to recruit back into the breeding population once they have fledged. The demographic effects of negative feedbacks between developmental stress and recruitment have been documented in other seabird species (e.g., Kitaysky et al. 2010). Linking these parameters is a necessary step toward understanding the long-term demographic consequences of perturbations in the developmental environment.

5.2 Daily Survival Rates: Gaillard and Cat Islands

During 2017–2018, we monitored 245 nests during incubation (2017: n = 97; 2018: n = 148) and 185 broods containing 279 chicks (2017: n = 85 broods, n = 128 chicks; 2018: n = 100 broods, n = 151 chicks). The DSR (± SE) of nests during incubation in 2017 and 2018 was 0.9940 ± 0.002 and 0.9138 ± 0.002, respectively, and the apparent survival of nests to hatching was 0.86 and 0.67, respectively. The DSR (± SE) of broods during chick-rearing in 2017 and 2018 was 0.9998 ± 0.0003 and 0.9952 ± 0.006, respectively, and the apparent survival of broods from hatch to fledge was 0.94 and 0.78, respectively.

In 2017, three highly supported models best predicted DSR during incubation (Table 5.2). Average barometric pressure appeared in all top models, average humidity appeared in two of the top models, and distance from nest to water appeared in one top model. Barometric pressure and humidity were negatively related to DSR during incubation in 2017 (Table 5.3), and distance to water was not related to DSR during incubation *(*i.e., 95% confidence interval overlapped zero). The odds of a nest surviving an additional day decreased by 0.5 times for each 1% decrease in average humidity and by 0.4 times for each 1 kPa decrease in average barometric pressure.

In 2018, the global model best predicted DSR during incubation (Table 5.2). DSR was significantly related to Julian date, distance from nest to water, nest elevation, barometric pressure, humidity, and maximum nest temperature (Table 5.3). The three weather variables had stronger negative effects on DSR of nests during 2018 compared to date or nest-based variables. The odds of a nest surviving an additional day decreased by 0.02 times for each one degree increase in maximum temperature, by 0.3 times for each 1 kPa decrease in average barometric pressure and each 1% decrease in average humidity. The odds of a nest surviving an additional day decreased by 0.3 times for each 1 m decrease in elevation of the nest site, decreased by 0.5 times for each 1 m in distance that a nest was closer to the shore, and decreased by 0.9 times for each day later the nest was initiated.

In 2017, two models best predicted DSR during brood-rearing (Table 5.2). Average barometric pressure and average humidity appeared in both top models, and distance from nest to water appeared in one top model. The 95% confidence intervals strongly overlapped zero for distance to water and did not overlap zero for barometric pressure or humidity. Barometric pressure was negatively related to DSR, humidity positively related to DSR, and distance to water not related to DSR during brood-rearing in 2017 (Table 5.3). The odds of a brood surviving an additional day increased by 11.8 times for each 1% increase in average humidity and decreased by 0.5 times for each 1 kPa decrease in average barometric pressure.

In 2018 a single model with 9 of the 10 variables available (average barometric pressure not included) best predicted DSR during brood-rearing and carried 99% cumulative weight (Table 5.2). Humidity and chick age^2 were positively related to DSR and date negatively related to DSR during brood-rearing in 2018 (Table 5.3). The odds of a brood surviving an additional day increased by 4.6 times for each 1% increase in average humidity and decreased by 0.8 times for each 1 day increase in date of hatching.

During both the 2017 and 2018 breeding seasons, DSR of brown pelican nests and broods was high, but the apparent survival from hatch or fledge appeared to vary by year and reproductive stage (incubation or brood) during the two years of our study. Several variables consistently appeared in top performing models in both years of the study during both incubation and chick-rearing. Weather variables (e.g., average barometric pressure and humidity) occurred more often and with more significance compared to habitat variables (e.g., nest height and vegetation cover) in the top performing models for both nest and brood success in 2017 and 2018. Previous studies on brown pelican nest selection in the GOM, including previous studies on the Gaillard Island colony, found that the reproductive (hatching, nest, and chick) success of brown pelicans was related to habitat variables including vegetation cover, nest height, and substrate beneath the nest (Ranglack et al. 1991, Robinson and Dindo 2011, Walter et al. 2013). Lamb (2016) found that among seven colonies in the Northern GOM, including Gaillard Island, chicks in

elevated nests were in better condition and had higher apparent fledging success than chicks in ground nests. Our results differed from these previous studies in that we did not find significant relationships between most habitat variables and survival of nests or broods. These differences could result from differences in the response variables being measured: our study examined nest success using DSR, but other studies focused on nest site selection, chick condition, or individual fledging success. The differences could also be due to the addition of weather variables in our modeling, which were not included in the previous studies. Our results suggest that the effects of habitat on reproductive success may be overwhelmed by the importance of weather variables, at least in some years.

Barometric pressure negatively affected daily survival rates of both eggs and broods, despite different requirements during these breeding stages. The negative relationship between success and barometric pressure we observed could be a result of cloudy, but not stormy, days having a positive effect on reproductive success. This may have occurred because barometric pressure was not indicative of storms and severe inclement weather in our study area, but instead was a signal of cloudy days with occasional rain. The barometric pressure range for storms is commonly considered to be 98.21–98.88 kPa (Breuner et al. 2013). The minimum average barometric pressure we recorded from weather station data was 100.77 kPa, much higher than the storm range, thus demonstrating that the barometric pressure we observed was not associated with storm conditions. The shading effect of clouds could reduce temperature and sun exposure of eggs and chicks during the summer breeding season and so increase their daily survival.

Average humidity also consistently appeared in top performing models and significantly affected nest survival in 2018 and brood survival in both years; however, the relationship differed among stages (a negative relationship with egg success but a positive relationship with brood success). During incubation, a negative relationship between nest survival and humidity could be caused by higher humidity and higher temperatures creating conditions where eggs can overheat, resulting in decreased survival (Sherley et al. 2011, Oswald and Arnold 2012).We observed a significant positive relationship between brood success and humidity in both years, in contrast to the negative relationship between brood success and humidity in both years. This could be due to an increased resilience of chicks to heat compared to eggs. The positive relationship we observed with humidity also may be due to higher air temperature (positively correlated with humidity) reducing any chilling effects from frequent rain (Konarzewski and Taylor 1989, Schreiber and Burger 2001).

Most habitat variables did not appear in top performing models for either nest or brood success in 2017 and 2018. However, the “distance to water” variable did appear in all the top models for both nest and brood survival during the study; it was significant only during incubation in 2018. We posit that the topography and structure of Gaillard Island, particularly the berm and the large rocks that surround the island, provided elevation and a physical barrier that limit the effects of flooding and storms on reproductive success. For example, following Tropical Storm Cindy and hurricanes Harvey, Irma, and Nate in 2018, vegetation and nesting material and/or substrate was reduced on Cat Island and brown pelicans did not nest there. Our data suggest that, regardless of storm activity, Gaillard Island may provide quality nesting habitat due to the elevated nesting, armored shoreline, and abundant shrub and nesting material. This unique set of habitat attributes may reduce the effect and strength of micro-scale habitat variables on breeding success.

5.3 Implications for Long-term Monitoring

Because of its ease of implementation and strong relationship to nestling survival, feather CORT is uniquely suited to detecting the sub-lethal stress effects on reproductive success and can be collected rapidly in response to unexpected environmental perturbations. Although measuring feather CORT requires more post-collection laboratory analysis than traditional reproductive success and chick health metrics, its advantages include minimal disturbance at breeding colonies, ease of collection and storage, and the ability to sample multiple colonies in a short time. However, interspecific differences in stress response may make this technique more suitable for some seabird species than others (e.g., Kitaysky et al. 2005). The existence of a detectable relationship between environmental covariates and nestling stress is a crucial prerequisite for using feather CORT as an indicator of environmental conditions. Moreover, to draw inferences at broad spatial scales (e.g., between colonies or planning areas), sampling regimes would need to account for the influence of varying habitat characteristics. Several recent studies of feather CORT, particularly Fairhurst et al. (2014), Lodjack et al. (2015), and López-Jiménez et al. (2016), have described the context-dependence of the stress-environment relationship and its sensitivity to local-scale habitat quality and climatic variation. Our results indicate that, though sibling dynamics do not confound variation in feather CORT in this species, nest height can affect both physiology and survival. These differences highlight the importance of understanding how different site- and individual-specific factors contribute to underlying variation in measured parameters, and how these factors could interact cumulatively or multiplicatively with environmental conditions to mask or exaggerate the effects of perturbations on reproduction.

We found variation within and among planning areas in colony-specific nestling health and reproductive success under baseline conditions across the Northern GOM. The foraging environment experienced by breeding seabirds depends on a variety of biotic and abiotic factors that can change across a species' range as well as between and within breeding seasons. Distinguishing the effects of environmental perturbations requires that the effects of short-term changes to foraging conditions be distinguished from the background noise of pre-existing variation. Endpoints that can be measured consistently across space and time provide a unifying approach for long-term monitoring efforts that can compare baseline measures to post-disturbance conditions.

Our study provides evidence that feather CORT can be used to detect differences in underlying nutritional quality and predict reproductive parameters in a free-living seabird population in which nestlings elevate stress hormone levels in response to nutritional constraints, making it an appropriate basis for long-term monitoring of population-wide reproductive health and, ultimately, detection of the indirect demographic effects of environmental change.

Table 5.1 Candidate Models for Brown Pelican Nest Productivity and Nestling Survival in the Northern GOM, 2014–2015

Terms		AIC_c	Δ_i (AIC_c)	w_i (AIC_c)	Σw	L_i (AIC_c)
Productivity						
	CORT	**4.17**	**0**	**0.94**	**0.94**	**1.00**
	BCI	11.14	6.97	0.03	0.97	0.03
	BCI + CORT	11.40	7.22	0.02	0.99	0.02
	Null model	13.06	8.88	0.01	1.00	0.01
Post-banding survival						
	CORT	**-17.66**	**0**	**0.96**	**0.96**	**1.00**
	BCI + CORT	-10.70	6.87	0.03	0.99	0.03
	BCI	-6.34	11.32	< 0.01	1.00	< 0.01
	Null model	-5.40	12.27	< 0.01	1.00	< 0.01
Post-dispersal survival						
	CORT	**-19.80**	**0**	**0.55**	**0.55**	**1.00**
	Null model	**-18.74**	**1.06**	**0.32**	**0.87**	**0.59**
	BCI	-16.53	3.27	0.11	0.98	0.19
	BCI + CORT	-13.00	6.81	0.02	1.00	0.03

Candidate models as a function of colony-average body condition (BCI) and feather CORT of 3- to 4-week-old chicks, ranked in order of increasing AIC values with model weights (wi), cumulative weights (Σw) and relative likelihoods (Li). Models in bold were considered strongly supported.

Table 5.2. Top Performing Models (△ AIC ≤ 2.0) of Daily Survival Rates of Nests and Broods of Brown Pelicans Breeding in Mobile Bay, Alabama, 2017 and 2018

Models	△ AIC	AIC Weight
2017 Incubation		
Average humidity + Average barometric pressure	0.00	0.36
Average barometric pressure	0.93	0.22
Average humidity + Average barometric pressure + Distance to water	1.90	0.14
2018 Incubation		
Nest height + Vegetation cover + Average humidity + Average barometric pressure + Julian date + Distance to water + Elevation of nest + Substrate + Location	0.00	0.99
2017 Brood-rearing		
Average humidity + Average barometric pressure	0.00	0.63
Average humidity + Average barometric pressure + Distance to water	1.14	0.36
2018 Brood-rearing		
Chick age^2 + Nest height + Vegetation cover + Average humidity + Julian date + Distance to water + Nest elevation + Substrate + Location	0.00	0.99

Table 5.3. Coefficient Estimates and 95% Confidence Intervals from Models of Daily Survival Rates of Nests and Broods of Brown Pelicans, Gaillard Island and Cat Island, Alabama, 2017–2018

	Coefficient Estimate	95% Confidence Interval
2017 Incubation		
Average barometric pressure	-0.98	-1.53, -0.43
Average humidity	-0.73	-1.47, 0.00
2017 Brood-rearing		
Average barometric pressure	-0.69	-1.12, - 0.28
Average humidity	2.47	1.47, 3.46
2018 Incubation		
Julian date	-0.08	-0.11, -0.05
Low elevation	-1.05	-1.97, -0.13
Distance to water	-0.73	-1.42, -0.03
Average barometric pressure	-1.11	-1.65, -0.58
Average humidity	-1.23	-1.69, -0.76
Maximum temperature	-3.69	-6.43, -0.95
2018 Brood-rearing		
Chick age^2	0.09	0.05, 0.12
Julian date	-0.22	-0.45, 0.00
Average humidity	1.53	0.95, 2.11

Coefficient estimates displayed are from highest-ranked model with that variable. Only coefficient estimates for which confidence intervals do not overlap zero (i.e., significant variables) are shown.

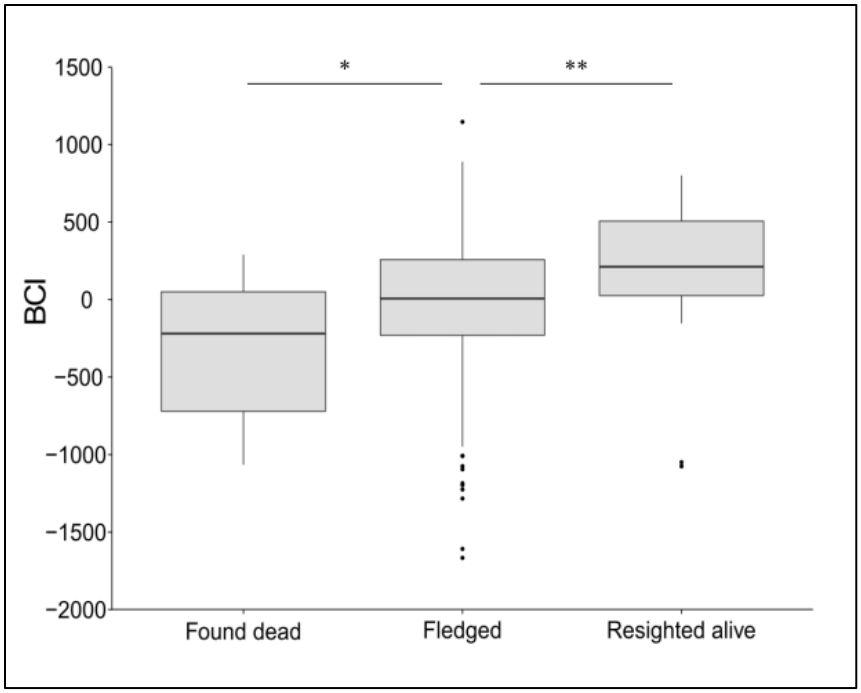


Figure 5.1.a. Distribution of individual measurements of BCI and feather CORT at 3–4 w post-hatch for brown pelican nestlings in the Northern GOM, 2013–2015: BCI.
Nestlings were later found dead after banding, presumed fledged, or re-sighted alive after leaving the breeding colony.

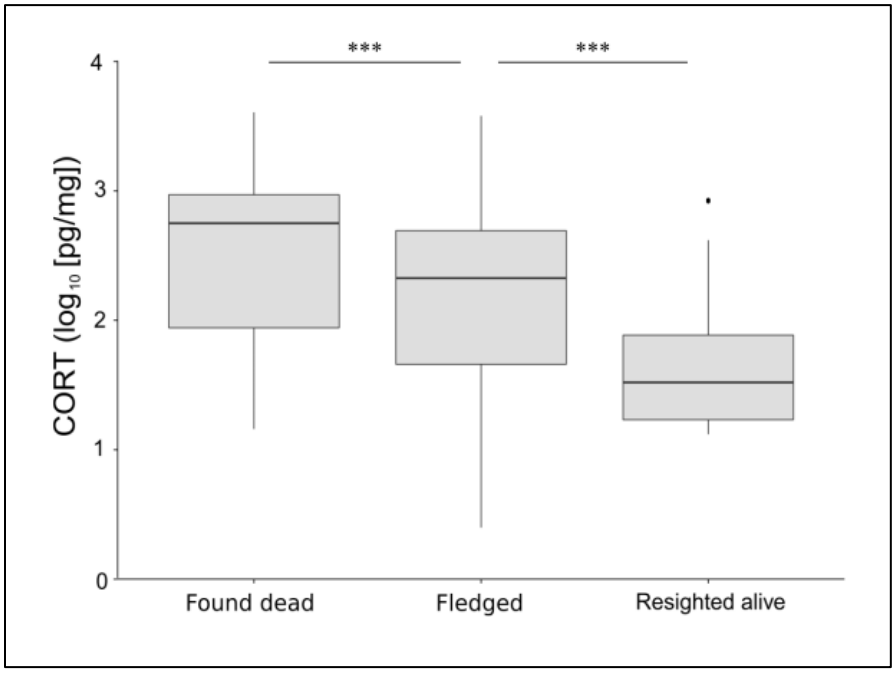


Figure 5.2.b. Distribution of individual measurements of BCI and feather CORT at 3–4 w post-hatch for brown pelican nestlings in the Northern GOM, 2013–2015: feather CORT.
Nestlings were later found dead after banding, presumed fledged, or re-sighted alive after leaving the breeding colony.

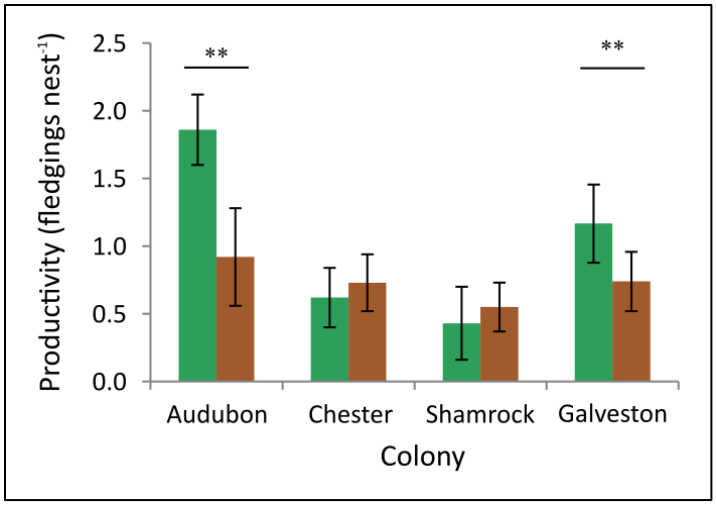


Figure 5.3.a. Relationship between brown pelican nest productivity, body condition index, and CORT of nestling, and nest elevation in the Northern GOM, 2014–2015: mean nest productivity.
In elevated (green) and ground (brown) nests.

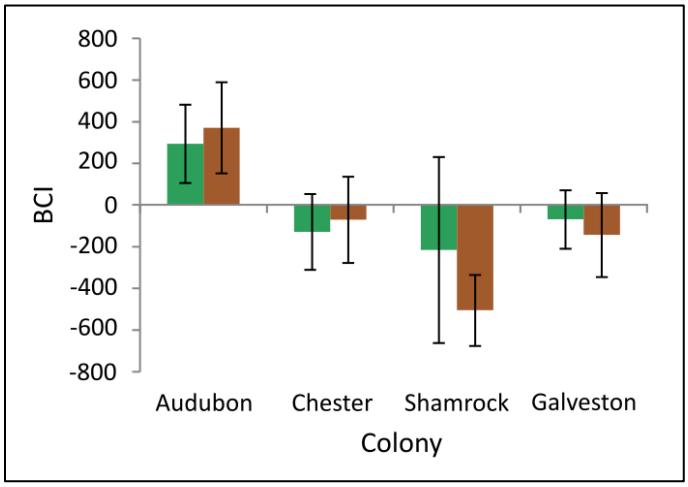


Figure 5.4.b. Relationship between brown pelican nest productivity, body condition index, and CORT of nestling, and nest elevation in the Northern GOM, 2014–2015: mean body condition index.
In elevated (green) and ground (brown) nests.

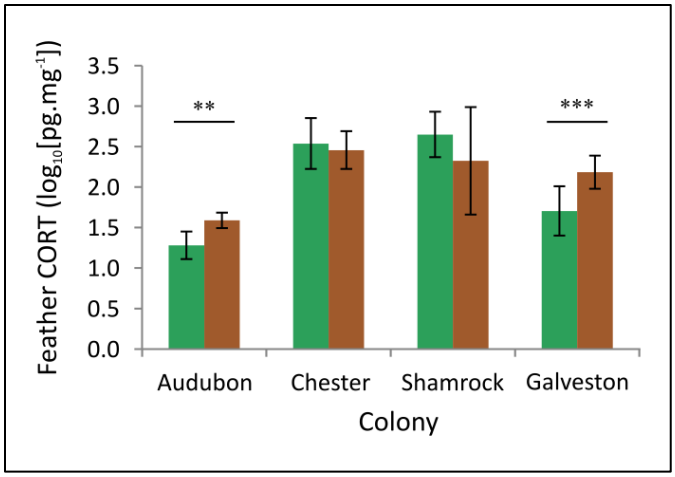


Figure 5.5.c. Relationship between brown pelican nest productivity, body condition index, and CORT of nestling, and nest elevation in the Northern GOM, 2014–2015: mean CORT concentration of nestlings. In elevated (green) and ground (brown).

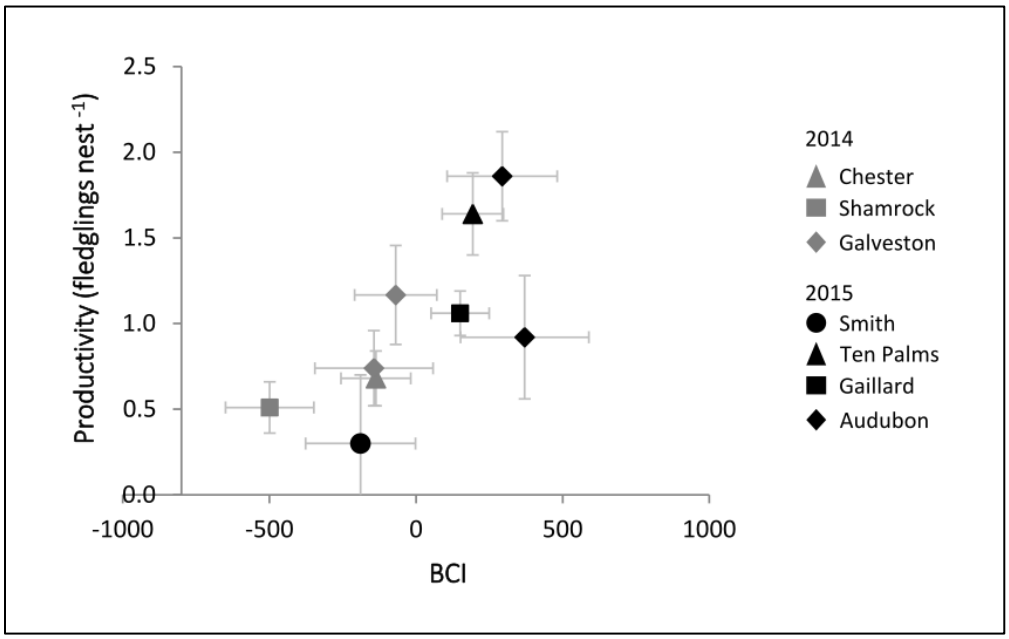


Figure 5.6.a. Correlation of mean brown pelican nest productivity to chick body condition index and feather CORT for colonies in the Northern GOM, 2014–2015: chick body condition index.

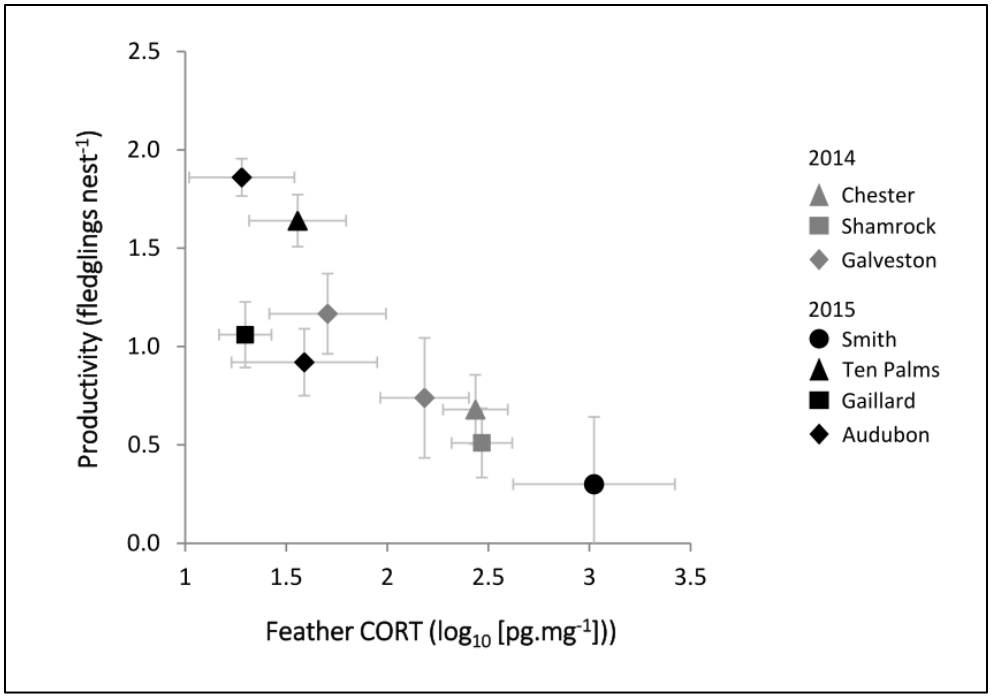


Figure 5.7.b. Correlation of mean brown pelican nest productivity to chick body condition index and feather CORT for colonies in the Northern GOM, 2014–2015: feather CORT.

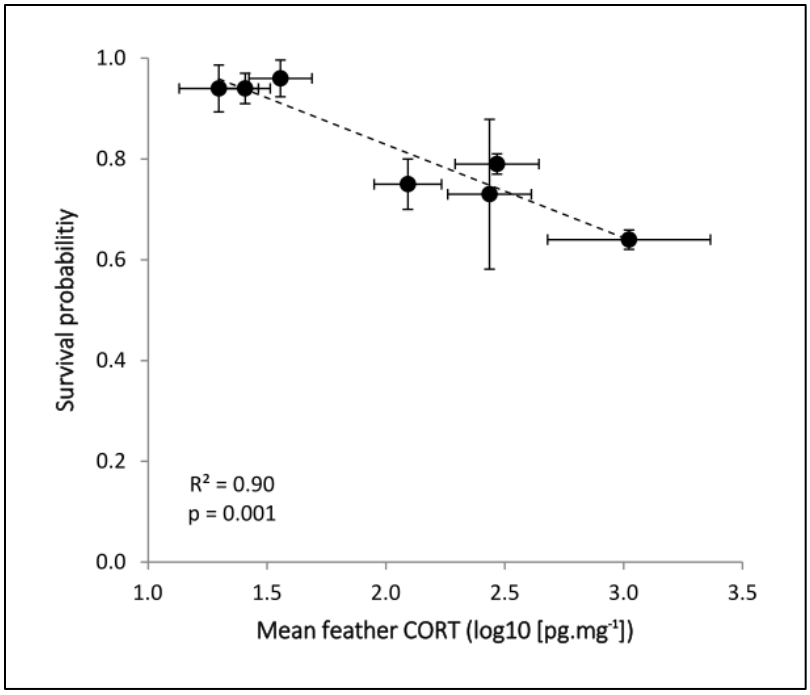


Figure 5.8.a. Relationship of colony-wide mean brown pelican nestling feather CORT to probability of survival to fledge and post-dispersal survival in the Northern GOM, 2014–2015: probability of survival to fledge.

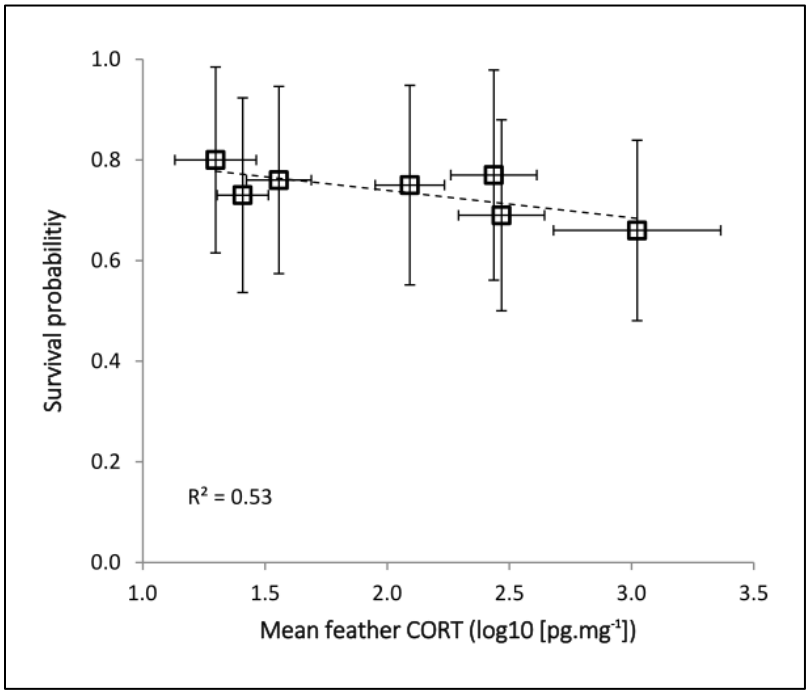


Figure 5.9.b. Relationship of colony-wide mean brown pelican nestling feather CORT to probability of survival to fledge and post-dispersal survival in the Northern GOM, 2014–2015: probability of post-dispersal survival.

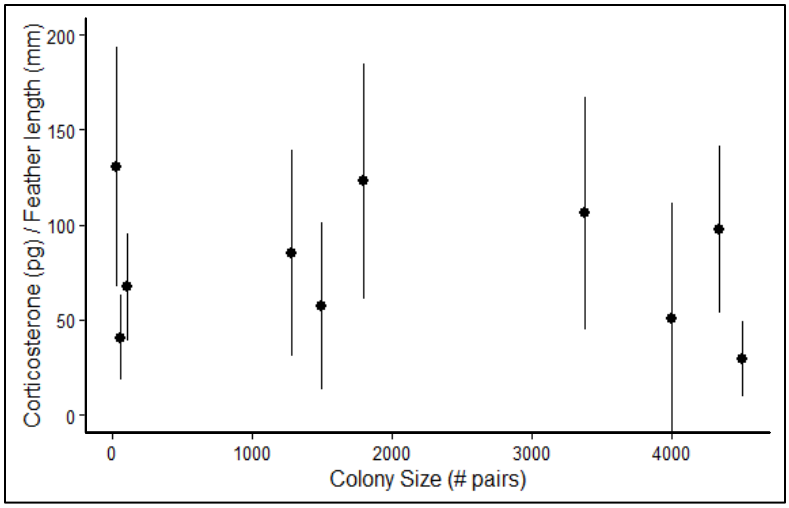


Figure 5.10.a. Brown pelican nestling CORT levels, and body condition index, Northern GOM, 2013–2015: CORT levels.
Colony mean values are shown ± standard deviations.

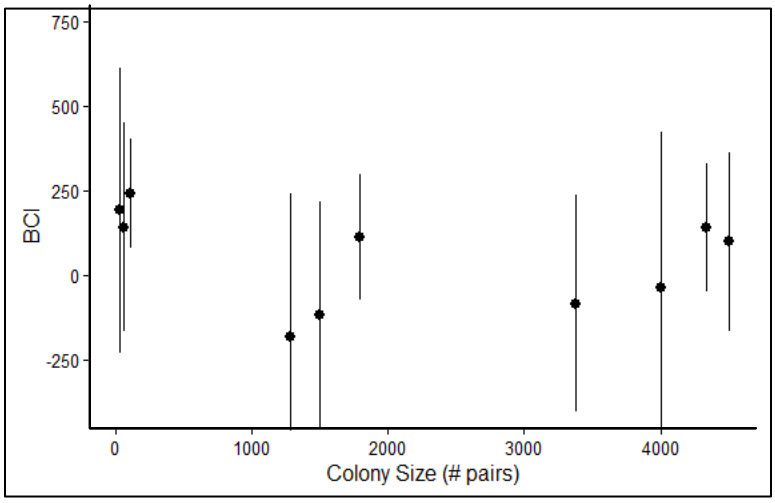


Figure 5.11.b. Brown pelican nestling CORT levels, and body condition index, Northern GOM, 2013–2015: BCI.
Colony mean values are shown ± standard deviations.

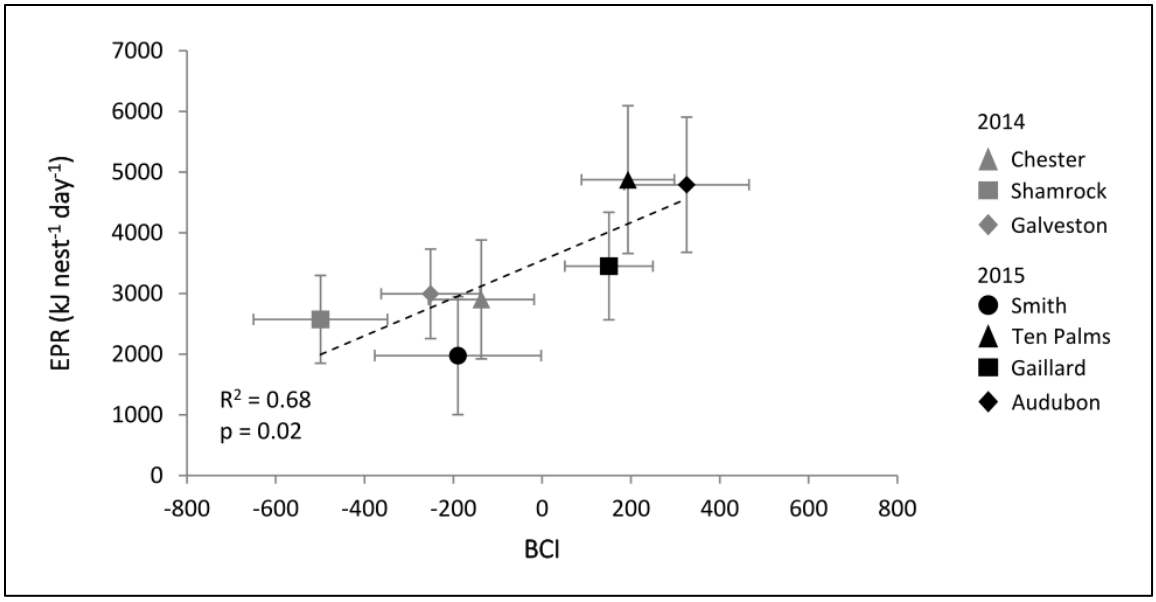


Figure 5.12.a. Relationship of brown pelican energy provisioning rate to chick health parameters BCI and feather CORT by colony in the Northern GOM, 2014–2015: BCI.

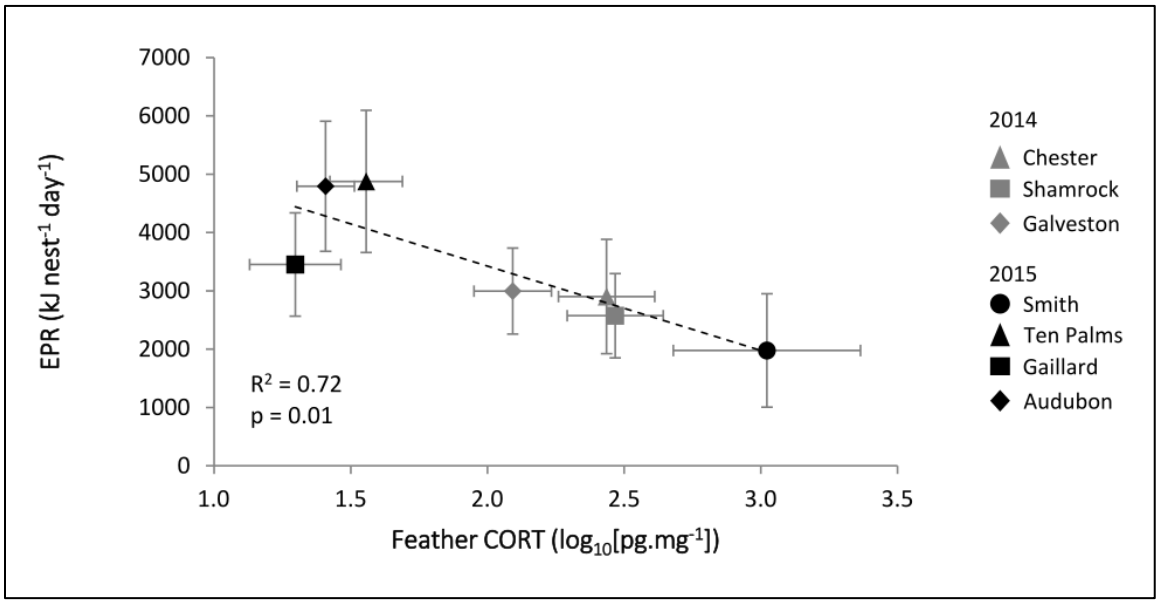


Figure 5.13.b. Relationship of brown pelican energy provisioning rate to chick health parameters BCI and feather CORT by colony in the Northern GOM, 2014–2015: feather CORT.

6 Nestling Diet

6.1 Taxonomic Composition of Diet

Over three years, we collected 641 chick meals (Year 1: N = 27; Year 2: N = 423; Year 3: N = 191), totaling 98 kg (212 lbs) of prey. We identified 46 prey species representing 25 families (Table 6.1). Thirty-six of the prey species represented less than 1% each of biomass collected; of these, 16 species represented less than 0.05% each of biomass collected (Table 6.1). Gulf menhaden was the most common prey species by weight overall, as well as at each study site. The proportion of menhaden in total biomass varied by colony, with higher proportions of menhaden within the central GOM (Figure 6.1). Other common prey species did not show a pattern of abundance in meals across sites, except for anchovy (*Anchoa spp.*), which increased from the western to the eastern GOM, and spot (*Leiostomus xanthurus*), which declined from the western to eastern GOM (Figure 6.2). The majority of meals (76%) contained a single fish species, and the maximum number of species in a meal was seven.

The overall proportion of menhaden in chick diets declined through the breeding season, (coefficient = -0.34 ± 0.10, $F_{1,596} = 12.3$, $p < 0.001$), driven by a decrease in juvenile menhaden < 110 mm (4.33 in) total length (coefficient = -0.75 ± 0.09, $F_{1,596} = 66.0$, $p < 0.001$). The proportions of adult menhaden, anchovies, and pinfish increased over the same period ($p < 0.01$ for all). The remaining prey species showed no seasonal trends in proportional occurrence.

Energetic content ranged from 3.3 to 5.5 kJ g^{-1} among all species with a mean (± SD) of 4.38 ± 0.98 kJ g^{-1} wet mass (Figure 6.3). Protein content had low variation across measured samples (CV = 8%) and correlated weakly with energy density per wet gram of fish ($F_{1,217} = 22.3$, $p < 0.001$, $r^2 = 0.09$); lipid content was variable both between and within species (CV = 75%) and was highly correlated with energy density ($F_{1,217} = 1929$, $p < 0.001$, $r^2 = 0.90$). First-year menhaden had significantly lower energy densities and lower lipid content than adult menhaden in the northeastern and northwestern Gulf of Mexico (Figure 6.3; $p < 0.1$ for all).

6.2 Meal Attributes

Average meal mass, meal delivery rate, and energy density of meals each differed significantly among colony sites (Figure 6.4). The two biomass components of EPR, feeding frequency and meal mass had similarly high levels of overall variation (CV frequency = 0.67; CV mass = 0.76), while energy density of meals was less variable (CV = 0.10). Relative to averages within planning areas, individual colony sites showed a generally opposing pattern between meal mass and meal delivery rates (Figure 6.5a). Colonies with below-average meal delivery rates tended to have above-average meal masses, and conversely. Energy densities followed a similar pattern to meal masses, but did not deviate more than 10% from the overall mean. Site-specific variation in all three provisioning metrics tended to covary (Figure 6.5b), with below-average variability toward the central and eastern Gulf and higher variability in the west.

Provisioning metrics also varied seasonally within the chick rearing period. Both meal mass and energy density increased over the course of the breeding season (meal mass: coefficient = 2.48 ± 0.24, $F_{1,596} = 104$, $p < 0.001$; energy density: coefficient = 0.007 ± 0.001, $F_{1,596} = 29.5$, $p < 0.001$), while meal delivery rate decreased during the same period (coefficient = -0.036 ± 0.005, $F_{1,135} = 46.1$, $p < 0.001$). However, rates of energy delivery, calculated as the product of daily average meal mass, energy density, and meal delivery rates, neither increased nor decreased during the breeding season ($F_{1,40} = 0.60$, $p > 0.20$).

Mean biomass provisioning rate (BPR) varied by colony from 454 ± 294 to 1106 ± 587 g day-1. Mean EPR varied by colony from 1977 to 4876 kJ day^{-1} (Table 6.2). BPR and EPR were highly correlated (coefficient = 4.48 ± 0.34, $F_{1,5} = 168.0$, $p < 0.001$). Of the individual provisioning covariates measured at each colony, meal delivery rate explained 38% of variance in energy provisioning rate, followed by meal mass (24%) and energy density of meals (1%). Both feeding frequency and meal mass improved model fit when added sequentially to the intercept-only model, but adding energy density did not significantly improve the fit of the model (Table 6.3).

Meal delivery rates increased with increasing proportions of menhaden and anchovy, which were also associated with decreasing energy density of meals (Figure 6.6a–c). By comparison, meals containing higher proportions of spot, croaker, and pinfish were associated with lower delivery rates and higher energy densities (Figure 6.6a–c). Meal masses were highest for meals containing striped mullet (*Mugil cephalus*) or Atlantic cutlassfish (*Trichiurus lepturus*) and lowest for meals containing anchovies (Figure 6.6b). The proportion of biomass represented by small size-class fish (< 110 mm (4.33 in) total length) at individual colonies correlated to feeding frequency ($F_{1,5} = 7.18$, $p = 0.04$, $r^2 = 0.59$, coefficient = 0.108 ± 0.04), but not to meal mass or energy density ($F_{1,5} = 1.82$, $p > 0.20$ for both).

Average fledging success (chicks $nest^{-1}$) was strongly correlated to both mean EPR and BPR at the colony level (Figure 6.7). Of the individual components of EPR, feeding frequency explained the largest portion of variance in nest productivity (49%), followed by meal mass (15%) and energy density of meals (0.1%). Both feeding frequency and meal mass significantly improved the fit of a null model for average fledging success by colony, while energy density did not improve model fit (Table 6.3). Diet composition (% menhaden) did not correlate with fledging success ($F_{1,5} = 0.89$; $p > 0.20$).

6.3 Nutritional Stress

We found that, in comparison to seabirds at high latitudes, brown pelicans in the GOM experience a narrow range of variation in energy content between prey species. Furthermore, our results suggest that nest productivity of brown pelicans is more closely associated with feeding frequency, followed by meal mass, and that species composition and energy content of meals have little effect on productivity. Combined, these results suggest that brown pelicans provisioning nestlings in this system use a feeding strategy that prioritizes frequent deliveries of highly available prey regardless of energy density. Though our results indicate that the junk-food hypothesis may not be useful for explaining the relationship between nestling provisioning and nest productivity in this system, our study also highlights the key importance of small, highly abundant schooling fish for breeding brown pelicans in the GOM.

Although brown pelicans delivered a wide variety of prey species to nestlings, both lipid content and overall energetic value of prey items in nestling diets varied within a narrow range. Compared to results from previous work in temperate and subpolar systems, average energetic content of prey species in our study was 15–30% lower, with 55–78% less variation between species (Figure 6.8). Our observations accord with previous work on mesopelagic fish species in the GOM (Stickney and Torres 1989) and the South Atlantic Bight (Jodice et al. 2011), which suggest that fish species in the tropical northwest Atlantic have relatively higher protein levels, lower lipid reserves, and lower overall energetic values than species at northern and southern latitudes characterized by cooler oceanic temperatures and higher inter-seasonal variability. Despite the wide longitudinal variation of our sampling area and the variation in prey species composition relative to prey distribution, energetic content of meals fed to pelican chicks varied little between colonies. As a result, colony-specific EPRs closely reflected a combination of meal mass and frequency of meal deliveries (i.e., BPR), but did not relate to energy content of meals. Our results suggest that prey energy content is not a significant driver of energy delivery rates to nestlings for brown pelicans in this system, given the lack of variation in energy density between prey species.

Our results support previous observations of the predominance of Gulf menhaden in brown pelican diets (e.g., Arthur 1919, Fogarty 1981); however, the proportions of menhaden consumed by pelicans in our study varied both spatially and temporally depending on underlying distribution and inferred availability. The proportion of juvenile menhaden in nestling diets declined over the course of the chick-rearing period, during which young-of-the year menhaden move gradually from shallow estuarine waters to offshore habitats, decreasing their availability to foraging pelicans (Ahrenholz 1991). Other prey, including pinfish, anchovy, and adult menhaden, increased proportionally during the same period, and overall rates of energy delivery to nestlings remained consistent throughout the breeding season. Gulf menhaden constituted 60–84% of pelican nestling diets in colonies at the core of its range (i.e., the central Northern GOM), but less than 40% of diets in colonies at the eastern and western margins of its range. Notably, first-year menhaden (individuals hatched during the previous winter) represented 56% of nestling pelican diets at the colony closest to the core of their range and 3% or less outside the range margins. As the proportion of menhaden in nestling diets declined, other prey species, principally anchovy in the eastern GOM and spot, croaker, and pinfish in the western GOM, contributed more significantly to nestling diets. The comparatively larger size of pelican breeding colonies at the core of the gulf menhaden range than at its margins may indicate that areas with high menhaden availability can support larger aggregations of breeding pelicans. However, further study is required to distinguish the effects of variation in prey availability among planning areas on population size from those of conservation history (e.g., King et al. 1985, Wilkinson et al. 1994) and breeding habitat availability (e.g., Walter et al. 2013).

We tested the effects of prey energy content on demographic rates by relating inter-colony variation in reproductive success to nutritional parameters. We found that the rate of biomass delivery alone explained over 90% of variation in nest productivity between sites, with a feeding rate of approximately 800 g d^{-1} (1.76 lbs d^{-1}) (approximately 56,000 g (123.46 lbs) total from hatch through fledging) required to successfully fledge one nestling. Despite variation in prey composition, energy density of meals varied little between colony sites, thus did not contribute to variation in fledging rates. The lack of relationship between energy density of meals and nestling survival indicates that the junk food hypothesis (JFH) may not be relevant in this context. Though support for the JFH to date has come from cold-water systems at high latitudes (Österblom et al. 2008), our results suggest that prey communities in the subtropical Northern GOM present top predators with a narrow range of energetic options, which may contribute to a lack of transferability of the JFH to warm-water systems. However, several previous studies in high-latitude systems have also found biomass provisioning metrics to be considerably better predictors of fledging success than energetic content of food items (e.g., Jodice et al. 2006, Hjernquist and Hjernquist 2010). Österblom et al. (2008) suggest that the negative influence of lower-energy food items is particularly pronounced in certain species of seabirds, especially species specialized to carry single prey items or small masses of prey, species with energetically expensive foraging strategies, and species with low digestive efficiency. Although plunge-diving is energetically demanding (Green et al. 2009), brown pelicans are able to capture and carry large volumes of prey, which may allow them to buffer the effects of reduced prey quality by increasing prey quantity with minimal increases in foraging effort.

In general, as meal delivery rates increased, meal masses decreased on a colony-wide basis. The relative magnitude of variation in these two metrics provides a useful basis for assessing how foraging conditions and strategies differ from site to site, indicating that there may be a trade-off between prey load maximization and time spent foraging. We found that differences in prey species composition helped to explain the negative relationship between meal mass and provisioning rates. Across species comprising > 1% of nestling diets, higher percentages of schooling fish of the order Clupeiformes (menhaden, Atlantic threadfin herring *Opisthonema oglinum*, and anchovies) were related to higher provisioning rates and generally lower meal masses, while spot, croaker, and pinfish (order Perciformes), as well as striped mullet (Mugiliformes), corresponded to lower feeding rates and higher meal masses. Clupeiformes are

typically schooling fish that occur in large aggregations in clear and relatively shallow water; the remaining species are bottom-dwellers that do not school and avoid waters where visibility is high (Nelson 1994). For a multiple-prey loader that can capture several prey items at once, targeting highly concentrated prey resources regardless of energetic content could be a means of maximizing biomass delivery.

Overall, we found that higher meal delivery rates were driven by the proportion of diet biomass composed of fish less than 110 mm (4.33 in) total length, regardless of species. Despite being among the least energy-rich prey items observed, juvenile menhaden constituted over 50% of pelican diets at the core of their range, suggesting that pelicans target accessible and highly aggregated prey without regard for energetic content. The importance of small, abundant schooling fish to brown pelican reproductive output is of potential conservation interest. Recruitment rates in gulf menhaden are highly sensitive to temperature and precipitation, with warmer and wetter winters producing comparatively fewer recruits in the next year class (Deegan 1990). Given that winter temperatures and precipitation are expected to rise under current climate change projections (Biasutti et al. 2012), the biomass of larval fish available to upper-level predators (e.g., Muhling et al. 2011) could become more limited or more variable in future climactic conditions. Additionally, pollution events can significantly depress survival of larval fish (Incardona et al. 2014) and could have indirect effects on prey dynamics that compound the direct effects of pollutants exposure to predators.

Table 6.1. Fish Species Occurring in the Diets of Brown Pelican Chicks in the Northern GOM, 2013–2015

Order	Family	Species	Common	Year	% biomass
Atheriniformes	Atherinidae	*Menidia beryllina*	Inland silverside	1,2,3	0.1
Aulopiformes	Synodontinae	*Sybodus foetens*	Inshore lizardfish	1,2	*
Beloniformes	Belonidae	*Tylosurus crocodilus*	Houndfish	3	*
	Hemiramphidae	*Hemiramphus brasiliensis*	Ballyhoo halfbeak	1,2	0.1
Clupeiformes	Clupeidae	*Brevoortia patronus*	Gulf menhaden	1,2,3	61.0
		Harengula jaguana	Scaled sardine	1	0.3
		Opisthonema oglinum	Atlantic threadfin Herring	2,3	1.7
	Engraulidae	*Anchoa hepsetus*	Striped anchovy	2,3	1.5
		Anchoa lyolepis	Dusky anchovy	3	2.2
		Anchoa mitchilli	Bay anchovy	1,2,3	7.5
Cyprinodontiformes	Cyprinodontidae	*Cyprinodon variegatus*	Sheepshead minnow	2	0.2
		Fundulus majalis	Striped killifish	2	*
Decapoda	Penaeidae	*Farfantepenaeus duorarum*	Pink shrimp	2,3	*
Mugiliformes	Mugilidae	*Mugil cephalus*	Striped mullet	2,3	4.8
Perciformes	Carangidae	*Caranx crysos*	Blue runner	1	0.1
		Chloroscombrus chrysurus	Atlantic bumper	1,2,3	0.6
		Decapterus punctatus	Round scad	3	0.1
		Hemicaranx amblyrhynchus	Bluntnose jack	2	*
		Selene setapinnis	Atlantic moonfish	2	*
	Gobiidae	*Gobioides broussonetii*	Violet goby	2	*
	Haemulidae	*Orthopristis chrysoptera*	Pigfish	1,2	*

Order	Family	Species	Common	Year	% biomass
	Lutjanidae	*Lutjanus campechanus*	Red snapper	15	0.3
	Sciaenidae	*Bairdiella chrysoura*	Silver perch	1,2	0.4
		Cynoscion arenarius	Sand seatrout	2,3	1.2
		Cynoscion nebulosus	Spotted seatrout	2,3	1.1
		Larimus fasciatus	Banded drum	2	*
		Leiostomus xanthurus	Spot	1,2,3	2.9
		Menticirrhus americanus	Southern kingfish	2	0.7
		Micropogonias undulatus	Atlantic croaker	1,2,3	3.8
		Sciaenops ocellata	Red drum	2,3	0.5
	Scombridae	*Auxis thazard*	Frigate mackerel	3	0.2
		Scomberomorus cavalla	King mackerel	2	0.1
		Scomberomorus maculatus	Spanish mackerel	2	0.3
	Serranicae	*Diplectrum formosun*	Sand perch	3	0.2
	Sparidae	*Calamus proridens*	Littlehead porgy	1	*
		Lagodon rhomboides	Pinfish	1,2,3	2.4
		Stenotomus caprinus	Longspine porgy	1	*
	Stromateidae	*Peprilus burti*	Gulf butterfish	2,3	0.1
		Peprilus paru	American harvestfish	2	0.1
	Trichiuridae	*Trichiurus lepturus*	Atlantic cutlassfish	1,2,3	3.6
Pleuronectiformes	Cynoglossidae	*Symphurus urospilus*	Spottail tonguefish	3	0.1
	Paralichthyidae	*Citharichthys spilopterus*	Bay whiff	2,3	0.1
Scorpaeniformes	Triglidae	*Prionotus tribulus*	Bighead searobin	2,3	*
Siluriformes	Ariidea	*Bagre marinus*	Gafftopsail catfish	1,2,3	0.3
Tetraodontiformes	Diodontidae	*Diodon holocanthus*	Longspine porcupinefish	2	*
Teuthida	Loliginidae	*Lolligunculla brevis*	Atlantic brief squid	1,3	*
Other			Isopod	3	*
			Bait (chicken)	3	*
			Unknown		1.2

An asterisk (*) in the biomass column denotes less than 0.05 % of total biomass. Year 1: 2013; Year 2: 2014; Year 3: 2015.

Table 6.2. Mean Values for Brown Pelican Nest Productivity, Chick Health Metrics, and Energy Provisioning Metrics by Colony in the Northern GOM, 2014–2015

	Colony	Productivity	Meals day^{-1}	g meal^{-1}	Energy g^{-1}	BPR	EPR
2014	Shamrock	0.51 ± 0.66	2.23 ± 1.28	205 ± 138	4.66 ± 0.50	552 ± 345	2574 ± 1618
2014	Chester	0.68 ± 0.79	3.10 ± 2.80	174 ± 136	4.53 ± 0.61	644 ± 559	2902 ± 2548
2014	Galveston	0.94 ± 0.86	5.68 ± 3.08	124 ± 91	3.99 ± 0.63	749 ± 446	2995 ± 1804
2015	Gaillard	1.06 ± 0.85	3.84 ± 1.89	175 ± 102	4.69 ± 0.36	758 ± 408	3451 ± 1879

2015	Audubon	1.42 ± 0.85	5.32 ± 2.33	191 ± 170	4.33 ± 0.38	1106 ± 587	4793 ± 2554
2015	Ten Palms	1.64 ± 0.95	5.84 ± 3.14	168 ± 105	4.59 ± 0.35	1042 ± 586	4876 ± 2722
2015	Smith	0.30 ± 0.64	4.21 ± 3.08	106 ± 78	4.35 ± 0.39	454 ± 294	1977 ± 1286

± standard deviations are shown.

Table 6.3. ANOVA Comparisons of Nested Models for Colony-specific Mean Brown Pelican Nestling Energy Provisioning Rates and Nest Productivity Based on Feeding Rate, Meal Mass, and Energy Density of Meals, Northern GOM, 2014–2015

	Terms	Residual df	Residual deviance	df	deviance	F	p
Energy provisioning rate							
	Intercept only	6	7236805				
	+ feeding rate	5	4498564	1,5	2738240	24.79	0.016
	+ meal mass	4	379699	1,5	4118866	37.3	0.009
	+ energy density	3	331316	1,5	48383	0.44	0.56
Nest productivity							
	Intercept only	6	1.397	1,5			
	+ feeding rate	5	0.714	1,5	0.683	47.83	0.006
	+ meal mass	4	0.056	1,5	0.658	46.12	0.007
	+ energy density	3	0.043	1,5	0.896	0.90	0.41

Terms are added sequentially, and a p-value of < 0.05 indicates a significant improvement in fit compared to the previous model.

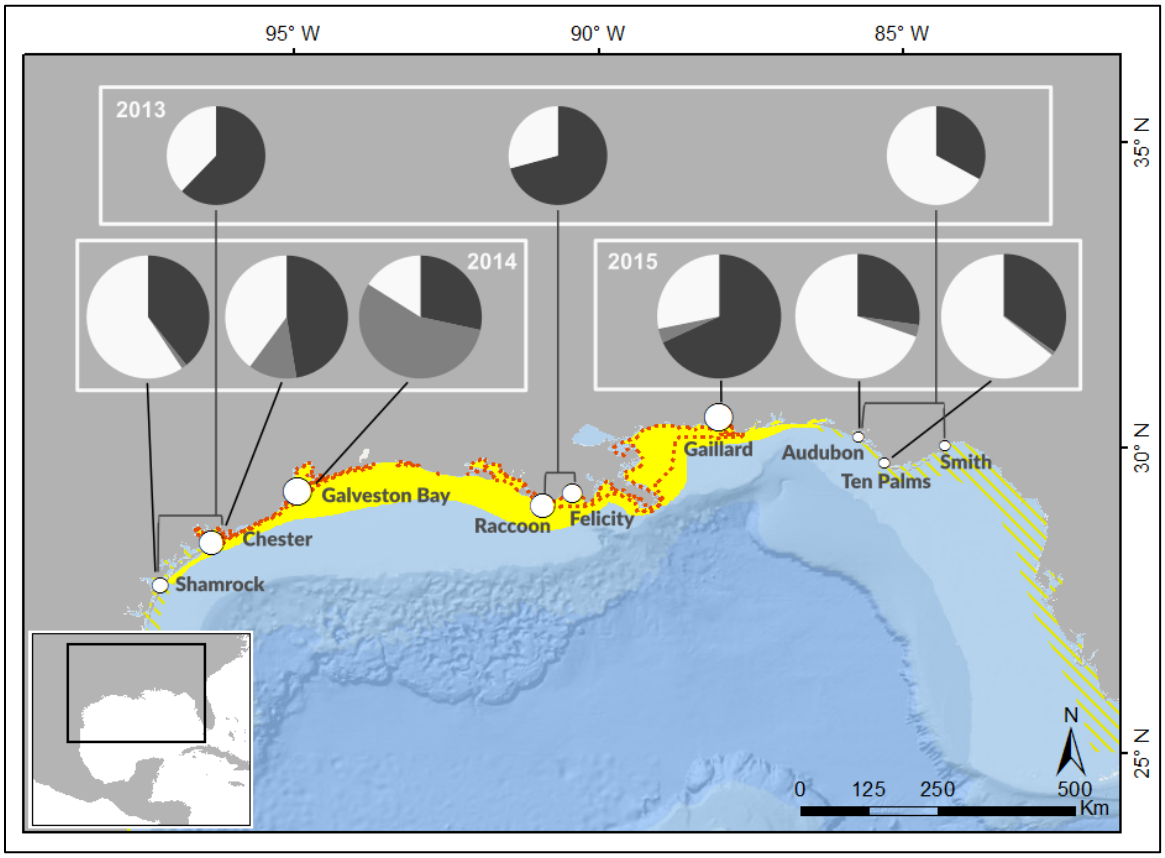


Figure 6.1. Percentage of Gulf menhaden in the diets of brown pelican nestlings, Northern GOM, 2013–2015.
Pie charts represent the portion by biomass of adult menhaden (dark grey), first year menhaden (light grey) and other prey species (white) in chick diets. Yellow shaded areas: summer distributions of adult (solid: major; hatched: minor) and first-year (red dashed outline) menhaden (Love et al. 2013) (Base layer: ESRI, DeLorme, GEBCO, NOAA, NGDC, and other contributors).

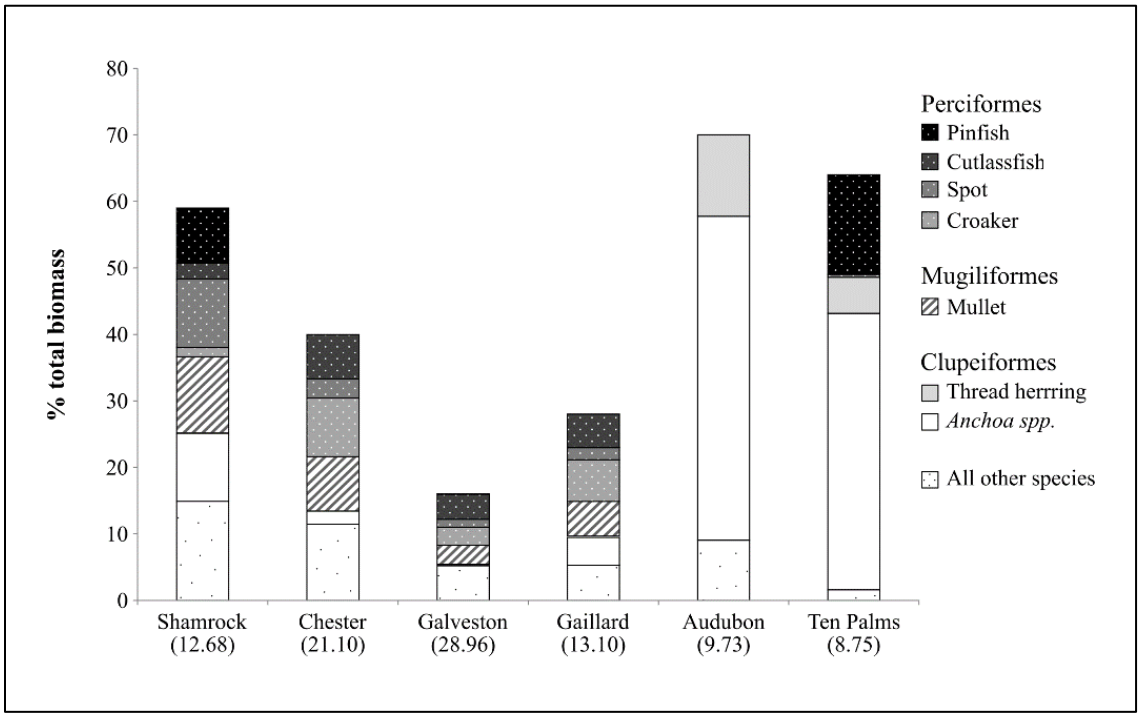


Figure 6.2. Proportion of biomass of brown pelican nestling diets represented by all prey species other than Gulf menhaden, Northern GOM, 2014–2015.
Species comprising <1% overall prey biomass are grouped. Parentheses: sample sizes (mass of recovered meals, kg) for each colony.

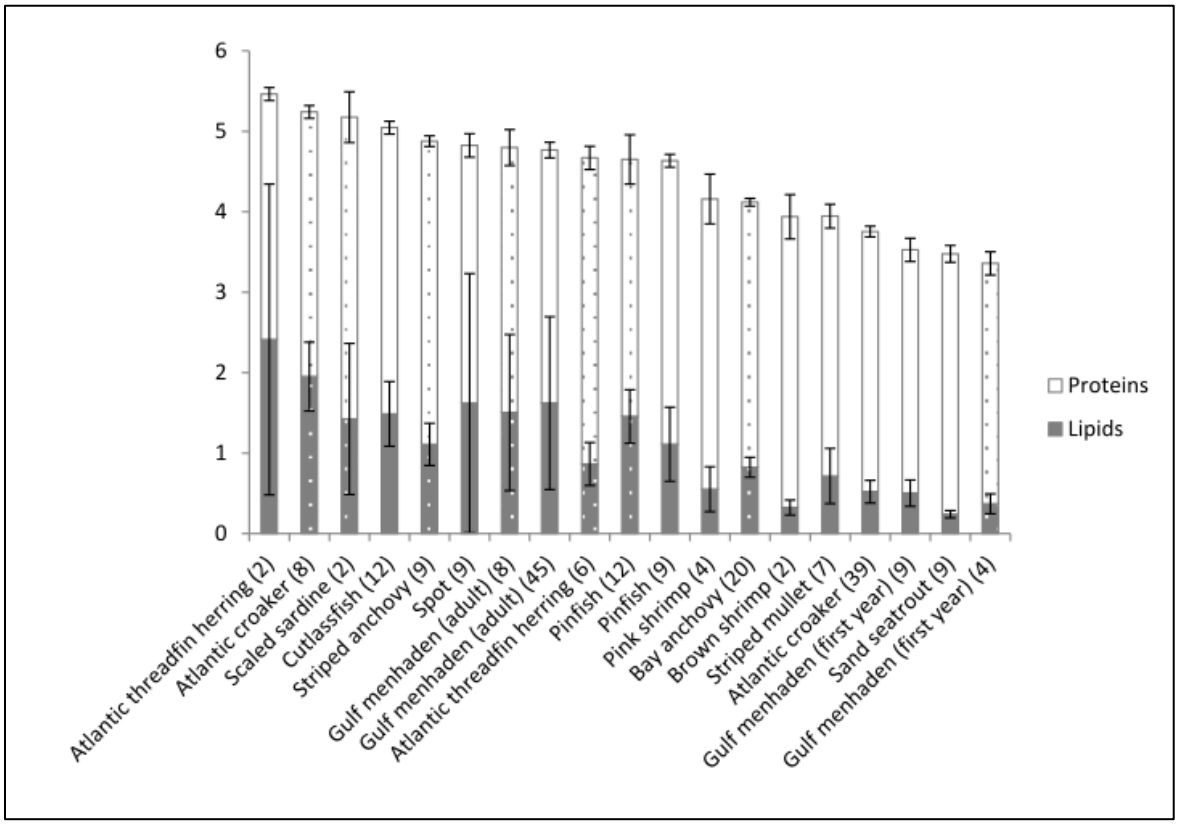


Figure 6.3. Mean energy densities of common prey items in the diet of brown pelican nestlings, Northern GOM, 2014–2015.
Only prey items each > 1% of total biomass are shown. Prey items collected from the northwestern (Corpus Christi Bay to Galveston Bay, TX: solid bars) and northeastern (Mobile Bay, AL to Apalachee Bay, FL: patterned bars). Error bars represent 95% confidence intervals. Sample sizes are listed in parentheses. Note error bars are specific to each segment of the stacked bar.

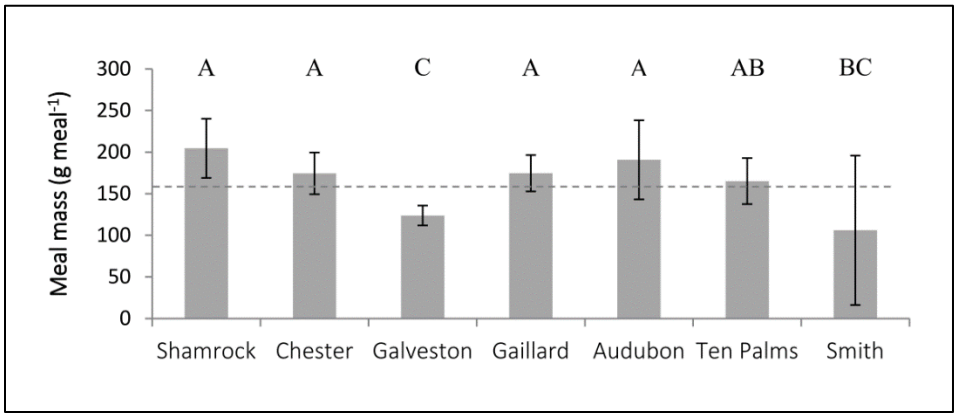


Figure 6.4.a. Comparison of average meal mass, provisioning rate, and energy density of meals between brown pelican colony sites, Northern GOM, 2014–2015: meal mass.
Letters denote Tukey post-hoc groups, error bars are 95% confidence intervals of means, and dashed lines are global mean values.

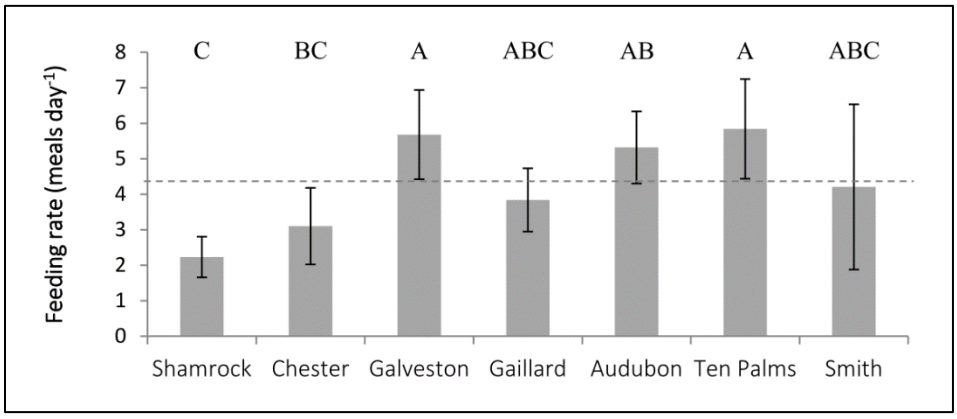


Figure 6.5.b. Comparison of average meal mass, provisioning rate, and energy density of meals between brown pelican colony sites, Northern GOM, 2014–2015: provisioning rate.
Letters denote Tukey post-hoc groups, error bars are 95% confidence intervals of means, and dashed lines are global mean values.

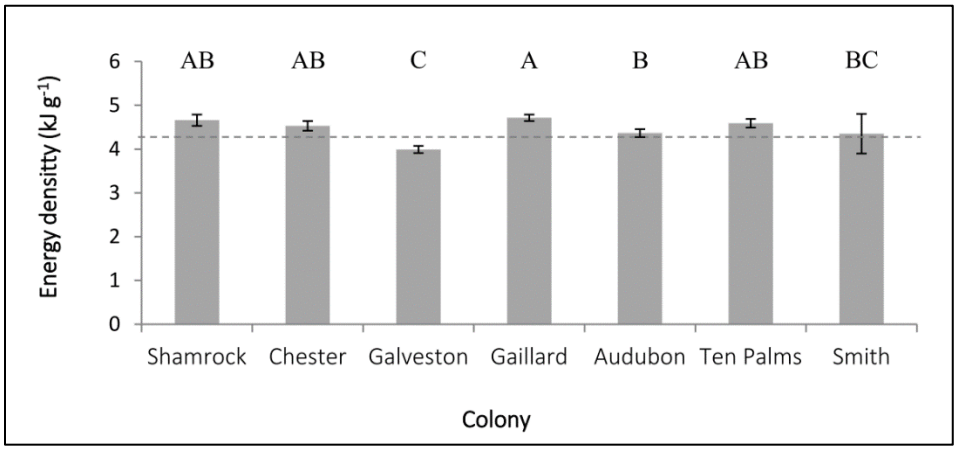


Figure 6.6.c. Comparison of average meal mass, provisioning rate, and energy density of meals between brown pelican colony sites, Northern GOM, 2014–2015: energy density of meals.
Letters denote Tukey post-hoc groups, error bars are 95% confidence intervals of means, and dashed lines are global mean values.

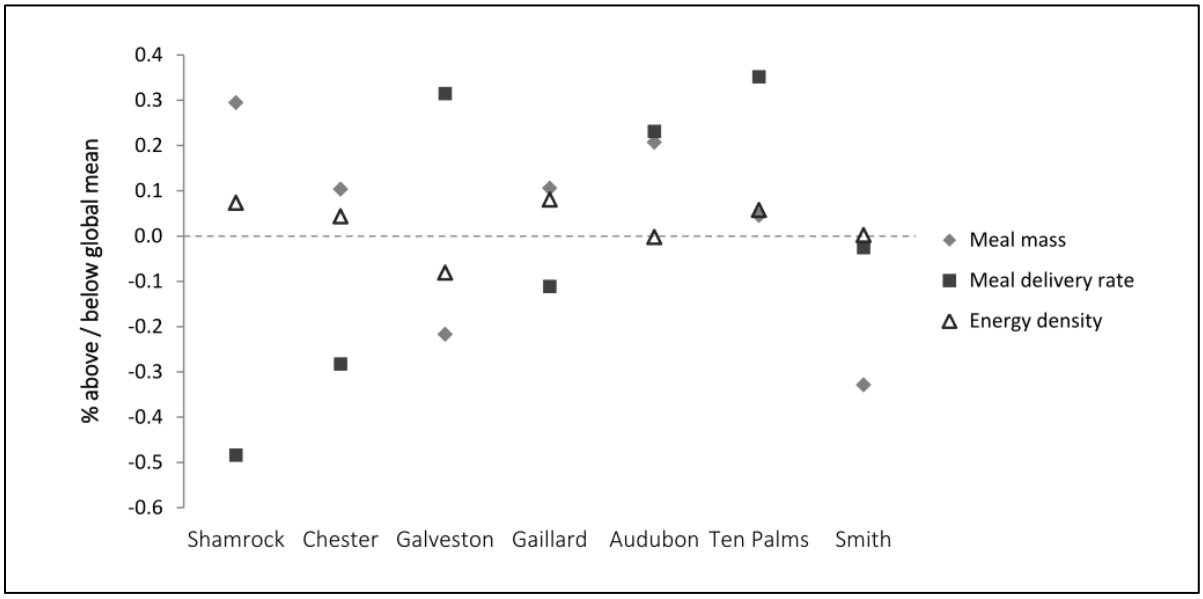


Figure 6.7.a. Drivers of between-colony variation in mean values of provisioning metrics and coefficients of variation for brown pelican colonies, Northern GOM, 2014–2015: mean values of provisioning metrics.
The mean value for each metric across all samples is set at zero, and individual points represent deviation from the global mean (as a percentage of global mean) at that colony site.

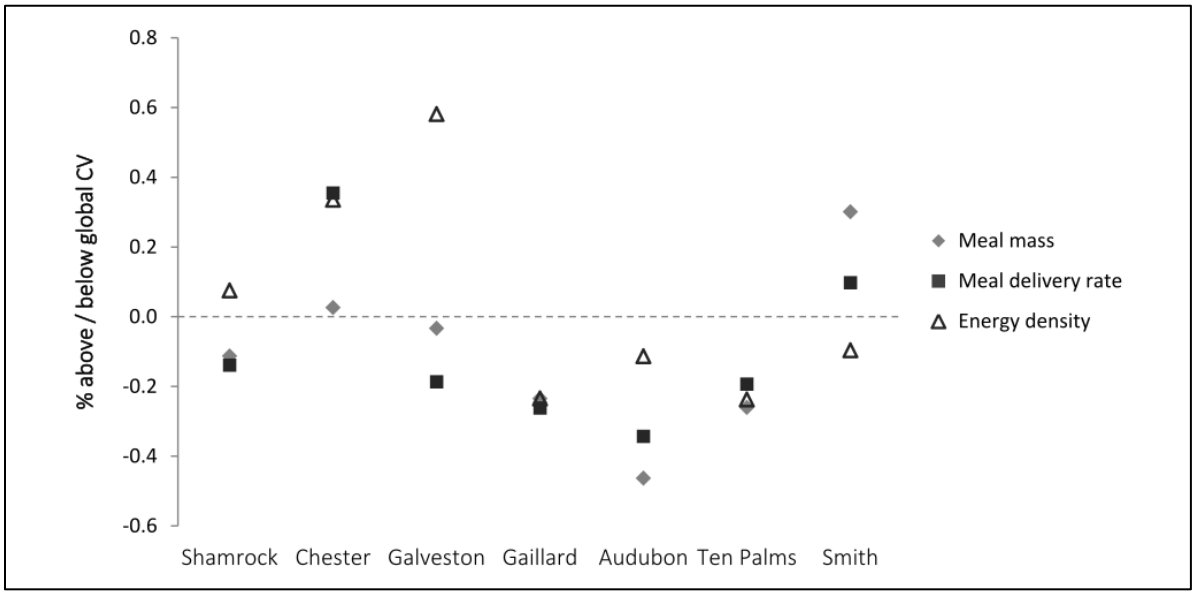


Figure 6.8.b. Drivers of between-colony variation in mean values of provisioning metrics and coefficients of variation for brown pelican colonies, Northern GOM, 2014–2015: coefficients of variation.

The mean value for each metric across all samples is set at zero, and individual points represent deviation from the global mean (as a percentage of global mean) at that colony site.

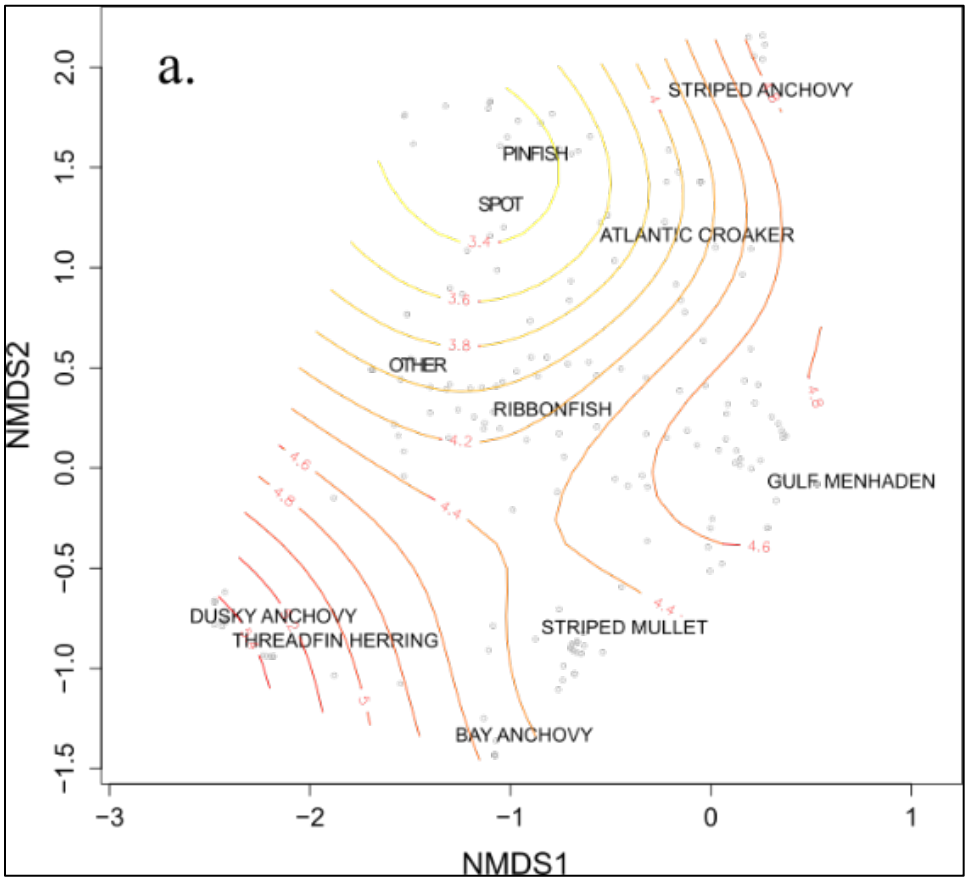


Figure 6.9.a. Non-metric multidimensional scaling plots showing the distribution of species composition of individual meals collected from brown pelican nestlings, Northern GOM, 2014–2015: meal delivery rate.
Grey dots represent individual meals. Surface plots of the three components of energy provisioning rate are overlaid to show isoclines; warmer colors represent direction of increase in ordination space.

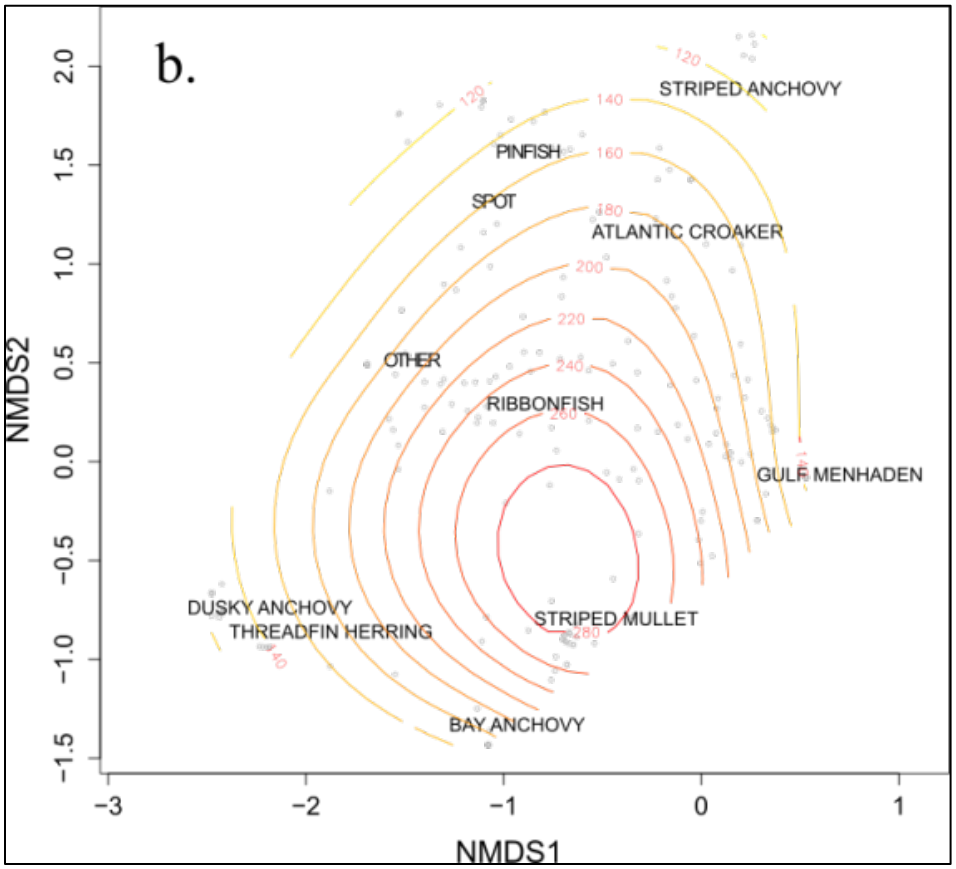


Figure 6.10.b. Non-metric multidimensional scaling plots showing the distribution of species composition of individual meals collected from brown pelican nestlings, Northern GOM, 2014–2015: mass.

Grey dots represent individual meals. Surface plots of the three components of energy provisioning rate are overlaid to show isoclines; warmer colors represent direction of increase in ordination space.

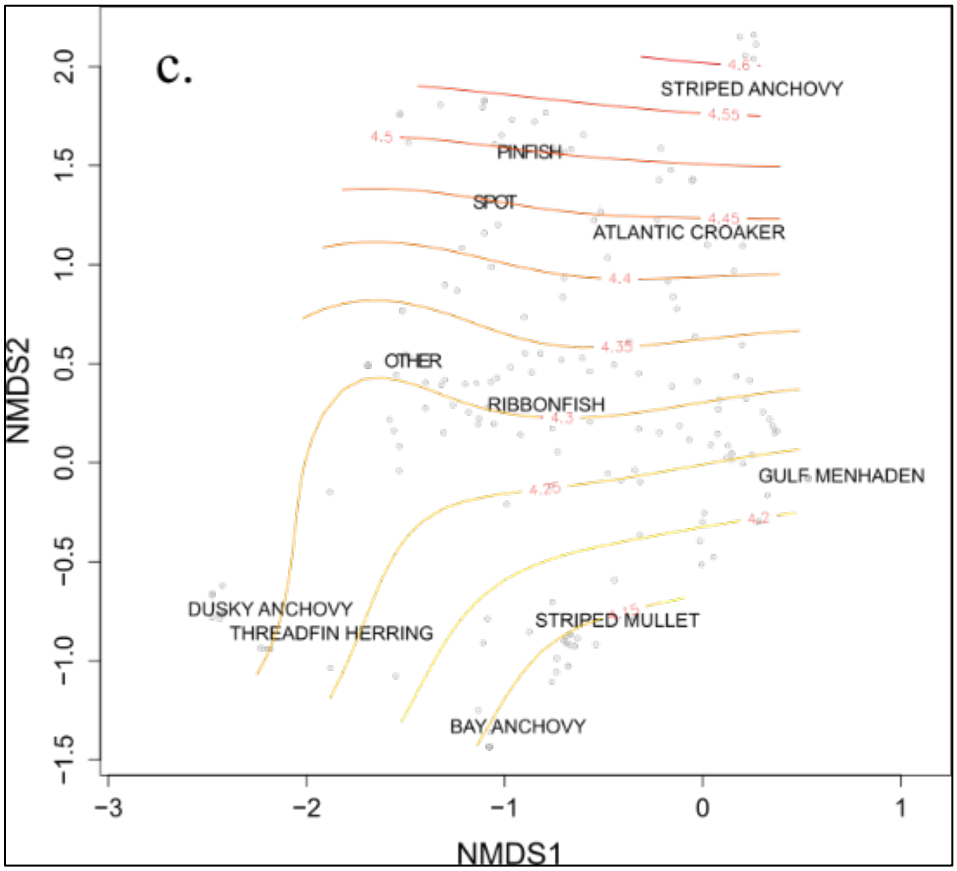


Figure 6.11.c. Non-metric multidimensional scaling plots showing the distribution of species composition of individual meals collected from brown pelican nestlings, Northern GOM, 2014–2015: energy density.
Grey dots represent individual meals. Surface plots of the 3 components of energy provisioning rate are overlaid to show isoclines; warmer colors represent direction of increase in ordination space.

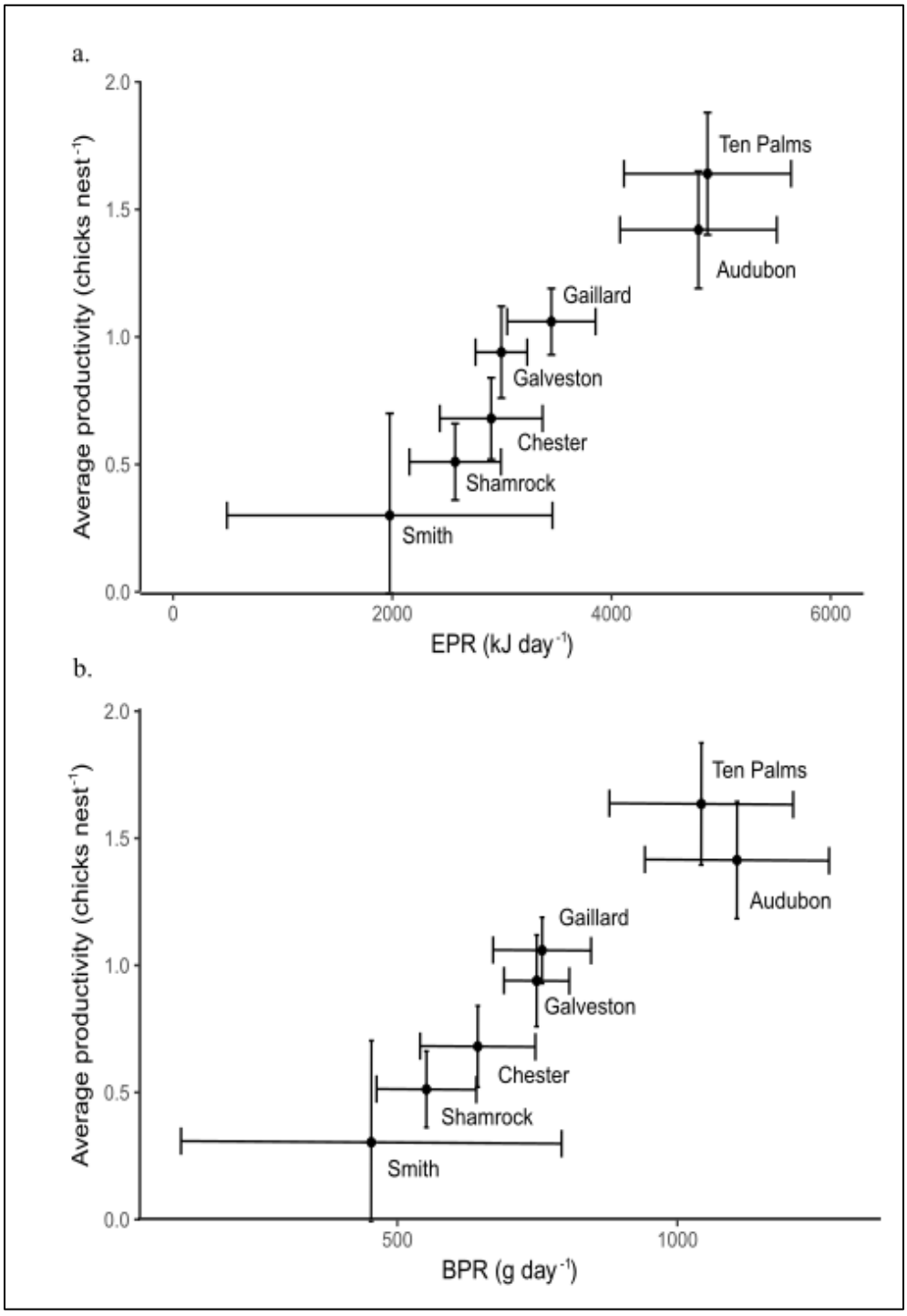
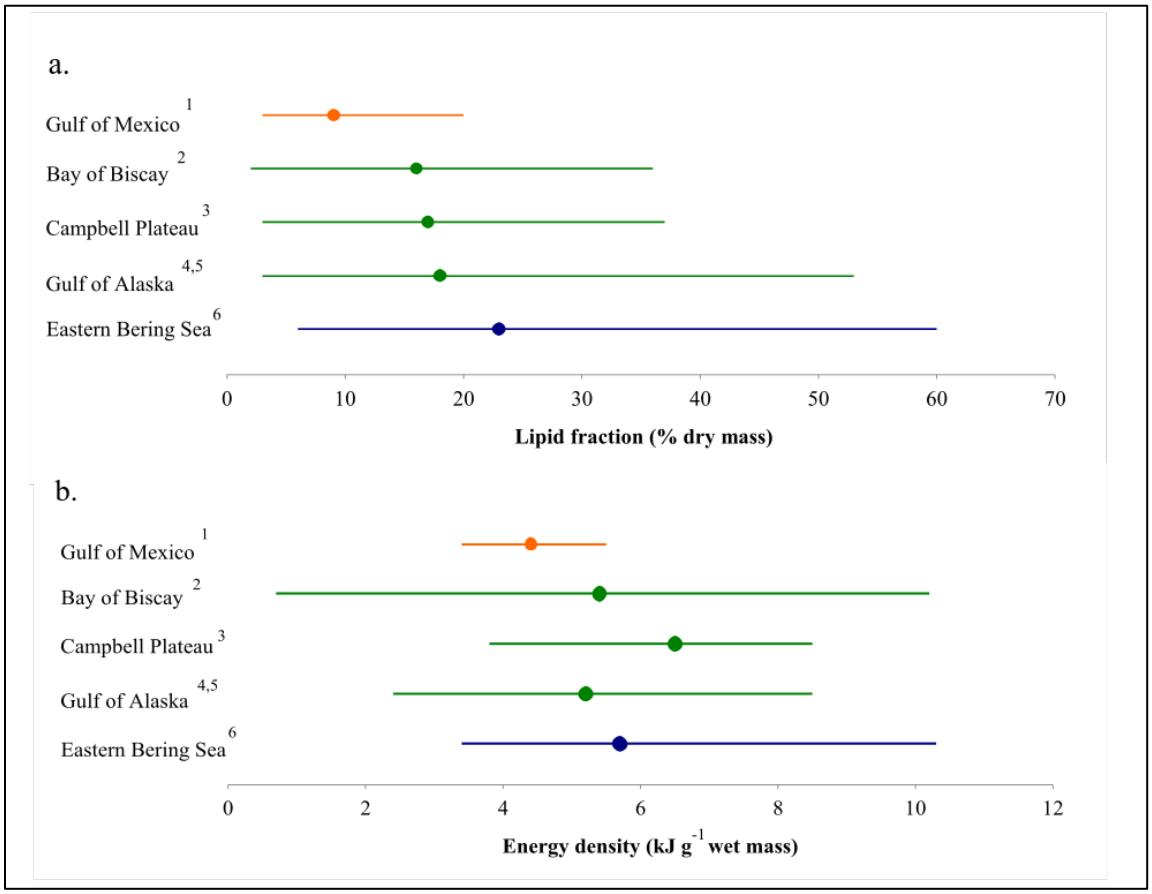


Figure 6.12. Linear relationship between energy provisioning rate and biomass provisioning rate, and nest productivity at brown pelican nesting colonies, Northern GOM, 2014–2015.
(a) Linear relationship between EPR and nest productivity ($y = 0.0004 x - 0.508$; $r^2 = 0.952$); (b) linear relationship between BPR and nest productivity ($y = 0.0019 x - 0.535$; $r^2 = 0.943$). Error bars represent 95% confidence interval of means.



[1] This study
[2] Spitz et al. 2010
[3] Meynier et al. 2008
[4] Anthony et al. 2000
[5] Van Pelt et al. 1997
[6] Payne et al. 1999

Figure 6.13. Comparison of lipid content and energy density of forage fish in this study with published values from other regions.
(a) Lipid content, (b) energy density of forage fish. Colors indicate marine regions (orange: tropical; green: temperate; blue: subpolar). Data sources are listed as footnotes.

7 Hematology, Plasma Chemistry, and PAHs

7.1 Hematology and Plasma Chemistry

CBCs provide a wealth of data within an individual and across populations. The half-life for red blood cells in birds is ~13 d (Maceda-Veiga et al. 2015), therefore blood samples provide insight into the recent condition of individuals (e.g., on the order of 2–4 w). For data in this study, analytes are indicative of condition during the incubation and early chick-rearing stage for adults, and for the early development stage for chicks. Furthermore, analytes of chicks may reflect nutritional conditions, and can be responsive to overall food quality as well as short-term changes in provisioning. It is not uncommon, therefore, to observe a substantial level of variability within an analyte among individuals (e.g., Ferguson et al. 2014, Fiorello 2019). Caution should be applied when interpreting such data, since attempting to provide detailed ecological explanations for the values of each analyte can be misleading due to the high levels of variability. We concentrated our interpretation on groups of analytes (e.g., plasma metabolites, enzymes) rather than individual analytes for each of the independent variables we assessed: BCI, planning area, sex, and home range size. This approach allows for a more ecologically-focused assessment of the data, in contrast to an analyte-specific clinical review. We also compare the reference levels from this study to other data available from brown pelicans.

7.1.1 Individual Attributes, Hematology, and Plasma Chemistry of Adults

7.1.1.1 Individual Attributes of Adults

BCI of adults ranged from -515.0–491.2 (mean = -6.3 ± 253.7). BCI of adults differed by sex ($F_{1,63} = 4.1$, $P = 0.04$) but not by planning area or sex * planning area ($P > 0.10$). Males had higher BCI compared to females (Figure 7.1a). The 50% core use area (i.e., home range) ranged from ~ 1km^2–909 km^2 (mean = 102.9 ± 157.9 km^2) (0.62–564.8 mi^2, mean = 63.9 ± 98.11 mi^2). Home range size differed by planning area ($P < 0.05$; Figure 7.1b). Home range did not differ with BCI, sex, or sex * planning area ($P > 0.10$). Correlated independent variables were not used within the same models, although all variables of interest were included in the overall suite of models.

7.1.1.2 Blood Analytes of Adults

Table 7.1 includes reference values for adults for all blood analytes. Sodium, which was the only analyte with a bimodal distribution, was treated as two separate analytes (see 2.8.1.3 Statistical Analysis). Of the 30 analytes examined, four had outliers removed (high values were removed for CORT, potassium, and alanine aminotransferase; a low value was removed for low-density lipoprotein cholesterol), 12 required transformation, and all had sufficient sample sizes to use a nonparametric reference interval (Table 7.1). Maximum sample sizes (i.e., the number of samples collected from each colony; not all samples provided data for all analytes) from each colony for blood analytes are summarized in Table 7.2.

Reference intervals were calculated for 30 blood analytes. Among the 30 analytes there were nine cases of moderate to strong correlation. Beta globulin was most commonly correlated with other analytes (n = 3 pair), followed by A:G, blood urea nitrogen, uric acid, and creatinine (n = 2 pair each). Pooled among all 30 blood analytes, the models that were most often highly supported or for which AICc ≤ 2.0 of the top-ranked model were (1) home range + sex (n = 13 analytes), (2) home range (n = 10 analytes), and (3) BCI + sex (n = 10 analytes; Table 7.3). Single-variable models for sex, BCI, and planning area were

infrequently ranked among top models ($n \leq 5$ for each), although the null model was more frequently ranked as a top model (n = 7 analytes) compared to single-variable models.

We calculated coefficient estimates using the value provided by the top-ranked model for an analyte (Table 7.4); coefficient estimates included only when estimate ± SE did not overlap zero).

7.1.1.3 Relationship of Planning Area with Blood Analytes of Adults

Among the independent variables we tested, coefficient estimates for the categorical variable "planning area" were most often strongly associated with the concentration of a blood analyte (Table 7.4, Figure 7.2). The eastern planning area was set as the reference level because it had the lowest level of oil and gas activity in coastal and marine waters. Concentrations of analytes were lower in both the central and western planning area compared to the eastern planning area for CPK, lipase, total protein, beta globulin, and gamma globulin. Concentrations of analytes were lower in the central or western planning area when compared to the eastern planning area for calcium (west), ALT (west), AST (central), albumin (west), and A1G (central). Concentrations of analytes were higher in both the central and western planning area compared to the eastern planning area for potassium and creatinine. Concentrations of analytes were higher in either the central or western planning area compared to the eastern planning area for calcium (central). Pelicans in the western planning area were likely to have lower levels of sodium than birds in either the eastern or central planning area ($\chi^2_2 = 29.0$, $P < 0.0001$).

7.1.1.4 Relationship of Body Condition Index, Sex, and Home Range with Blood Analytes of Adults

BCI was positively related to potassium and negatively related to creatinine, uric acid, and BUN:CRE (Figure 7.3). Differences in analytes by sex occurred for seven analytes. Levels of BUN, uric acid, and BUN:CRE were higher in females compared to males, but levels of calcium, lipase, cholesterol, and HDLc were higher in males compared to females (Figure 7.4). We found a negative relationship between home range size and CPK, lactate dehydrogenase, lipase, BUN, creatinine, and uric acid; and a positive relationship between home range size and HDLc (Figure 7.5).

7.1.1.5 White Blood Cells from Adults

Reference values were calculated for the counts ($10^3\,ml^{-1}$) of WBC for adults (Table 7.5). Outliers (n = 2) were removed for the count of WBC, heterophils, and lymphocytes. Each of the WBC types including the total count were sufficient in sample size to use a nonparametric reference interval (Table 7.2). Heterophils were the most common WBC type and were observed in all samples. Samples frequently failed to include monocytes (n = 24), eosinophils (n = 38), and basophils (n = 66); the modal value for each = 0.

Because WBC data did not fit a normal distribution (either as raw data or when transformed), we performed nonparametric analyses (Kruskal-Wallis or Kendall correlation) to assess the relationships between WBC data and sex, state, BCI, and home range size. Monocytes were slightly less common (Kruskal Wallis $H_1 = 2.8$, $P = 0.09$) in males (median = 0.18, quartiles = 0, 0.36) compared to females (median = 0.3, quartiles = 0.07, 0.8; Figure 7.6a). No other significant relationships occurred between sex and WBC counts. WBC counts were higher in the western planning area (median = 13, quartiles = 9–15) than in the central planning area (median = 7, quartiles = 5.7–12) (Kruskal Wallis $H_2 = 5.3$, $P = 0.07$; (Figure 7.6b). Heterophils were higher in the eastern planning area (median = 8.3, quartiles = 6.7–10.0) than in the central planning area (median = 5.7, quartiles = 3.8–7.6) (Kruskal Wallis $H_2 = 6.8$, $P = 0.03$; Figure 7.6c). No other significant relationships occurred among between planning area and WBC counts. Monocyte counts were negatively correlated to BCI (Kendall tau = -0.17, P = 0.04; Figure 7.6d). When

analyzed separately by sex (i.e., because monocyte count differed by sex), there was a moderate negative correlation between monocyte counts and BCI in females (Kendall tau =-0.23) but no correlation between monocyte counts and BCI in males (Kendall tau = -0.01). Lymphocyte counts declined moderately with home range size (Kendall tau = -0.15, P = 0.07; (Figure 7.6e). No other significant correlations were found for BCI or home range size with WBC counts. Hematocrit (i.e., packed cell volume, PCV) was higher in males compared to females ($F_{1,62}$= 8.1, P = 0.006; Figure 7.6f). Hematocrit did not vary with planning area, sex, home range size, or BCI (P > 0.3 for each).

7.1.2 Individual Attributes, Hematology, and Plasma Chemistry of Chicks

7.1.2.1 Individual Attributes of Chicks

The two independent variables (BCI and planning area) were interrelated and therefore not used within the same models. BCI ranged from -976.9–1148.2 (mean = -13.9 ± 584.5). BCI of chicks differed by planning area ($F_{2,32}$ = 11.4, P = < 0.0002). BCI of chicks differed between the western and central planning areas (Tukey HSD P = 0.003) and between the western and eastern planning areas (Tukey HSD P = 0.001; Figure 7.7).

7.1.2.2 Blood Analytes from Chicks

Reference values for chicks appear in Table 7.6. Of the 30 analytes examined, four had outliers removed (high values were removed for BUN, BUN:CRE, CPK, and GGT, and seven required transformation. Sample sizes were insufficient for calculating nonparametric reference intervals and therefore we instead calculated reference intervals using the robust method with a Box-Cox transformation. For cases where a better fit was provided by an untransformed robust estimator (CO_2, amylase, and CORT) or a Box-Cox standard estimator (pre-albumin, A1G, and gamma globulin) (Table 7.6), these estimators were used instead. Maximum sample sizes from each colony for blood analytes and for WBC counts (i.e., the number of samples collected from each colony; not all samples provided data for all analytes) are shown in Table 7.2**.**

Reference intervals were calculated for 30 blood analytes. Among the 30 analytes there were 19 cases of moderate to strong correlation. Gamma globulin and total protein were most commonly correlated with other analytes (n = 5 pair each), followed by AST and A:G (n = 4 pair), A2G and beta globulin (n = 3 pair each).

Pooled among all 30 blood analytes, the models that were most often highly supported included the null model (n = 21 analytes), planning area (n = 17 analytes), and BCI (n = 12 analytes; Table 7.7). Both the null model and the planning area model ranked as the top model for 13 analytes, while BCI ranked as the top model in four analytes. Planning area appeared as the only ranked model for six analytes, BCI appeared as the only ranked model for one analyte, and the null appeared as the only ranked model for four analytes.

7.1.2.3 Relationship of Planning area with Blood Analytes of Chicks

Coefficient estimates for the categorical variable "planning area" were more frequently found to be associated with the concentration of a blood analyte than BCI (Table 7.8). The eastern planning area was set as the reference level because it had the lowest level of oil and gas activity in coastal and marine waters. Relationships among blood analytes and planning area are displayed in Figure 7.8. Concentrations of analytes were lower in both the central and western planning areas compared to the eastern planning area for amylase and A1G. Concentrations of analytes were lower in either the central or western planning area compared to the eastern planning area for CO_2 (west), calcium (west), ALT (central), AST (central), glucose (west), BUN:CRE (central), albumin (west), gamma globulin (central), and A:G (west). Concentrations of analytes were never found to be higher in both the central and western planning area compared to the eastern planning area. Concentrations of analytes were higher in either the central and western planning areas compared to the eastern planning area for AST (west), lactate dehydrogenase (west), triglycerides (west), BUN (west), creatinine (central), BUN:CRE (west), A2G (west), prealbumin (west), and A:G (central).

7.1.2.4 Relationship of Body Condition Index with Blood Analytes of Chicks

BCI was positively related to amylase, VLDLc, albumin, A1G and negatively related to potassium, AST, CPK, triglycerides, and CORT (Figure 7.9).

7.1.2.5 White Blood Cells from Chicks

Reference values were calculated for the counts (10^3 ml^{-1}) of WBC for chicks (Table 7.9). No outliers were identified for the count of total WBC or any WBC type. Sample sizes (n = 35 for all WBC types) were insufficient for calculating nonparametric reference intervals and therefore we instead calculated reference intervals using the robust method with a Box-Cox transformation (WBC count, heterophils, lymphocytes) or with an untransformed standard estimator (monocytes, eosinophils, and basophils) (Table 7.9). Heterophils were the most common WBC type and were observed in all samples. Samples frequently failed to include monocytes (n = 14), eosinophils (n = 20), and basophils (n = 23); the modal value for each = 0.

Because WBC data did not fit a normal distribution (either as raw data or when transformed), we performed nonparametric analyses (Kruskal-Wallis or Kendall correlation) to assess the relationships between WBC data and planning area and BCI. No significant relationships occurred for any WBC counts with either planning area (Kruskal Wallis H $P > 0.21$ for each) or BCI ($|r| < 0.18$ for each). Hematocrit also did not vary with planning area ($F_{2,31} = 1.1$, $P = 0.3$) or BCI ($F_{1,32} = 0.06$, $P = 0.8$).

7.1.3 Ecological Relationships and Intraspecific Comparisons

7.1.3.1 Hematology of Adults and Chicks

Reference values from our study for PCV, counts of WBCs, and counts of each type of WBC were all within the reference intervals of previously published data for the species for adults and chicks (Ferguson et al. 2014, Fiorello 2019). In both adults and chicks, heterophils were the most common type of WBC, although in chicks the difference between heterophil and lymphocyte counts was less substantial. Fiorello (2019) notes that pelicans may be heterophilic and our data appear to support that observation. Within chicks we found no difference in any WBC count or PCV by planning area or BCI. A negative relationship between monocyte counts in adults and BCI is consistent with an increase in monocyte activity with infection or stress, both of which are likely to increase with lower BCI. Caution should be applied when comparing WBC data among planning areas for adults as all values were well within normal ranges.

7.1.3.2 Ecological Relationships in Adults

Two previously published data sets present measures of blood analytes in adult brown pelicans (Wolf et al. 1985, Zaias et al. 2000). Wolf et al. (1985) included captive birds from sub-adult to adult. Zaias et al. (2000) included captive, healthy, but flightless pelicans in a rehabilitation center and wild caught birds during the non-breeding season (presumably from the Atlantic coast of South Florida). Zaias et al. (2000) found no differences between captive and wild individuals, or between sub-adults and adults, for any analytes. Neither data set provided reference levels, presenting values as means ± SE. Compared to these data, we identify five analytes for which our mean values appeared to differ from those reported in Wolf et al. (1985) and Zaias et al. (2000). AST appeared lower by ~ 50% in our sample, but the means reported in the other two studies were within the upper end of our reference intervals. Our measures of ALT, albumin, A1G, and A2G all appeared lower by ~ 50% and mean values from the aforementioned studies did not occur within our reference intervals, suggesting a substantial difference. Lower levels of ALT and albumin in our sample may be indicative of nutritional or physiological stress relative to captive birds or those during the nonbreeding season when foraging effort is less demanding (Dean et al. 2017, Fiorello 2019). Higher values of A1G and A2G in the aforementioned studies may be indicative of infection or parasitism, particularly in captive birds (Ferguson et al. 2014).

7.1.3.2.1 Effects of Sex in Adults

Differences in blood analytes are not uncommon between sexes (e.g., Maness et al. 2017). During this study, sex appeared as a variable in a top-performing model for 17 analytes but in only seven cases did the relationship between sex and the analyte concentration appear to be ecologically relevant. The differences we observed in analytes between males and females appear to be consistent with requirements of egg-laying and with body condition. For example, lower levels of calcium and cholesterols in females compared to males in our study may indicate sex-specific deficits from egg formation and egg laying (Nisbet 1997, Bauch et al. 2010). Lower levels of lipase and cholesterols, and higher levels of BUN, uric acid, and BUN:CRE can all be indicative of dehydration and nutritional stress (Alonso-Alvarez et al. 2007, Fiorello 2019). In our study, males had higher BCI compared to females, and we also found lower levels of lipase and cholesterols, and higher levels of BUN, uric acid, and BUN:CRE in females than in males. Uric acid and BUN:CRE were also negatively related to BCI across both sexes in our study, further supporting the contention that these differences may be indicative of overall condition at the time of sampling.

7.1.3.2.2 Effects of Body Condition Index in Adults

BCI is used as a relative and coarse descriptor of the condition of an individual based on its body mass and body size. Because body mass can fluctuate substantially within an individual over short periods of time (e.g., due to recent feeding), caution should be applied when applying and interpreting BCIs. Within our data set BCI did not differ by planning area, suggesting that the condition of the adults we sampled, although variable, was not related to any region-wide conditions in the Northern GOM. Males did have higher BCI compared to females. A sex-based difference in BCI is not uncommon during early breeding due to the physiological stress experienced by females from egg-laying (Kalmbach et al. 2004). During this study, BCI appeared as a variable in a top-performing model for 15 analytes. For adult pelicans in the Northern GOM, 20% of the analytes measured were substantially influenced by BCI. The positive relationship that we observed between BCI and potassium indicates that pelicans in better condition likely had higher levels of electrolytes and hence were less likely to be nutritionally stressed. We also observed negative relationships between BCI and BUN:CRE, creatinine, and uric acid. These three analytes often indicate dehydration and kidney function (Fiorello 2019). A negative relationship of each with BCI would therefore be consistent with individuals presenting with lower body mass (i.e., lower total body water).

7.1.3.2.3 Effects of Planning Area in Adults

We collected our data from colonies across three planning areas of BOEM that represented different levels of oil and gas activity (eastern = least activity, central = most activity, western = intermediate activity). These areas can be considered as surrogates for exposure to oil and associated chemicals based on the level of infrastructure within each planning area. Other sources of petrochemicals may, however, exist. Such sources include but are not limited to pipelines, shipping lanes, and industrial ports and refineries (see 2.4 and 4.2). Therefore, a strong signature of certain analytes to planning area may indicate exposure to oil and gas activity and a weaker signature may suggest that exposure to toxins is more regionally widespread or not only linked to oil and gas activity. Planning area can also serve as a surrogate for many other factors that may be undefined or highly variable within the study set. For example, in our sample we found that home range size differed among planning areas, and data from other aspects of this study demonstrate that diet can differ among planning areas as well (Chapters 4 and 6). Planning area effects can be further confounded because samples were collected from different planning areas in different years. Therefore, it would be prudent to use caution when seeking to interpret differences or a lack of differences in analytes among planning areas.

Within each grouping of blood analytes (electrolytes, enzymes, metabolites, and plasma proteins), greater than 50% of the individual analytes showed some relationship with planning area. The most consistent pattern we observed was for plasma metabolites to be higher in the eastern planning area compared to the central and/or western planning areas. Lower levels of plasma metabolites can indicate nutritional stress and/or oiling (Alonso-Alvarez et al. 2007, Ibañez et al. 2015, Dean et al. 2017). In our study area, exposure to oil from oil and gas activity would be expected to be higher in the central and western planning areas, and as such would be consistent with these results. While it is difficult to assess the levels of nutritional stress among planning areas, the fact that we did not observe a difference in BCI by planning area suggests consistency in nutrition across the study area. We did, however, find that in this data set the size of home ranges was smaller in the eastern planning area compared to the central and western planning areas. Home range size is often inversely related to food availability and, in seabirds, to colony size (see Chapter 3). Therefore, lower levels of plasma metabolites might be expected in areas with larger home range sizes, which is consistent with our results. Lower levels of total proteins and creatinine (metabolites) are also indicative of nutritional or physiological stress (Alonso-Alvarez et al. 2007, Fiorello 2019). During our study, each were lower in the central and western planning areas compared to the eastern planning area, consistent with the patterns we observed in plasma proteins.

Potential mechanisms underlying the higher levels of enzyme activity in birds from the eastern planning area are not clear. Higher levels of AST, ALT, and CPK are often noted as being indicative of muscle damage, hepatic damage, and/or oil exposure (Fiorello 2019, Alonso-Alvarez et al. 2007). The smaller home ranges of birds in the eastern planning area are inconsistent with high levels of exercise (flight) and possibly subsequent muscle damage. Inherently lower levels of exposure to oil and gas activity would also appear inconsistent with high enzyme levels. We did, however, find that blood samples of birds in the eastern planning area were more likely to increase in the concentration of parent PAHs and alkylated PAHs compared to birds in the central planning area (see section 8.3). Such elevations in PAHs may therefore explain the higher levels of enzyme activity in the eastern planning area. Nonetheless, Harr (2002) notes that while these enzymes are sensitive to the stressors, they are not specific and therefore caution should be applied when interpreting patterns in these enzymes.

7.1.3.2.4 Effects of Home Range in Adults

Data comparing home range sizes to blood profiles in birds appear to be lacking in the published literature. In our samples, home ranges are measured following the collection of the blood sample over a period of days to months. In contrast, the blood samples reference the time-period before blood sampling over a period of days to weeks, Therefore, attempts to relate home range size to blood analyte levels assume that the two can be linked despite the difference in the temporal frame of reference.
In our samples, three of five metabolites appeared to be related to the size of the home range (BUN, creatinine, and uric acid). For each analyte, the relationship with home range size was negative. Higher levels of creatinine are common with increased energetic reserves and nutritional condition, and therefore would be consistent with smaller home ranges if smaller home ranges are indicative of higher food quantity/quality near the breeding site. High levels of uric acid and BUN are typically associated with nutritional stress or dehydration and are therefore inconsistent with other patterns we observed (e.g., increased creatinine with smaller home ranges).

We also observed higher levels of enzyme activity with smaller home range sizes. Higher enzyme values are indicative of muscle damage among other issues, so they might signal increased effort, but this would appear to be inconsistent with a smaller home range size. The higher levels of enzyme activity we observed with smaller home ranges may also be confounded with other factors. For example, hemolysis can result in enzyme activity appearing higher in a sample. Coincidentally, we found that the home range size of pelicans from which blood samples were characterized as hemolyzed (48.4 ± 57.1 km^2) appeared lower compared to those that were not characterized as hemolyzed (116.7 ± 172.3 km^2). It is possible, therefore, that the pattern we observed in enzyme activity was not ecologically based but instead may have been an artifact of sample condition. Such a finding also would be consistent with higher enzyme levels in birds from the eastern planning area, where home ranges were smaller than those in the central or western planning areas s.

One possible explanation for the observed increase in enzyme activity and metabolites with smaller home range sizes may be that active flight styles (e.g., flapping flight) comprise a higher proportion of flight within smaller home ranges compared to larger home ranges. For example, larger home ranges may require more commuting flight which can include less active flight styles such as soaring. A second explanation for the observed increase in enzyme activity and metabolites with smaller home range sizes may be that the driver of the relationship has been misidentified. For example, individuals experiencing muscle damage or other physiological stress would be expected to present with high enzyme activity and high levels of certain metabolites such as BUN and uric acid. Individuals in poor condition might also have smaller foraging ranges due to their reduced condition. Therefore, it may be that home range does

not drive the pattern in the blood analytes but rather that the blood analytes drive the reduced size of the home range. Because of the confounding nature of the data herein with respect to home range size, the lack of studies explicitly designed to examine the relationship between home range size and blood analytes, and the potential temporal mismatch between blood samples and home range size, a study designed to specifically assess this relationship appears warranted.

7.1.3.3 Ecological Relationships in Chicks

The most relevant data set for a comparison to ours appears in Ferguson et al. (2014) and includes similar data from brown pelican chicks sampled at colonies in South Carolina. Most of the analytes common to both studies were similar in magnitude and range, with means from each study occurring well within the reference intervals from the other study. Three exceptions occurred. HDLc values from the Gulf were above the reference interval for the South Carolina sample. CO_2 and VLDLc values from the Gulf were each below the reference interval provided for the South Carolina samples. Lipids and cholesterol (e.g., VLDLc and HDLc) are highly sensitive to current nutritional state and therefore may reflect time since feeding or food type, and therefore the opposing patterns in VLDLc and HDLc should not be over-interpreted. For example, we found no correlation in the measures of HDLc and VLDLc in either chicks or adults during our study. Furthermore, the level of amylase from the Gulf samples was at the extreme upper end of the reference interval of the sample from South Carolina. A lack of detailed studies on the role of amylase in birds (Fiorello 2019) makes an interpretation of this comparison challenging, but the disparate data from these two samples suggests that the analyte should be measured in future studies to establish a more robust reference interval for the species. The difference in CO_2 between the two studies is also not clear. CO_2 is an indicator of respiratory function. One hypothesis to consider is that chicks in the Gulf are exposed to higher levels of airborne toxins from oil and gas activity compared to the South Carolina coast, and this may impair CO_2 levels. Our data also showed reduced CO_2 levels in chicks from the western GOM compared to the eastern GOM (BCI also was higher in the eastern gulf compared to the western GOM), a pattern that would be consistent with this hypothesis. We did not, however, observe differences in CO_2 levels in adults among planning areas.

Only two variables were considered for the assessment of blood analytes for chicks, planning area and BCI. BCI differed by planning area, with BCI being least in the western planning area. This result is consistent with a similar analysis of a larger sample from our study (see Chapter 5) and is attributed to higher levels of nutritional stress in the western planning area. Caution should be applied, however, when comparing the results of analyses suggesting that both planning area and BCI are strong predictors of a blood analyte because the two explanatory variables are related to each other. Although planning area appeared as a top model for 17 analytes and BCI as a top model for 12 analytes, the null model appeared most frequently as a top model (n = 21 analytes) suggesting that in many cases there were no strong patterns of influence of BCI or planning area, or that measurable levels of influence were slight.

7.1.3.3.1 Effects of Body Condition Index in Chicks

Only one electrolyte, potassium, was related to BCI. The negative relationship we observed is consistent with electrolyte levels decreasing with nutritional status and hydration. Two enzymes, AST and CPK, showed a negative relationship with BCI while one (amylase) showed a positive relationship. CPK increases with stress (Maceda-Veiga et al. 2015) and therefore higher levels of CPK would be consistent with poorer BCI. AST increases with hepatic and muscular damage as well as with inflammation, and therefore higher levels of AST would be consistent with poorer BCI. A lack of detailed studies on the role of amylase in birds (Fiorello 2019) makes an interpretation of its negative relationship with BCI challenging, although the pattern appears to be consistent with the difference observed in amylase by planning area (i.e., amylase highest in the eastern planning area where BCI was highest).

The negative relationship we observed between triglycerides and BCI is challenging to interpret. Triglycerides typically decline with poor nutrition; however, levels of triglycerides can also increase with hepatic damage or soon after nutritional stress ensues (Alonso-Alvarez and Ferrer 2001). Therefore, the negative relationship we observed between BCI and triglycerides may suggest the onset of nutritional stress for the chicks in this sample. The positive but relatively weak relationship we observed between BCI and VLDLc suggests that energy stores increase as BCI increases. Similarly, lower levels of A1G (a plasma protein) in relation to BCI are also consistent with nutritional stress (Alanso-Alvarez et al. 2007). Last, higher levels of CORT are indicative of stress, and stress is negatively correlated with BCI in pelican chicks (see Chapter 5).

7.1.3.3.2 Effects of Planning Area in Chicks

We observed some patterns that suggest chicks in the west and/or central planning area were in poorer condition compared to those in the east. Two of three electrolytes, calcium and sodium, were highest in the eastern planning area and each tends to decline with nutritional stress or dehydration (Maceda-Veiga et al. 2015). Lower levels of glucose (metabolite) in the western planning area suggest poorer nutrition there compared to the east and central planning areas, and the highest levels of BUN (metabolite) in the west also suggest dehydration which is consistent with lower BCIs (Fiorello 2019). We also observed patterns in plasma proteins that support a regional pattern in BCIs. Albumin was lowest in the western planning area, gamma globulin and A1G were both least in the central planning area, and A1G was lower in the western compared to the eastern planning area. These patterns are also consistent with a gradient of BCIs across the planning areas. The patterns in enzymes are more difficult to interpret. Four enzymes appeared to differ among planning areas, but the pattern was inconsistent. ALT, AST, and amylase were all lowest in the central planning area, although the coefficient estimate for AST was weak and for ALT the null model held the most weight. Enzymes also can represent reactions to capture and therefore could also be depressed in the central planning area if capture efforts there were for some reason less stressful to chicks. Ultimately, enzyme levels represent short-term reactions and therefore differences may be difficult to relate to larger scale variables such as planning area.

7.2 Polycyclic Aromatic Hydrocarbons

7.2.1 PAHs in Adult Blood

There was no correlation between home range size (either the 50% core area or the 95% use area) and BCI ($r < -0.18$ for each) within adults sampled for PAH in blood. We also failed to detect any relationships among home range size (either the 50% core area or the 95% use area) and sex or planning area, and between BCI and sex or planning area ($P > 0.11$ for all) within adults sampled for PAH in blood.

7.2.1.1 PAH Profiles in Adult Blood

We analyzed blood for PAHs from 33 adult pelicans. The occurrence and concentrations of each PAH are summarized in Table 7.10 and reported as wet weight (ng g^{-1}). The most frequently occurring PAHs were of intermediate molecular weight (Figure 7.10). The PAH with the highest concentration detected was Fluorene (165.4 and 161.1 ng g^{-1}; both birds from Audubon Island, Florida). We failed to detect two alkylated compounds and eight parent compounds out of the full test set. The two most frequently detected PAHs, 1,3-dimethylnaphthalene and 2,3,5-trimethylnaphthalene, also had the widest range in measured concentrations (~ 80 ng g^{-1} - ~ 128 ng g^{-1}; Table 7.10).

Of the 24 PAHs assessed, 14 were detected in at least one individual (Table 7.10). Alkylated PAHs were detected in 48% of individuals and parent PAHs were detected in 30% of individuals. Three alkylated compounds were each detected in > 10% of individuals; 2,6-dimethyl naphthalene (n = 4), 1,3-dimethylnaphthalene (n = 5), and 2,3,5-trimethylnaphthalene (n = 6).

Of 33 birds sampled, 21 (63.6%) had at least 1 PAH detected (Table 7.11; 1 PAH: n = 10; 2 PAHs: n = 10; 4 PAHs: n = 1). Parent compounds were detected in 10 of 33 birds, alkylated compounds were detected in 16 of 33 birds, and both parent and alkylated PAHs were detected in 5 of 33 birds. The proportion of birds sampled with detectable limits of PAHs in blood was 50% in the central planning area, 63% in the western planning area, and 80% in the eastern planning area (Table 7.11). PAHs were detected in 75% of females sampled and in 57% of males sampled (Table 7.11). The occurrence of each PAH detected in blood is summarized by planning area and sex in Table 7.12.

Among birds with detectable limits of PAHs, the sum of all PAHs ranged from 42.44 - 463.75 ng g^{-1}, the sum of alkylated PAHs ranged from 58.46 - 220.51 ng g^{-1}, and the sum of parent PAHs ranged from 42.44 - 245.47 ng g^{-1} (Figure 7.11a). There was no significant difference in the concentration of parent compared to alkylated PAHs using either the full data set or using only data from birds above detectable limits (Wilcoxon rank sum test P > 0.13 for each; Figure 7.11b). When all individuals were considered, there was no correlation between summed concentrations of alkylated and parent PAHs (Kendall tau r = -0.05, Pearson r = -0.09). Similarly, when only individuals with detectable limits of PAHs were considered, there was no correlation between summed concentrations of alkylated and parent PAHs (Pearson r = 0.25). The individual with the highest concentration of summed parent PAHs (245.47 ng g^{-1}) did, however, present with the 2nd highest level of alkylated PAHs (218.28 ng g^{-1}; female, Audubon Island, Florida).

7.2.1.2 Total PAHs (Parent PAHs + Alkylated PAHs) in Adult Blood

Five models for the presence of sumPAH in pelican blood received support, and these included each of the main variables we assessed except planning area (Table 7.13a). There was little separation among these five models, with the most supported model only carrying an AICc weight = 0.21. The only variable that appeared to have a measurable relationship with sumPAH was sex (coefficient estimate = -1.12 ± 0.95). Females were 3.1 times more likely to be detected with a PAH compared to males although there was substantial variability around the estimate (90% CI for odds ratio = 0.7, 16.7).

The concentration of sumPAH in pelican blood was best described by a single model that included sex and home range size (Table 7.13b). There was substantial separation among the first and second ranked model, with the most supported model carrying 90% of the AICc weight. There was a strong relationship between sumPAH concentrations and sex (coefficient estimate = -0.73 ± 0.23) and a weak negative relationship between sumPAH concentrations and home range size which was strongly leveraged by a single individual and therefore discounted (coefficient estimate = -0.00022 ± 0.000099). The odds of the sumPAH concentration increasing by 1 ng g^{-1} increased by 2.1 times for females compared to males (90% CI for odds ratio = 1.4, 3.0).

7.2.1.3 Parent PAHs in Adult Blood

Three models for the presence of sumPAR in pelican blood received support, and these included home range, sex, and BCI (Table 7.13c). There was little separation among these three models, with the most supported model only carrying an AICc weight = 0.28. Sex was weakly associated with sumPAR (coefficient estimate = -0.94 ± 0.89). Females were approximately 2.5 times more likely to be detected with a PAR compared to males, although there was substantial variability around the estimate (90% CI

for odds ratio = 0.6, 11.1). Coefficient estimates for home range size and BCI had standard errors that overlapped zero indicating no relationship.

Four models for the concentration of sumPAR in pelican blood received support, and these included each of the main variables we assessed (Table 7.13d). There was little separation among these four models, with the most supported model only carrying an AICc weight = 0.38. The only variable with a measurable, yet weak, effect on sumPAR was planning area. Coefficient estimates indicated that the concentrations of sumPAR were lower in the central compared to the eastern planning area (coefficient estimate = -0.70 ± 0.41; Figure 7.12a). The odds of the sumPAR concentration increasing by 1 ng g^{-1} increase by 2.0 times for birds in the eastern compared to the central planning area, although there was substantial variability around the estimate (90% CI for odds ratio = 1.0, 4.0).

7.2.1.4 Alkylated PAHs in Adult Blood

Two models for the presence of sumALK in pelican blood received support, and these included the variables sex and home range (Table 7.13e). There was little separation among these two models, with the most supported model being 1.5x as likely to be the best model compared to the second-ranked model. Sex had a measurable relationship with sumALK (coefficient estimate = -1.45 ± 0.91). Females were 4.3 times more likely to be detected with an ALK compared to males, although there was substantial variability around the estimate (90% CI for odds ratio = 1.1, 25.0).

Only the full model for the concentration of sumALK in pelican blood, which included each main variable and carried an AICc weight = 0.86, received support (Table 7.13f). Coefficient estimates indicated that the concentrations of ALK were likely to decrease in the central compared to the eastern planning area (coefficient estimate = -0.36 ± 0.24; Figure 7.12b), decrease in males compared to females (coefficient estimate = -0.67 ± 0.21), decrease with an increase in BCI (coefficient estimate = -0.0011 ± 0.0004), and decrease with an increase home range size (coefficient estimate = -0.00019 ± 0.00011). The odds of the sumALK concentration increasing by 1 ng g^{-1} increase by 1.4 times for birds in the eastern compared to the central planning area (90% CI for odds ratio = 1.0, 2.2), and increase by 1.9 times for females compared to males (90% CI for odds ratio = 1.4, 2.8). The odds of a change in sumALK for BCI and home range do not differ from 1.0 even when each independent variable is scaled up one order of magnitude.

7.2.2 PAHs in Adult Feathers

There was no correlation between home range size (either the 50% core area or the 95% use area) and BCI ($r < 0.11$ for each). We also failed to detect any relationships among home range size (either the 50% core area or the 95% use area) and sex or planning area ($P > 0.39$ for each). BCI was moderately related to sex ($t_{77} = 1.68$, $P = 0.10$; BCI males > BCI females). BCI was lower in the central planning area compared to the western planning area ($t_{76} = -2.2$, $P = 0.03$). Home range size was related to migration class ($t_{63} < -4.6$, $P < 0.0001$ for each).

7.2.2.1 PAH Profiles in Adult Feathers

We analyzed feathers for PAHs from 92 adult pelicans. The occurrence and concentrations of each PAH are summarized in Table 7.14 and reported as dry weight (ng g^{-1}). The most frequently occurring PAHs were of intermediate molecular weight (Figure 7.13). The PAHs with the highest concentrations detected were 1,3-dimethylnaphthalene (256.2 and 221.8 ng g^{-1}; both birds from Felicity Island, Louisiana) and 2-methyl naphthalene (229.0 ng g^{-1}; Shamrock Island, Texas).

All of the alkylated compounds were detected in ≥ 2 birds while nine parent compounds were not detected. 1,3-dimethylnaphthalene, the most frequently detected PAH, also had the widest range in measured concentration (~ 72 ng g^{-1} - ~ 256 ng g^{-1}; Table 7.14). Of the 24 PAHs assessed, 15 were detected in at least one individual. Alkylated PAHs were detected in 46% of individuals and parent PAHs were detected in 26% of individuals. Three alkylated compounds were detected in > 10% of individuals (2,6-dimethyl naphthalene (n = 10), 1,3-dimethylnaphthalene (n = 11), and 2,3,5-trimethylnaphthalene (n = 10).

Of 92 birds sampled, 56 (60.8%) had at least 1 PAH detected (Table 7.15) (1 PAH: n = 39; 2 PAHs: n = 13; 3 PAHs: n = 2; 4 and 6 PAHs: n = 1). Parent compounds were detected in 24 of 92 birds, alkylated compounds were detected in 42 of 92 birds, and both parent and alkylated PAHs were detected in 10 of 92 birds (Table PAH blood 2). The proportion of birds sampled with detectable levels of PAHs in feathers was 45% in the central planning area, 16% in the western planning area, and 17% in the eastern planning area (Table 7.15). PAHs were detected in 67% of females sampled and in 55% of males sampled. The occurrence of each PAH in feathers is summarized by planning area and sex in Table 7.16.

7.2.2.2 Total PAHs (Parent PAHs + Alkylated PAHs) in Adult Feathers

Among birds with detectable limits of PAHs, the sum of all PAHs ranged from 60.20–623.80, the sum of alkylated PAHs ranged from 71.50–479.00, and the sum of parent PAHs ranged from 32.40–166.70 (Figure 7.14a). The sum of alkylated PAHs was greater than the sum of parent PAHs for both the full data set (W = 3135.5, p-value = 0.0004) and data from birds above detectable limits (W = 235.5, p-value = 0.0003; Figure 7.14b). When all individuals were considered, there was no correlation between summed concentrations of alkylated and parent PAHs (Kendall tau r = -0.06, Pearson r = -0.03). When only individuals with detectable limits of PAHs were considered, there was a moderate positive correlation between summed concentrations of alkylated and parent PAHs (Pearson r = 0.57).

One model for the presence of sumPAH in pelican feathers received support, and it included BCI and migration class (Table 7.17a). The migration class “long distance” was set as the reference level. This 2-variable model carried 63% of the AIC weight and was 3x as likely to be the best model compared to the second ranked model (which was a single variable model for migration class). Both BCI (coefficient estimate = -0.002 ± 0.001) and migration class (coefficient estimates: medium -1.58 ± 0.77, short -1.38 ± 0.76) appeared to have a measurable relationship with sumPAH. The odds of a bird having a PAH increased 1.002 times (90% CI for odds ratio = 1.0006, 1.004) for every unit decrease in BCI (i.e., 1.2 times for every 100 unit decrease in BCI). The odds of a bird having a PAH decreased 4.8 times for medium v. long distance migrants (90% CI for odds ratio = 1.4, 20.0) and decreased 4.0 times for short v. long distance migrants (90% CI for odds ratio = 1.2, 16.7).

One model for the concentration of sumPAH in pelican feathers received support, and it included BCI and migration class (Table 7.17b). Although the best-performing model carried 94% of the AIC weight, neither BCI nor migration class had a measurable effect on the concentration of sumPAH (i.e., SE > coefficient estimate).

7.2.2.3 Parent PAHs in Adult Feathers

Three models for the presence of sumPAR in pelican feathers received support (Table 7.17c). The top ranked model carried 31% of the AIC weight and was 1.2 times as likely to be the best model compared to the second ranked model. Home range size appeared to have a measurable relationship with sumPAR (coefficient estimate = 0.00081 ± 0.0003). The odds of a bird having a PAR increased 1.0008 times (90% CI for odds ratio = 1.0004, 1.001) for every 1 km^2 (0.62 mi^2) increase in home range size (i.e., 1.08 times for every 100 km^2 unit increase in home range). There was a marginal increase in the odds of a bird

having a PAR for females compared to males (2.4 times, 90% CI for odds ratio = 0.8, 7.1). The odds of a bird having a PAR decreased 4.3 times for medium compared to long distance migrants (90% CI for odds ratio = 1.4, 20.0). The odds of a bird having a PAR increased 4.4 times for birds in the central compared to the eastern planning area (90% CI for odds ratio = 1.3, 15.9).

One model for the concentration of sumPAR in pelican feathers received support, and it included migration class and BCI (Table 7.17d). This two-variable model carried 70% of the AIC weight and was 4.4x as likely to be the best model compared to the second ranked model which was > 2 AIC points removed. Only migration class (coefficient estimates: medium -0.31 ± 0.21, short -0.39 ± 0.15) had a measurable relationship with sumPAR (Figure 7.15). The odds of the sumPAR concentration increasing by 1 ng g^{-1} increased by 1.4 times for birds in the long-distance compared to medium-distance migrant class (90% CI for odds ratio = 0.9, 2.0) while the odds of the sumPAR concentration increasing by 1 ng g^{-1} increased by 1.5 times for birds in the long-distance compared to short-distance migrant class (90% CI for odds ratio = 1.1, 1.9).

7.2.2.4 Alkylated PAHs in Adult Feathers

Two models for the presence of sumALK received support, and both included migration class (Table 7.17e). The first-ranked model carried 68% of the model weights. This top ranked model included migration class and BCI and was 2.6 times as likely to be the best model compared to the second ranked model which included only migration class. BCI was negatively related to the presence of sumALK (coefficient estimate = -0.0014 ± 0.0009). The odds of a bird having an ALK increased 1.001 times (90% CI for odds ratio = 1.0002, 1.003) for every 1 unit decrease in BCI (i.e., 1.15 times for every 100 unit decrease in BCI). Migration class did not have a measurable effect on sumALK.

The concentration of sumALK in pelican feathers was represented by one model that included variables for migration class and planning area (Table 7.17f). The best performing model carried 74% of the AIC weight and was 5.7 times as likely to be the best model compared to the second ranked model. Neither variable, however, had a measurable effect on the concentration of sumALK.

7.2.3 PAHs in Chick Feathers

BCI of chicks differed among planning area ($F_{2,32}$ = 10.3, P = 0.0003) and was highest in the central planning area (502.3 ± 614.9), intermediate in the eastern planning area (204.4 ± 434.2), and lowest in the western planning area (-530.8 ± 584.5).

7.2.3.1 PAH Profiles in Chick Feathers

We analyzed feathers for PAHs from 35 pelican chicks. The occurrence and concentrations of each PAH are summarized in Table 7.18 and reported as wet weight (ng g^{-1}). The most frequently occurring PAHs were of intermediate molecular weight (Figure 7.16). The PAH with the highest concentration detected was 2,6-dimethyl naphthalene (250.0 ng g^{-1}; Galveston Bay).

All of the alkylated compounds were detected in ≥ 1 bird while 13 parent compounds were not detected. 2,6-dimethyl naphthalene, one of two most frequently detected PAH, also had the widest range in measured concentration (~ 50 ng g^{-1} - ~ 250 ng g^{-1}; Table 7.18).

Of the 24 PAHs assessed, 11 were detected in at least one individual (Table 7.18). Alkylated PAHs were detected in 34% of individuals and parent PAHs were detected in 9% of individuals. Two alkylated compounds were each detected in > 10% of individuals; 2,6-dimethyl naphthalene (n = 4) and 2,3,5-trimethylnaphthalene (n = 4).

Of 35 birds sampled, 13 (37.1%) had at least 1 PAH detected (Table 7.19) (1 PAH n = 8; 2 PAHs n = 5). Parent compounds were detected in 3 of 35 birds, alkylated compounds were detected in 12 of 35 birds, and both parent and alkylated PAHs were detected in 2 of 35 birds (Table PAH feathers 2). The proportion of birds sampled with detectable limits of PAHs in feathers was 80% in the central planning area, 25% in the western planning area, and 40% in the eastern planning area (Table 7.19). The occurrence of each PAH in blood is summarized by region in Table 7.20.

7.2.3.2 Total PAHs (Parent PAHs + Alkylated PAHs) in Chick Feathers

Among birds with detectable levels of PAHs, the sum of all PAHs ranged from 100.5–309.6, the sum of alkylated PAHs ranged from 50.3–265.3, and the sum of parent PAHs ranged from 57.9–193.5 (Figure 7.17a). The sum of alkylated PAHs was not significantly different from the sum of parent PAHs when using the full data set (W = 458, P = 0.01) and did not differ when only birds above detectable limits were examined (W = 21.0, P = 0.7; Figure 7.17b). When all individuals are considered, there was no correlation between summed concentrations of alkylated and parent PAHs (Kendall tau r = 0.13, Pearson r = 0.05). Sample sizes were insufficient (n = 3 birds) to assess the correlation between alkylated and parent PAHs when only individuals with detectable limits of PAHs were considered.

Two models for the presence of sumPAH in chick feathers received support. The top ranked model included planning area and the null model also was supported (Table 7.21a) The planning area model carried 54% of the AIC weight and was 1.9 times as likely to be the best model compared to the second ranked model. Birds in the central planning area were 6 times as likely to have a PAH compared to birds in the eastern planning area (coefficient estimates = 1.79 ± 1.29) although the variability on the estimate was wide (90% CI for odds ratio = 0.9, 75.9).

All three models received support for the concentration of sumPAH in chick feathers (Table 7.21b). The model including planning area carried 41% of the AIC weight and was 1.1 times as likely to be the best model compared to the null model which ranked second. Planning area (coefficient estimates: central = -0.59 ± 0.29, western = -0.36 ± 0.27) had a measurable relationship with sumPAH. Birds in the eastern planning area were 1.8 times (90% CI for odds ratio = 1.1, 2.9) more likely to have elevated sumPAH concentrations with respect to birds in the central planning area and birds in the eastern planning area were 1.4 times (90% CI for odds ratio = 0.9, 2.3) more likely to have elevated sumPAH concentrations with respect to birds in the western planning area.

7.2.3.3 Parent PAHs in Chick Feathers

Only three birds had detectable levels of sumPAR. Although the model including BCI received support for the presence of sumPAR, it ranked second to the null model which was 2.6 times as likely to be the best model (Table 7.21c). The SE on the estimate of BCI was superior to the coefficient estimate, indicating no measurable relationship. A hurdle model was not conducted for sumPAR due to insufficient sample size.

7.2.3.4 Alkylated PAHs in Chick Feathers

Only one model supported the presence of sumALK in chick feathers. The top ranked model included planning area (Table 7.21d). The planning area model carried 70% of the AIC weight and was 3.5 times

as likely to be the best model compared to the null model which ranked second. Birds in the central planning area were 6 times more likely (90% CI for odds ratio = 0.9, 75.9) to have a PAH compared to birds in the eastern planning area (coefficient estimate = 1.79 ± 1.29) while birds in the eastern planning area were 2.6 times more likely (90% CI for odds ratio = 0.7, 11.1) to have a PAH compared to birds in the western planning area (coefficient estimates = -0.98 ± 0.85).

Although the model including BCI received support for the concentration of sumALK, it ranked second to the null model which was 1.9 times as likely to be the best model (Table 7.21e).

7.2.4 Ecological relationships

7.2.4.1 PAHs in Adult Blood

7.2.4.1.1 PAH Profiles in Adult Blood

PAHs in blood likely derive from consumption of contaminated prey or ingestion of preen oil, although bioaccumulation through food webs is thought to be low (Paruk et al. 2014, Paruk et al. 2016, Acampora et al. 2018). Furthermore, blood samples provide a recent assessment of exposure and represent substances currently circulating within an individual (Paruk et al. 2014, Paruk et al. 2016). The most commonly occurring PAHs and the PAHs with the highest summed concentration included 2,3,5-trimethylnaphthalene, 1,3-dimethylnaphthalene, and 2,6-dimethyl naphthalene. Analysis for 2,6-dimethyl naphthalene was recommended following the DWH oil spill due to developments in sourcing of PAHs from the spill (Seegar et al. 2015). The two highest within-individual concentrations and the highest average concentration were for fluorene. The two individuals from which these samples were taken were both nesting adults on Audubon Island, Florida, with home ranges centered in and proximate to bays surrounding Panama City, Florida. Within adult blood samples, alkylated PAHs were detected in 48% of individuals and parent PAHs were detected in 30% of individuals. Alkylated PAHs are more abundant in crude oil, more persistent, and less prone to metabolization compared to parent PAHs (Seegar et al. 2015). Alkylated PAHs also were more common in blood samples of common loons (*Gavia immer*) wintering in the Northern GOM compared to parent PAHs (Paruk et al. 2014, Paruk et al. 2016). Liu et al. (2012) found that alkylated PAHs had a stronger signature in DWH crude oil, weathered oil, and oil mousse compared to parent PAHs. The sum of both parent and alkylated PAHs in blood appears to be higher in the brown pelicans we sampled compared to blood samples collected from migratory common loons (2011–2013) and migratory tundra peregrine falcons (*Falco peregrinus tundrius*; 2011), the two data sets that currently appear to be the most comparable to ours. Similarly, the maximum individual values for blood samples from brown pelicans also appear to be an order of magnitude higher than for blood samples collected from migratory common loons and migratory tundra peregrine falcons.

7.2.4.1.2 Effects of Sex on PAHs in Adult Blood

The presence or absence of PAHs in adult blood samples was most frequently predicted by sex. On average, females were roughly three times more likely to have either type of PAH compared to males, although this relationship varied from strong (sumALK) to moderate (sumPAH and sumPAR) and the confidence interval on each estimate was wide. We also assessed which variables best predicted an increase in PAH concentrations among individuals with PAH greater than zero. For both sumPAH and sumALK, sex was likely to be related to an increase in concentration. Given that blood reflects a relatively recent signature, our results suggest that females are being exposed to PAHs more frequently or perhaps more recently than males during incubation and early chick-rearing. A dimorphic result based on sex could occur through differential resource selection by males and females, in terms of habitat occupied and/or prey consumption (Seegar et al. 2015). Sex is not a predictor for either the presence or

concentration levels of PAHs in feathers of adults, further suggesting that the sex-effect observed in blood samples may be indicative of recent exposure.

7.2.4.1.3 Effects of Planning Area on PAHs in Adult Blood

Planning area was never a strong predictor of the presence of PAHs in pelican blood, and only moderately appeared to affect the level of PAHs in those individuals identified with PAHs. A slight increase in levels of sumPAR in the eastern planning area was driven by two individuals from Florida, each with a high level of fluorene. Similarly, the three highest levels of sumALK occurred in birds nesting in Florida. Caution needs to be applied to interpreting these results as sample sizes are small. Nonetheless, even a conservative interpretation suggests that the levels of PAHs in pelican blood are not driven by differences in oil and gas activity among planning areas.

7.2.4.2 PAH in Adult Feathers

7.2.4.2.1 PAH Profiles in Adult Feathers

The profile of PAHs in adult feathers was similar to the profile of PAHs in adult blood. For example, alkylated PAHs were detected in 46% of feather samples (48% in adult blood) and parent PAHs were detected in 26% of feather samples (30% in adult blood). The most commonly occurring PAHs and the PAHs with the highest summed concentrations included 2,3,5-trimethylnaphthalene, 1,3-dimethylnaphthalene, and 2,6-dimethyl naphthalene. 1,3-dimethylnaphthalene and 2-methyl naphthalene were found in the highest individual concentrations from birds nesting in Louisiana and Texas, respectively. PAHs detected from feathers may provide a different spatial, temporal, or source signature compared to PAHs detected in blood or other fluids that turnover relatively quickly (Jaspers et al. 2004, Acampora et al. 2018). For example, sources of PAHs in feathers may include blood supply (during feather growth), contact with the external environment, or contact with contaminated preen oil (Jaspers et al. 2004, Acampora et al. 2018). Feather samples may thus provide an assessment of local and/or transboundary contamination in migratory species with a longer temporal signature compared to blood (Acampora et al. 2018). The higher frequency of alkylated PAHs in feathers suggests a petrogenic source. Alkylated PAHs are more abundant in crude oil, more persistent, and less prone to metabolization compared to parent PAHs (Seegar et al. 2015). Comparisons of PAH levels in feathers of adult pelicans to other studies of PAH levels in feathers of free-ranging birds from this region are, to the best of our knowledge, unavailable at this time.

7.2.4.2.2 Effects of Migration Class on PAHs in Adult Feathers

The presence or absence of PAHs in adult feathers was predicted most often by migration class. Three of the six model steps showed that longer distance migrants were more likely to be found with a PAH (sumPAH and sumPAR) and that the level of PAHs was likely to increase in that group (sumPAR). Given that feathers represent a longer-term signature of PAHs compared to blood, our results suggest that birds that migrate longer distances may experience increased exposure to PAHs away from the colony (Acampora et al. 2018). Most long-distance migrants in our study departed the Northern GOM and occupied wintering areas in the southern GulfGOM southwestern GOM, or Cuba. However, an assessment of molting locations may also be warranted to better understand PAH levels. Many individuals also attended distinct molting sites separate from both their breeding and wintering areas, and approximately 75% of birds in our sample occupied ranges in the Louisiana Delta during the post-breeding period. An investigation into potential sources of parent PAHs in molting and wintering areas may be warranted but likely would include combustion processes (which could be quite varied) as opposed to exposure to crude oil.

7.2.4.2.3 Effects of Body Condition Index on PAHs in Adult Feathers

The presence or absence of PAHs in adult feathers was also partially explained by BCI. Individuals in poorer body condition were more likely to be found with a PAH, and it was more likely that the PAH was from the alkylated group. BCI represents a current measure of condition and therefore caution should be applied when interpreting these results given their potential temporal mismatch with PAHs on feathers and the frequency with which BCI appeared as an influential variable among the model sets (i.e., only 2 of 6 model sets). Nonetheless, our data suggest that individuals with high levels of PAHs over time may experience reduced physical condition.

7.2.4.2.4 Effect of Other Independent Variables on PAHs in Adult Feathers

Three of the independent variables we assessed (home range, planning area, sex) did not frequently or reliably predict PAH presence or concentrations in adult feathers. Because home range reflects activity of individuals post-sampling, and feathers represent the pre-sample time period, the lack of a pattern is not surprising. The lack of a relationship between feather PAHs and planning area also suggests that the levels of PAHs in pelican feathers is driven by a complex set of factors that cannot be distilled solely to the planning area within which the colony occurs. The lack of a sex effect suggests that males and females may not experience different levels of contact exposure to these specific PAHs. Other pollutants, however, may still present a differential risk to males and females (see Chapter 5).

7.2.4.3 PAH in Chick Feathers

7.2.4.3.1 PAH Profiles in Chick Feathers

Chick feathers likely represent contact transfer of PAHs from adults, deposition from aerial sediments, or contact with PAHs in ground/nesting material or prey. Alkylated PAHs were detected in 34% of samples and parent PAHs were detected in 9% of samples. Alkylated PAHs are more abundant in crude oil, more persistent, and less prone to metabolization compared to parent PAHs (Seegar et al. 2015). The most commonly occurring PAHs were 2,3,5-trimethylnaphthalene, 1,3-dimethylnaphthalene, and 2,6-dimethyl naphthalene, the same common PAHs found in adult feathers. 2,6-dimethyl naphthalene and pyrene were found in the highest individual concentrations from birds nesting in Louisiana and Texas, respectively. Two of the three highest concentrations of PAHs in chick feathers were recorded from Galveston Bay, Texas, and the third from a colony on the Florida Panhandle. The ratio of alkylated to parent PAHs also appeared to be higher in chick feathers compared to adult blood or adult feathers, suggesting that PAHs in chick feathers may reflect a petrogenic source of PAHs. A petrogenic source may be more likely if contamination occurs from contact with recently foraging parents. Further, we posit that the location from which feathers are sampled may reflect different sources of contact, e.g., scapular feathers contacting adults and chest feathers contacting nesting material. We are not aware, however, of any efforts to analyze data to assess this hypothesis.

7.2.4.3.2 Effects of Body Condition Index on PAHs in Chick Feathers

BCI was not a predictor of PAH levels in chick feathers. Planning area irregularly and weakly predicted PAH levels in feathers of chicks. The presence of PAHs, and particularly sumALK, was more likely in the central planning area. Alkylated PAHs tend to be associated with petrogenic sources (Seegar et al. 2015, Paruk et al. 214) in the Northern GOM and the central planning area has a higher concentration of oil and gas activity compared to the western and eastern planning areas. Because of relative infrequency of PAHs in chick feathers, however, caution should be applied when interpreting these results. Comparable data sets assessing PAH loads in chicks are, to the best of our knowledge, not available for other nearshore seabirds within the region. Given that the route of contamination for PAHs on chick feathers is not entirely clear, we suggest that additional assessments be considered to determine if short- or long-term changes may occur in PAH loads dependent upon chick age or parental activity such as provisioning or brooding (i.e., activities that may enhance contact with chicks).

Table 7.1. Statistical Values for Mass and Serum Chemistry for Adult Brown Pelicans Sampled from Breeding Colonies in the Northern GOM, 2013–2014

Analyte (units)	n	Mean	Median	SD	Min	Max	Reference Interval	Lower 90% CI	Upper 90% CI
Sodium (mEq L^{-1})	72	205.9	250.0	54.5	111	250	116.8–250.0	111.0–130.0	250.0–250.0
Potassium (mEq L^{-1}) *^	72	3.95	3.65	1.79	1.2	10.9	1.37–9.66	1.20–1.65	6.42–10.90
CO_2 (mEq L^{-1})	73	16.2	16.0	3.5	9	24	9.0–24.0	9.0–10.7	22.2–24.0
Calcium (mg dL^{-1}) ^	72	8.30	8.55	1.54	4.5	13.1	4.83–11.20	4.50–5.64	10.09–13.10
Phosphorus (mg dL^{-1}) ^	71	4.98	4.70	1.63	2.5	12.6	2.74–9.88	2.50–3.18	7.00–12.60
Glucose (mg dL^{-1})	73	204.8	210.0	43.4	25	307	98.1–293.4	25.0–145.8	264.9–307.0
Blood urea nitrogen (mg dL^{-1})	73	4.3	3.0	3.9	1	18	1.0–16.3	1.0–1.0	13.2–18.0
Creatinine (mg dL^{-1}) ^	71	0.7	0.7	0.3	0.2	1.9	0.28–1.42	0.20–0.38	1.20–1.90
Blood urea nitrogen:Creatinine ratio^	68	6.0	5.0	4.32	1.7	23.3	1.70–19.46	1.70–1.92	13.38–23.30
Amylase (U L^{-1})	72	1166.2	1171.0	145.2	760	1637	801.3–1553.7	760.0–942.0	1377.4–1637.0
Lipase (U L^{-1}) ^	73	23.8	19.0	16.1	1	74	3.6–62.9	1.0–5.0	55.8–74.0
Cholesterol (mg dL^{-1})	73	151.9	153.0	31.7	80	252	86.8–223.1	80.0–103.4	199.4–252.0
Triglycerides (mg dL^{-1}) ^	72	57.4	49.0	29.2	27	142	28.7–140.4	27.0–30.0	134.4–142.0
High density lipoprotein cholesterol (mg dL^{-1})	72	83.5	84.5	15.1	50	111	52.5–110.2	50.0–58.0	104.0–111.0
Low density lipoprotein cholesterol (mg dL^{-1}) *^	72	11.4	10.0	5.8	5	28	5.8–28.0	5.0–6.0	27.0–28.0
Uric acid (mg dL^{-1}) ^	72	12.15	9.55	7.81	0.7	32.6	2.19–32.19	0.70–3.27	27.73–32.60
Total protein (g dL^{-1})	74	4.34	4.20	0.90	2.4	6.7	2.93–6.26	2.40–3.19	5.90–6.70
Aspartate aminotransferase (U L^{-1}) ^	72	175.9	163.5	57.1	71	380	93.3–371.8	71.0–109.0	265.9–380.0
Alanine aminotransferase (U L^{-1}) *	70	28.5	28.5	7.3	12	44	12.0–43.2	12.0–15.9	39.1–44.0
Lactate dehydrogenase (U L^{-1})	72	4674.3	4592.5	1403.3	1764	7960	1953.8–7521.1	1764.0–2632.8	7218.1–7960.0
Creatine phosphokinase (U L^{-1})	72	964.4	942.0	442.5	48	1854	143.7–1737.7	48.0–256.3	1617.3–1854.0
Gamma-glutamyl transferase (U L^{-1})	72	10.2	7.0	6.9	5	34	5.0–32.4	5.0–5.0	24.9–34.0
Albumin:Globulin ratio	74	0.57	0.55	0.18	0.21	1.01	0.27–1.01	0.21–0.32	0.90–1.01

Analyte (units)	n	Mean	Median	SD	Min	Max	Reference Interval	Lower 90% CI	Upper 90% CI
Pre-albumin (mg dL^{-1})	74	0.25	0.25	0.07	0.09	0.42	0.12–0.40	0.09–0.15	0.36–0.42
Albumin (mg dL^{-1})	74	1.24	1.24	0.21	0.78	1.67	0.79–1.66	0.78–0.93	1.59–1.67
Alpha-1 globulin (mg dL^{-1})	74	0.14	0.13	0.03	0.09	0.27	0.09–0.23	0.09–0.09	0.18–0.27
Alpha-2 globulin (mg dL^{-1})	74	0.68	0.64	0.16	0.40	1.18	0.43–1.11	0.40–0.49	1.00–1.18
Beta globulin (mg dL^{-1}) ^	74	1.18	1.10	0.37	0.47	2.24	0.61–2.22	0.47–0.74	1.84–2.24
Gamma globulin (mg dL^{-1}) ^	74	0.85	0.70	0.50	0.24	2.13	0.24–2.02	0.24–0.32	1.79–2.13
CORT (mg dL^{-1}) *	73	36.13	35.80	13.86	11.9	78.0	12.41–65.08	11.90–15.77	59.61–78.00

* outlier(s) removed

^required box-cox transformation

Sample size (n), mean, median, standard deviation (SD), minimum (Min), and maximum (Max) values with reference intervals and 90% confidence intervals (CI) of reference limits.

Table 7.2. Number of Blood Samples and Blood Smears Collected from Adult and Chick Brown Pelican Chicks in the Northern GOM, 2013–2015

State and Colony	Adult CBC			Adult WBC counts			Chick CBC	Chick WBC counts
	Female	Male	Unknown	Female	Male	Unknown	Unknown	Unknown
Florida								
Audubon Island	4	7	0	4	7	3	5	5
Smith Island	3	8	3	3	8	3	-	-
Ten Palms Island	-	-	-	-	-	-	5	5
Alabama								
Gaillard Island	-	-	-	-	-	-	5	5
Louisiana								
Felicity Island	4	4	1	5	5	1	-	-
Raccoon Island	2	5	0	4	6	6	-	-
Texas								
Chester	4	5	3	7	5	3	5	5
Galveston Bay	-	-	-	-	-	-	10	10
Shamrock	8	11	2	9	11	3	5	5

Blood samples were used for complete blood counts (CBC) and blood smears for white blood cell counts (WBC). Actual number of samples for CBC and WBC varied by analyte because not all samples resulted in a successful or complete CBC or WBC. Sex for adults (Female, Male, or Unknown) was determined post-capture from collected blood and therefore sex could not be balanced throughout the sampling effort.

Table 7.3. Summary of Model Selection Results Assessing Relationships between Blood Analytes of Adult Brown Pelicans Breeding in the Northern GOM and Four Independent Variables, 2013–2014

Analyte	Category	Sex	BCI	Planning area	HR50	HR50 + sex	BCI + planning area	HR50 + BCI	Null
Carbon dioxide	Blood gas				1	2		3	
Calcium	Electrolytes & minerals				3	1	2		
Potassium	Electrolytes & minerals						1		
Phosphorous	Electrolytes & minerals				1	2			
Sodium*	Electrolytes & minerals								
Alanine aminotransferase	Enzyme		1		2	4	3	5	
Amylase	Enzyme				1				
Aspartate aminotransferase	Enzyme			1					2
Creatine phosphokinase	Enzyme				1	2	3		
Gamma-glutamyl transferase	Enzyme		2		1				
Lactate dehydrogenase	Enzyme				1			2	
Lipase	Enzyme					1	2		
High density lipoprotein cholesterol	Lipids					1			
Triglycerides	Lipids	1							2
Low density lipoprotein cholesterol	Lipids	2		3					1
Blood urea nitrogen	Metabolite					1			
Cholesterol	Metabolite					1			
Creatinine	Metabolite						1	2	
Glucose	Metabolite				1	2			
Ratio BUN:CRE	Metabolite-Ratio		2			1			
Total protein	Metabolite						1		
Uric acid	Metabolite					1		2	
Albumin	Plasma protein			1					2
Alpha 1 globulin	Plasma protein	3		2					1
Alpha 2 globulin	Plasma protein								1
Beta globulin	Plasma protein						1		
Gamma globulin	Plasma protein						1		
Pre-albumin	Plasma protein								1
Ratio Albumin:Globulin	Plasma protein			1					

Analyte	Category	Sex	BCI	Planning area	HR50	HR50 + sex	BCI + planning area	HR50 + BCI	Null
CORT	Stress hormone				1	2			
Count of analytes for which model was ranked highly		3	3	5	10	13	10	5	7

*see section 2.7 for details of analysis process for sodium

Body condition index and 50% kernel home range size (HR50) are continuous variables and are defined in the methods. Sex and planning area (East = Florida, Central = Alabama and Louisiana, West = Texas) are categorical variables with Female and East as the reference levels, respectively. Null = null model with only an intercept term. Cell values indicate the rank of that model for a given blood analyte. Only rankings for models with AIC values ≤ 2.0 are shown.

Table 7.4. Summary of Coefficient Estimates from Model Selection Process Assessing Relationships between Blood Analytes of Adult Brown Pelicans Breeding in the Northern GOM and Four Independent Variables, 2013–2014

Analyte	Group	Body condition index	50% home range	Sex	Planning area
Calcium*	Electrolytes & minerals			1.50 ± 0.82	W = -2.30 ± 0.91 C = -1.50 ± 1.07
Potassium	Electrolytes & minerals	0.16 ± 0.09			W = 0.59 ± 0.20 C = 0.25 ± 0.23
Sodium	Electrolytes & minerals				W = -71.8 ± 13.2 C = -33.7 ± 15.6
Alanine aminotransferase	Enzyme				W = -3.87 ± 2.12
Aspartate aminotransferase*	Enzyme				C = $-1.4x10^4 \pm 6.3x10^5$
Creatine phosphokinase	Enzyme		-115.9 ± 54.7		W = -317.0 ± 123.4 C = -326.2 ± 145.6
Lactate dehydrogenase	Enzyme		-279.4 ± 165.6		
Lipase*	Enzyme		-0.38 ± 0.20	0.96 ± 0.41	W = -1.02 ± 0.44 C = -2.07 ± 0.53
High density lipoprotein cholesterol	Lipids		3.33 ± 1.80	11.23 ± 3.67	
Blood urea nitrogen	Metabolite		-1.25 ± 0.45	-2.51 ± 0.91	
Cholesterol	Metabolite			16.9 ± 8.2	
Creatinine*	Metabolite	-0.09 ± 0.04	-0.12 ± 0.04		W = -0.30 ± 0.10 C = -0.34 ± 0.12
Total protein	Metabolite				W = -0.88 ± 0.22 C = -1.05 ± 0.26
Uric acid*	Metabolite	-0.34 ± 0.15	-0.62 ± 0.15	-0.79 ± 0.30	
Ratio BUN:CRE*	Metabolite-Ratio	-0.27 ± 0.12		-0.64 ± 0.23	
Albumin	Plasma protein				W = -0.11 ± 0.06
Alpha 1 globulin	Plasma protein				C = -0.02 ± 0.01
Beta globulin*	Plasma protein				W = -0.26 ± 0.07 C = -0.32 ± 0.08
Gamma globulin*	Plasma protein				W = -0.60 ± 0.16 C = -0.74 ± 0.19

Analyte	Group	Body condition index	50% home range	Sex	Planning area
Ratio ALB:Globulin	Plasma protein				W = 0.10 ± 0.04 C = 0.20 ± 0.05

Body condition index and 50% kernel home range size are continuous variables and are defined in the methods. Sex and planning area (West = Texas, Central = Louisiana, East = Florida) are categorical variables with Female and East as the reference levels, respectively. Only coefficients where the SE < coefficient estimate (i.e., an ecological relationship between the analyte and the independent variable is more likely) are reported. Analytes marked with * were transformed before analysis and coefficient estimates are presented on the transformed scale. No interactions of the independent variables returned coefficients likely to be ecologically relevant (i.e., SE > mean in all cases).

Table 7.5. Statistical Values for Packed Cell Volume (PCV, Averaged over 3 Readings) and Leukocyte Profiles for Adult Brown Pelicans Sampled from Breeding Colonies in the Northern GOM, 2013–2014

Analyte	n	Mean	Median	SD	Min	Max	Reference Interval	Lower	Upper
PCV average *	73	45.4	46.0	4.3	30	54.0	32.1–54.0	30.0–39.0	52.1–54.0
White blood cell count *	82	11.5	11.0	4.9	3	27.0	5.0–25.0	3.0–5.1	21.0–27.0
Heterophil (10^3/ml) *	82	8.1	7.7	3.2	1	15.0	1.9–14.7	1.0–3.6	13.3–15.0
Lymphocytes (10^3/ml) *	82	2.9	2.2	2.6	0.3	12.7	0.5–12.3	0.3–0.8	8.6–12.7
Monocyte(10^3/ml)	84	0.3	0.2	0.3	0	1.6	0.0–1.3	0.0–0.0	0.9–1.6
Eosinophil(10^3/ml)	84	0.16	0.09	0.2	0	1.1	0.0–1.0	0.0–0.0	0.7–1.1
Basophil(10^3/ml)	84	0.05	0.0	0.1	0	0.6	0.0–0.5	0.0–0.0	0.3–0.6

* outlier(s) removed

Sample size (n), mean, median, standard deviation (SD), minimum (Min), and maximum (Max) values with reference intervals and 90% confidence intervals of reference limits.

Table 7.6. Statistical Values for Mass and Serum Chemistry for Chicks of Brown Pelicans Sampled from Breeding Colonies in the Northern GOM, 2013–2015

Analyte (units)	n	Mean	Median	SD	Min	Max	Reference Interval	Lower 90% CI	Upper 90% CI
Sodium (mEq L^{-1})	34	146.5	147.0	4.7	136	157	136.3–155.7	133.6–139.5	15378–157.7
Potassium (mEq L^{-1}) *^	34	3.52	3.45	0.62	2.4	5.3	2.44–5.00	2.25–2.70	4.57–5.56
CO2 (mEq L^{-1})	34	15.4	16.0	3.0	9	19	6.0–20.2	7.7–10.1	19.3–21.0
Calcium (mg dL^{-1}) ^	34	10.75	10.75	0.79	8.9	12.1	8.95–12.44	8.50–9.48	11.92–12.54
Phosphorus (mg dL^{-1}) ^	34	7.21	7.05	1.22	5.4	10.4	5.19–10.14	4.93–5.57	9.19–11.27
Glucose (mg dL^{-1})	34	182.4	182.0	30.3	100	248	119.7–244.3	104.3–137.3	225.7–260.7
Blood urea nitrogen (mg dL^{-1})	33	3.2	3.0	1.0	1	6	1.00–5.33	0.6–1.6	4.7–5.9
Creatinine (mg dL^{-1}) ^	34	0.48	0.40	0.20	0.1	0.9	0.15–1.00	0.11–0.22	0.81–1.15
Blood urea nitrogen:Creatinine ratio ^	31	7.05	6.70	2.54	2.5	13.3	2.45–12.82	1.88–3.40	11.26–14.29
Amylase (U L^{-1})	34	1293.0	1268.0	209.2	919	1756	826.0–1694.6	720.7–922.3	1555.9–1839.5
Lipase (U L^{-1}) ^	34	27.6	28.0	8.8	13	61	13.9–50.0	11.4–16.9	41.7–59.2
Cholesterol (mg dL^{-1})	34	203.1	201.5	35.2	140	284	139.3–283.6	129.3–154.1	260.9–309.3
Triglycerides (mg dL^{-1}) ^	34	99.3	95.5	37.3	42	177	27.2–180.9	14.7–42.0	159.3–203.2
High density lipoprotein cholesterol (mg dL^{-1})	34	80.7	77.5	13.8	57	110	54.8–112.1	50.9–60.5	103.4–120.4
Low density lipoprotein cholesterol (mg dL^{-1}) *^	34	19.8	19.0	7.5	8	35	5.8–36.7	3.4–8.6	32.1–41.5
Uric acid (mg dL^{-1}) ^	34	15.77	14.90	8.24	5.4	46	4.67–38.71	3.65–6.65	31.16–48.90

Analyte (units)	n	Mean	Median	SD	Min	Max	Reference Interval	Lower 90% CI	Upper 90% CI
Total protein (g dL^{-1})	34	4.23	4.20	0.56	3.3	5.6	3.26–5.57	3.13–3.47	5.15–6.01
Aspartate aminotransferase (U L^{-1}) ^	34	167.5	149.0	57.6	97	339	92.4–332.2	85.6–101.3	262.7–423.2
Alanine aminotransferase (U L^{-1}) *	34	31.0	30.0	8.3	19.0	51.0	17.8–51.8	16.1–20.3	45.5–59.3
Lactate dehydrogenase (U L^{-1})	34	5629.3	5455.5	1623.7	801	9663	2076.9–8793.2	1079.7–3170.6	7747.4–9696.5
Creatine phosphokinase (U L^{-1})	33	1308.7	1357.0	261.0	466	1687	631.1–1727.2	219.7–885.3	1641.3–1793.8
Gamma-glutamyl transferase (U L^{-1})	32	7.3	7.0	1.6	5	10	4.27–11.12	3.9–4.9	10.2–11.8
Albumin:Globulin ratio	34	0.76	0.79	0.14	0.43	1.06	0.44–1.03	0.36–0.55	0.98–1.09
Pre-albumin (mg dL^{-1})	34	0.27	0.25	0.06	0.18	0.39	0.16–0.42	0.14–0.18	0.38–0.47
Albumin (mg dL-1)	34	1.53	1.54	0.21	0.98	1.92	1.04–1.90	0.87–1.20	1.82–1.97
Alpha-1 globulin (mg dL-1)	34	0.13	0.12	0.03	0.09	0.18	0.08–0.20	0.07–0.09	0.18–0.23
Alpha-2 globulin (mg dL-1)	34	0.73	0.73	0.16	0.47	1.27	0.48–1.15	0.44–0.54	1.01–1.31
Beta globulin (mg dL-1) ^	34	0.98	0.96	0.15	0.76	1.26	0.70–1.33	0.66–0.75	1.24–1.43
Gamma globulin (mg dL-1) ^	34	0.58	0.51	0.18	0.34	1.02	0.33–1.08	0.31–0.37	0.88–1.32
CORT (mg dL-1) *	34	57.31	57.45	22.80	16.6	128.2	7.99–101.9	0.01–21.14	87.37–115.8

* outlier(s) removed
^ required box-cox transformation
Sample size (n), mean, median, standard deviation (SD), minimum (Min), and maximum (Max) values with reference intervals and 90% confidence intervals (CI) of reference limits. Untransformed robust values reported when available, otherwise untransformed standard data reported.

Table 7.7. Summary of Model Selection Results Assessing Relationships between Blood Analytes of Brown Pelican Chicks in the Northern GOM and Two Independent Variables, 2013–2015

Analyte	Category	Planning area	BCI	Null
Carbon dioxide	Blood gas	1		2
Calcium	Electrolytes & minerals	1		
Potassium	Electrolytes & minerals		2	1
Phosphorous	Electrolytes & minerals			1
Sodium	Electrolytes & minerals	1		2
Alanine aminotransferase	Enzyme	1		1
Amylase	Enzyme	3	1	2
Aspartate aminotransferase	Enzyme	1	2	
Creatine phosphokinase	Enzyme		1	2
Gamma-glutamyl transferase	Enzyme		2	1
Lactate dehydrogenase	Enzyme	1		
Lipase	Enzyme		2	1
High density lipoprotein cholesterol	Lipids	2	1	3
Triglycerides	Lipids		2	1
Very low density lipoprotein cholesterol	Lipids		2	1
Blood urea nitrogen (BUN)	Metabolite	2		1
Cholesterol	Metabolite		2	1
Creatinine	Metabolite	1		2
Glucose	Metabolite	1		
Ratio BUN/Creatinine	Metabolite-Ratio	1		
Total protein	Metabolite			1
Uric acid	Metabolite			1
Albumin	Plasma protein			
Alpha 1 globulin	Plasma protein	3	2	1
Alpha 2 globulin	Plasma protein	1		2
Beta globulin	Plasma protein			1
Gamma globulin	Plasma protein	1		2
Pre-albumin	Plasma protein	1		
Ratio Albumin/Globulin	Plasma protein	1		

Analyte	Category	Planning area	BCI	Null
CORT	Stress hormone		1	
Count of analytes for which model was ranked highly		17	12	21

BCI is a continuous variable and is defined in the methods. Planning area is a categorical variable (East = reference level and includes Florida, Central includes Alabama and Louisiana, and West includes Texas). Null = null model with only an intercept term. Cell values indicate the rank of that model for a given blood analyte. Only rankings for models with AIC values ≤ 2.0 are shown.

Table 7.8. Summary of Coefficient Estimates from Model Selection Process Assessing Relationships between Blood Analytes of Brown Pelican Chicks in the Northern GOM and Two Independent Variables, 2013–2014

Analyte	Group	Body condition index	Central planning area	Western planning area
Carbon dioxide*	Blood gas		0.3 ± 1.7	-2.4 ± 1.1
Calcium	Electrolytes & minerals			-0.83 ± 0.27
Potassium	Electrolytes & minerals	$-3.0 \times 10^{-4} \pm 2.0 \times 10^{-4}$		
Sodium	Electrolytes & minerals		-5.0 ± 2.6	-3.3 ± 1.7
Alanine aminotransferase	Enzyme		-9.5 ± 4.6	
Amylase	Enzyme	0.11 ± 0.06	-212.8 ± 119.3	-140.7 ± 78.1
Aspartate aminotransferase	Enzyme	-0.032 ± 0.017	-49.8 ± 31.6	25.5 ± 20.7
Creatine phosphokinase	Enzyme	-0.12 ± 0.07		
Lactate dehydrogenase	Enzyme			1672.7 ± 548.5
Triglycerides	Lipids	$-8.0 \times 10^{-3} \pm 4.0 \times 10^{-3}$		
Low density lipoprotein cholesterol	Lipids	$3.0 \times 10^{-3} \pm 2.0 \times 10^{-3}$		
Blood urea nitrogen	Metabolite			0.62 ± 0.40
Creatinine	Metabolite		0.25 ± 0.11	
Glucose	Metabolite			-36.9 ± 9.5
Ratio BUN:CRE	Metabolite-Ratio		-1.79 ± 0.85	0.60 ± 0.58
Albumin	Plasma protein			-0.14 ± 0.08

Analyte	Group	Body condition index	Central planning area	Western planning area
Alpha 1 globulin*	Plasma protein	2.5x10-4 ± 1.8x10-4	-0.56 ± 0.35	-0.35 ± 0.23
Gamma globulin*	Plasma protein		-0.49 ± 0.25	
Ratio Albumin:Globulin	Plasma protein			0.08 ± 0.02
CORT	Stress hormone	-0.019 ± 0.006		

BCI is a continuous variable and is defined in the methods. Planning area (West = Texas, Central = Louisiana and Alabama, East = Florida) is a categorical variable with east as the reference level. Only coefficients where the SE < coefficient estimate (i.e., an ecological relationship between the analyte and the independent variable is more likely) are reported. Analytes marked with * were transformed before analysis and coefficient estimates are presented on the transformed scale. No interactions of the independent variables returned coefficients likely to be ecologically relevant (i.e., SE > mean in all cases).

Table 7.9. Statistical Values for Packed Cell Volume (PCV, Averaged over 3 Readings) and Leukocyte Profiles for Chicks of Brown Pelicans Sampled from Breeding Colonies in the Northern GOM, 2013–2015

Analyte	n	Mean	Median	SD	Min	Max	Reference Interval	Lower	Upper
PCV average *	34	40.5	40.0	4.8	30	48.7	30.3–50.2	28.1–32.7	47.7–52.6
White blood cell count *	35	22.1	17.0	16.1	5.0	71.0	6.5–84.1	5.6–7.9	48.7–139.9
Heterophil (10^3/ml) *	35	11.9	8.6	9.6	2.3	46.2	3.07–48.9	2.6–3.8	27.1–88.2
Lymphocytes (10^3/ml) *	35	9.5	6.3	7.3	2.7	34.1	2.7–47.7	2.3–3.2	23.3–115.9
Monocyte(10^3/ml)	35	0.3	0.1	0.7	0	3.7	0.0–1.7	0.0	0.7–2.7
Eosinophil(10^3/ml)	35	0.2	0.0	0.4	0	1.6	0.0–1.1	0.0	0.5–1.4
Basophil(10^3/ml)	35	0.1	0.0	0.3	0	1.3	0.0–0.7	0.0	0.4–1.0

* outlier(s) removed

Sample size (n), mean, median, standard deviation (SD), minimum (min), and maximum (Max) values with reference intervals and 90% confidence intervals of reference limits.

Table 7.10. Frequency of Detection of Individual PAHs from Blood of Adult Brown Pelicans Breeding in the Northern GOM, 2013–2014

	Number birds > detection limit	Number birds < detection limit	Measured values [ng/g wet weight] (% total PAH burden)
Alkylated Compounds			
2-methyl naphthalene	3	30	[80.7] [86.0] [86.3] **Σ252.9 (8.2%)**
2,6-dimethyl naphthalene	4	29	[79.3] [84.4] [92.9] [98.1] **Σ354.7 (11.5%)**
1,3-dimethylnaphthalene	5	28	[82.8] [86.8] [122.4] [125.3] [128.1] **Σ545.2 (17.7%)**
1,5-dimethylnaphthalene	0	33	-
2,3,5-trimethylnaphthalene	6	27	[81.4] [84.4] [86.2] [90.2] [90.5] [127.6] **Σ560.3 (18.2%)**
1-methylfluorene	0	33	-
3-methylphenanthrene	1	32	[78.0] **Σ78.0 (2.5%)**
9-methylphenanthrene	2	30	[58.5] [61.9] **Σ120.4 (3.9%)**
Parent Compounds			
Naphthalene	2	31	[83.9] [102.2] **Σ186.1 (6.1%)**
Acenaphthalene	0	33	-
Acenapthene	2	31	[102.2] [108.5] **Σ210.7 (6.8%)**
Fluorene	2	31	[161.1] [165.4] **Σ326.6 (10.6%)**
Phenanthrene	1	32	[48.9] **Σ48.9 (1.6%)**
Anthracene	3	29	[73.9] [80.5] [84.3] **Σ238.7 (7.8%)**
Fluoranthene	1	32	[42.4] **Σ42.4 (1.4%)**
Pyrene	1	32	[50.0] **Σ50.0 (1.6%)**
Benzo(a)anthracene	1	32	[57.8] **Σ57.8 (1.9%)**
Chrysene	0	33	-
benzo(b)fluoranthene	0	33	-
Benzo(k)fluoranthene	0	33	-
benzo(a)pyrene	0	33	-
Indeno(1,2,3-cd)pyrene	0	33	-
Dibenz(a,h)anthracene	0	33	-
Benzo(g,h,i)perylene	0	33	-

(n = 33)

Table 7.11. Frequency of Cccurrence of Parent and Alkylated PAHs by Planning Area and Sex from Blood of Adult Brown Pelicans Breeding in the Northern GOM, 2013–2014.

Category	Number birds sampled	Number of birds ≥ 1 parent *or* alkylated PAH	Number of birds ≥ 1 parent *and* alkylated PAH	Number of birds with parent PAHs	Number of birds with alkylated PAHs
Planning area					
East	10	8	1	4	5
Central	12	6	2	2	6
West	11	7	2	4	5
Total	33	21	5	10	16
Sex					
Female	12	8	4	5	8
Male	21	12	1	5	8
Total	33	20	5	10	16

Table 7.12. Frequency of Occurrence of Individual PAHs by Planning Area and Sex from Blood of Adult Brown Pelicans Breeding in the Northern GOM, 2013–2014

	Number birds ≥ detectable limit	East (n = 10)	Central (n =12)	West (n = 11)	Female	Male
Alkylated Compounds						
2-methyl naphthalene	3	0	2	1		3
2,6-dimethyl naphthalene	4	2	2	1	2	2
1,3-dimethylnaphthalene	5	2	2	1	2	3
1,5-dimethylnaphthalene	0					
2,3,5-trimethylnaphthalene	6	2	2	2	6	
1-methylfluorene	0					
3-methylphenanthrene	1			1	1	
9-methylphenanthrene	2	1	1		1	1
Parent Compounds						
Naphthalene	2			2	2	
Acenaphthalene	0					
Acenapthene	2	1	1			2
Fluorene	2	2			1	1
Phenanthrene	1		1		1	
Anthracene	3	1		2	2	1
Fluoranthene	1	1				1
Pyrene	1			1		1
Benzo(a)anthracene	1	1				1
Chrysene	0					
Benzo(b)fluoranthene	0					
Benzo(k)fluoranthene	0					
Benzo(a)pyrene	0					
Indeno(1,2,3-cd)pyrene	0					
Dibenz(a,h)anthracene	0					
Benzo(g,h,i)perylene	0					

(n = 33)

Table 7.13.a–f. Model Results from Logistic and Gamma Regressions Assessing the Relationships between PAHs Detected in Blood of Adult Brown Pelicans Breeding in the Northern GOM and a Suite of Independent Variables, 2013–2014

K = number of parameters, AICc = Akaike Information Criteria, Delta AICc = difference in AIC values between indicated model and top ranked model. AICc weight = probability of model being the best model given the models tested and data analyzed. sumPAH = sum of all PAHs, sumPAR = sum of Parent PAHs, sumALK = sum of alkylated PAH.

(a) Logistic regression models for sumPAH (response variable = presence or absence of sumPAH; n = 33). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Home range	2	42.29		0.21
Sex + home range	3	42.97	0.49	0.17
Home range + BCI	3	43.62	1.13	0.12
BCI	2	43.78	1.29	0.11
Sex + BCI	3	44.11	1.62	0.09

(b) Gamma regression models for sumPAH (response variable = concentration of sumPAH; only individuals with sumPAH > 0 included in analyses, n = 21). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Sex + home range	3	203.67		0.90

(c) Logistic regression models for sumPAR (response variable = presence or absence of sumPAR; n = 33). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Home range	2	39.92		0.28
Sex + home range	3	40.80	0.89	0.45
Home range + BCI	3	41.89	1.97	0.10

(d) Gamma regression models for sumPAR (response variable = concentration of sumPAR; only individuals with sumPAR > 0 included in analyses, n = 10). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Home range	3	103.18		0.38
Planning area + home range	5	104.28	1.11	0.22
Home range + BCI	4	104.86	1.68	0.16
Sex + home range	4	104.94	1.76	0.16

(e) Logistic regression models for sumALK (response variable = presence or absence of sumALK; n = 33). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Sex + home range	3	43.15		0.35
Home range	2	43.89	0.74	0.24

(f) Gamma regression models for sumALK (response variable = concentration of sumALK; only individuals with sumALK > 0 included in analyses, n = 16). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Sex + home range + BCI + planning area	7	137.7		0.86

Table 7.14. Frequency of Detection of Individual PAHs from Feathers of Adult Brown Pelicans Breeding in the Northern GOM, 2013–2014

	Number birds > detection limit	Number birds < detection limit	Measured values (ng/g dry weight) (% total PAH burden)
Alkylated Compounds			
2-methyl naphthalene	6	86	[56.3] [108.9] [113.7] [118.6] [138.1] [229.0] **Σ764.6 (7.9%)**
2,6-dimethyl naphthalene	10	82	[71.5] [84.9] [98.5] [98.5] [126.9] [130.3] [144.3] [151.2] [152.7] [208.9] **Σ126.7 (13.1%)**
1,3-dimethylnaphthalene	11	81	[71.7] [77.6] [94.6] [128.9] [135.5] [146.1] [168.3] [188.3] [205.6] [221.8] [256.2] **Σ1694.6 (17.5%)**
1,5-dimethylnaphthalene	6	86	[84.0] [131.0] [132.4] [142.0] [184.0] [190.0] **Σ863.4 (8.9%)**
2,3,5-trimethylnaphthalene	10	82	[50.3] [52.7] [82.3] [82.8] [100.8] [103.2] [116.6] [129.1] [166.7] [183.1] **Σ1067.6 (11.0%)**
1-methylfluorene	7	85	[49.7] [74.5] [85.0] [92.5] [103.5] [105.3] [146.3] **Σ656.8 (6.8%)**
3-methylphenanthrene	2	90	[120.5] [181.5] **Σ302.0 (3.1%)**
9-methylphenanthrene	3	89	[124.4] [180.3] [261.8] **Σ566.5 (5.8%)**
Parent Compounds			
Naphthalene	4	88	[90.7] [95.1] [130.9] [132.2] **Σ448.9 (4.6%)**
Acenaphthalene	2	90	[101.3] [137.2] **Σ238.5 (2.5%)**
Acenapthene	3	89	[89.3] [121.3] [166.7] **Σ377.3 (3.9%)**
Fluorene	0	92	-
Phenanthrene	4	88	[32.4] [73.8] [84.3] [100.0] **Σ290.5 (3.0%)**
Anthracene	2	90	[63.2] [70.5] **Σ133.7 (1.4%)**
Fluoranthene	6	86	[60.2] [71.6] [75.5] [78.3] [106.4] [121.6] **Σ513.6 (5.3%)**
Pyrene	5	87	[55.8] [59.7] [98.8] [126.1] [160.5] **Σ500.9 (5.2%)**
Benzo(a)anthracene	0	92	-
Chrysene	0	92	-
Benzo(b)fluoranthene	0	92	-
Benzo(k)fluoranthene	0	92	-
Benzo(a)pyrene	0	92	-
Indeno(1,2,3-cd)pyrene	0	92	-
Dibenz(a,h)anthracene	0	92	-
Benzo(g,h,i)perylene	0	92	-

(n = 92)

Table 7.15. Frequency of Occurrence of Parent and Alkylated PAHs by State and Sex from Feathers of Adult Brown Pelicans Breeding in the Northern GOM, 2013–2014

Category	Number of birds sampled	Number of birds ≥ 1 parent or alkylated PAH	Number of birds ≥ 1 parent and alkylated PAH	Number of birds with parent PAHs	Number of birds with alkylated PAHs
Planning area					
East	25	16	2	5	16
Central	36	25	7	16	13
West	31	15	1	3	13
Total	92	56	10	24	42
Sex					
Female	43	29	3	14	18
Male	49	27	7	10	24
Total	92	56	10	24	42

Table 7.16. Frequency of Occurrence of Individual PAHs by Planning Area and Sex from Feathers of Adult Brown Pelicans Breeding in the Northern GOM, 2013–2014

	Number birds ≥ detectable limit	East (n = 10)	Central (n =12)	West (n = 11)	Female	Male
Alkylated Compounds						
2-methyl naphthalene	6	1	4	1	2	4
2,6-dimethyl naphthalene	10	6	2	2	3	7
1,3-dimethylnaphthalene	11	1	4	6	7	4
1,5-dimethylnaphthalene	6	2	4	0	1	5
2,3,5-trimethylnaphthalene	10	4	3	3	4	6
1-methylfluorene	7	1	2	4	2	5
3-methylphenanthrene	2	1	1	0	2	0
9-methylphenanthrene	3	1	2	0	2	1
Parent Compounds						
Naphthalene	4	4	0	0	3	1
Acenaphthalene	2	1	0	1	2	0
Acenapthene	3	3	0	0	1	2
Fluorene	0	0	0	0	0	0
Phenanthrene	4	2	2	0	2	2
Anthracene	2	2	0	0	1	1
Fluoranthene	6	3	2	1	2	4
Pyrene	5	4	0	1	3	2
Benzo(a)anthracene	0	0	0	0	0	0
Chrysene	0	0	0	0	0	0

	Number birds ≥ detectable limit	East (n = 10)	Central (n =12)	West (n = 11)	Female	Male
Benzo(b)fluoranthene	0	0	0	0	0	0
Benzo(k)fluoranthene	0	0	0	0	0	0
Benzo(a)pyrene	0	0	0	0	0	0
Indeno(1,2,3-cd)pyrene	0	0	0	0	0	0
Dibenz(a,h)anthracene	0	0	0	0	0	0
Benzo(g,h,i)perylene	0	0	0	0	0	0

(n = 92)

Table 7.17.a–f. Model Results from Logistic and Gamma Regressions Assessing the Relationships between PAHs Detected in Feathers of Adult Brown Pelicans Breeding in the Northern GOM and a Suite of Independent Variables, 2013–2014

K = number of parameters, AICc = Akaike Information Criteria, Delta AICc = difference in AIC values between indicated model and top ranked model. AICc weight = probability of model being the best model given the models tested and data analyzed. sumPAH = sum of all PAHs, sumPAR = sum of Parent PAHs, sumALK = sum of alkylated PAHs.

(a) Logistic regression models for sumPAH (response variable = presence or absence of sumPAH; n = 92). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
BCI + migration class	4	86.41		0.63

(b) Gamma regression models for sumPAH (response variable = concentration of sumPAH; only individuals with sumPAH > 0 included in analyses, n = 56). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
BCI + migration class	5	522.89		0.94

(c) Logistic regression models for sumPAR (response variable = presence or absence of sumPAR; n = 92). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Migration class + planning area	5	83.10		0.31
Migration class + planning area + sex	6	83.54	0.45	0.25
Home range	2	84.74	1.64	0.14

(d) Gamma regression models for sumPAR (response variable = concentration of sumPAR; only individuals with sumPAR > 0 included in analyses, n = 24). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
BCI + migration class	5	206.15		0.69

(e) Logistic regression models for sumALK (response variable = presence or absence of sumALK; n = 92). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
BCI + migration class	4	98.22		0.68
Migration class	3	100.12	1.90	0.26

(f) Gamma regression models for sumALK (response variable = concentration of sumALK; only individuals with sumALK > 0 included in analyses, n = 42). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Planning area + migration class	6	391.17		0.74

Table 7.18. Frequency of Detection of Individual PAHs from Feathers of Brown Pelican Chicks in the Northern GOM, 2014–2015.

	Number birds > detection limit	Number birds < detection limit	Measured values (ng/g dry weight) (% total PAH burden)
Alkylated Compounds			
2-methyl naphthalene	1	86	[69.0] **Σ69.0 (3.2%)**
2,6-dimethyl naphthalene	4	82	[50.3] [164.1] [178.4] [250.0] **Σ642.8 (30.2%)**
1,3-dimethylnaphthalene	2	81	[62.7] [116.1] **Σ178.8 (8.4%)**
1,5-dimethylnaphthalene	1	86	[140.7] **Σ140.7 (6.6%)**
2,3,5-trimethylnaphthalene	4	82	[69.0] [72.3] [101.6] [124.7] **Σ367.6 (17.3%)**
1-methylfluorene	1	85	[104.3] **Σ104.3 (4.9%)**
3-methylphenanthrene	1	90	[81.3] **Σ81.3 (3.8%)**
9-methylphenanthrene	1	89	[100.5] **Σ100.5 (4.7%)**
Parent Compounds			
Naphthalene	1	88	[186.9] **Σ186.9 (8.8%)**
Acenaphthalene	0	90	-
Acenapthene	0	89	-
Fluorene	0	92	-
Phenanthrene	1	88	[57.9] **Σ57.9 (2.7%)**
Anthracene	0	90	-
Fluoranthene	0	86	-
Pyrene	1	87	[193.5] **Σ193.5 (9.1%)**
Benzo(a)anthracene	0	92	-
Chrysene	0	92	-
Benzo(b)fluoranthene	0	92	-
Benzo(k)fluoranthene	0	92	-
Benzo(a)pyrene	0	92	-
Indeno(1,2,3-cd)pyrene	0	92	-
Dibenz(a,h)anthracene	0	92	-
Benzo(g,h,i)perylene	0	92	-

(n = 35)

Table 7.19. Frequency of Occurrence of Parent and Alkylated PAHs by Planning Area from Feathers of Brown Pelican Chicks in the Northern GOM, 2014–2015

Planning area	Number birds sampled	Number of birds ≥ 1 parent *or* alkylated PAH	Number of birds ≥ 1 parent *and* alkylated PAH	Number of birds with parent PAHs	Number of birds with alkylated PAHs
East	10	4	1	1	4
Central	5	4	0	0	4
West	20	5	1	2	4
Total	35	13	2	3	12

(n = 35)

Table 7.20. Frequency of Occurrence of Individual PAHs by Planning Area from Feathers of Brown Pelican Chicks in the Northern GOM, 2014–2015

	Number birds ≥ detectable limit	East (n = 10)	Central (n = 5)	West (n = 20)
Alkylated Compounds				
2-methyl naphthalene	1	1		
2,6-dimethyl naphthalene	4	1	1	2
1,3-dimethylnaphthalene	2	1	0	1
1,5-dimethylnaphthalene	1	1	0	0
2,3,5-trimethylnaphthalene	4	2	1	1
1-methylfluorene	1	0	1	0
3-methylphenanthrene	1	0	0	1
9-methylphenanthrene	1	0	1	0
Parent Compounds				
Naphthalene	1	0	0	1
Acenaphthalene	0	0	0	0
Acenapthene	0	0	0	0
Fluorene	0	0	0	0
Phenanthrene	1	0	0	1
Anthracene	0	0	0	0
Fluoranthene	0	0	0	0
Pyrene	1	1	0	0
Benzo(a)anthracene	0	0	0	0
Chrysene	0	0	0	0
Benzo(b)fluoranthene	0	0	0	0
Benzo(k)fluoranthene	0	0	0	0
Benzo(a)pyrene	0	0	0	0
Indeno(1,2,3-cd)pyrene	0	0	0	0
Dibenz(a,h)anthracene	0	0	0	0
Benzo(g,h,i)perylene	0	0	0	0

(n=35)

Table 7.21. a–e. Model Results from Logistic and Gamma Regressions Assessing the Relationships between PAHs Detected in Feathers of Brown Pelican Chicks in the Northern GOM and a Suite of Independent Variables, 2014–2015

K = number of parameters, AICc = Akaike Information Criteria, Delta AICc = difference in AIC values between indicated model and top ranked model. AICc weight = probability of model being the best model given the models tested and data analyzed. sumPAH = sum of all PAHs, sumPAR = sum of Parent PAHs, sumALK = sum of alkylated PAHs.

(a) Logistic regression models for sumPAH (response variable = presence or absence of sumPAH; n = 35). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Planning area	3	46.96		0.54
Null	1	48.18	1.22	0.29

(b) Gamma regression models for sumPAH (response variable = concentration of sumPAH; only individuals with sumPAH > 0 included in analyses, n = 13). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Planning area	4	150.21		0.41
Null	2	150.51	0.31	0.36
BCI	3	151.37	1.17	0.23

(c) Logistic regression models for sumPAR (response variable = presence or absence of sumPAR; n = 35). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Null	1	22.48		0.63
BCI	2	24.41	1.94	0.24

(d) Logistic regression models for sumALK (response variable = presence or absence of sumALK; n = 35). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Planning area	3	44.48		0.70

(e) Gamma regression models for sumALK (response variable = concentration of sumALK; only individuals with sumALK > 0 included in analyses, n = 12). Only models ≤ delta AICc 2.0 are included.

Variables	K	AICc	Delta AICc	AICc Weight
Null	2	135.13		0.55
BCI	3	136.40	1.27	0.29
Home range + BCI	4	420.52	1.07	0.19
Home range + sex	4	421.28	1.82	0.13

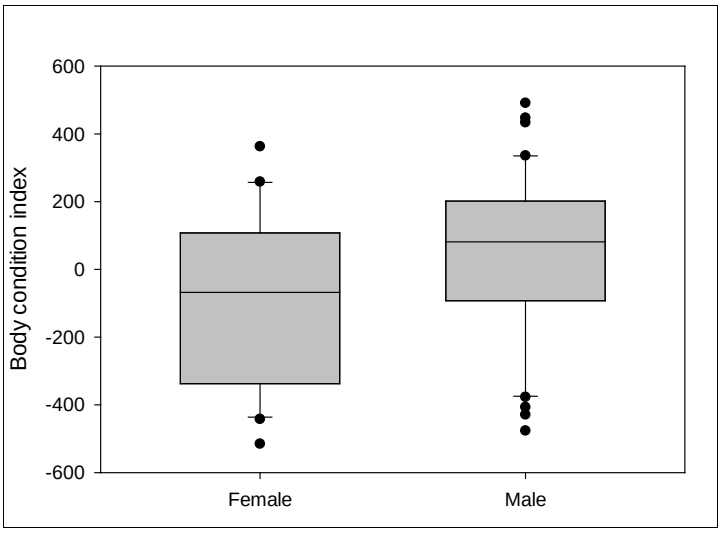


Figure 7.1.a Relationships among independent variables used in modeling blood analytes of adult brown pelicans breeding in the Northern GOM, 2013–2015, BCI for female and male pelicans.

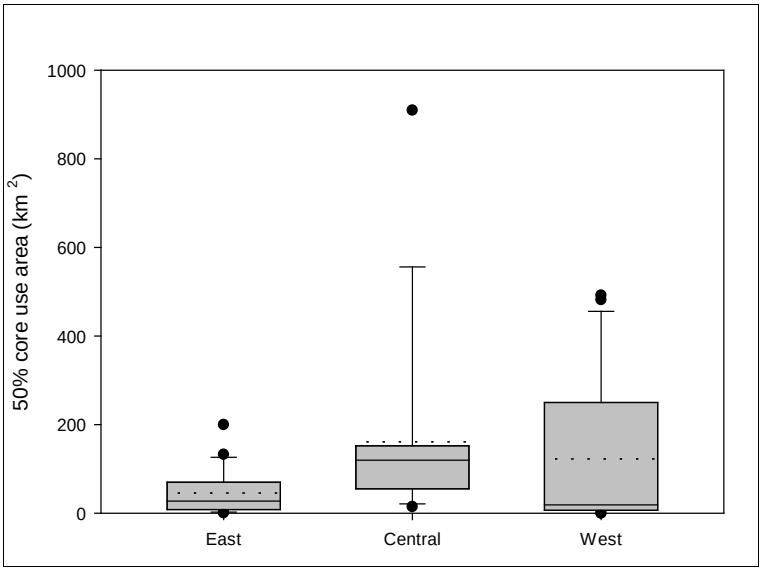


Figure 7.2.b. Relationships among independent variables used in modeling blood analytes of adult brown pelicans breeding in the Northern GOM, 2013–2015, home range size.
Home range size is the 50% core use area for adult brown pelicans in the eastern, central, and western planning areas of the GOM.

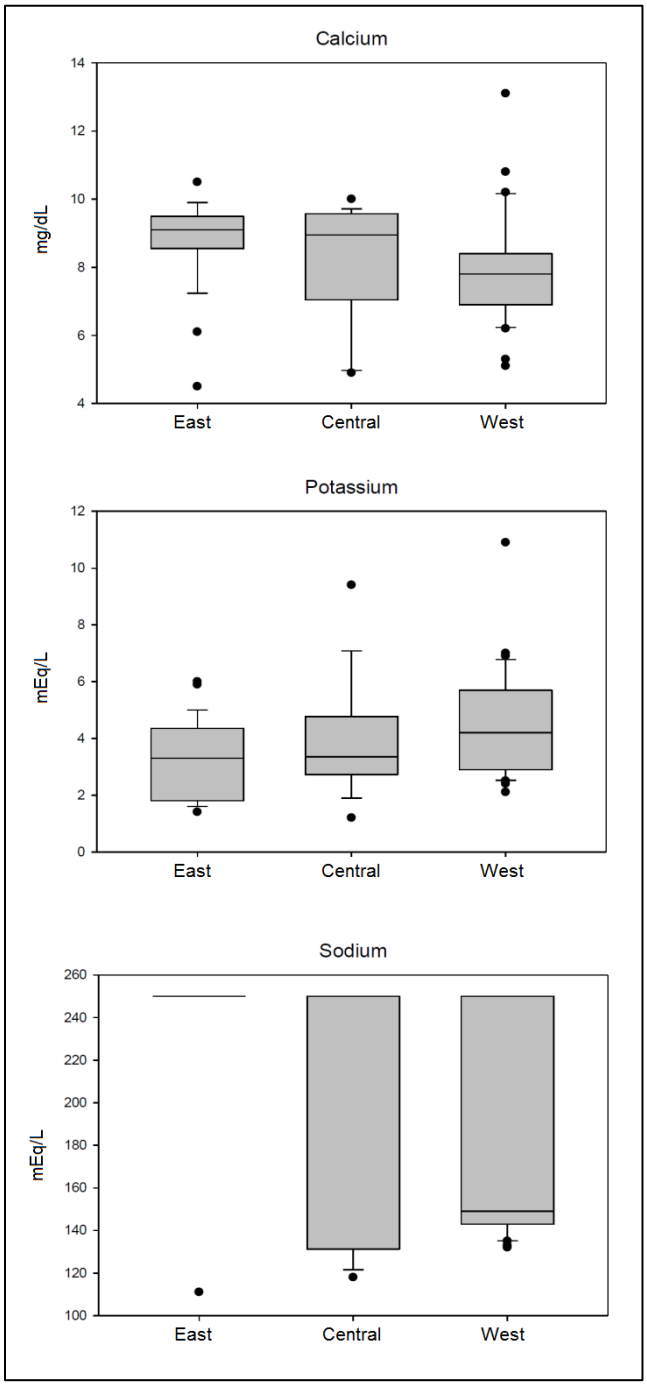


Figure 7.3.a. Box plots of blood analytes of adult brown pelicans breeding in the Northern GOM, in relation to planning area, 2013–2015, electrolytes, calcium, potassium, and sodium.
Only analytes found to be related to planning area (coefficient estimate > SE) from highly ranked models are displayed. In all cases, the eastern planning area is set as the reference level.

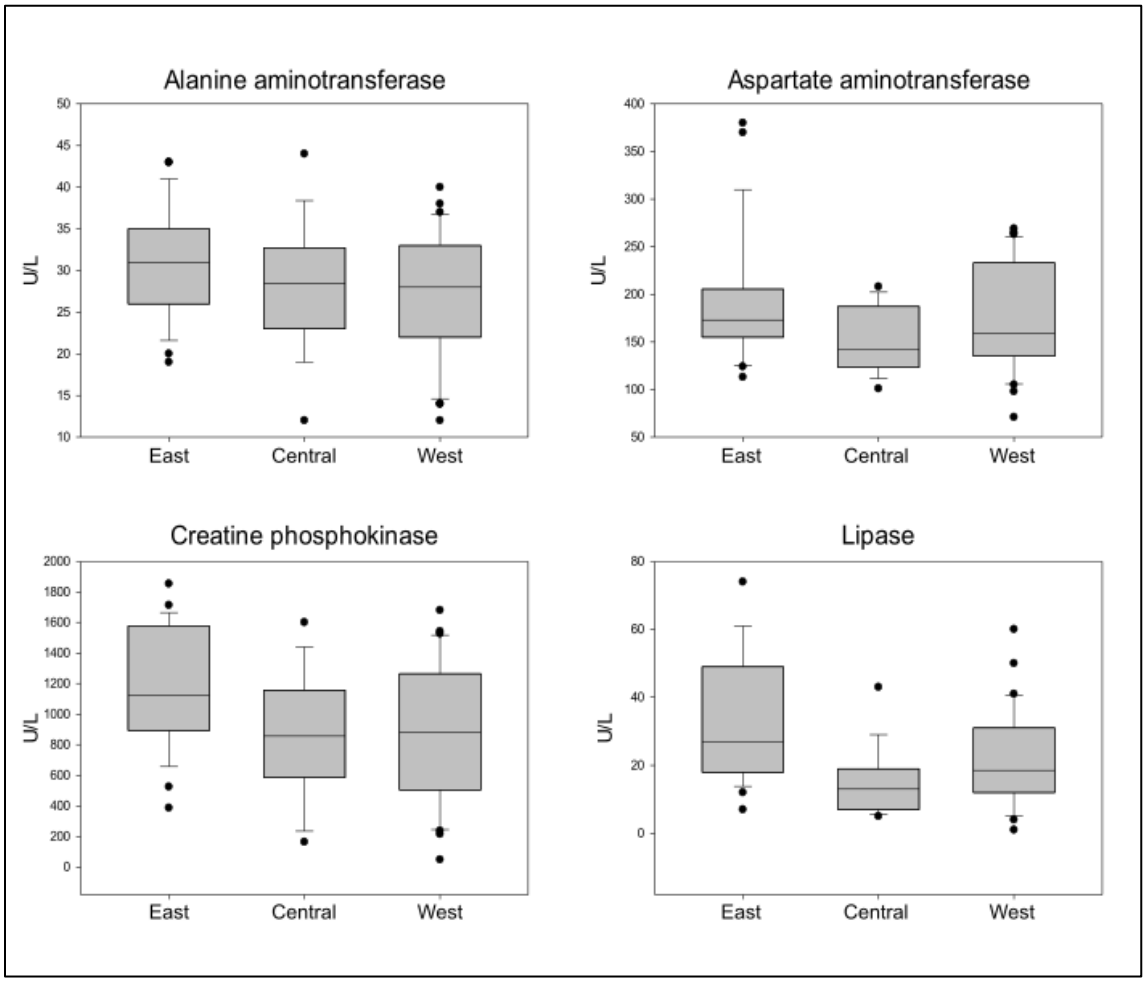


Figure 7.4.b. Box plots of blood analytes of adult brown pelicans breeding in the Northern GOM, in relation to planning area, 2013–2015: enzymes: alanine aminotransferase, aspartate aminotransferase, creatine phosphokinase, lipase.
Only analytes found to be related to planning area (coefficient estimate > SE) from highly ranked models are displayed. In all cases, the eastern planning area is set as the reference level.

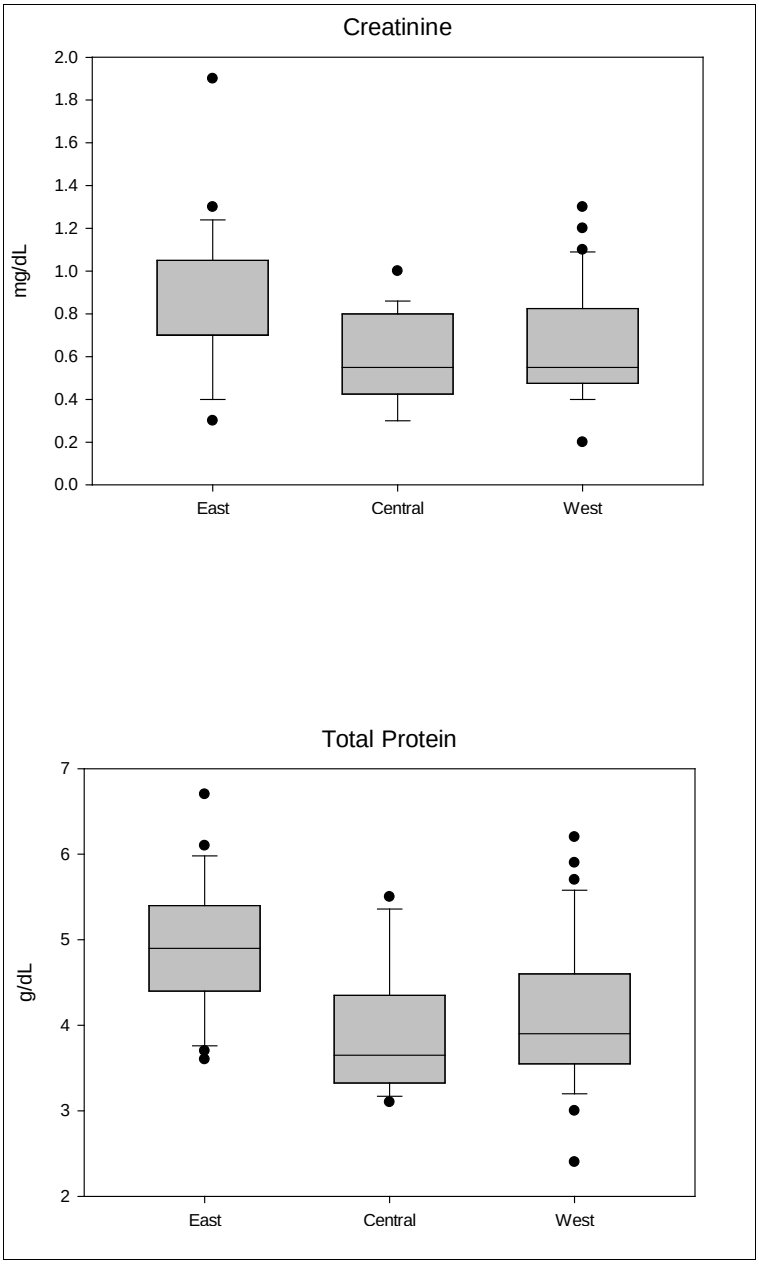


Figure 7.5c. Box plots of blood analytes of adult brown pelicans breeding in the Northern GOM, in relation to planning area, 2013–2015, metabolites: creatinine, total protein.
Only analytes found to be related to planning area (coefficient estimate > SE) from highly ranked models are displayed. In all cases, the eastern planning area is set as the reference level.

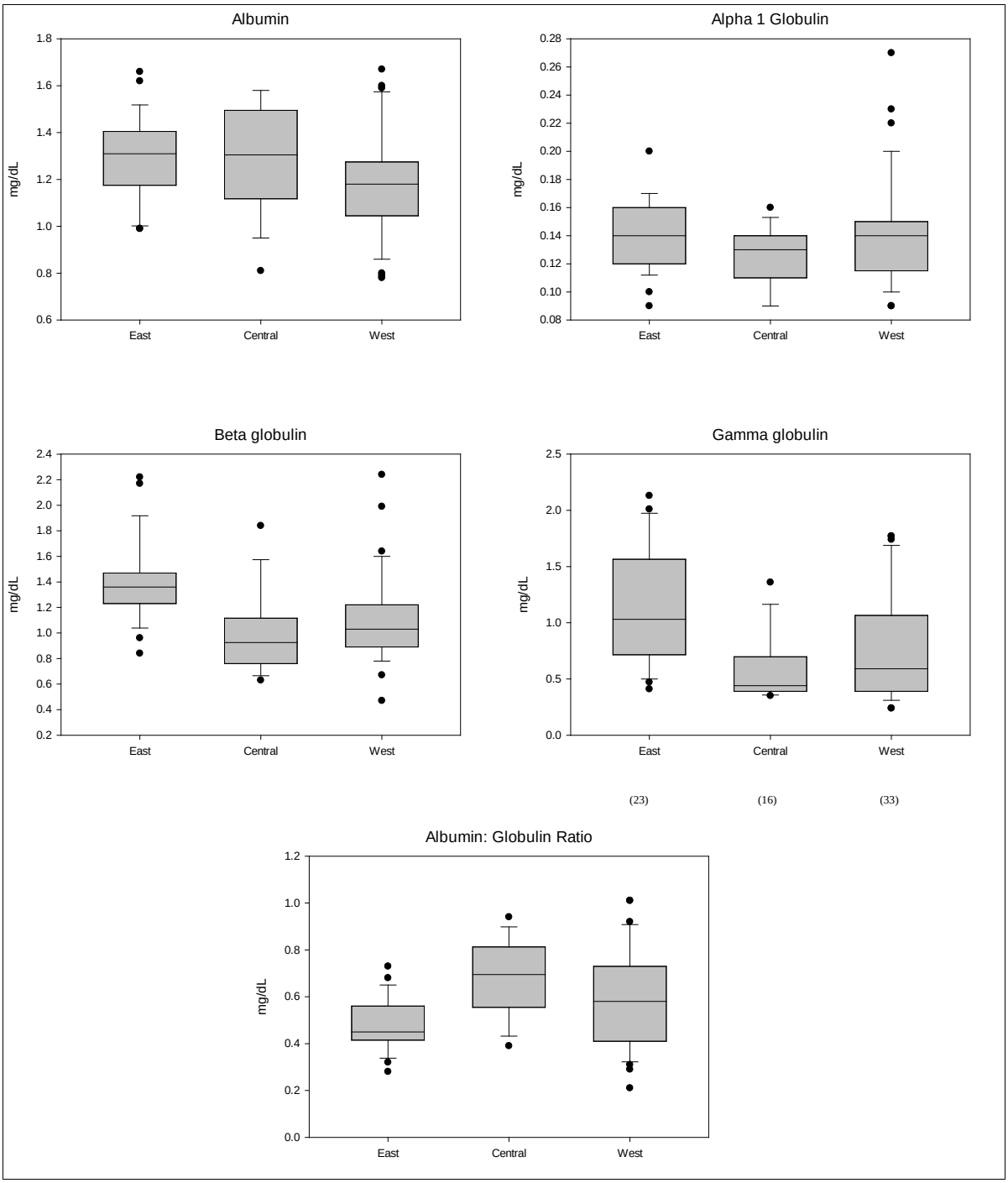


Figure 7.6.d. Box plots of blood analytes of adult brown pelicans breeding in the Northern GOM, in relation to planning area, 2013–2015: plasma proteins: albumin, alpha 1 globulin, beta globulin, ratio albumin:globulin.
Only analytes found to be related to planning area (coefficient estimate > SE) from highly ranked models are displayed. In all cases, the eastern planning area is set as the reference level.

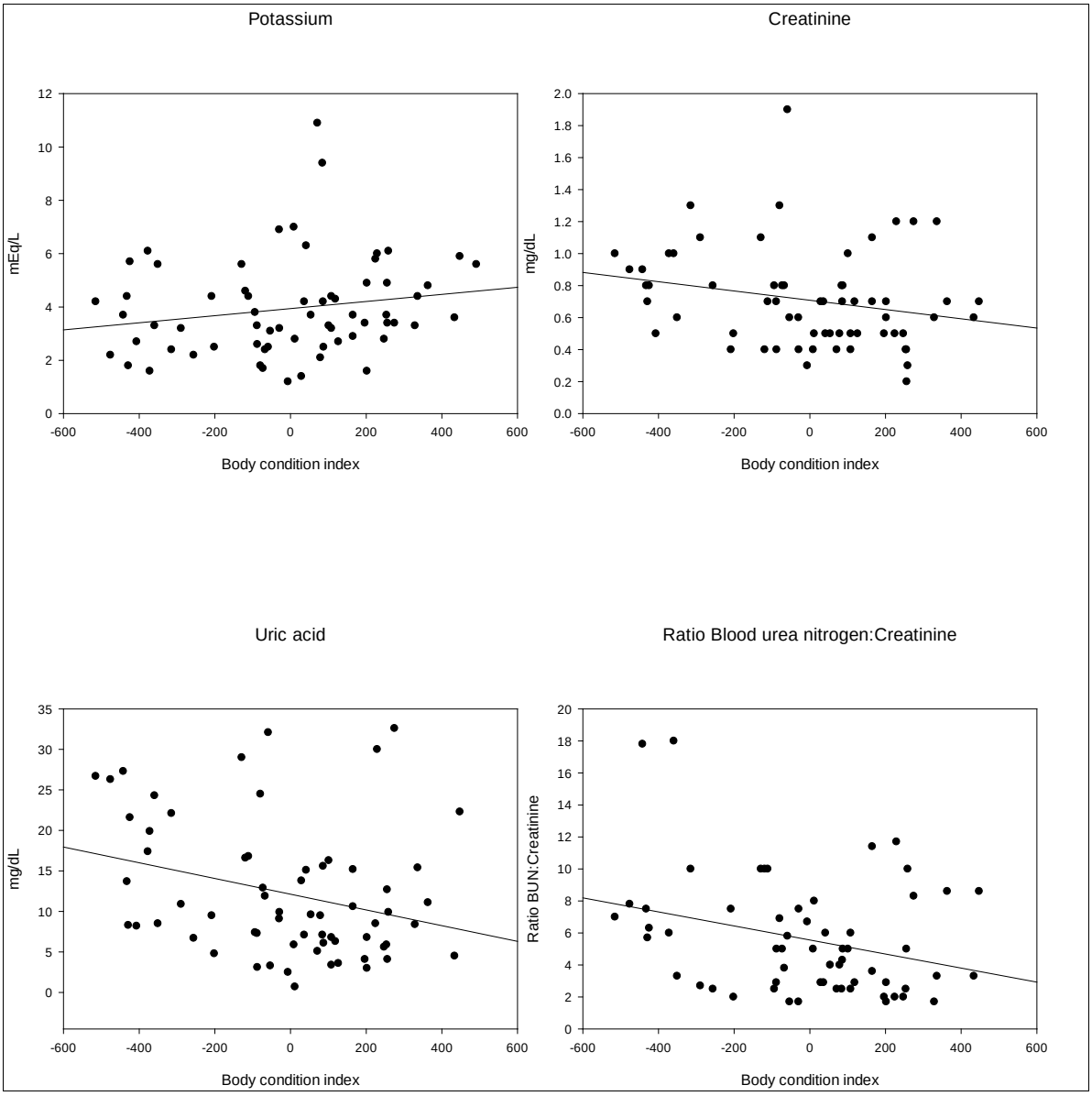


Figure 7.7. Body condition index of adult brown pelicans breeding in the Northern GOM, in relation to four blood analytes, 2013–2015.

Only analytes found to be strongly related to BCI based on coefficient estimates from highly ranked models are displayed.

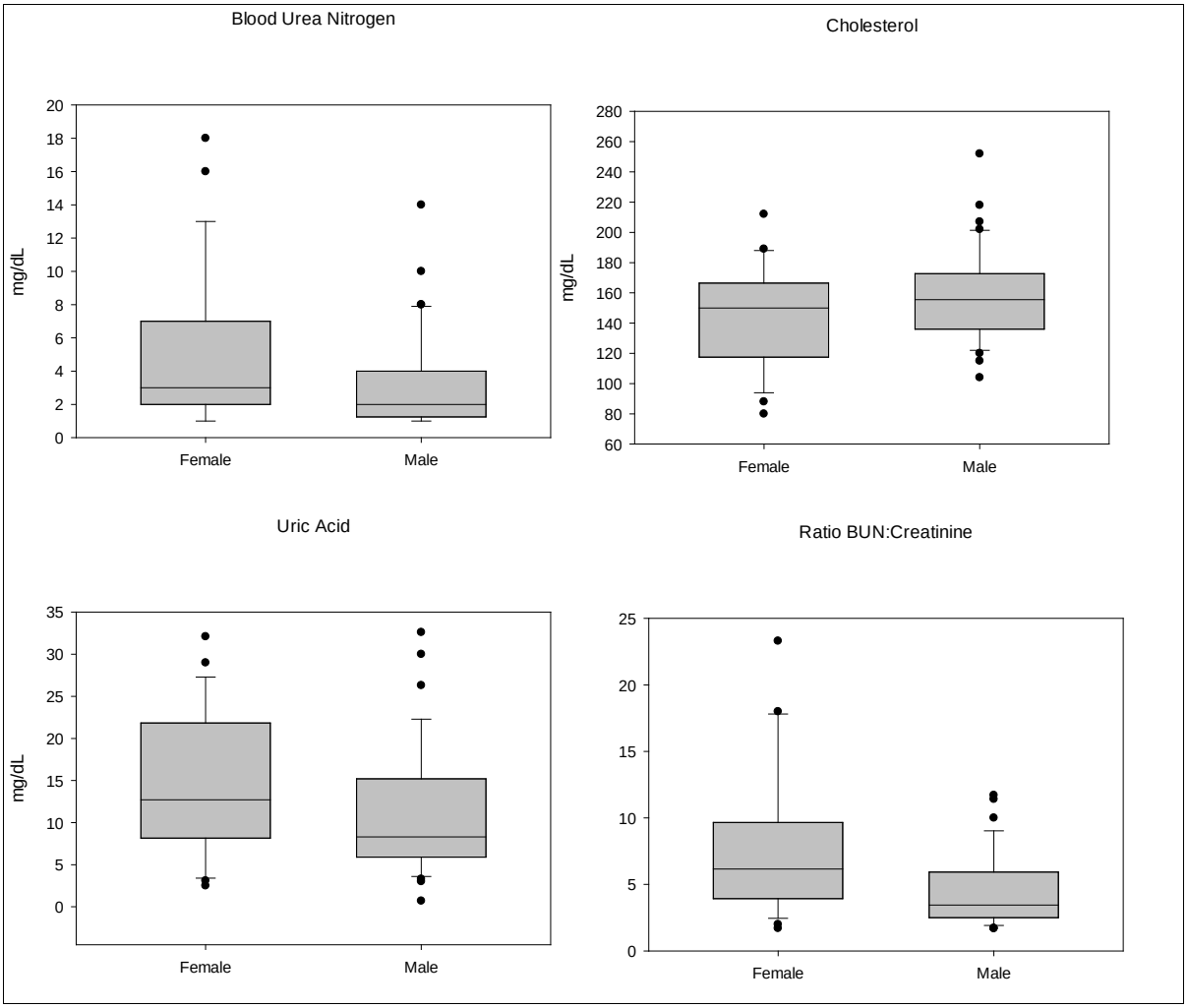


Figure 7.8.a. Sex of adult brown pelicans breeding in the Northern GOM, in relation to seven blood analytes, 2013–2015: metabolites.
Only analytes found to be strongly related to BCI based on coefficient estimates from highly ranked models are displayed.

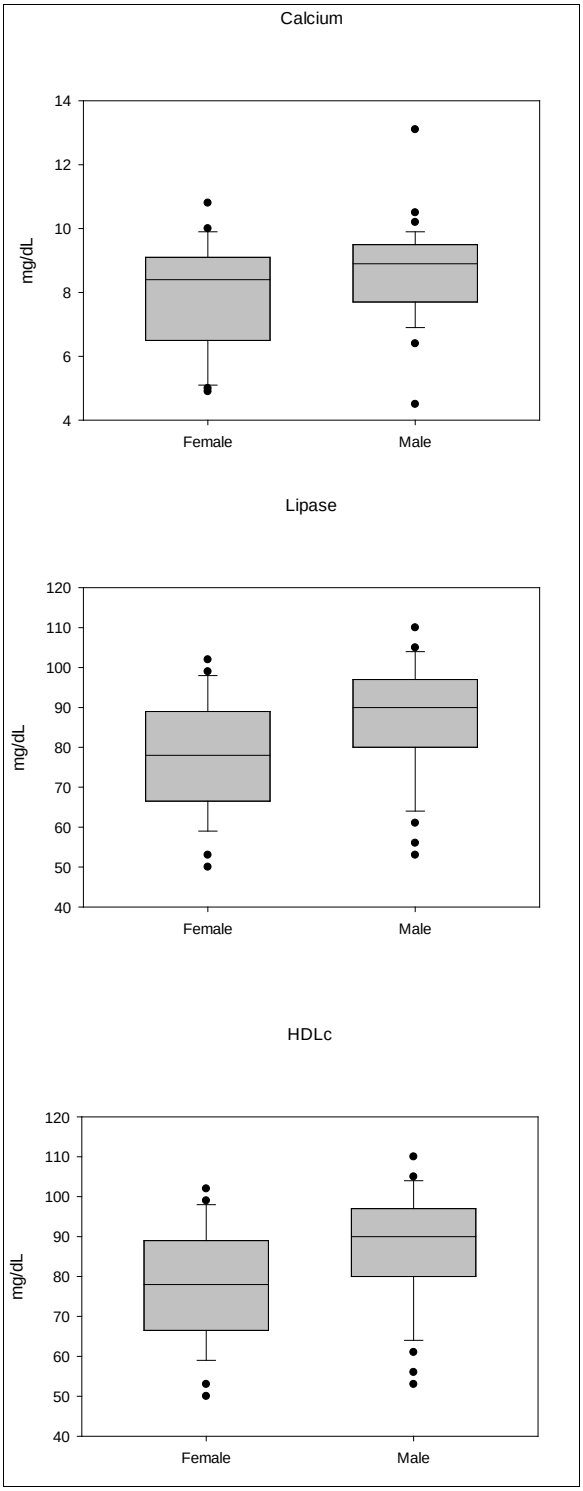


Figure 7.9.b. Sex of adult brown pelicans breeding in the Northern GOM, in relation to seven blood analytes, 2013–2015: Electrolyte (n = 1), Enzyme (n = 1), Lipid (n = 1).
Only analytes found to be strongly related to BCI based on coefficient estimates from highly ranked models are displayed.

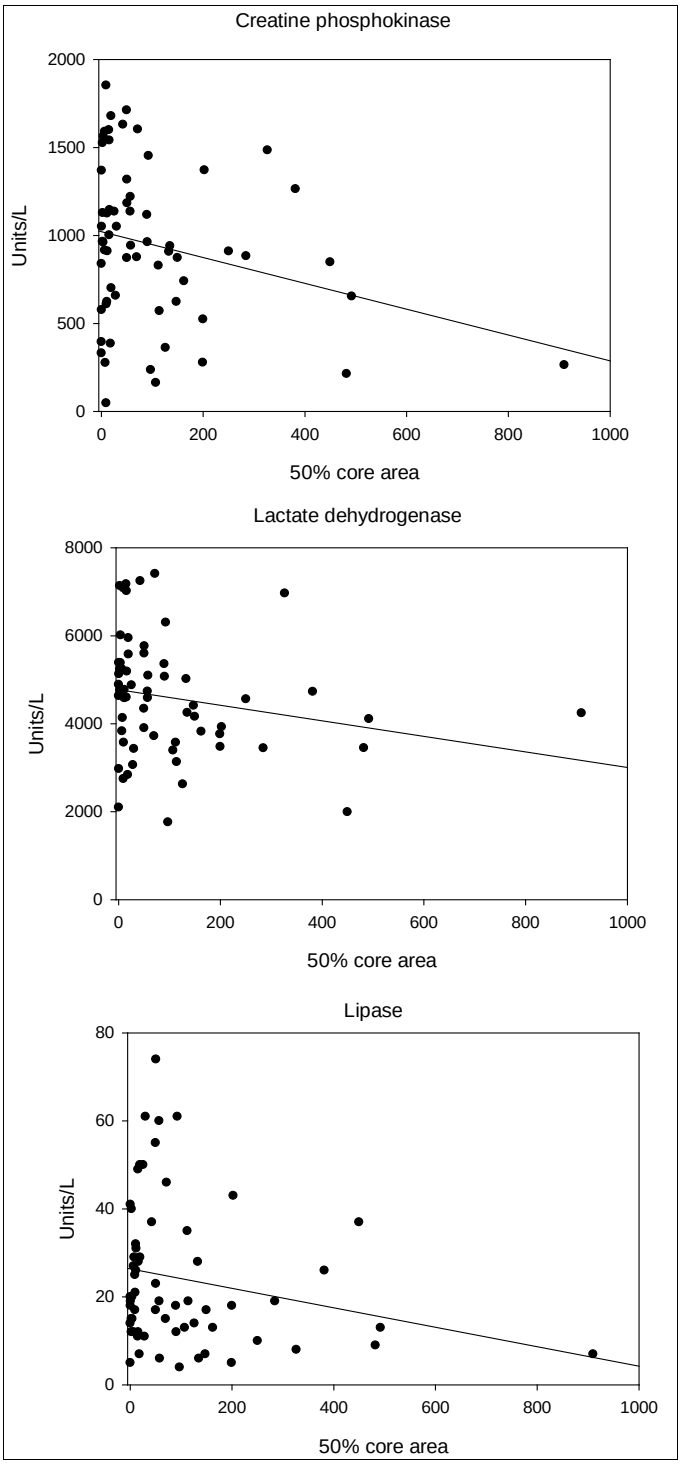


Figure 7.10.a. Home range size (50% core area) of adult brown pelicans breeding in the Northern GOM, in relation to seven blood analytes: 2013–2015, enzymes.
Only analytes found to be strongly related to home range based on coefficient estimates from highly ranked models are displayed.

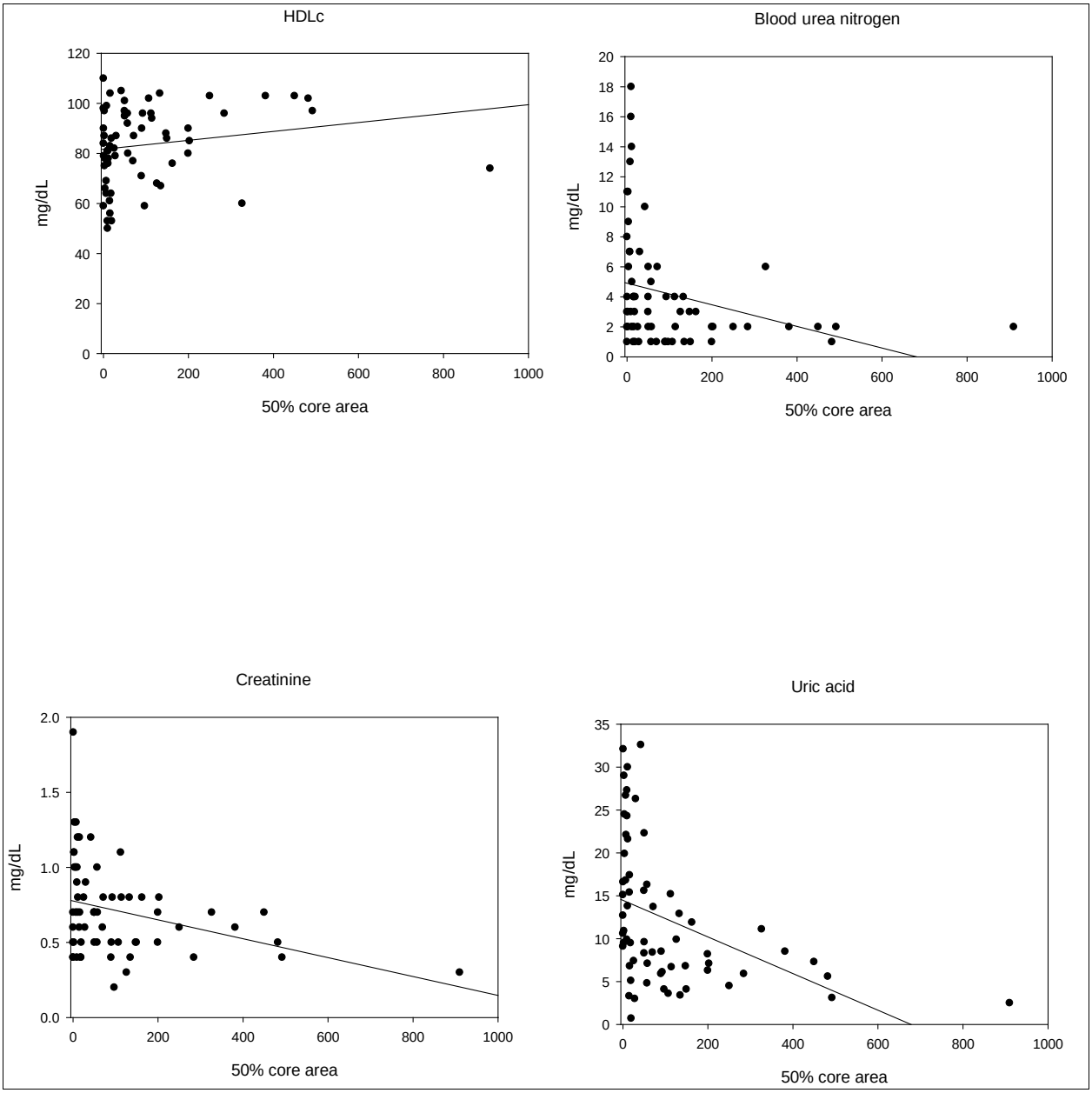


Figure 7.11.b. Home range size (50% core area) of adult brown pelicans breeding in the Northern GOM, in relation to seven blood analytes, 2013–2015: metabolites and lipids.
Only analytes found to be strongly related to home range based on coefficient estimates from highly ranked models are displayed.

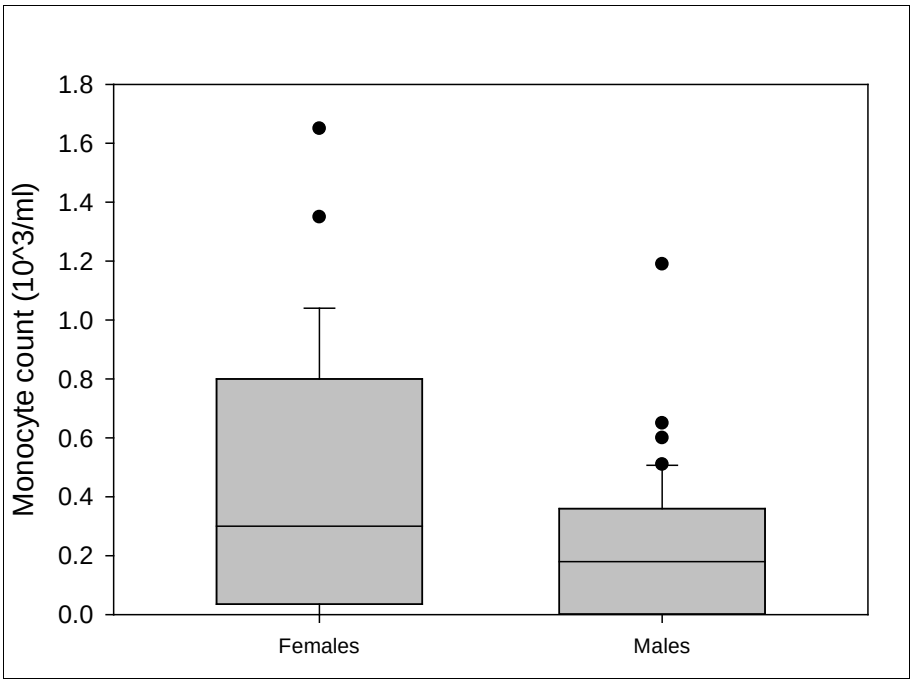


Figure 7.12.a. Concentrations of white blood cells of adult brown pelicans breeding in the Northern GOM, 2013–2015: count of monocytes for males and females.

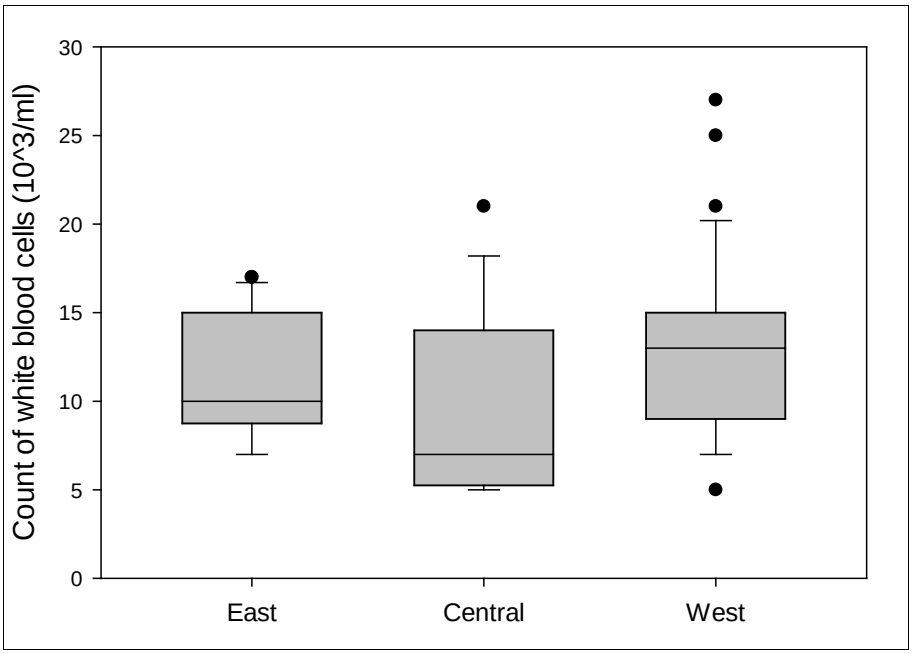


Figure 7.13.b. Concentrations of white blood cells of adult brown pelicans breeding in the Northern GOM, 2013–2015: count of all white blood cells by planning area.

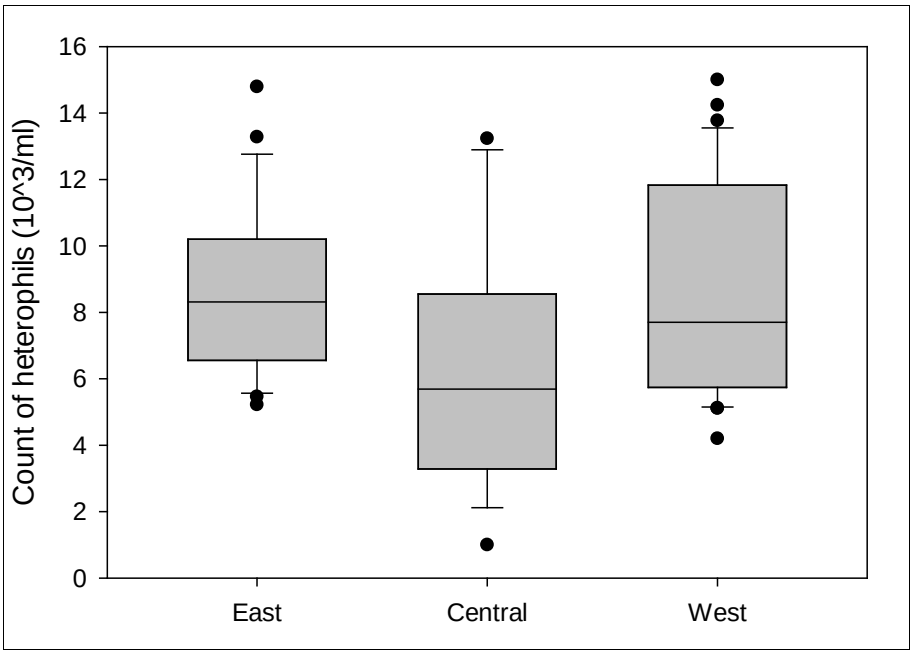


Figure 7.14.c. Concentrations of white blood cells of adult brown pelicans breeding in the Northern GOM, 2013–2015: count of heterophils by planning area.

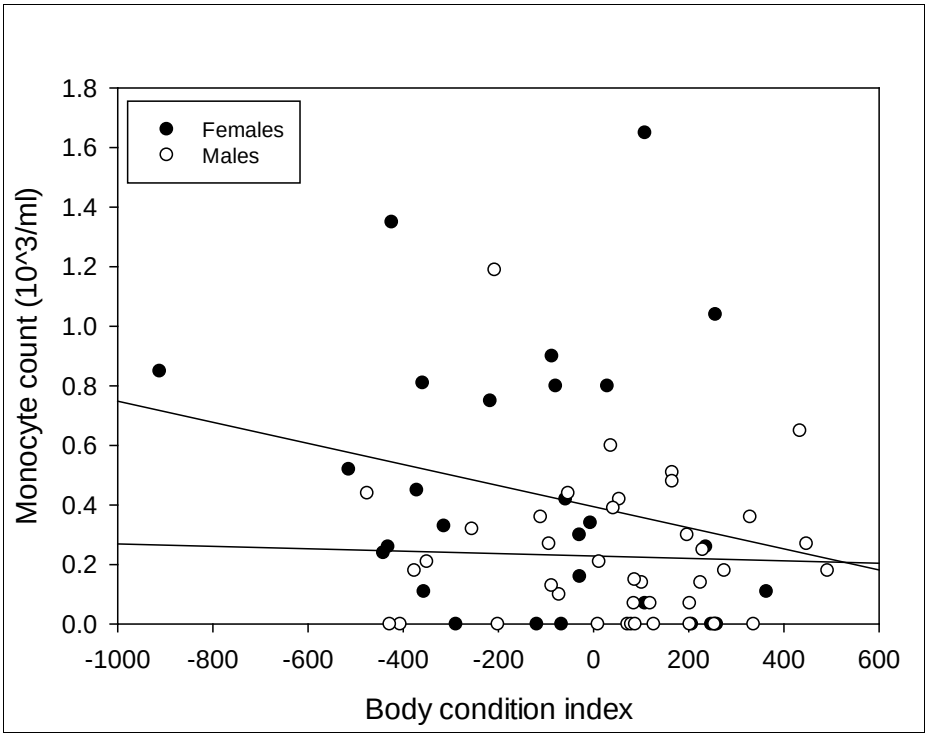


Figure 7.15.d. Concentrations of white blood cells of adult brown pelicans breeding in the Northern GOM, 2013–2015: count of monocytes in relation to BCI for females and males.

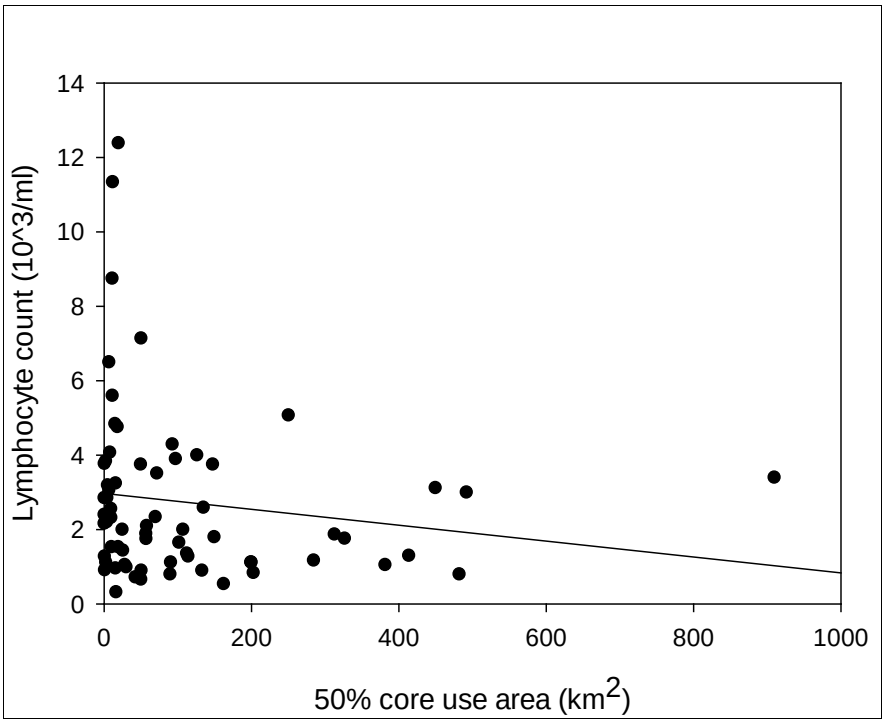


Figure 7.16.e. Concentrations of white blood cells of adult brown pelicans breeding in the Northern GOM, 2013–2015: count of lymphocytes in relation to size of home range (50% core area; km^2).

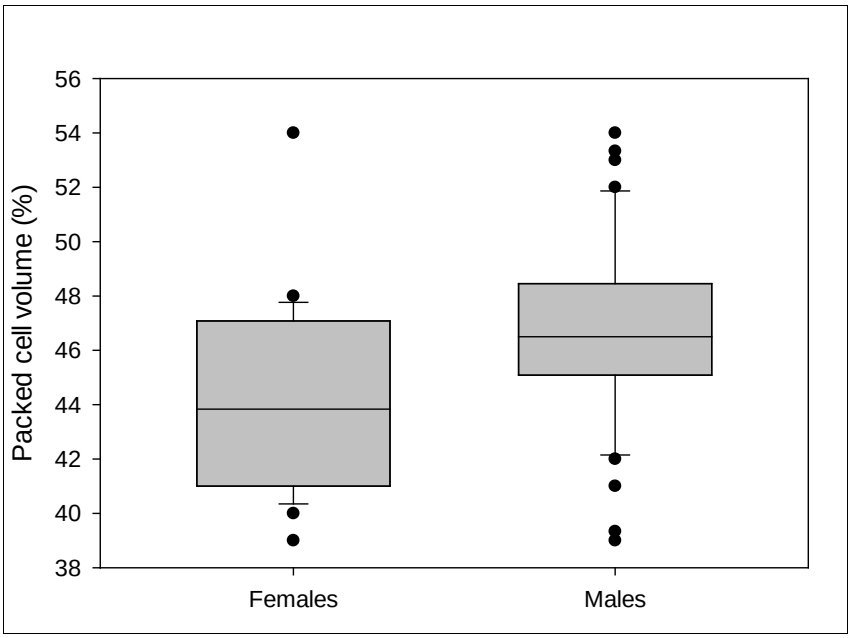


Figure 7.17.f. Concentrations of white blood cells of adult brown pelicans breeding in the Northern GOM, 2013–2015: packed cell volume (%) for females and males.

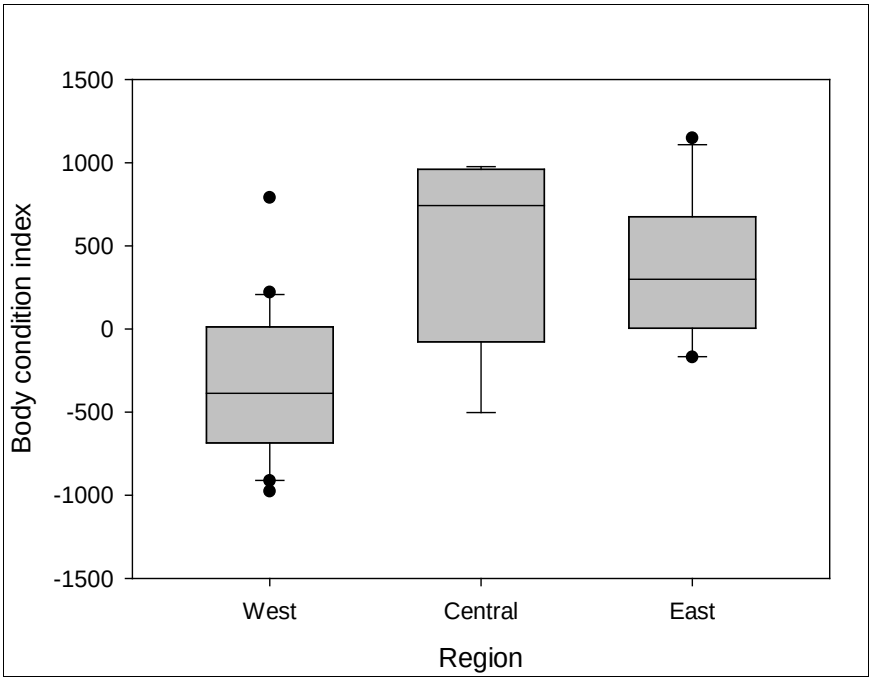


Figure 7.18. Box plots of body condition index of brown pelican chicks in the Northern GOM, in relation to planning area of study, 2014–2015.

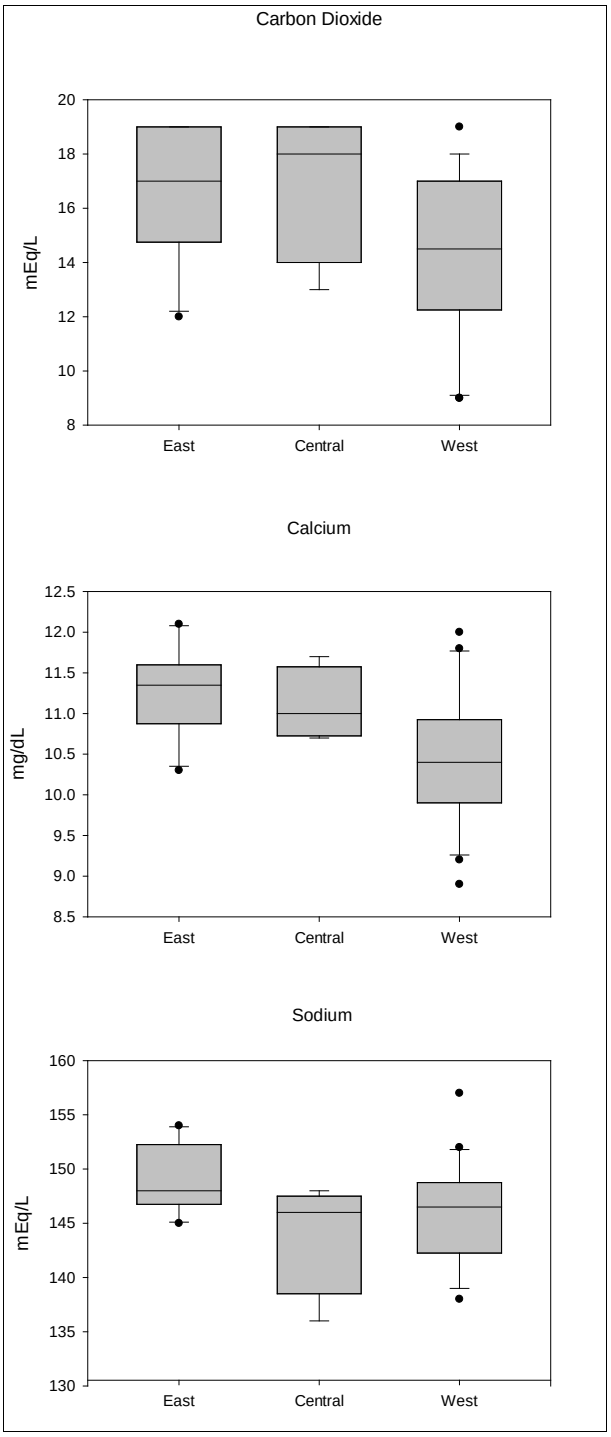


Figure 7.19.a. Box plots of blood analytes of adult brown pelican chicks in the Northern GOM, in relation to planning area, 2014–2015: blood gas (CO2) and electrolytes and minerals (calcium, sodium).
Only analytes found to be strongly related to planning area based on coefficient estimates from highly ranked models are displayed. In all cases, the eastern region is set as the reference level.

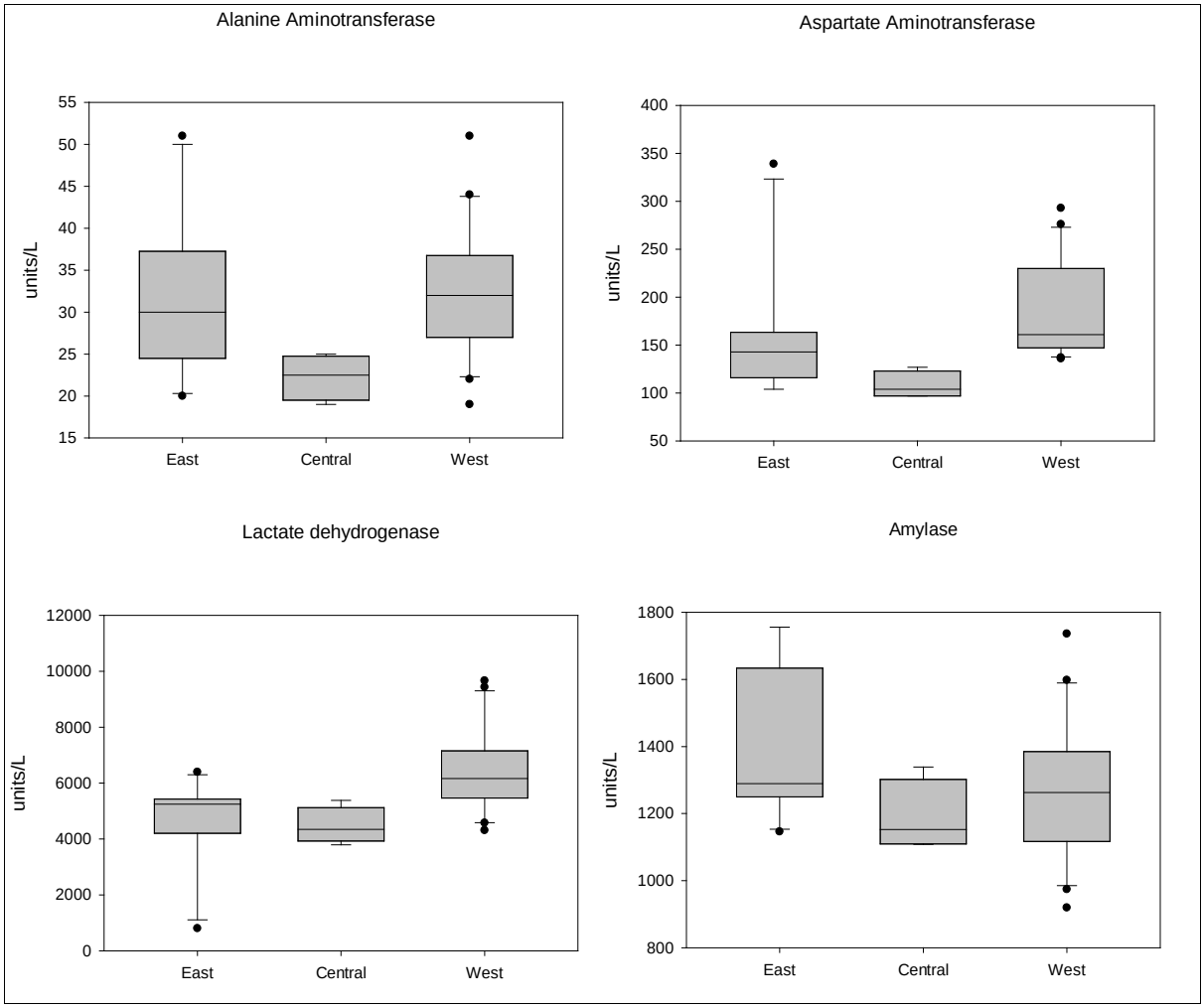


Figure 7.20.b. Box plots of blood analytes of adult brown pelican chicks in the Northern GOM, in relation to planning area, 2014–2015: enzymes: alanine aminotransferase, aspartate aminotransferase, lactate dehydrogenase, amylase.
Only analytes found to be strongly related to planning area based on coefficient estimates from highly ranked models are displayed. In all cases, the eastern planning area is set as the reference level.

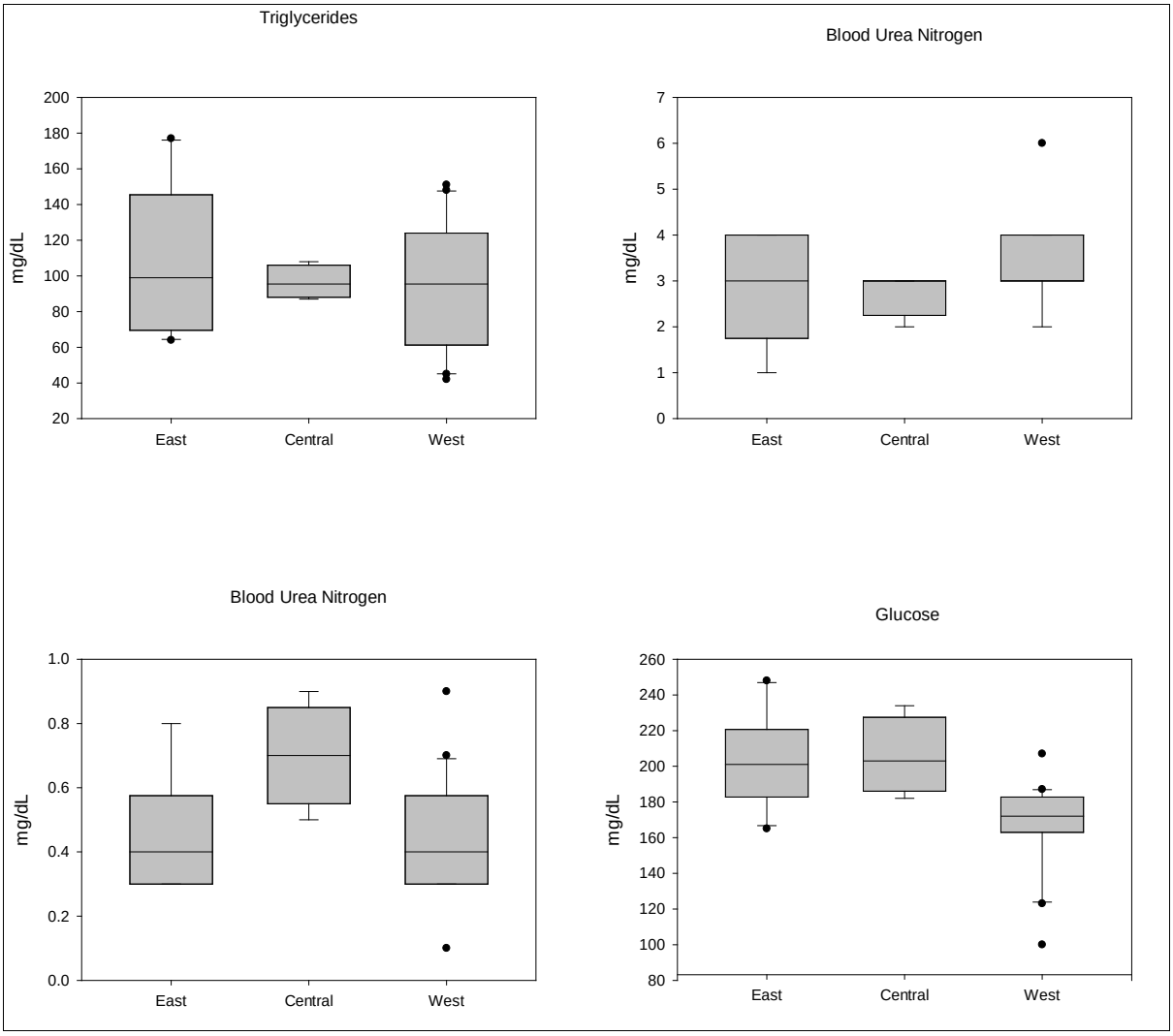


Figure 7.21.c. Box plots of blood analytes of adult brown pelican chicks in the Northern GOM, in relation to planning area, 2014–2015: lipids (triglycerides) and metabolites (blood urea nitrogen, creatinine, glucose).

Only analytes found to be strongly related to planning area based on coefficient estimates from highly ranked models are displayed. In all cases, the eastern planning area is set as the reference level.

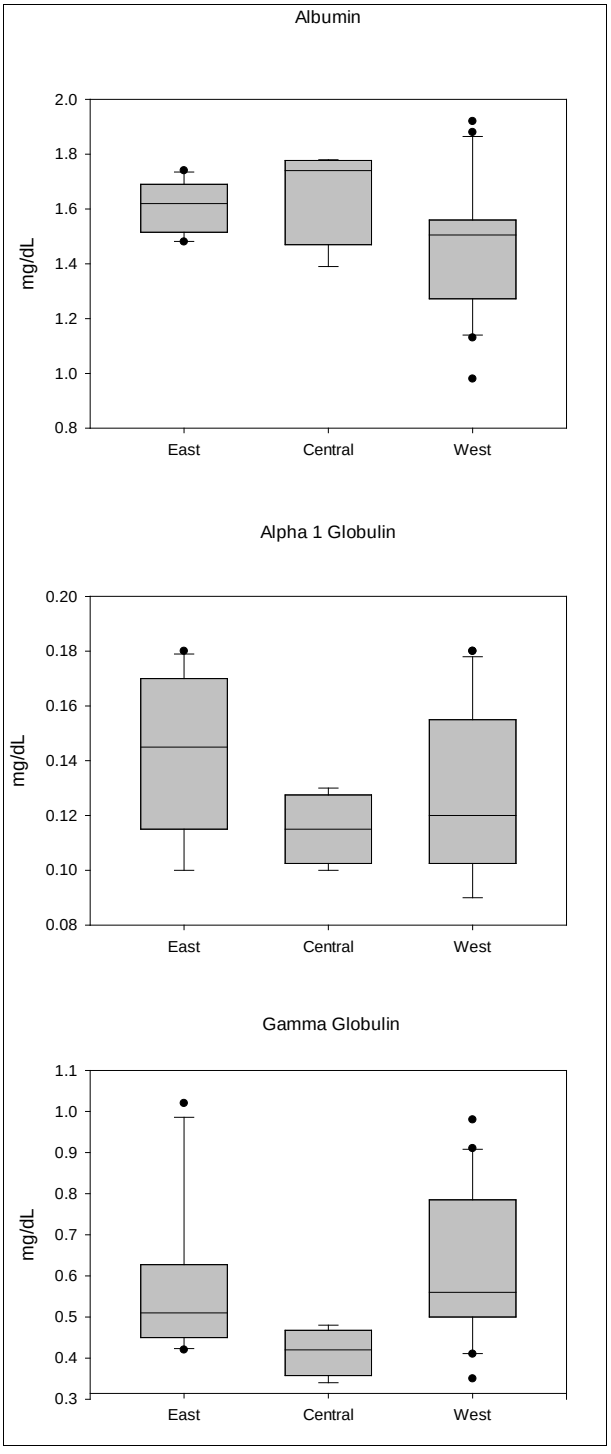


Figure 7.22.d. Box plots of blood analytes of adult brown pelican chicks in the Northern GOM, in relation to planning area, 2014–2015: plasma proteins: albumin, alpha 1 globulin, gamma globulin.
Only analytes found to be strongly related to planning area based on coefficient estimates from highly ranked models are displayed. In all cases, the eastern planning area is set as the reference level.

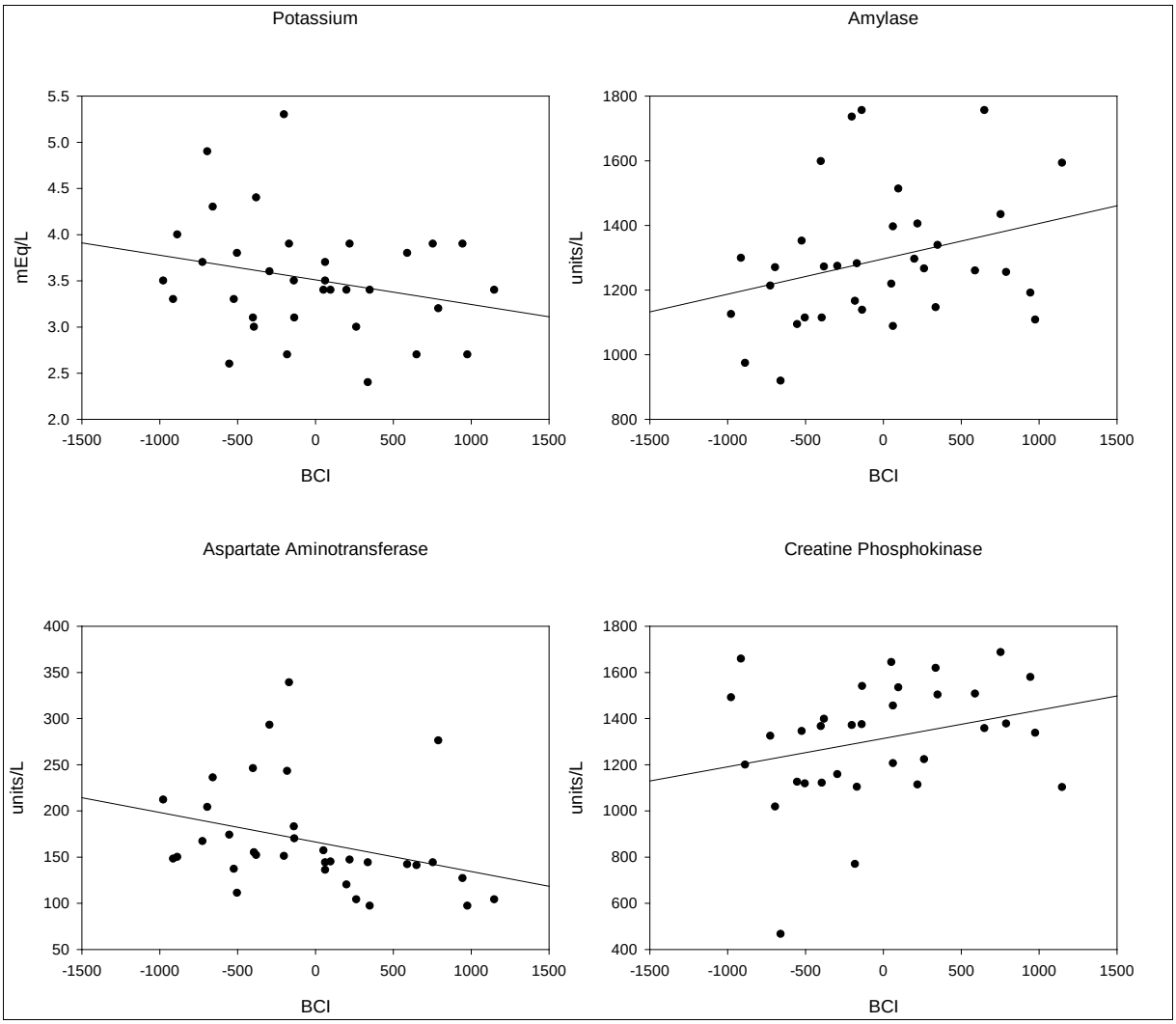


Figure 7.23.a. Body condition index of brown pelican chicks in the Northern GOM, in relation to eight blood analytes, 2014–2015: potassium, amylase, aspartate aminotransferase, and creatinine phosphokinase.
Only analytes found to be strongly related to BCI based on coefficient estimates from highly ranked models are displayed.

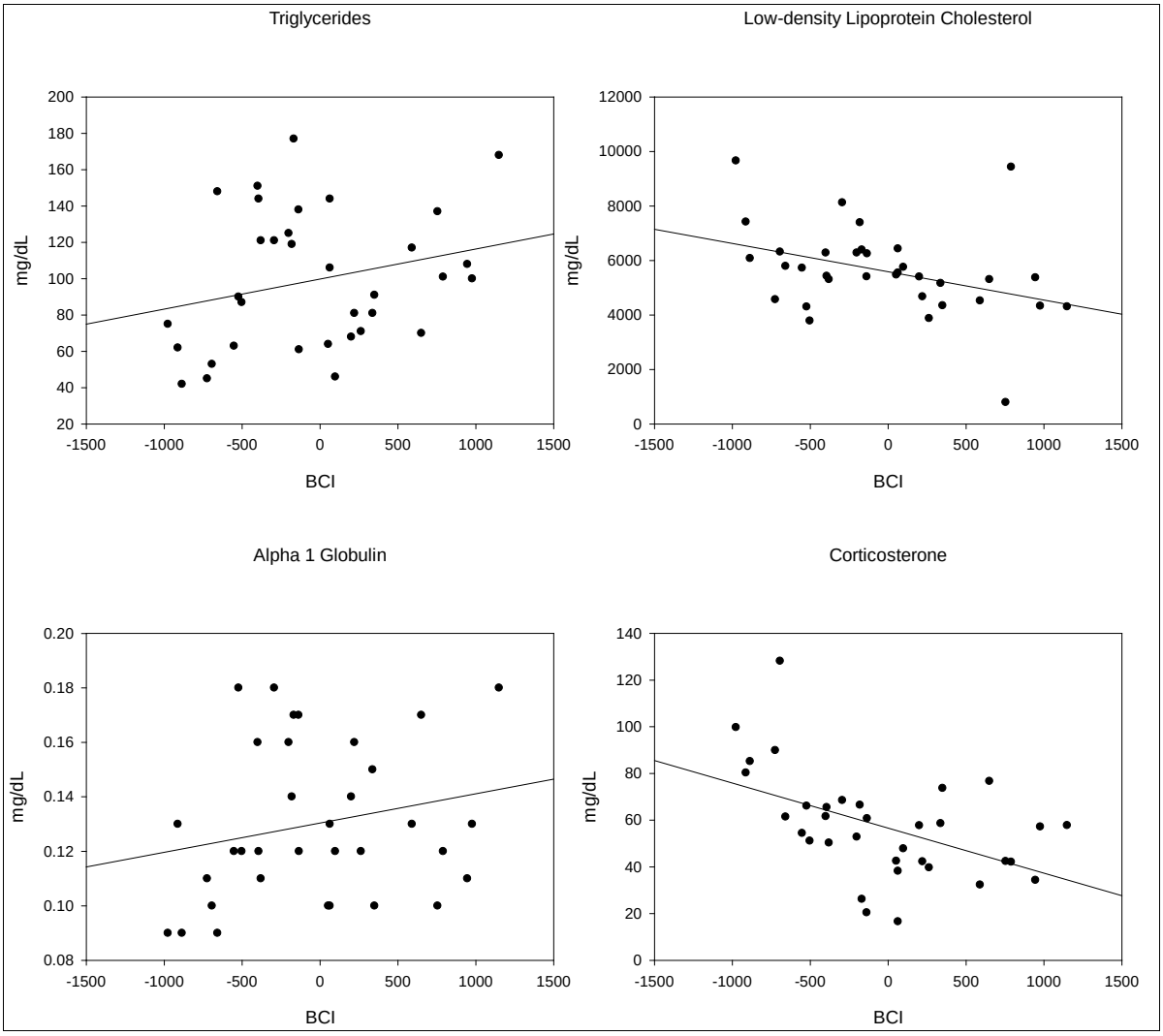


Figure 7.24.b. Body condition index of brown pelican chicks in the Northern GOM, in relation to eight blood analytes, 2014–2015: triglycerides, low density lipoprotein cholesterol, alpha 1 globulin, and CORT.
Only analytes found to be strongly related to BCI based on coefficient estimates from highly ranked models are displayed.

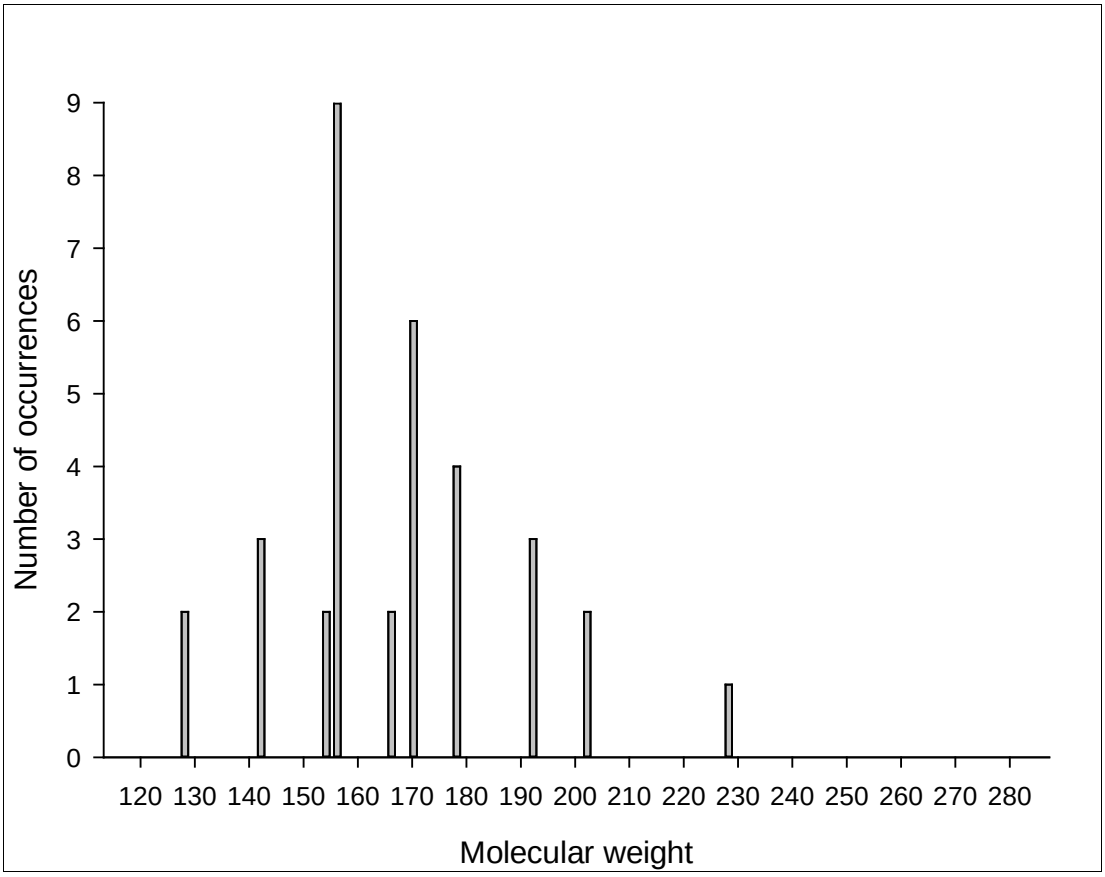


Figure 7.25. Count of PAHs by molecular weight from blood samples of adult brown pelicans breeding in the Northern GOM, 2013–2015.

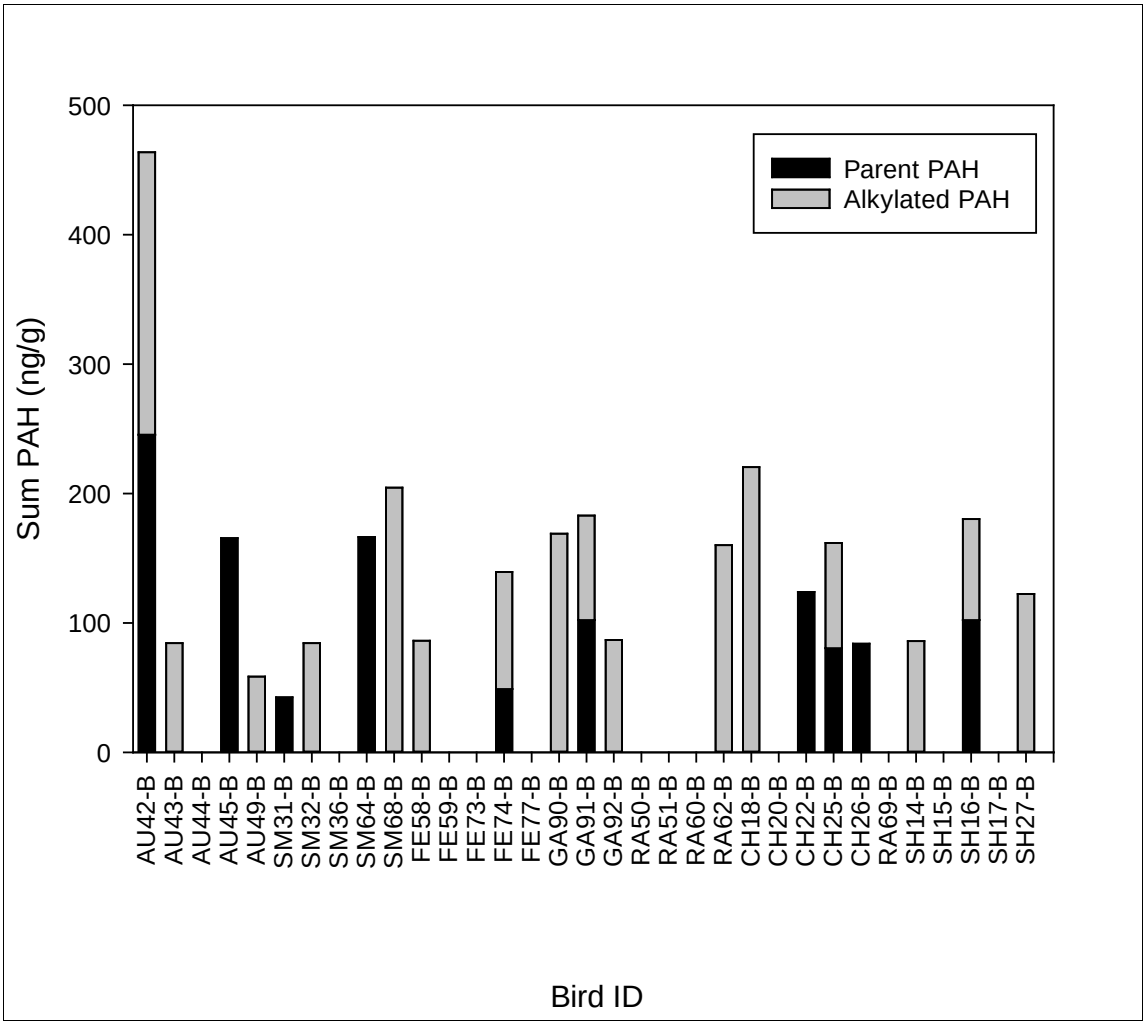


Figure 7.26.a. Summation of PAHs by individual from blood samples of adult brown pelicans breeding in the Northern GOM, 2013–2015: total PAH concentration (ng g-1; wet weight) of parent and alkylated PAHs in blood samples.

Bird ID = two letter abbreviation for the colony of origin of the sample (AU = Audubon Island, SM = Smith Island, FE = Felicity Island, GA = Gaillard Island, RA = Raccoon Island, CH = Chester Island, SH = Shamrock Island; see Figs. 2.1 and 2.2), a unique identification number, and B = blood sample).

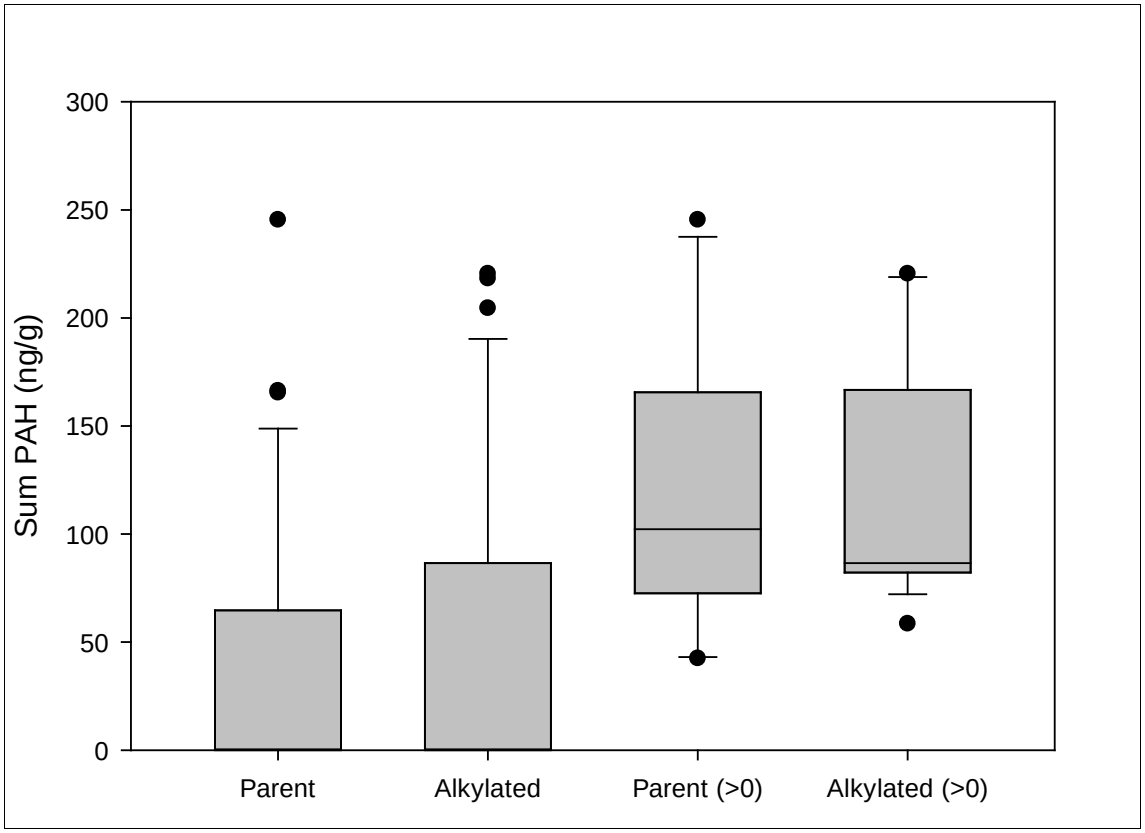


Figure 7.27.b. Summation of PAHs by individual from blood samples of adult brown pelicans breeding in the Northern GOM, 2013–2015: box plots of PAH concentration (ng g^{-1}; wet weight) of parent and alkylated PAHs in blood samples.
The two left-side boxes include data from all individuals. The two right-side boxed include only data where PAHs were > detectable limit (i.e., non-zero data). Bird ID = two letter abbreviation for the colony of origin of the sample (AU = Audubon Island, SM = Smith Island, FE = Felicity Island, GA = Gaillard Island, RA = Raccoon Island, CH = Chester Island, SH = Shamrock Island; see Figs. 2.1 and 2.2), a unique identification number, and B = blood sample).

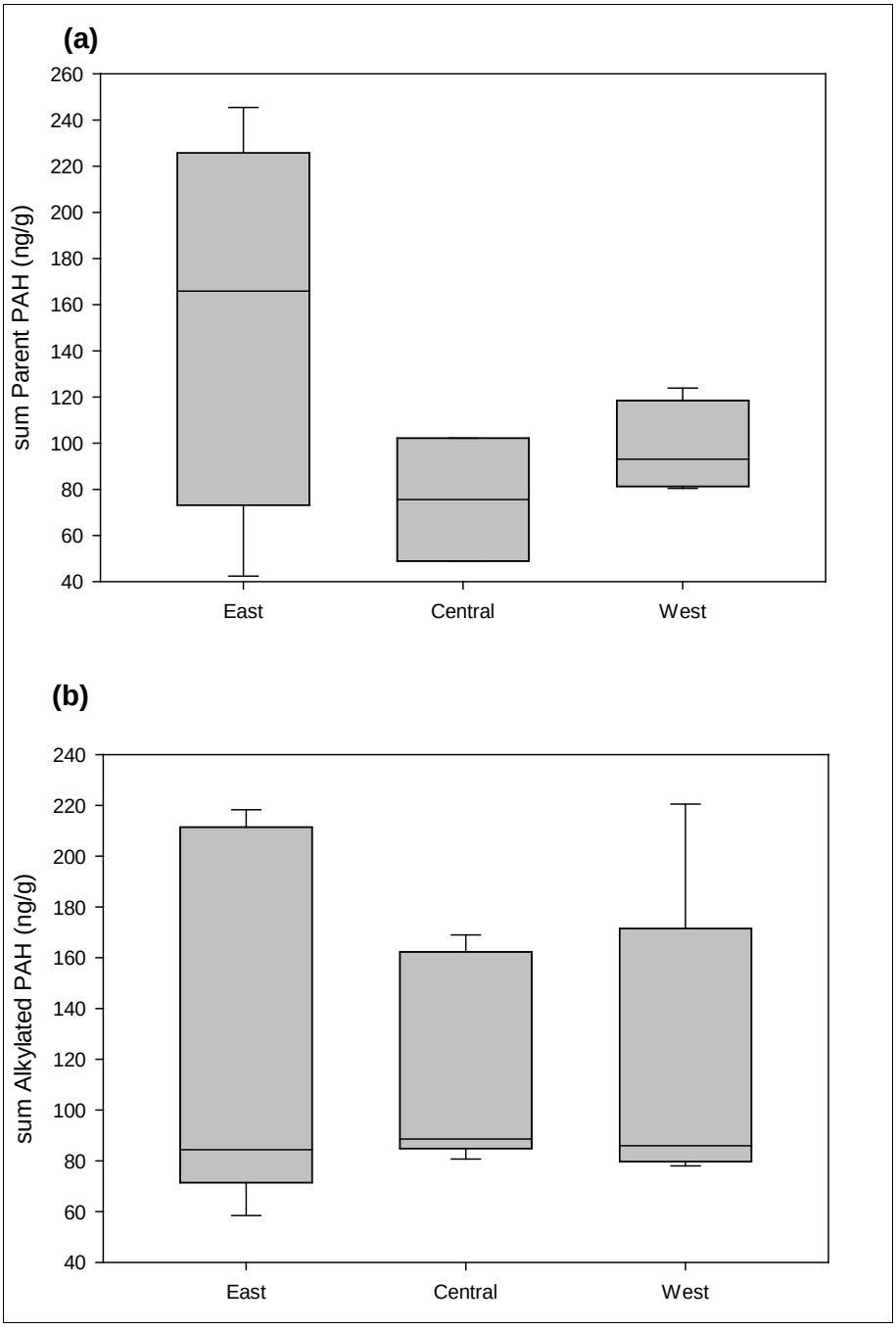


Figure 7.28. Concentrations of PAHs by planning area from blood samples of adult brown pelicans breeding in the Northern GOM, 2013–2015.
Only samples above detectable limits are included (i.e., zeros are excluded)
(a) Total concentration of parent PAHs (ng g^{-1}; wet weight) for all samples above detectable limits. (b) Total concentration of alkylated PAHs (ng g^{-1}; wet weight) for all sample above detectable limits.

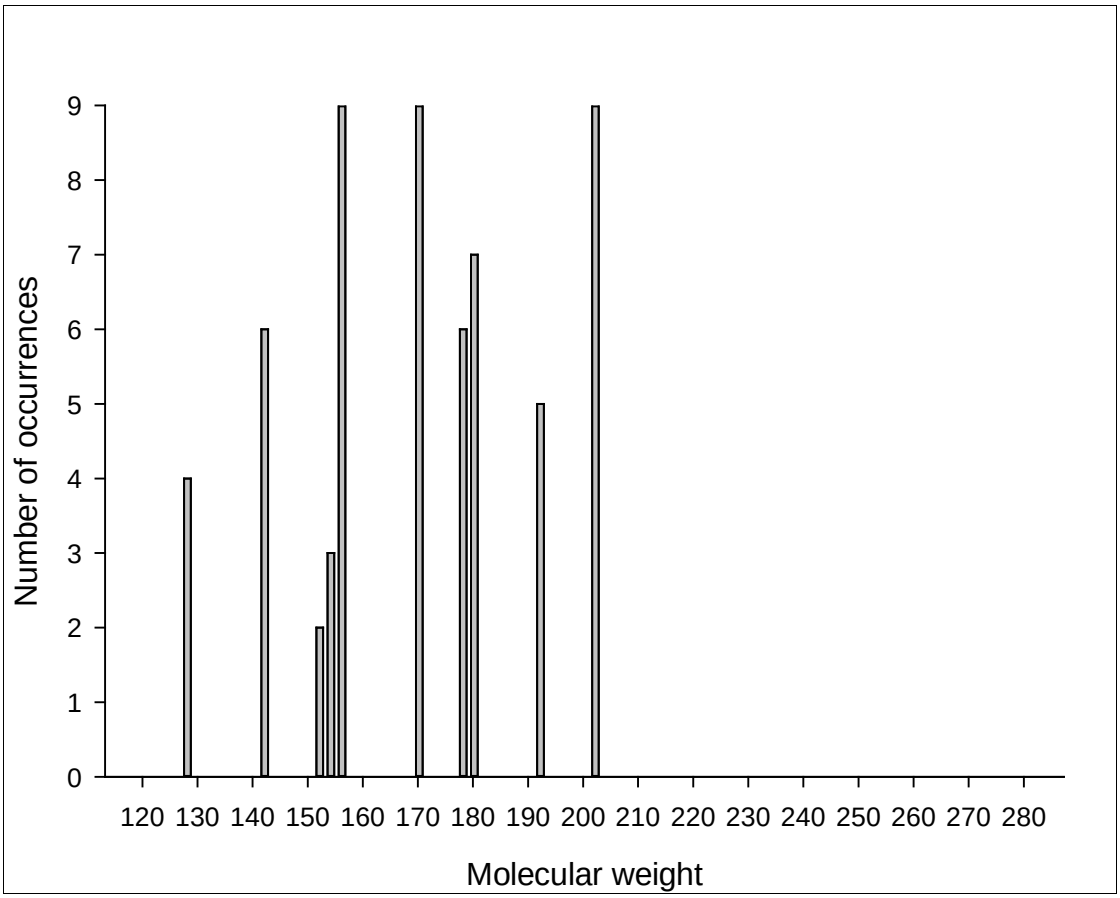


Figure 7.29. Count of PAHs by molecular weight from samples of feathers of adult brown pelicans breeding in the Northern GOM, 2013–2015.

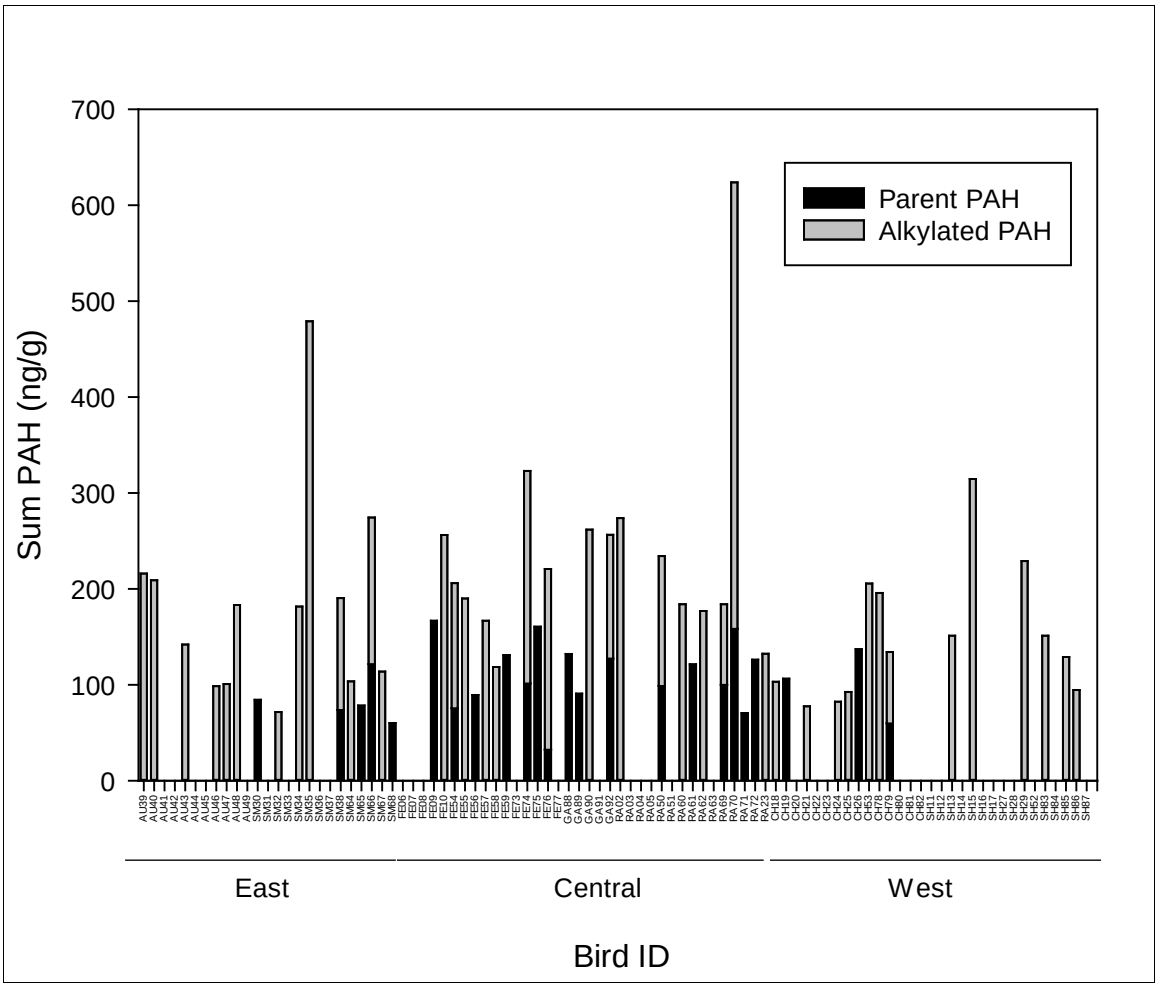


Figure 7.30.a. Summation of PAHs by individual from feather samples of adult brown pelicans breeding in the Northern GOM, 2013–2015: total PAH concentration (ng g^{-1}; dry weight) of parent and alkylated PAHs from adult feathers.

Bird ID = two letter abbreviation for the colony of origin of the sample (AU = Audubon Island, SM = Smith Island, FE = Felicity Island, GA = Gaillard Island, RA = Raccoon Island, CH = Chester Island, SH = Shamrock Island; see Figs. 2.1 and 2.2, and a unique identification number).

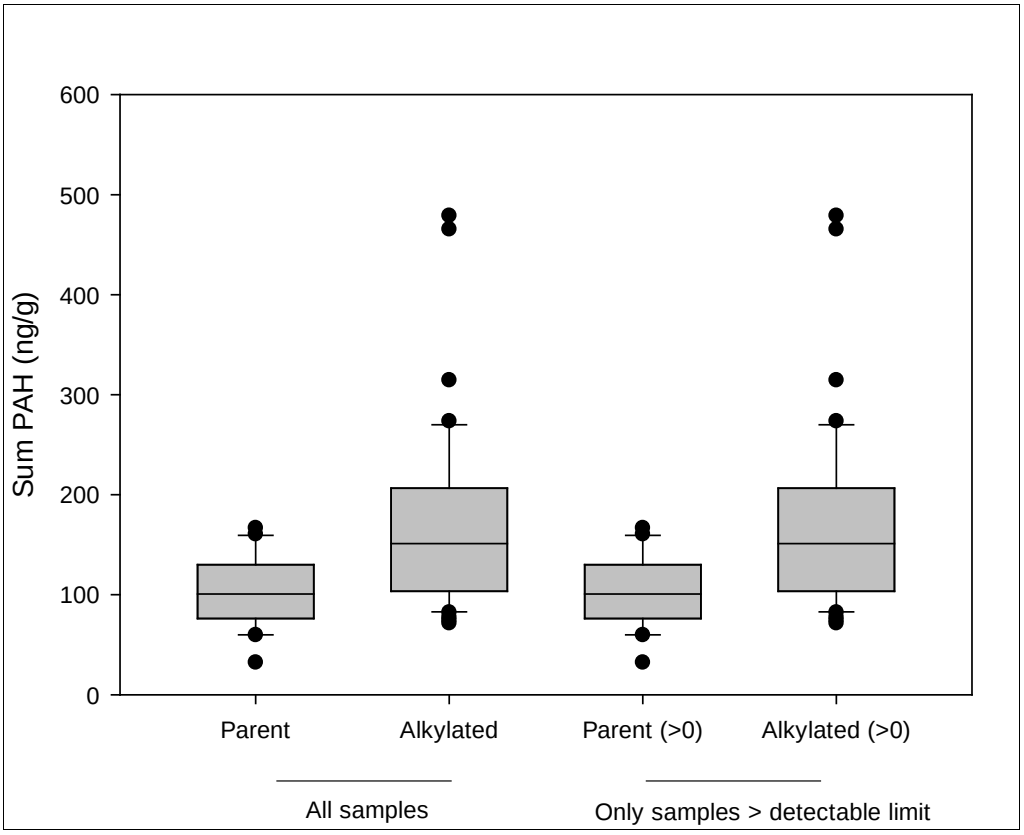


Figure 7.31.b. Summation of PAHs by individual from feather samples of adult brown pelicans breeding in the Northern GOM, 2013–2015: box plots of PAH concentration (ng g^{-1}; dry weight) of parent and alkylated PAHs from adult feathers.

The two left-side boxes include data from all individuals. The two right-side boxed include only data where PAHs were > detectable limit (i.e., non-zero data). Bird ID = two letter abbreviation for the colony of origin of the sample (AU = Audubon Island, SM = Smith Island, FE = Felicity Island, GA = Gaillard Island, RA = Raccoon Island, CH = Chester Island, SH = Shamrock Island; see Figs. 2.1 and 2.2, and a unique identification number).

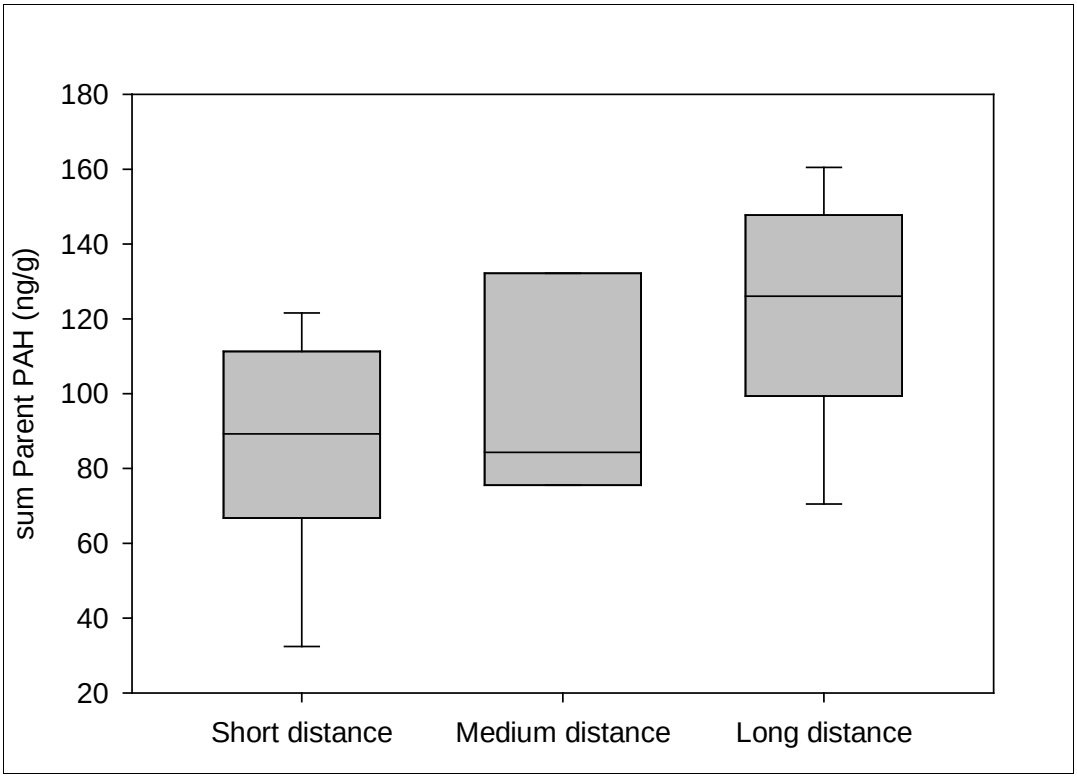


Figure 7.32. Concentrations of Parent PAHs by migration class from feather samples of adult brown pelicans breeding in the Northern GOM, 2013–2015.
Only samples above detectable limits are included (i.e., zeros are excluded). Concentrations are in ng g^{-1} (wet weight).

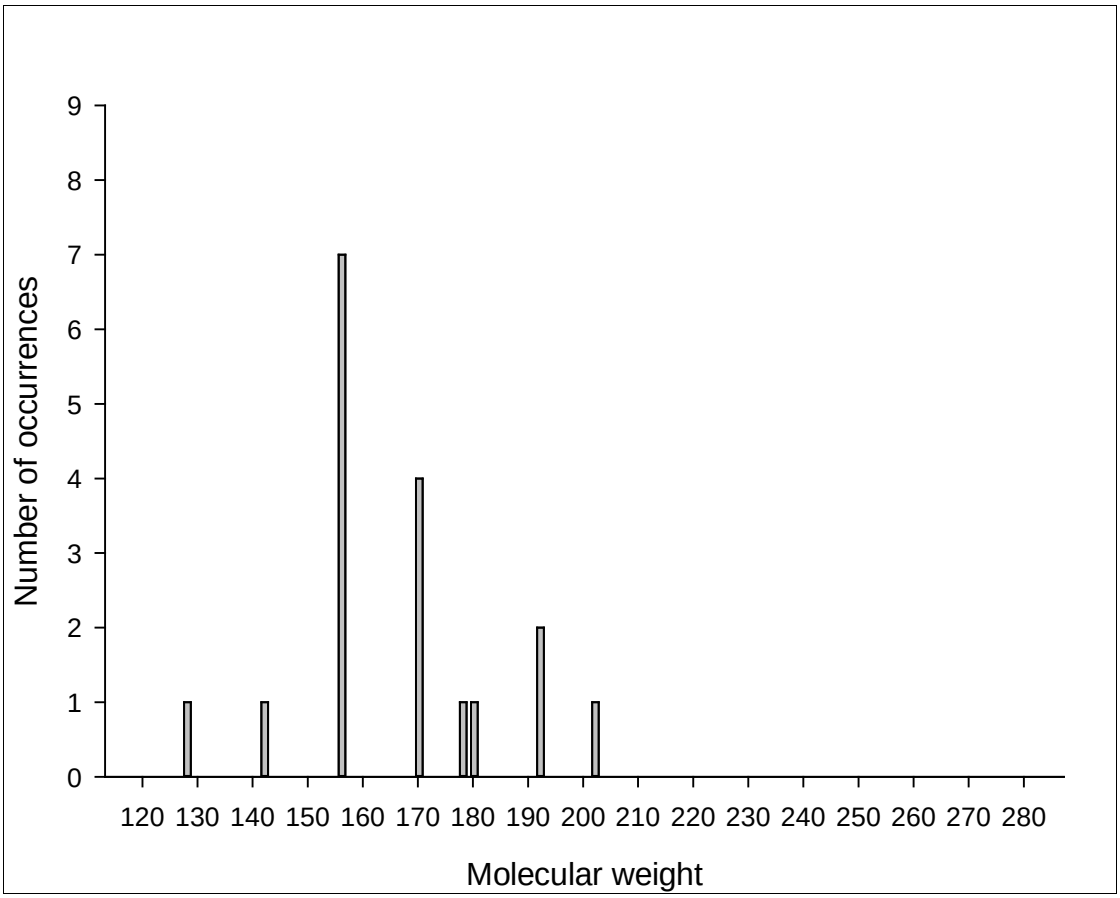


Figure 7.33. Count of PAHs by molecular weight from samples of feathers of brown pelican chicks in the Northern GOM, 2014–2015.

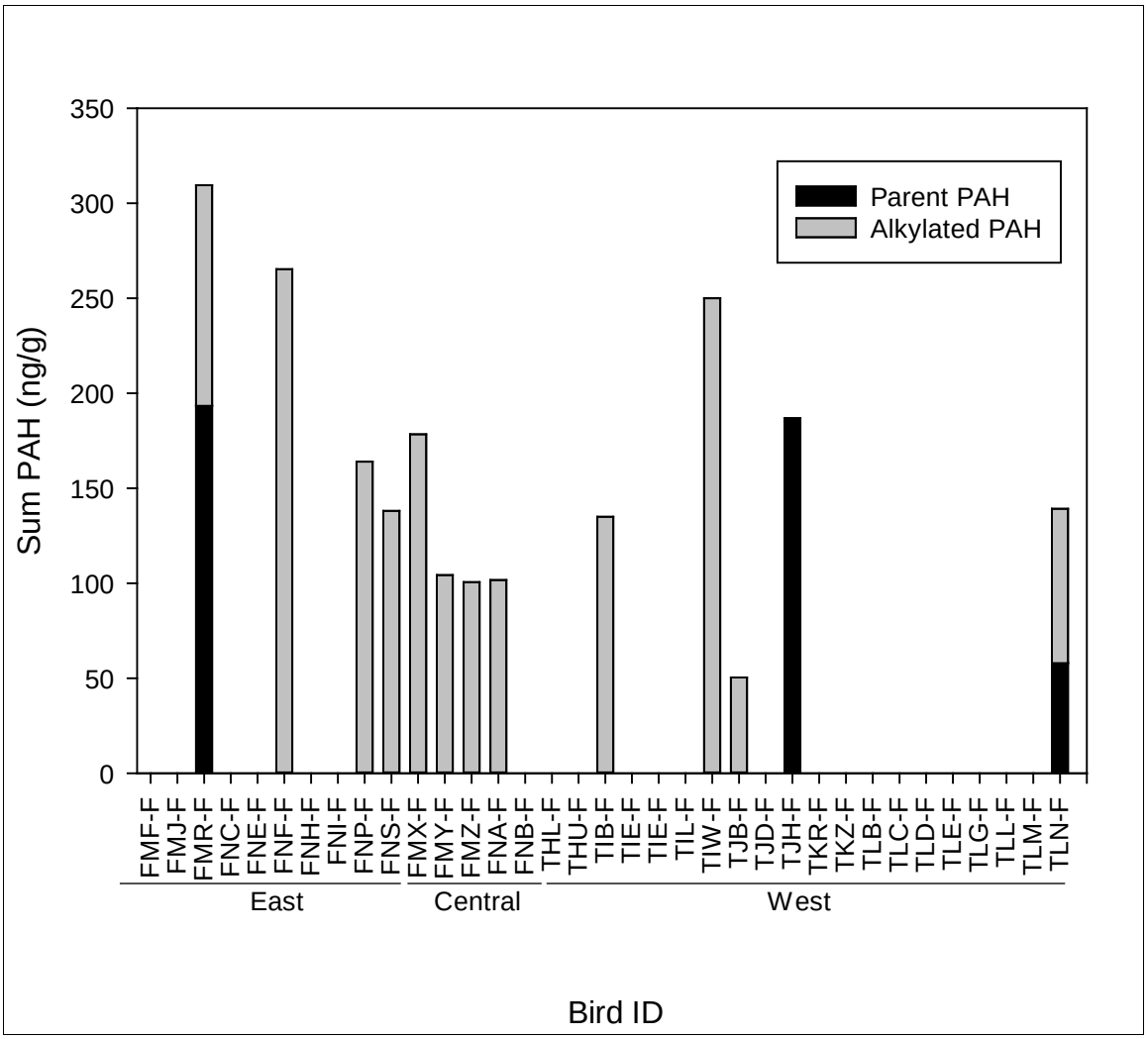


Figure 7.34.a. Summation of PAHs by individual from feather samples of brown pelican chicks in the Northern GOM, 2014–2015: total PAH concentration (ng g^{-1}; dry weight) of parent and alkylated PAHs in feathers of chicks.

Bird ID = the three-letter combination from the field-readable plastic leg band applied to the chick. F = feather sample.

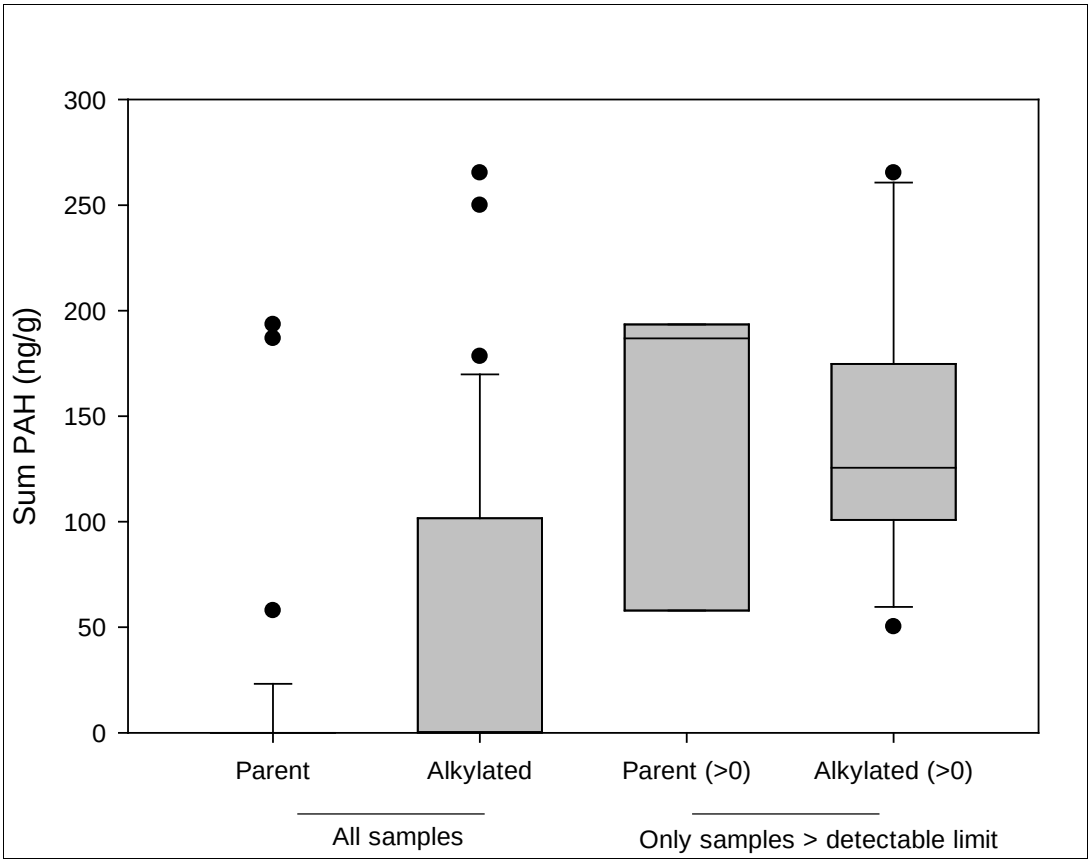


Figure 7.35.b. Summation of PAHs by individual from feather samples of brown pelican chicks in the Northern GOM, 2014–2015: box plots of PAH concentration (ng g^{-1}; dry weight) of parent and alkylated PAHs in feathers of chicks.

The two left-side boxes include data from all individuals. The two right-side boxed include only data where PAHs were > detectable limit (i.e., non-zero data).

8 Conclusions and Future Directions

To date, the research described in this report is one of the most spatially and temporally extensive research efforts conducted on the Eastern brown pelican. Although the brown pelican has been a species of conservation concern in the GOM for decades, the species has been relatively understudied in the Northern GOM until research was initiated in approximately 2010 and after (e.g., Walter et al. 2013, 2014; this report). For example, before 2010, there were substantial data gaps on productivity, chick survival, and chick condition, and on the variability within each of those parameters both within and among colonies and years. Our understanding of movement patterns during breeding and nonbreeding was limited to band return studies and anecdotal evidence of home range sizes, often from areas outside the GOM. These data gaps set the context for the research described herein. We focused on three primary areas of pelican ecology: (a) reproductive ecology, (b) spatial ecology and movement, and (c) health and exposure to contaminants.

To date (February 2020), our research effort has contributed, either in whole or in part, to the following theses, dissertations, and published manuscripts (listed chronologically):

Lamb JS. 2016 Ecological drivers of brown pelican movement patterns and reproductive success in the Gulf of Mexico [dissertation]. Clemson (SC): Clemson University.

Lamb JS, O'Reilly KM, Jodice PGR. 2016. Physical condition and stress levels during early development reflect feeding rates and predict pre- and post-fledging survival in a nearshore seabird. Conserv Physiol. 4(1): cow060. doi:10.1093/conphys/cow060

Lamb JS, Satgé YG, Fiorello CV, Jodice PGR. 2016. Behavioral and reproductive effects of bird-borne data logger attachment on Brown Pelicans on three temporal scales. J Ornith. 158: 617-627.

Haney JC, Jodice PGR, Montevecchi WA, Evers DC. 2017. Challenges to oil spill assessment for seabirds in the deep ocean. Arch Environ Contam Toxicol. 73: 33-39.

Lamb JS, Satgé YG, Jodice PGR. 2017. Diet composition and provisioning rates of nestlings determine reproductive success in a subtropical seabird. Mar Ecol Prog Ser. 581:149-164.

Lamb JS, Satgé YG, Jodice PGR. 2017. Influence of density-dependent competition on foraging and migratory behavior of a subtropical colonial seabird. Ecol Evol.7(16):1–13. DOI: 10.1002/ece3.3216

Lamb JS, Newstead DJ, Koczur LM, Ballard BM, Green CM, Jodice PGR. 2018. A bridge between oceans: Overland migration of marine birds in a wind energy corridor. J Avian Biol. 49(2): e01474. doi: 10.1111/jav.01474

Streker R. 2019. Reproductive ecology and diet of brown pelicans in the Gulf of Mexico [thesis]. Clemson (SC): Clemson University.

Lamb JS, Satgé YG, Jodice PGR. 2019. Seasonal variation in environmental and behavioral drivers of annual-cycle habitat selection in a nearshore seabird. Divers Distrib. 00:1–13. doi.org/10.1111/ddi.13015

The remainder of this section provides a summary of key findings, data gaps, and potential directions for future research, particularly because each may relate to decision-making. Summaries are grouped into four topics and discussed in turn: spatial ecology, diet and forage fish, risk exposure, and long-term monitoring.

8.1 Spatial Ecology: Home Range, Migration, and Movement

Tracking individual pelicans using GPS-equipped satellite tags allowed us to accumulate several locations per day per bird. Tag duration was typically sufficient to allow us to calculate home range sizes during the breeding season and migration patterns during the nonbreeding season. We assessed characteristics of movement patterns during both breeding and nonbreeding in relation to colony and individual characteristics, with a particular emphasis on the potential role that density of breeding birds might have on spatial ecology.

Data from GPS tracking revealed that colony characteristics more so than individual characteristics determined the foraging ranges of breeding pelicans, and that foraging locations were not unique or specific to a given colony. For example, 50% core areas for individuals ranged from < 10 km^2 (6.21 mi^2) to ca. 500 km^2 (310.69 mi^2) and 95% use areas for individuals ranged from < 10 km^2 (6.21 mi^2) to ca. 3500 km^2 (2175 mi^2). The home range size of pelicans during the breeding was not consistent among colonies and we found a positive relationship between both 50% and 95% use areas and the abundance of breeding birds at a colony, suggesting a density dependent effect on movement. We did not detect any effect of sex, body size, or body condition on home range size. We also found that individuals from different colonies overlapped in their space use during the breeding season in all three planning areas of the GOM. Therefore, in the event of an acute stress event that may occur off colony, such as an oil spill, the probability of an individual from a given colony interacting with that stressor will not be based strictly on the distance from the point-event to the nearest colony, but also will need to consider colony size and the distribution of colonies in the area. For example, our data demonstrated that individuals may forage > 100 km (62.1 mi) from their breeding colony and in a locale also frequented by birds from neighboring colonies.

Our data demonstrated that brown pelicans in the GOM are partially migratory. As a population, partial migration leads to migration probabilities and distances that are inconsistent even within a single colony. In our study we found that migration distance of individuals ranged from < 50 km (31 mi) to approximately 2500 km (1553 mi). At the colony level the proportion of migrants ranged from approximately 25% to approximately 75%. Both migration distance and migration probability were positively related to the abundance of breeding birds at a colony, suggesting a positive effect of density on migration. Migration strategies also varied with individual characteristics, including sex and body size. As with home ranges during the breeding season we also found that individuals from different colonies and even different planning areas of the GOM overlapped spatially and temporally during staging and migration. For example, pelicans from all three planning areas overlapped in the Mississippi River Delta region of Louisiana during staging, suggesting that this area presents a hot spot for migrating pelicans at a specific time of year (migration) when birds may be physically stressed. Birds from the western and central GOM also overlapped on wintering grounds along the Yucatan Peninsula (an area not used by pelicans from the eastern GOM). As with the breeding season, therefore, our ability to predict the probability of birds from a specific colony being affected by a localized stressor event is complicated by the intra- and inter-colony differences observed in migration patterns. Furthermore, our data showed that pelicans breeding in Texas and Louisiana also winter along the Pacific coast of Mexico. Movement between ocean basins are uncommon for seabirds and, for pelicans, such migratory routes may facilitate genetic mixing and help distribute risk across populations.

We also documented some unique attributes of migration paths of pelicans during our study. Over-water migrations were not uncommon. These included north-south transits across the GOM from the Louisiana Delta region to the Yucatan Peninsula, and from the Florida Keys to Cuba. During these transits, individuals were using pelagic waters. Additional data on pelicans' use of GOM pelagic waters is being collected by vessel-based surveys of the Gulf of Mexico Marine Assessment Program for Protected Species (GoMMAPPS). Combining tracking data from our study with observation-based data from those vessel surveys may provide a unique opportunity to explorepelicans' use of GOM pelagic waters. The migration of GOM pelicans to Cuba also suggests that spatial overlap occurs with pelicans that breed along the Atlantic coast of the US and also migrate to Cuban waters (Poli 2015). Whether pelicans that breed in other areas of the Caribbean also migrate to Cuban waters is not well known, but it appears that Cuba could represent an overlap in migration among multiple populations of pelicans.

The movement data we collected clearly demonstrates a wide range of patterns within and among colonies. Such variability presents numerous challenges with respect to our ability to link a specific colony to a specific location that may experience an acute stress event such as an oil spill. Our data demonstrate that proximity from a colony to a localized stress event cannot be used as the sole predictor of the probability of a bird encountering that stress event. The spatial and temporal overlap in use areas by birds from different colonies furthers that concept. Several factors related to colony and individual dynamics will also affect that probability. Our data suggest that the continued development of maps of use areas specific to colonies are an important step in our ability to assess risk or damage to specific colonies. In the context of linking environmental attributes or stress events to specific colonies, our data demonstrate that colonies and the individuals that occupy them are being affected by conditions that range spatially over three orders of magnitude during the breeding season (1s–100s km) and over four orders of magnitude during the nonbreeding season (1s–1000s km).

8.2 Diet and Forage Fish

Although the diet of pelicans in the GOM has been broadly defined as being focused on menhaden, details pertaining to diet and its effect on productivity have been less clear. We collected diet data from chicks during the breeding season from pelican colonies throughout the Northern GOM. Our analysis sought to define the diet composition of pelican chicks and the relative quantity and quality of the diet. We assessed the contribution of provisioning rates, meal size, and energy density of meals to productivity, and did so within the context of the nutritional-stress and junk-food hypotheses. Our study marks one of the first to do so for subtropical seabirds, with most previous assessments occurring in temperate or cold-water systems.

We found that menhaden made up 60–85% of the diet of pelican chicks at colonies within the summer range of menhaden, but < 40% at colonies outside of the core summer range of menhaden. Other primary prey included fish from the Perciformes, Mugiliformes, and Clupeiformes. Our data suggest that diet composition is not uniform throughout the Northern Gulf and therefore that any efforts to assess the availability of forage fish as it may relate to pelican foraging or breeding need to consider species beyond menhaden and colonies from throughout the region.

We also examined the primary components of meals fed to chicks and related those to productivity. Meal delivery rate, meal size, and energy density of meals all were positively related to productivity. Of these, however, the rate at which meals were provisioned had the strongest effect on chick survival. We found that the lipid density of prey was not as important as the provisioning rate or the size of the meal. Our results indicate, therefore, that the biomass of food provisioned rather than the energy content of the food provisioned was a more important driver of reproductive success in pelicans. Most previous studies that have examined the relationship of the quantity and quality of diet to reproductive success have occurred

in colder water systems and our data suggest that applying concepts from such studies to pelicans in subtropical waters could be misleading. In the Northern GOM, therefore, it appears that reproductive success of pelicans is strongly linked to their ability to locate and successfully forage on abundant, small, schooling fish and in so doing maintain a high rate of meal provisioning. Any stressors that would reduce the availability of such prey could subsequently have a detrimental effect on reproductive success of pelicans and hence population dynamics.

Despite the spatially and temporally extensive nature of our diet assessment, several important aspects of pelican diet remain unknown or unclear. Here we summarize three issues that may warrant attention.

(1) The frequency, timing, and location of interactions between pelicans and commercial fisheries throughout the GOM are relatively unclear. Our diet data included several species of fish that were likely sourced from discarded bycatch at trawlers (e.g., Perciformes not typically found in the upper meters of the water column). The abundance of these prey in the diet appears to differ among planning areas in the GOM, being more predominant in the western colonies that are located on the edge or outside of the range of menhaden. Improving our understanding of the role these prey items have in the diet of pelicans during the breeding season may be particularly important in the western planning area of the GOM, and in other locations if menhaden availability declined or if changes in trawling activity (e.g., intensity or location) occurred.

(2) The diet of pelicans during migration and wintering seasons remains understudied. Given the wide range in migration strategies and endpoints, and the potential stress that individuals encounter outside of the breeding season, an assessment of diet throughout their nonbreeding range would be an important contribution to better understanding their annual cycle.

(3) It is unclear how natural and anthropogenic stressors, either acute or chronic, may affect the availability of prey or the quality of prey. For example, acute stress events (e.g., oil spill) may inhibit recruitment of year classes of prey, and chronic stress events (e.g., continued exposure to a pollutant) may increase contaminant loads in prey. Our diet data, as well as the features of the diet that are less clear, all suggest that a monitoring program for diet throughout the Northern GOM would provide useful baseline and longitudinal data for managers and decision-makers. The opportunity to collect diet samples directly, as well as to assess diet composition using fecal DNA signatures and analysis of stable isotopes, provides a range of techniques with which to undertake such long-term monitoring.

8.3 Risk Exposure

For brown pelicans in the Northern GOM, risk exposure is a complex response that considers spatial and temporal dynamics as well as characteristics of individual birds. We set our risk exposure models within the three BOEM planning areas: oil and gas development was highest in the central planning area and least in the eastern planning area. We expanded our assessment of risk exposure, however, beyond oil and gas infrastructure and also included exposure to surface pollutants and shipping lanes, two additional stressors of potential significance for pelicans that forage and move primarily in nearshore waters.

Exposure was least in the eastern planning area and higher but similar between the central and western planning areas. The similarity in exposure between the central and western planning areas is due to the inclusion of multiple sources of risk. Had our assessment of risk been based solely on the abundance of oil and gas platforms within a planning area, pelicans in the central planning area would have been exposed to higher levels of risk compared to pelicans in the eastern or western planning areas. By adding risk associated with shipping lanes, however, the western and central planning areas became more similar with respect to exposure. The similarity in exposure between the western and central planning areas also

was based in part on movement patterns of individual birds. Our tracking data revealed that pelicans that were breeding in the western planning area often migrated through the central planning area (e.g., Louisiana delta) and therefore they became exposed to each of the three sources of risk we modeled in that planning area. In general, males experienced higher levels of risk compared to females due in large part to the lower probability of migration in males.

Spatially, we found that each planning area had some overlap between preferred habitat of pelicans and surface pollutants at some time of the year. We also detected hot spots of overlap between preferred habitat and surface pollutants year-round within the areas of the Louisiana delta and Galveston Bay. Temporally, exposure tended to be highest when individuals were constrained spatially within a location that had higher levels of pollutants. For example, individuals constrained by central place foraging during the breeding season or by molt during the nonbreeding season tended to have higher exposure to the risks we modeled. In terms of the avian annual cycle, post breeding was the time of maximum exposure and this was due in part to the overlap of use of the central planning area (i.e., Louisiana delta) by birds from all three planning areas during the physiologically stressful process of molt.

Many models of risk exposure for seabirds are limited to assessing spatial and temporal overlap of birds with sources of risk, particularly those based on data obtained by surveys (e.g., aerial or vessel-based surveys of specific locations). An advantage to the models we present is the inclusion of behavior to further refine the level of risk an individual is experiencing. We used detailed aspects of movement available from tracking data to determine the behavioral state (i.e., transient or resident) of birds and by doing so were able to weight risk more towards birds that were resident. By considering the spatial and temporal resolution at which tracking data are collected (e.g., by recording more locations in a shorter amount of time), researchers and decision-makers could enhance the short-term accuracy of the classified behaviors and therefore model the exposure risk at different scales.

Our risk exposure model does not consider pelican use of the southern GOM or Cuba during the nonbreeding season. For example, females in our model were predicted to be exposed to lower levels of risk compared to males, and this was due in part to the greater probability of females migrating out of the Northern GOM, compared to males. Our models were not able to readily parameterize risk outside of the Northern GOM, however, creating a data gap that may alter the risk experienced by migrating birds. Risk models also can be enhanced by including exposure to potential development of wind power infrastructure, an aspect of risk not assessed during this study. Our research was also not focused on assessing risk to natural stressors. For example, pelicans appear to be susceptible to acute spells of cold weather and modeling the risk associated with such exposure both spatially and temporally could enhance the ability of managers to predict injury to birds during the nonbreeding season. Recent research in the Atlantic is also assessing the behavioral and spatial response of pelicans to tropical storms (Wilkinson et al. 2019). Developing such a model for the Northern GOM also could inform managers to potential seasonal risks. Our risk assessment models also do not explicitly consider the extended breeding season for pelicans in the GOM, and the asynchronous nature of their breeding within a season. For example, an acute stressor (e.g., flood event) could occur during a time when, even within a colony, breeding effort ranged from early incubation to mid chick-rearing. The reproductive cost of such an event could easily be misinterpreted if it were assumed all pairs were at the same stage of breeding.

The PAH profile of brown pelicans in the Northern GOM was diverse and comprised predominantly of alkylated PAHs, suggesting petrogenic sources. Of the 24 PAHs assessed, 17 occurred at least once when data were pooled among all three sample sets (i.e., adult blood, adult feathers, chick feathers). Each of the eight alkylated PAHs was observed at least once among the three sample sets, and nine of the 16 parent PAHs were detected at least once. Six of the eight alkylated PAHs were found in all three sample sets and only three of the 16 parent PAHs were detected in all three data sets. There were no PAHs found in chicks that were not also found in adults, suggesting that chicks represent a subset of the adult data.

Three alkylated PAHs were the most frequently occurring among all three data sets: 2,3,5-trimethylnaphthalene, 1,3-dimethylnaphthalene, and 2,6-dimethyl naphthalene. In contrast, seven parent PAHs were never detected: chrysene, benzo(b)fluoranthene, benzo(k)fluoranthene, benzo(a)pyrene, indeno(1,2,3-cd)pyrene, dibenz(a,h)anthracene, benzo(g,h,i)perylene. Among parent PAHs that were detected, there was no clear pattern in the frequency of their occurrence among the three sample sets.

8.4 Methodological and Monitoring Assessments

Two aspects of our study design that are relevant for the development of future research and monitoring are (1) the effects of loggers on individual behavior and (2) the potential use of biomarkers for long-term monitoring. Each are briefly reviewed in turn.

The use of GPS tracking loggers is common in all aspects of wildlife research yet direct examinations of the effects of capture and attachment are still lacking. We used both field data and captive trials to assess the short-term effects of loggers on pelican behavior, and season-long monitoring to assess impacts of tagging on attendance and abandonment of nests. We found no strong effects of tagging on individual behavior or nest abandonment, but did find that the duration of handling during the tagging event was an important factor in the short- and long-term response of individuals. Our data suggest that efforts to minimize handling time will reduce negative effects of tagging on breeding birds in both the short- and long-term. One aspect of tagging that we did not investigate was the use of harness materials other than Teflon ribbon. Such an assessment was beyond the scope of this study but other studies of plunge-diving birds have used or are experimenting with implanted transmitters and silicone harnesses. Results from such assessments should be considered in future study design.

Biomarkers can be used to establish baselines of overall health for a population, or to investigate specific aspects of a stressor on a population. Here we used a specific biomarker, CORT, to assess levels of baseline stress in chicks. The use of CORT is widespread in wildlife conservation research although the use of feathers as a medium is more recent. Feathers have the advantage of incorporating stress over a longer period of time compared to blood, and are less invasive to collect. We found that the concentration of CORT in feathers served as a viable predictor for a suite of relevant ecological and biological parameters including nutritional stress and ultimately survival of chicks to fledging. Given the relative ease with which feathers can be collected, our data suggest that a long-term monitoring program could be established using this physiological marker. Doing so would allow for the long-term assessment of environmental conditions on pelican chicks, and may also serve as an index for productivity, typically a time-consuming parameter to measure in pelicans. If similar relationships were established between feather CORT and condition and survival in other coastal species (e.g., terns, skimmers), a region-wide, long-term, multi-species monitoring plan could be established.

Reference levels for hematology and plasma chemistry also can provide a tool for long-term tracking of individual health as well as changing relationships between blood analytes and among environmental variables of interest (e.g., planning area, sex, BCI). Our data provide reference levels for a time period following a major spill event, and therefore a further assessment conducted additional years out from the

event (e.g., 5 and 10-years post spill) may also provide context for the stability of reference levels. Long-term tracking of PAHs, as well as an assessment of sublethal effects of PAHs on pelicans, can also enhance our understanding of the persistence and effects of this contaminant in the Northern GOM. We assessed PAH loads in blood and feathers, but recent studies also suggest that preen oil can also be used to assess PAH levels (Acampora et al. 2018). Assessing PAH levels through multiple matrices (e.g., blood, feathers, preen oil) may provide a more complete picture of contamination (Acampora et al. 2018). Further, the expansion or establishment of time series monitoring of ecosystem components likely to be exposed to petroleum releases, including the incorporation of alkylated PAHs into analyses to reflect exposure to crude oil, has been recommended (National Research Council 2003).

8.5 Additional Information Needs

8.5.1 Colony Atlas and Nonbreeding Surveys

A current registry or colony atlas for pelicans in the Northern GOM that is region-wide and accessible to the broader avian conservation community is an important but currently missing tool and/or data source (Jodice et al. 2019, Ferguson et al. 2018). Such an atlas could also include the entire suite of coastal seabirds that nest in the region. Although each state collects some level of data on abundance of breeding seabirds, the timing, frequency, type, and protocols associated with surveys are not consistent, inhibiting effective and efficient regional assessments. Furthermore, such a product would provide a useful tool for response to future anthropogenic or natural stressors such as oil spills, contamination events, hurricanes, or flooding events. Periodic assessments of variables beyond nest counts (e.g., productivity, provisioning rates, chick condition, nestling diets) also are lacking. Such colony-level attributes would enhance our understanding of mechanisms underlying colony dynamics and also would be a valuable resource when responding to acute or chronic stress events (Jodice et al. 2019).

Similarly, data on the distribution and abundance of pelicans and their allies during the nonbreeding season are lacking. Although tracking data such as ours can inform managers and stakeholders regarding habitat use during the nonbreeding season, a coordinated survey effort of the coastal zone that emphasized nearshore species would provide longer-term data that could be used in a manner similar to that contained in a breeding atlas. Such data would allow for the assessment of distribution and abundance of migrants and an identification of roosting and foraging sites that may not be a focus during the breeding season. Given that pelicans range extensively throughout the GOM, declines observed at any single colony may not be due strictly to on-colony factors, but rather may be a function of environmental conditions or threats experienced at wintering sites (Szostek and Becker 2015). Therefore, assessment of environmental conditions and stressors in core areas of the wintering range appear warranted.

8.5.2 Colony-based Monitoring

For brown pelicans, data are still lacking on various components of their reproductive ecology, particularly given the spatial extent of nesting in the region. For example, the measurement of growth rates of chicks can provide substantial levels of detail for long-term monitoring strategies or for assessment of stressors. Chick growth can be measured repeatedly on the same individuals to provide growth curves that can be assessed, for example, in relation to environmental stressors or diet (Eggert et al. 2008), or single measures of chick size when collected on many chicks at once can be used to make comparisons among colonies or across time and space (Benson et al. 2003). Results described herein also have demonstrated that biomarkers, such as the measure of CORT in chick feathers, can be used to compare reproductive success among colonies and can be correlated with body condition or fledging success. A monitoring program that included all or some of the above tools would enhance our

understanding of baseline measures of reproductive parameters and provide useful methods for assessing responses to natural and anthropogenic stressors.

For brown pelicans, and for other seabirds that nest in the region, data on adult and juvenile survival are lacking (Shields 2014). Seabirds are long lived (commonly > 20 yrs) and adult survival rates tend to be drivers of population dynamics and recovery in long-lived species (Champagnon et al. 2018). Though banding and extensive band-resight efforts can inform estimates of survival, these approaches can also be challenging. For example, the extensive spatial distribution of colonies throughout the region, the remoteness of some colonies, the ability of individuals to move among colonies within or between years, and delayed maturity that results in a multi-year state of non-residency and multiple transition probabilities among sub-adults makes the detailed estimation of survival using band-resighting challenging and requires a long-term commitment of resources. Therefore, measures of juvenile survival are also difficult to obtain. An alternative or additional approach can include the continuation of long-term tracking studies using various tracking devices. For example, the recent advance in nano-tag technology could allow for the marking of 1000s of individuals throughout the GOM and these could subsequently be "re-captured" by nano-tag arrays deployed throughout the region (Loring et al. 2017). Such a design would overcome the sample size issue associated with deploying expensive satellite tags and the logistical issues associated with manually resighting individuals throughout remote areas.

8.5.3 Prey Monitoring

Our data demonstrated the importance of provisioning rates, and hence prey availability, to reproductive success. Long-term monitoring of prey resources in the Northern GOM would therefore benefit not only our understanding of population dynamics of brown pelicans but also trends in other avian taxa within the region. For example, developing diet databases for focal avian species would allow for long-term assessments in changes of diet composition, diet quality, and diet quantity (Sydeman et al. 2001). A variety of tools including direct observation of chick feeding, stable isotope analysis of blood and feathers, and examination of fecal material for DNA signatures of prey items could be used to develop and maintain a diet database. Further, pelicans and other nearshore and pelagic seabirds interact regularly with commercial fisheries (Jodice et al. 2011). It is likely that discarded bycatch from trawlers in the GOM provides some proportion of the diet but the extent of this has yet to be determined. Without such data, it is difficult to fully understand how changes in commercial fishing activity might affect local populations of prey and their predators. Assessing contaminant loads in prey, such as PAHs, also would allow for longitudinal assessments within food webs.

8.5.4 Expanded Scope: Taxonomic and Spatial

Although our research provided a substantial increase in the quantity and quality of data available on the ecology of brown pelicans, it is important to note that other avian taxa within the guild of nearshore seabirds are understudied and that numerous and substantial data gaps exist. Though some are addressed indirectly above, here we highlight the potential value of expanding data collection focused on spatial ecology and tracking.

The renewed interest in research on brown pelicans during the past decade has not been surprising given their former status as endangered, their focus during oil spill events, and the general interest the species has with stakeholders and the public. Nonetheless, the life history of pelicans and their ecology is somewhat unique among coastal seabirds in the region. Although their breeding sites overlap spatially with many other species, their foraging style and breeding strategy differ from other species in significant ways. For example, pelicans plunge dive and capture large quantities of fish at once, whereas most coastal seabirds that overlap spatially with pelicans in the Northern GOM are surface feeders that capture single prey items (e.g., terns, gulls, and skimmers). Pelicans also have altricial young and a protracted breeding

season. In contrast, terns and skimmers have precocial young and a compact breeding season, relative to pelicans. Taken together, these two differences in life-history strategies suggest that foraging behavior, home range size, provisioning rates, and attendance patterns all may differ among this suite of coastal seabirds and that, as a result, spatial ecology data of pelicans may not be entirely representative of other coastal seabirds. Therefore, expanding tracking efforts to include other coastal seabirds (e.g., terns and skimmers) would enhance our ability to understand the effects of natural and anthropogenic stressors on the coastal seabird community of the Northern GOM. Beyond an expansion of tracking efforts to other coastal seabirds, stakeholders also would benefit from research efforts to simultaneously tag and track apex marine predators across taxonomic classes. For example, examining the spatial and temporal overlap of seabirds and coastal sharks or marine mammals may provide insight into coastal hot spots or forage bases that support multiple predators. Such multi-species assessments can provide a more broad-based view of the structure and function of coastal and marine ecosystems (Harrison et al. 2018).

Two additional opportunities also exist to expand tracking efforts specifically for pelicans. To date, little is known about movement patterns, foraging behavior, and spatial ecology of sub-adult pelicans in the Northern GOM. Efforts to tag and track birds immediately post-fledging could provide important data streams about an individual's initial exposure to natural and anthropogenic threats in the region. For example, it appears that young-of-year birds forage upon discarded bycatch from trawlers, but the extent to which this occurs is unclear and the impact it may have on first-winter survival also remains unknown. Furthermore, although our study area was extensive, there were still spatial gaps in the Northern Gulf that warrant coverage. Two of note include Gaillard Island, Alabama, and the Florida peninsula. Gaillard Island is the largest colony of pelicans in the Northern GOM and a tracking study specifically focused on that area would provide critical data on a core portion of the breeding range. The Florida peninsula also supports pelican colonies and that portion of the GOM, because it is not currently impacted by oil and gas activities, can provide important baseline data for colonies less likely to be affected by such anthropogenic stressors.

Works Cited

Acampora H, White P, Lyashevska O, O'Connor I. 2018. Contrasting congener profiles for persistent organic pollutants and PAH monitoring in European storm petrels (Hydrobates pelagicus) breeding in Ireland: a preen oil versus feathers approach. Environ Sci Pollut Res. 25(17):16933-16944.

Ahrenholz DW. 1991. Population biology and life history of the North American menhadens, Brevoortia spp. Mar Fish Rev. 53(4):3-19.

Ainley DG, Ford RG, Brown ED, Suryan RM, Irons DB. 2003. Prey resources, competition, and geographic structure of kittiwake colonies in Prince William Sound. Ecol. 84(3):709-723.

Ainley DG, Ribic CA, Ballard G, Heath S, Gaffney I, et al. 2004. Geographic structure of Adélie Penguin populations: overlap in colony-specific foraging areas. Ecol Monogr. 74(1):159-178.

Almasi B, Roulin A, Jenni-Eiermann S, Breuner CW, Jenni L. 2009. Regulation of free corticosterone and CBG capacity under different environmental conditions in altricial nestlings. General Comp Endocrinol 164(2-3):117-124.

Alonso-Alvarez C, Ferrer M. 2001. A biochemical study of fasting, subfeeding, and recovery processes in yellow-legged gulls. Physiol Biochem Zool. 74(5):703-713.

Alonso-Alvarez C, Munilla I, López-Alonso M, Velando A. 2007. Sublethal toxicity of the Prestige oil spill on yellow-legged gulls. Environ Int. 33(6):773-781.

Anderson DJ, Ricklefs RE. 1992. Brood size and food provisioning in Masked and Blue-footed Boobies (Sula spp.). Ecology. 73(4):1363-1374.

Angelier F, Shaffer SA, Weimerskirch H, Trouvé C, Chastel O. 2007. Corticosterone and foraging behavior in a pelagic seabird. Physiol Biochem Zool. 80(3):283-292.

Anthony JA, Roby DD, Turco KR. 2000. Lipid content and energy density of forage fishes from the northern Gulf of Alaska. J Exp Biol Ecol. 248(1):53-78.

Arthur SC. 1919. The emblematic bird of Louisiana. Louisiana. Hist Q. 2:255-256.

Ashmole NP. 1971. Seabird ecology and the marine environment. Avian Biol. 1:223-286.

Ballance L, Pitman R. 1999. S34. 4: Foraging ecology of tropical seabirds. In: Adams NJ, Slotow RH, editors. Proceedings of the 22nd International Ornithological Congress, 16–22 August 1998. Durban (ZA): International Ornithological Congress. p. 2057-2071.

Ballance LT. 2007. Understanding seabirds at sea: why and how. Mar Ornith. 35:127-135.

Ballance LT, Ainley DG, Ballard G, Barton K. 2009. An energetic correlate between colony size and foraging effort in seabirds, an example of the Adélie penguin Pygoscelis adeliae. J Avian Biol. 40(3):279-288.

Balseiro A, Espi A, Marquez I, Perez V, Ferreras MC, et al. 2005. Pathological features in marine birds affected by the Prestige's oil spill in the north of Spain. J Wildl Dis. 41(2):371-378.

Barron DG, Brawn JD, Weatherhead PJ. 2010. Meta-analysis of transmitter effects on avian behaviour and ecology. Methods Ecol Evol. 1(2):180-187.

Bauch C, Kreutzer S, Becker PH. 2010. Breeding experience affects condition: blood metabolite levels over the course of incubation in a seabird. J Compar Physiol B. 180(6):835-845.

Bearhop S, Phillips RA, McGill R, Cherel Y, Dawson DA, et al. 2006. Stable isotopes indicate sex-specific and long-term individual foraging specialisation in diving seabirds. Mar Ecol Prog Ser. 311:157-164.

Beaudry F, Demaynadier PG, Hunter Jr ML. 2010. Identifying hot moments in road-mortality risk for freshwater turtles. J Wildl Manage. 74(1):152-159.

Becker BH, Beissinger SR. 2003. Scale-dependent habitat selection by a nearshore seabird, the marbled murrelet, in a highly dynamic upwelling system. Mar Ecol Prog Ser. 256:243-255.

Behrenfeld MJ, Falkowski PG. 1997. Photosynthetic rates derived from satellite-based chlorophyll concentration. Limnol Oceanogr. 42(1):1-20.

Belthoff JR, Gauthreaux Jr SA. 1991. Partial migration and differential winter distribution of House Finches in the eastern United States. The Condor: Ornith Appl. 93(2): 374-382. DOI: 10.2307/1368953

Benson J, Suryan RM, Piatt JF. 2003. Assessing chick growth from a single visit to a seabird colony. Mar Ornith. 31:181-184.

Biasutti M, Sobel AH, Camargo SJ, Creyts TT. 2012. Projected changes in the physical climate of the Gulf Coast and Caribbean. Clim Change. 112(3-4):819-845.

Binford LC. 1989. A distributional survey of the birds of the Mexican state of Oaxaca (No. 598.2 AME). Ornith Monogr. (43):1-418.

Blas J, Baos R, Bortolotti GR, Marchant T, Hiraldo F. 2005. A multi-tier approach to identifying environmental stress in altricial nestling birds. Funct Ecol. 19(2):315-322.

Blus LJ. 1982. Further interpretation of the relation of organochlorine residues in brown pelican eggs to reproductive success. Environ Pollut Ser A. 28(1):15-33.

Boesch DF, Rabalais NN, eds. 1987. Long-term environmental effects of offshore oil and gas development. London (GB): Taylor & Francis.

Bonal R, Aparicio JM. 2008. Evidence of prey depletion around lesser kestrel Falco naumanni colonies and its short-term negative consequences. J Avian Biol. 39(2):189-197.

Bonier F, Martin PR, Sheldon KS, Jensen JP, Foltz SL, et al. 2006. Sex-specific consequences of life in the city. Behav Ecol. 18(1):121-129.

Bonier F, Moore IT, Martin PR, Robertson RJ. 2009. The relationship between fitness and baseline glucocorticoids in a passerine bird. General Comp Endocrinol. 163(1-2):208-213.

Bonter DN, MacLean SA, Shah SS, Moglia MC. 2014. Storm-induced shifts in optimal nesting sites: a potential effect of climate change. J Ornith. 155(3): 631-638.

Börger L, Dalziel BD, Fryxell JM. 2008. Are there general mechanisms of animal home range behaviour? A review and prospects for future research. Ecol Lett. 11(6):637-650.

Bortolotti GR, Marchant TA, Blas J, German T. 2008. Corticosterone in feathers is a long-term, integrated measure of avian stress physiology. Funct Ecol. 22(3):494-500.

Boyer TP, Biddle M, Hamilton M, Mishonov AV, Paver CR, et al. 2011. Gulf of Mexico regional climatology [dataset]. Washington (DC): National Oceanic and Atmospheric Administration, National Centers for Environmental Information. NCEI Accession 0123320. National Centers for Environmental Information. [accessed 2016 February 1]. https://doi.org/10.7289/V5C53HSW .

Breuner CW, Sprague RS, Patterson SH, Woods HA. 2013. Environment, behavior and physiology: do birds use barometric pressure to predict storms? J Experim Biol. 216(11):1982-1990.

Briggs KT, Lewis DB, Tyler WB, Hunt Jr GL. 1981. Brown pelicans in southern California: habitat use and environmental fluctuations. The Condor: Ornith Appl. 83(1):1-15.

Britton JC, Morton B. 1989. Shore ecology of the Gulf of Mexico. 396 p. Austin: University of Texas Press.

Brown CR, Brown MB. 1996. Coloniality in the cliff swallow: the effect of group size on social behavior. 580 p. Chicago (IL): University of Chicago Press.

Brown S, Gratto-Trevor C, Porter R, Weiser EL, Mizrahi D, et al. 2017. Migratory connectivity of Semipalmated Sandpipers and implications for conservation. The Condor: Ornith Appl. 119(2): 207-224.

Bureau of Ocean Energy Management. Platforms [dataset]. Washington (DC): Bureau of Ocean Energy Management, Data Center. Vector digital data [accessed 2016 February 1]. https://www.data.boem.gov/Main/Mapping.aspx

Burger AE. 1993. Estimating the mortality of seabirds following oil spills: effects of spill volume. Mar Poll Bull. 26(3):140-143.

Burke CM, Montevecchi WA, Wiese FK. 2012. Inadequate environmental monitoring around offshore oil and gas platforms on the Grand Bank of Eastern Canada: Are risks to marine birds known? J Environ Manage. 104:121-126.

Burnham KP, Anderson DR. 2004. Multimodel inference: understanding AIC and BIC in model selection. Socio Methods Res. 33(2):261-304.

Burnham KP. 1993. A theory for combined analysis of ring recovery and recapture data. In: Lebreton J-D, North PM, editors. Marked individuals in the study of bird population. 397 p. Basel (CH): Birkhauser Verlag. p.199-213.

Butler MW, Leppert LL, Dufty Jr AM. 2009. Effects of small increases in corticosterone levels on morphology, immune function, and feather development. Physiol Biochem Zool. 83(1):78-86.

Butler RG, Harfenist A, Leighton FA, Peakall DB. 1988. Impact of sublethal oil and emulsion exposure on the reproductive success of Leach's storm-petrels: short and long-term effects. J Appl Ecol. 25(1):125-143.

Cabrera-Cruz SA, Cervantes-Pasqualli JA, Inzunza ER, Hernandez-Morales T Villegas-Patraca R. 2017. Raptor and large soaring bird migration across the Isthmus of Tehuantepec, Mexico: distribution, seasonality, and phenology. Bird Conserv Int. 27(1):111-126.

Cairns DK. 1992. Population regulation of seabird colonies. In: Power DM, editor. Current ornithology, vol. 9. Boston (MA): Springer. p. 37-61.

Calenge C. 2006. The package “adehabitat” for the R software: a tool for the analysis of space and habitat use by animals. Ecol Modell. 197(3-4): 516-519.

Calenge C, Darmon G, Basille M, Loison A, Jullien JM. 2008. The factorial decomposition of the Mahalanobis distances in habitat selection studies. Ecology. 89(2):555-566.

Campagna C, Short FT, Polidoro BA, McManus R, Collette BB, et al. 2011. Gulf of Mexico oil blowout increases risks to globally threatened species. BioScience. 61(5):393-397.

Catry T, Ramos JA, Le Corre M, Phillips RA. 2009. Movements, at-sea distribution and behaviour of a tropical pelagic seabird: the wedge-tailed shearwater in the western Indian Ocean. Mar Ecol Prog Ser. 391:231-242.

Champagnon J, Lebreton JD, Drummond H, Anderson DJ. 2018. Pacific Decadal and El Niño oscillations shape survival of a seabird. Ecology. 99(5): 1063-1072.

Chapman BB, Brönmark C, Nilsson JÅ, Hansson LA. 2011. The ecology and evolution of partial migration. Oikos. 120(12): 1764-1775.

Cheng S, Kong J, Song H. 2009. Wenchuan 512 earthquake and giant panda habitat in Wolong, China: a review of strong earthquake effects. Front Forestry China. 4(4):388-393.

Clark JD, Dunn JE, Smith KG. 1993. A multivariate model of female black bear habitat-use for a geographic information system. J Wildl Manage. 57(3):519-526.

Cohen LA, Pichegru L, Grémillet D, Coetzee J, Upfold L, et al. 2014. Changes in prey availability impact the foraging behaviour and fitness of Cape gannets over a decade. Mar Ecol Prog Ser. 505: 281-293.

Coleman FC, Baker PB, Koenig CC. 2004. A review of Gulf of Mexico marine protected areas: successes, failures, and lessons learned. Fisheries. 29(2):10-21.

Colibri Ecological Consulting and R.G. Ford Ecological Consulting. (2015). Analysis of 2010-2013 photographic census data from waterbird breeding colonies in the vicinity of the Deepwater Horizon Oil Spill. Draft Final Report prepared for U.S. Fish and Wildlife Service.

Cristol DA, Baker MB, Carbone C. 1999. Differential migration revisited: latitudinal segregation by age and sex class. In: Nolan V, Ketterson ED, Thompson CF, (eds). Current ornithology, vol. 15. Boston (MA): Springer. p. 33-88.

Croxall JP, Butchart SH, Lascelles BEN, Stattersfield AJ, Sullivan BEN, et al. 2012. Seabird conservation status, threats and priority actions: a global assessment. Bird Conserv Intl. 22(1): 1-34.

Daan R, Mulder M. 1996. On the short-term and long-term impact of drilling activities in the Dutch sector of the North Sea. ICES J Mar Sci. 53(6):1036-1044.

Daunt F, Afanasyev V, Silk JRD, Wanless S. 2006. Extrinsic and intrinsic determinants of winter foraging and breeding phenology in a temperate seabird. Behav Ecol Sociobiol. 59(3):381-388.

Davis RW, Evans WE, Würsig B, editors (Texas A&M University at Galveston). 2000. Cetaceans, sea turtles and seabirds in the Northern Gulf of Mexico: distribution, abundance and habitat associations Volume I: executive summary. 40 p. New Orleans (LA): Department of the Interior Minerals Management Service, and Washington (DC): US Geological Survey Biological Resources Division. OCS Study MMS 2000-002. Contract No.: 1445-CT09-96-0004 and 1445-IA09-96-0009.

Day RH, Nigro DA, Prichard AK. 2000. At-sea habitat use by the Kittlitz's murrelet Brachyramphus brevirostris in nearshore waters of Prince William Sound, Alaska. Mar Ornith. 28:105-114.

Dean KM, Bursian SJ, Cacela D, Carney MW, Cunningham FL, et al. 2017. Changes in white cell estimates and plasma chemistry measurements following oral or external dosing of double-crested cormorants, Phalacocorax auritus, with artificially weathered MC252 oil. Ecotoxicol Environ Saf. 146:40-51.

Deegan LA. 1990. Effects of estuarine environmental conditions on population dynamics of young-of-the-year Gulf Menhaden. Mar Ecol Prog Ser. 68):195-205.

Deepwater Horizon Natural Resource Damage Assessment Trustees. 2016. Deepwater Horizon oil spill: Final Programmatic Damage Assessment and Restoration Plan and Final Programmatic Environmental Impact Statement. Retrieved from http://www.gulfspillrestoration.noaa.gov/restoration-planning/gulf-plan

Desholm M, Kahlert J. 2005. Avian collision risk at an offshore wind farm. Biol Lett. 1(3): 296-298.

Diamond AW. 1978. Feeding strategies and population size in tropical seabirds. Am Nat. 112(983): 215-223.

Dolédec S, Chessel D, Gimaret-Carpentier C. 2000. Niche separation in community analysis: a new method. Ecology. 81(10): 2914-2927.

Drent RH, Daan S. 1980. The prudent parent: energetic adjustments in avian breeding. Ardea. 68: 225-252.

Drewitt AL, Langston RH. 2006. Assessing the impacts of wind farms on birds. Ibis. 148(s1): 29-42.

Duncan CD, Havard RW. 1980. Pelagic birds of the northern Gulf of Mexico. Am Birds. 34 (March):122-132.

Dunstan TC. 1972. A harness for radio-tagging raptorial birds. Inland Bird Band News. 44:4-8.

Duong T. 2015. Ks: kernel smoothing. In: R Package Version 1.10.1. https://CRAN.R-project.org/package=ks

Eggert LM, Jodice PG. 2008. Growth of Brown Pelican nestlings exposed to sublethal levels of soft tick infestation. The Condor: Ornith Appl. 110(1):134-142.

Eggert LM, Jodice PG, O'Reilly KM. 2010. Stress response of brown pelican nestlings to ectoparasite infestation. Gen Compar Endocrinol. 166(1):33-38.

Eppley ZA, Rubega MA. M.A., 1990. Indirect effects of an oil spill: Reproductive failure in a population of south Polar skuas following the "Bahia Paraiso" oil spill in Antarctica. Mar Ecol Prog Ser. 67(1): 1-6.

Eppley ZA. 1992. Assessing indirect effects of oil in the presence of natural variation: the problem of reproductive failure in South Polar skuas during the Bahia Paraiso oil spill. Mar Poll Bull. 25(9-12): 307-312.

Erwin RM. 1977. Foraging and breeding adaptations to different food regimes in three seabirds: the Common Tern, Sterna hirundo, Royal Tern, Sterna maxima, and Black Skimmer, Rynchops niger. Ecology. 58(2): 389-397.

Fairhurst GD, Dawson RD, van Oort H, Bortolotti GR. 2014. Synchronizing feather-based measures of corticosterone and carotenoid-dependent signals: what relationships do we expect? Oecologia. 174(3): 689-698.

Fairhurst GD, Marchant TA, Soos C, Machin KL, Clark RG. 2013. Experimental relationships between levels of corticosterone in plasma and feathers in a free-living bird. J Exper Biol. (Nov 1): 216(Pt 21):4071-4081. doi:10.1242/jeb.091280

Fairhurst GD, Navarro J, González-Solís J, Marchant TA, Bortolotti GR. 2012. Feather corticosterone of a nestling seabird reveals consequences of sex-specific parental investment. Proc R Soc London Ser B. 279(1726):177-184.

Ferguson LM, Norton TM, Cray C, Oliva M, Jodice PG. 2014. Health assessments of brown pelican (Pelecanus occidentalis) nestlings from colonies in South Carolina and Georgia, USA. J Zoo Wildl Med. 45(4):802-812.

Ferguson LM, Satgé YG, Tavano J, Jodice PGR. 2018. Seabird colony registry and atlas for the Southeastern US Final report. 26 p. Clemson (SC): US Fish and Wildlife Service and South Carolina Cooperative Fish and Wildlife Research Unit. https://docs.wixstatic.com/ugd/641a0f_b95253e3f0354ec1a93fadec782a8950.pdf

Fiorello C. 2019. Seabirds and waterfowl. In: Heatley JJ, Russell KE, editors. Exotic animal laboratory diagnosis. 664 p. New York: John Wiley & Sons. p. 585-606.

Fogarty MJ, Nesbitt SA, Gilbert CR. 1981. Diet of nestling brown pelicans in Florida. Florida Field Nat. 9(3):38-40.

Ford RG, Ainley DG, Brown ED, Suryan RM, Irons DB. 2007. A spatially explicit optimal foraging model of Black-legged Kittiwake behavior based on prey density, travel distances, and colony size. Ecol Modell. 204(3-4):335-348.

Frederiksen M, Edwards M, Richardson AJ, Halliday NC, Wanless S. 2006. From plankton to top predators: bottom-up control of a marine food web across four trophic levels. J Animal Ecol. 75(6): 1259-1268.

Freudenburg WR, Gramling R. 1994. Oil in troubled waters: Perceptions, politics, and the battle over offshore drilling. 179 p. Albany (NY): State University of New York Press.

Friesen VL, Burg TM, McCoy KD. 2007. Mechanisms of population differentiation in seabirds. Mol Ecol. 16(9): 1765-1785.

Furness RW, Greenwood JJD, Jarvis PJ. 1993. Can birds be used to monitor the environment? In: Furness RW, Greenwood JJD, editors. Birds as monitors of environmental change. 356 p. Dordrecht (GB): Springer Science+Business Media. p. 1-41.

Furness RW, Wade HM, Masden EA. 2013. Assessing vulnerability of marine bird populations to offshore wind farms. J Environ Manage. 119:56-66.

Gannon MR, Willig MR. 1994. The effects of Hurricane Hugo on bats of the Luquillo Experimental forest of Puerto Rico. Biotropica. 26(3): 320-331.

García LV. 2004. Escaping the Bonferroni iron claw in ecological studies. Oikos. 105(3): 657-663.

Garthe S, Hüppop O. 2004. Scaling possible adverse effects of marine wind farms on seabirds: developing and applying a vulnerability index. J Applied Ecol. 41(4): 724-734.

Gaston AJ, Chapdelaine G, Noble DG. 1983. The growth of Thick-billed Murre chicks at colonies in Hudson Strait: inter-and intra-colony variation. Can J Zool. 61(11):2465-2475.

Gaston AJ, Ydenberg RC, Smith GJ. 2007. Ashmole's halo and population regulation in seabirds. Mar Ornith. 35(2):119-126.

Geffré A, Concordet D, Braun JP, Trumel C. 2011. Reference Value Advisor: a new freeware set of macroinstructions to calculate reference intervals with Microsoft Excel. Vet Clin Pathol. 40(1): 107-112.

Gitzen RA, Millspaugh JJ, Kernohan BJ. 2006. Bandwidth selection for fixed-kernel analysis of animal utilization distributions. J Wildl Manage. 70(5): 1334-1344.

Golet GH, Kuletz KJ, Roby DD, Irons DB. 2000. Adult prey choice affects chick growth and reproductive success in pigeon guillemots. The Auk: Ornithol Adv. 117(1): 82-91.

Goutte A, Angelier F, Chastel CC, Trouvé C, Moe B, et al. 2010. Stress and the timing of breeding: glucocorticoid-luteinizing hormones relationships in an arctic seabird. General Comp Endocrinol. 169(1):108-116.

Gray JS. 1997. Marine biodiversity: patterns, threats and conservation needs. Biodivers Conserv. 6(1):153-175.

Green JA, White CR, Bunce A, Frappell PB, Butler PJ. 2009. Energetic consequences of plunge diving in gannets. Endanger Species Res. 10: 269-279.

Grémillet D, Dell'Omo G, Ryan PG, Peters G, Ropert-Coudert Y, et al. 2004. Offshore diplomacy, or how seabirds mitigate intra-specific competition: a case study based on GPS tracking of Cape gannets from neighbouring colonies. Mar Ecol Prog Ser. 268: 265-279.

Halpern BS, Walbridge S, Selkoe KA, Kappel CV, Micheli F, et al. 2008. A global map of human impact on marine ecosystems. Science. 319(5865):948-952.

Haney JC. 1985. Wintering phalaropes off the southeastern United States: application of remote sensing imagery to seabird habitat analysis at oceanic fronts. J Field Ornith. 56(4):321-333.

Haney JC, Geiger HJ, Short JW. 2014. Bird mortality from the Deepwater Horizon oil spill. II. Carcass sampling and exposure probability in the coastal Gulf of Mexico. Mar Ecol Prog Ser. 513: 239-252.

Harms NJ, Fairhurst GD, Bortolotti GR, Smits JE. 2010. Variation in immune function, body condition, and feather corticosterone in nestling tree swallows (Tachycineta bicolor) on reclaimed wetlands in the Athabasca oil sands, Alberta, Canada. Environ Pollut. 158(3):841-848.

Harr KE. 2002. Clinical chemistry of companion avian species: a review. Vet Clin Pathol. 31(3):140-151.

Harrison AL, Costa DP, Winship AJ, Benson SR, Bograd SJ, et al. 2018. The political biogeography of migratory marine predators. Nat Ecol Evol. 2(10):1571.

Hebblewhite M, Haydon DT. 2010. Distinguishing technology from biology: a critical review of the use of GPS telemetry data in ecology. Philos Trans Royal Soc London, Ser B. 365(1550): 2303-2312.

Herrera-Alsina L, Villegas-Patraca R, Eguiarte LE, Arita HT. 2013. Bird communities and wind farms: a phylogenetic and morphological approach. Biodivers Conserv. 22(12): 2821-2836.

Hill MO, Smith AJE. 1976. Principal component analysis of taxonomic data with multi-state discrete characters. Taxon. 25(2/3): 249-255.

Hjernquist B, Hjernquist MB. 2010. The effects of quantity and quality of prey on population fluctuations in three seabird species. Bird Study. 57(1):19-25.

Hunt Jr GL. 1990. The pelagic distribution of marine birds in a heterogeneous environment. Polar Res. 8(1):43-54.

Hunt Jr GL, Eppley ZA, Schneider DC. 1986. Reproductive performance of seabirds: the importance of population and colony size. The Auk: Ornithol Adv. (103): 306-317.

Ibañez AE, Najle R, Larsen K, Montalti D. 2015. Hematology, biochemistry and serum protein analyses of Antarctic and non-Antarctic Skuas. Waterbirds. 38(2):153-162.

Incardona JP, Gardner LD, Linbo TL, Brown TL, Esbaugh AJ, et al. 2014. Deepwater Horizon crude oil impacts the developing hearts of large predatory pelagic fish. Proc Natl Acad Sci USA. Apr 15; 111(115):E1510-18. doi.org/10.1073/pnas.1320950111

Itoh Y, Suzuki M, Ogawa A, Munechika I, Murata K, et al. 2001. Identification of the sex of a wide range of Carinatae birds by PCR using primer sets selected from chicken EE0. 6 and its related sequences. J Heredity. 92(4):315-321.

Jaeger JA, Bowman J, Brennan J, Fahrig L, Bert D, et al. 2005. Predicting when animal populations are at risk from roads: an interactive model of road avoidance behavior. Ecol Modell. 185(2-4): 329-348.

Jakob EM, Marshall SD, Uetz GW. 1996. Estimating fitness: a comparison of body condition indices. Oikos. 77:61-67.

JaspersV, Dauwe T, Pinxten R, Bervoets L, Blust R, et al. 2004. The importance of exogenous contamination on heavy metal levels in bird feathers. A field experiment with free-living great tits, Parus major. J Environ Monit. 6(4): 356-360.

Jodice PG, Roby DD, Turco KR, Suryan RM, Irons DB, et al. 2006. Assessing the nutritional stress hypothesis: relative influence of diet quantity and quality on seabird productivity. Mar Ecol Prog Ser. 325:267-279.

Jodice PG, Wickliffe LC, Sachs EB. 2011. Seabird use of discards from a nearshore shrimp fishery in the South Atlantic Bight, USA. Mar Biol. 158(10):2289.

Jodice, PGR, Adams EM, Lamb JS, Satgé YG. 2019. Strategic Avian Monitoring Plan for the Gulf of Mexico: Seabirds. In Woodrey et al. (eds). Gulf of Mexico Avian Monitoring Network Strategic Monitoring Plans. Starkville (MS): Mississippi State University Press.

Jodice PGR, Roby DD, Suryan RM, Irons DB, Kaufman AM, et al. 2003. Variation in energy expenditure among black-legged kittiwakes: effects of activity-specific metabolic rates and activity budgets. Physiol Biochem Zool. 76(3):375-388.

Johnson ML, Gaines MS. 1990. Evolution of dispersal: theoretical models and empirical tests using birds and mammals. Annu Rev Ecol Syst. 21(1):449-480.

Kadin M, Österblom H, Hentati-Sunberg J, Olsson O. 2012. Contrasting effects of food quality and quantity on a marine top predator. Mar Ecol Prog Ser. 444:239-249.

Kalmbach E, Griffiths R, Crane JE, Furness RW. 2004. Effects of experimentally increased egg production on female body condition and laying dates in the great skua Stercorarius skua. J Avian Biol. 35(6): 501-514.

Kaltenberg AM, Emmett RL, Benoit-Bird KJ. 2010. Timing of forage fish seasonal appearance in the Columbia River plume and link to ocean conditions. Mar Ecol Prog Ser. 419:171-184.

King DT, Goatcher BL, Fischer JW, Stanton J, Lacour JM, et al. 2013. Home ranges and habitat use of brown pelicans (Pelecanus occidentalis) in the northern Gulf of Mexico. Waterbirds. 36(4): 494-500.

King KA, Blankenship DR, Payne E, Krynitsky AJ, Hensler GL. 1985. Brown pelican populations and pollutants in Texas 1975-1981. Wilson Bull. 97(2): 201-214.

Kitaysky AS, Kitaiskaia EV, Piatt JF, Wingfield JC. 2003. Benefits and costs of increased levels of corticosterone in seabird chicks. Horm Behav. 43(1): 140-149.

Kitaysky AS, Kitaiskaia EV, Wingfield JC, Piatt JF. 2001. Dietary restriction causes chronic elevation of corticosterone and enhances stress response in red-legged kittiwake chicks. J Compar Physiol B. 171(8): 701-709.

Kitaysky AS, Piatt JF, Hatch SA, Kitaiskaia EV, Benowitz-Fredericks ZM, et al. 2010. Food availability and population processes: severity of nutritional stress during reproduction predicts survival of long-lived seabirds. Funct Ecol. 24(3):625-637.

Kitaysky AS, Romano MD, Piatt JF, Wingfield JC, Kikuchi M. M., 2005. The adrenocortical response of tufted puffin chicks to nutritional deficits. Horm Behav. 47(5): 606-619.

Kochert MN, Fuller MR, Schueck LS, Bond L, Bechard MJ, et al. 2011. Migration patterns, use of stopover areas, and austral summer movements of Swainson's Hawks. The Condor: Ornith Appl. 113(1):89.

Konarzewski M, Taylor JR. 1989. The influence of weather conditions on growth of little auk Alle alle chicks. Ornis Scand. 20(2):112-116.

Krebs CT, Burns KA. 1977. Long-term effects of an oil spill on populations of the salt-marsh crab Uca pugnax. Science. 197(4302): 484-487.

Kristan III WB. 2006. Sources and expectations for hierarchical structure in bird-habitat associations. The Condor: Ornith Appl. 108(1):5-12.

Laake J, Rexstad E. 2008. RMark–an alternative approach to building linear models in MARK. In: Cooch EG, White GC. Program MARK: a gentle introduction. Fort Collins (CO): Colorado State University. p. C1–C113.

Lack D. 1944. The problem of partial migration. Br Birds. (37):122-130.

Lamb JS. 2016. Ecological drivers of Brown Pelican movement patterns and reproductive success in the Gulf of Mexico [dissertation]. Clemson (SC): Clemson University.

Lamb JS, Newstead DJ, Koczur LM, Ballard BM, Green MC, et al. 2018. A bridge between oceans: overland migration of marine birds in a wind energy corridor. J Avian Biol. 49(2): jav-01474.

Lamb JS, O'Reilly KM, Jodice PG. 2016. Physical condition and stress levels during early development reflect feeding rates and predict pre-and post-fledging survival in a nearshore seabird. Conserv Physiol. 4(1).

Lamb JS, Satgé YG, Fiorello CV, Jodice PG. 2017. Behavioral and reproductive effects of bird-borne data logger attachment on Brown Pelicans (Pelecanus occidentalis) on three temporal scales. J Ornith. 158(2):617-627.

Langrock R, King R, Matthiopoulos J, Thomas L, Fortin D, et al. 2012. Flexible and practical modeling of animal telemetry data: hidden Markov models and extensions. Ecology. 93(11): 2336-2342.

Lattin CR, Reed JM, DesRochers DW, Romero LM. 2011. Elevated corticosterone in feathers correlates with corticosterone-induced decreased feather quality: a validation study. J Avian Biol. 42(3): 247-252.

Le Corre M, Jaeger A, Pinet P, Kappes MA, Weimerskirch H, et al. 2012. Tracking seabirds to identify potential Marine Protected Areas in the tropical western Indian Ocean. Biol Conserv. 156:83-93.

Lewis S, Sheratt TN, Hamer KC, Wanless S. 2001. Evidence of intra-specific competition for food in a pelagic seabird. Nature. 412(6849):816.

Liedvogel M, Åkesson S, Bensch S. 2011. The genetics of migration on the move. Trends Ecol Evol. 26(11):561-569.

Liu, Z, Liu J, Zhu Q, Wu W. 2012. The weathering of oil after the Deepwater Horizon oil spill: insights from the chemical composition of the oil from the sea surface, salt marshes and sediments. Environ Res Lett. 7(3): 035302.

Lodjak J, Mägi M, Rooni U, Tilgar V. 2015. Context-dependent effects of feather corticosterone on growth rate and fledging success of wild passerine nestlings in heterogeneous habitat. Oecologia. 179(4):937-946.

López-Jiménez L, Blas J, Tanfera A, Cabeezas S, Marchant T, et al. 2016. Ambient temperature, body condition and sibling rivalry explain feather corticosterone levels in developing black kites. Funct Ecol. 30(4):605-613.

Loring P, Ronconi R, Welch L, Taylor P, Mallory M. 2017. Postbreeding dispersal and staging of Common and Arctic Terns throughout the western North Atlantic. Avian Conserv Ecol. 12(2):20.

Lormée H, Jouventin P, Trouve C, Chastel O. 2003. Sex-specific patterns in baseline corticosterone and body condition changes in breeding Red-footed Boobies Sula sula. Ibis. 145(2): 212-219.

Love MS, Baldera A, Yeung C, Robbins C. 2013. The Gulf of Mexico ecosystem: a coastal & marine atlas. 232 p. New Orleans (LA): Ocean Conservancy, Gulf Restoration Center. https://oceanconservancy.org/wp-content/uploads/2017/05/gulf-atlas.pdf

Love OP, Shutt LJ, Silfies JS, Bord DM. 2003. Repeated restraint and sampling results in reduced corticosterone levels in developing and adult captive American kestrels (Falco sparverius). Physiol Biochem Zool. 76(5):753-761.

MacArthur RH, Pianka ER. 1966. On optimal use of a patchy environment. Am Nat. 100(916):603-609.

Macdonald CA, McKinnon EA, Gilchrist HG, Love OP. 2016. Cold tolerance, and not earlier arrival on breeding grounds, explains why males winter further north in an Arctic-breeding songbird. J Avian Biol. 47(1):7-15.

Maceda-Veiga A, Figuerola J, Martínez-Silvestre A, Viscor G, Ferrari N, et al 2015. Inside the Redbox: applications of haematology in wildlife monitoring and ecosystem health assessment. Sci Total Environ. 514:322-332.

MacQueen J. 1967. Some methods for classification and analysis of multivariate observations. In: Le Cam LM, Neyman J, editors. Proceedings of the Fifth Berkeley Symposium on Mathematical Statistics and Probability, Volume 1: Statistics. Berkeley (CA): University of California Press, p. 281-297.

Maness TJ, Anderson DJ. 2017. Serum chemistry of free-ranging nazca boobies (sula granti). J Zoo Wildl Med. 48(4):1234-1238.

Marra PP, Holberton RL. 1998. Corticosterone levels as indicators of habitat quality: effects of habitat segregation in a migratory bird during the non-breeding season. Oecologia. 116(1-2):284-292.

Martin TG, Chadès I, Arcese P, Marra PP, Possingham HP, et al. 2007. Optimal conservation of migratory species. PloS ONE. 2(8):e751.

Masden EA, Haydon DT, Fox AD, Furness RW. 2010. Barriers to movement: modelling energetic costs of avoiding marine wind farms amongst breeding seabirds. Mar Poll Bull. 60(7):1085-1091.

Matyjasiak P. Rubolini D, Romano M, Saino N. 2016. No short-term effects of geolocators on flight performance of an aerial insectivorous bird, the Barn Swallow (Hirundo rustica). J Ornith.157(3):653-661.

Mazerolle, M.J. 2016. AICcmodavg: Model selection and multimodel inference based on (Q)AIC(c). R package version 2.1.0. https://cran.r-project.org/package=AICcmodavg.

McCune B, Grace J. 2002. MRPP (Multi-response permutation procedures) and related techniques. In: Analysis of ecological communities. Chapter 24. Gleneden Bach (OR): MjM Software Design. p.188-197.

McEachran JD, Fechhelm JD. 2010. Fishes of the Gulf of Mexico: volume 1: Myxiniformes to Gasterosteiformes. 1120 p. Austin (TX): University of Texas Press.

McEachran JD, Fechhelm JD. 2010. Fishes of the Gulf of Mexico: volume 2: Scorpaeniformes to Tetraodontiformes. Austin (TX): University of Texas Press.

McEwen BS, Biron CA, Brunson KW, Bulloch K, Chambers WH, et al. 1997. The role of adrenocorticoids as modulators of immune function in health and disease: neural, endocrine and immune interactions. Brain Res Rev. 23(1-2):79-133.

McLeay LJ, Page B, Goldsworthy SD, Paton DC, Teixeira C, et al. 2010. Foraging behaviour and habitat use of a short-ranging seabird, the crested tern. Mar Ecol Prog Ser. (411):271-283.

McNease L, Richard D, Joanen T. 1992. Reintroduction and colony expansion of the Brown Pelican in Louisiana. In: Eversole AG, Overacre KC, Jones E, Garman GC, Hailey WF, editors. (n.p., n.p.) Proceedings of the Forty-Sixth Annual Conference, Southeastern Association of Fish and Wildlife Agencies. p. 223-229.

Meynier L, Morel PCH, Mackenzie DDS, MacGibbon A, Chilvers BL, et al. 2008. Proximate composition, energy content, and fatty acid composition of marine species from Campbell Plateau, New Zealand. N Z J Mar Freshwater Res. 42(4):425-437.

Michelot T, Langrock R, Patterson T, Rexstad E. 2015. moveHMM: animal movement modelling using hidden Markov models. R Package Version 1.1.

Mikuska T, Kushlan JA, Hartley S. 1998. Key areas for wintering North American herons. Colonial Waterbirds. 21(2): 125-134.

Møller AP, Mousseau TA. 2011. Conservation consequences of Chernobyl and other nuclear accidents. Biol Conserv. 144(12):2787-2798.

Montevecchi WA, Hedd A, Tranquilla LM, Fifield DA, Burke CM, et al. 2012. Tracking seabirds to identify ecologically important and high-risk marine areas in the western North Atlantic. Biol Conserv. 156: pp.62-71.

Moran MD. 2003. Arguments for rejecting the sequential Bonferroni in ecological studies. Oikos. 100(2):403-405.

Morrison ML, Marcot B, Mannan W. 2012. Wildlife-habitat relationships: concepts and applications. 520 p. Washington (DC): Island Press.

Muhling BA, Lee SK, Lamkin JT, Liu Y. 2011. Predicting the effects of climate change on bluefin tuna (Thunnus thynnus) spawning habitat in the Gulf of Mexico. ICES J Mar Sci. 68(6):1051-1062.

Müller C, Jenni-Eiermann S, Jenni L. 2009. Effects of a short period of elevated circulating corticosterone on postnatal growth in free-living Eurasian kestrels Falco tinnunculus. J Exp Biol. 212(9):1405-1412.

Myers JP. 1981. A test of three hypotheses for latitudinal segregation of the sexes in wintering birds. Can J Zool. 59(8):1527-1534.

Nakagawa S. 2004. A farewell to Bonferroni: the problems of low statistical power and publication bias. Behav Ecol. 15(6):1044-1045.

National Research Council (NRC). 2003. Oil in the sea III: Inputs, fates, and effects. Nat Acad Press. doi.org/10.17226/10388.

[NOAA] National Oceanic and Atmospheric Administration, National Centers for Environmental Information. 2006. 2-minute Gridded Global Relief Data (ETOPO2) v2 [dataset]. Washington (DC): NOAA, National Geophysical Data Center. doi:10.7289/V5J1012Q.

Nelson, JB. 2005. Pelicans, Cormorants and their relatives. 661p. Oxford: Oxford University Press.

Nelson JS. 1994. Fishes of the world. 3rd ed. 234 p. New York: John Wiley and Sons, Inc.

Nisbet IC. 1997. Female Common Terns Sterna hirundo eating mollusc shells: evidence for calcium deficits during egg laying. Ibis 139(2):400-401.

NOAA Incident news. c2016. Raw incident data. Washington (DC): National Oceanic and Atmospheric Administration, Office of Response and Restoration. IncidentNews 3.3.2. [accessed 2016 March 10]. http://incidentnews.noaa.gov/raw/index.

O'Malley R. 2014. Ocean roductivity. Corvallis (OR): Oregon State University. [accessed 2016 February 1]. http://www.science.oregonstate.edu/ocean.productivity/index.php .

Österblom H, Olsson O, Blenckner T, Furness RW. 2008. Junk-food in marine ecosystems. Oikos. 117(7):967-977.

Oswald SA, Arnold JM. 2012. Direct impacts of climatic warming on heat stress in endothermic species: seabirds as bioindicators of changing thermoregulatory constraints. Integr Zool. 7(2):121-136.

OttoniEB. 2000. EthoLog 2.2: a tool for the transcription and timing of behavior observation sessions. Behav Res Meth Instrum Comput. 32(3):446-449.

Paruk JD, Adams EM, Uher-Koch H, Kovach KA, Long IV D, et al. 2016. Polycyclic aromatic hydrocarbons in blood related to lower body mass in common loons. Sci Total Environ 565:360-368.

Paruk JD, Long D, Perkins C, East A, Sigel BJ, et al. 2014. Polycyclic aromatic hydrocarbons detected in Common Loons (Gavia immer) wintering off coastal Louisiana. Waterbirds. 37(sp1):85-94.

Patterson AG, Kitaysky AS, Lyons DE, Roby DD. 2014. Nutritional stress affects corticosterone deposition in feathers of Caspian tern chicks. J Avian Biol. 46(1):18-24.

Patterson TA, Basson M, Bravington MV, Gunn JS. 2009. Classifying movement behaviour in relation to environmental conditions using hidden Markov models. J Animal Ecol. 78(6):1113-1123.

Payne SA, Johnson BA, Otto RS. 1999. Proximate composition of some north-eastern Pacific forage fish species. Fish Oceanogr. 8(3):159-177.

Pelc R, Fujita RM. 2002. Renewable energy from the ocean. Mar Pol. 26(6):471-479.

Pennycuick CJ, Fast PL, Ballerstädt N, Rattenborg N. 2012. The effect of an external transmitter on the drag coefficient of a bird's body, and hence on migration range, and energy reserves after migration. J Ornith. 153(3):633-644.

Pérez C, Grandeiro JP, Dias MP, Alonso H, Catry P. 2013. When males are more inclined to stay at home: insights into the partial migration of a pelagic seabird provided by geolocators and isotopes. Behav Ecol. 25(2):313-319.

Pérez C, Velando A, Munilla I, López-Alonso M, Oro D. 2008. Monitoring polycyclic aromatic hydrocarbon pollution in the marine environment after the Prestige oil spill by means of seabird blood analysis. Environ Sci Technol. 42(3):707-713.

Peterson CH 2001. The "Exxon Valdez" oil spill in Alaska: acute, indirect and chronic effects on the ecosystem. Adv Mar Biol. 39:1-103.

Peterson CH, Rice SD, Short JW, Esler D, Bodkin JL, et al. 2003. Long-term ecosystem response to the Exxon Valdez oil spill. Science.302(5653):2082-2086.

Phillips RA, Bearhop S, Mcgill RA, Dawson DA. 2009. Stable isotopes reveal individual variation in migration strategies and habitat preferences in a suite of seabirds during the nonbreeding period. Oecologia. 160(4): 795-806.

Phillips RA, Xavier JC, Croxall JP. 2003. Effects of satellite transmitters on albatrosses and petrels. The Auk: Ornithol Adv. 120(4):1082-1090.

Piatt JF, Lensink CJ, Butler W, Kendziorek M, Nysewander DR. 1990. Immediate impact of the 'Exxon Valdez' oil spill on marine birds. The Auk: Ornithol Adv. 107(2):387-397.

Pinaud D, Weimerskirch H. 2005. Scale-dependent habitat use in a long-ranging central place predator. J Animal Ecol. 74(5):852-863.

Poli, C. 2015. Variability in movement patterns and habitat use of two species of Pelecaniformes [thesis]. Clemson (SC): Clemson University.

R Core Team. 2014. R: A language and environment for statistical computing. Vienna (AT): R Foundation for Statistical Computing. https://www.R-project.org/.

Ramos JA, Maul AM, Ayrton V, Bullock I, Hunter J, et al. 2002. Influence of local and large-scale weather events and timing of breeding on tropical roseate tern reproductive parameters. Mar Ecol Prog Ser. 243:271-279.

Ranglack GS, Angus RA, Marion KR. 1991. Physical and temporal factors influencing breeding success of Cattle Egrets (Bubulcus ibis) in a West Alabama colony. Colonial Waterbirds. 14(2):140-149.

Renner M, Kuletz KJ. 2015. A spatial–seasonal analysis of the oiling risk from shipping traffic to seabirds in the Aleutian Archipelago. Mar Poll Bull. 101(1):127-136.

Ricklefs RE, Day CH, Huntington CE, Williams JB. 1985. Variability in feeding rate and meal size of Leach's storm-petrel at Kent Island, New Brunswick. J Animal Ecol. 54(3):883-898.

Robinson OJ, Dindo JJ. 2011. 2011. Egg success, hatching success, and nest-site selection of Brown Pelicans, Gaillard Island, Alabama, USA. Wilson J Ornith. 123(2):386-390.

Romano MD, Piatt JF, Roby DD. 2006. Testing the junk-food hypothesis on marine birds: effects of prey type on growth and development. Waterbirds. 29(4): 407-414.

Romero LM, Reeds JM. 2005. Collecting baseline corticosterone samples in the field: is under 3 min good enough? Comp Biochem Physiol A. 140(1):73-79.

Romero LM, Wikelski M. 2001. Corticosterone levels predict survival probabilities of Galapagos marine iguanas during El Nino events. Proc Natl Acad Sci USA. 98(13):7366-7370.

Rosen DA, Trites AW. 2000. Pollock and the decline of Steller sea lions: testing the junk-food hypothesis. Can J Zool. 78(7) 1243-1250.

Rosen DA, Trites AW. 2004. Satiation and compensation for short-term changes in food quality and availability in young Steller sea lions (Eumetopias jubatus). Can J Zool. 82(7):1061-1069.

Sachs EB, Jodice PG. 2009. Behavior of parent and nestling Brown Pelicans during early brood rearing. Waterbirds. 32(2):276-281.

Sammarco PW, Atchinson AD, Boland GS. 2004. Expansion of coral communities within the Northern Gulf of Mexico via offshore oil and gas platforms. Mar Ecol Prog Ser. 280:129-143.

Sapolsky RM, Romero LM, Munck AU. 2000. How do glucocorticoids influence stress responses? Integrating permissive, suppressive, stimulatory, and preparative actions. Endocr Rev. 21(1):55-89.

Schmidt-Nielsen, K., 1997. Animal physiology: adaptation and environment. Cambridge University Press.

Schnell GD, Hellack JJ. 1978. Flight speeds of Brown Pelicans, Chimney Swifts, and other birds. Bird-banding. 49(2):108-112.

Schreiber EA, Burger J. 2001. Biology of marine birds (eds). Boca Raton (FL): CRC press.

Schreiber RW, Mock PJ. 1988. Eastern Brown Pelican: what does [sic] 60 years of banding tell us? J Field Ornith. 59(2):171-182.

Schreiber RW. 1980. Nesting chronology of the eastern brown pelican. The Auk: Ornithol Adv. 97(3):491-508.

Seegar WS, Yates MA, Doney GE, Jenny JP, Seegar TC, et al. 2015. Migrating Tundra Peregrine Falcons accumulate polycyclic aromatic hydrocarbons along Gulf of Mexico following Deepwater Horizon oil spill. Ecoltoxicol Environ Saf. 24(5):1102-1111.

Sherley RB, Ludynia K, Underhill LG, Jones R, Kemper J. 2012. Storms and heat limit the nest success of Bank Cormorants: implications of future climate change for a surface-nesting seabird in southern Africa. J Ornith. 153(2):441-455.

Shields M M. 2014. Brown Pelican (Pelecanus occidentalis). The Birds of North America Online. Version 2.0. Published July 15, 2014. Ithaca, NY: Cornell Lab of Ornithology. [accessed 2016 February 1]. http://bna.birds.cornell.edu/bna/species/609 .

Smith M, Bolton M, Okill DJ, Summers RW, Ellis P, et al. 2014. Geolocator tagging reveals Pacific migration of Red-necked Phalarope Phalaropus lobatus breeding in Scotland. Ibis. 156(4):870-873.

Smits JE, Fernie KJ. 2013. Avian wildlife as sentinels of ecosystem health. Comp Immun Microbiol Infect Dis. 36(3):333-342.

Soanes LM, Atkinson PW, Gauvin RD, Green JA. 2013. Individual consistency in the foraging behaviour of Northern Gannets: Implications for interactions with offshore renewable energy developments. Mar Pol. 38:507-514.

Spear LB, Ainley DG. 1998. Morphological differences relative to ecological segregation in petrels (Family: Procellariidae) of the Southern Ocean and tropical Pacific. The Auk: Ornithol Adv. 115(4):1017-1033.

Spencer KA, Evans NP, Monaghan P. 2008. Postnatal stress in birds: a novel model of glucocorticoid programming of the hypothalamic-pituitary-adrenal axis. Endocrinol. 150(4):1931-1934.

Spitz J, Mourocq E, Schoen V, Ridoux V. 2010. Proximate composition and energy content of forage species from the Bay of Biscay: high-or low-quality food? ICES J Mar Sci. 67(5):909-915.

State of Alabama Oil and Gas Board [OGB]. OGB GIS data. [dataset]. Tuscaloosa (AL): Geological Survey of Alabama. [accessed 2016 February 1]. https://www.ogb.state.al.us/ogb/gisdata

Steeves TE, Anderson DJ, Friesen VL. 2005. A role for nonphysical barriers to gene flow in the diversification of a highly vagile seabird, the masked booby (Sula dactylatra). Mol Ecol. 14(12):3877-3887.

Stefan SJ. 2008. An analysis of recovery data of brown pelicans (Pelecanus occidentalis) and royal terns (Sterna maxima) banded in South Carolina [thesis]. Charleston (SC): College of Charleston.

Stickney DG, Torres JJ. 1989. Proximate composition and energy content of mesopelagic fishes from the eastern Gulf of Mexico. Mar Biol. 103(1):13-24.

Strategic Online Natural Resources Information System. c2016. Access data. Baton Rouge (LA): Louisiana Department of Natural Resources. 2016. [accessed 2016 February 1]. http://sonris.com/ .

Streker RA. 2019. Reproductive ecology of Brown Pelicans in the northern Gulf of Mexico [thesis]. Clemson (SC): Clemson University.

Suryan RM, Irons DB, Benson J. J., 2000. Prey switching and variable foraging strategies of black-legged kittiwakes and the effect on reproductive success. The Condor: Ornith Appl. 102(2):374-384.

Suryan RM, Irons DB, Brown ED, Jodice PG, Roby DD. 2006. Site-specific effects on productivity of an upper trophic-level marine predator: Bottom-up, top-down, and mismatch effects on reproduction in a colonial seabird. Prog Oceanogr. 68(2-4):303-328.

Suryan RM, Santora JA, Sydeman WJ. 2012. New approach for using remotely sensed chlorophyll a to identify seabird hotspots. Mar Ecol Prog Ser. 451:213-225.

Sydeman WJ, Hester MM, Thayer JA, Gress F, Martin P, et al. 2001. Climate change, reproductive performance and diet composition of marine birds in the southern California Current system, 1969–1997. Prog Oceanogr. 49(1-4):309-329.

Szostek KL, Becker PH. 2015. Survival and local recruitment are driven by environmental carry-over effects from the wintering area in a migratory seabird. Oecologia. 178(3):643-657.

Teal JM, Howarth RW. 1984. Oil spill studies: a review of ecological effects. Environ Manag. 8(1):27-43.

Terrill SB. 1987. Social dominance and migratory restlessness in the dark-eyed junco (Junco hyemalis). Behav Ecol Sociobiol. 21(1):1-11.

Tew-Kai E, Rossi V, Sudre J, Weimerskirch H, Lopez C, et al. 2009. Top marine predators track Lagrangian coherent structures. Proc Natl Acad Sci USA. 106(20):8245-8250.

Thaxter CB, Lascelles B, Sugar K, Cook AS, Roos S, et al. 2012. Seabird foraging ranges as a preliminary tool for identifying candidate Marine Protected Areas. Biol Conserv. 156:53-61.

Texas General Land Office. 2016. GIS Maps & Data. Offshore oil & gas structures. [accessed 2016 February 1]. Austin (TX): Texas General Land Office. http://www.glo.texas.gov/land/land-management/gis/index.html

Thompson DR, Furness RW, Monteiro LR. 1998. Seabirds as biomonitors of mercury inputs to epipelagic and mesopelagic marine food chains. Sci Total Environ. 213(1-3):299-305.

Tranquilla LAM, Montevecchi WA, Hedd A, Fifield DA, Burke CM, et al. 2013. Multiple-colony winter habitat use by murres *Uria* spp. in the Northwest Atlantic Ocean: implications for marine risk assessment. Mar Ecol Prog Ser. 472:287-303.

Tremblay Y, Bertrand S, Henry RW, Kappes MA, Costa DP, et al. 2009. Analytical approaches to investigating seabird–environment interactions: a review. Mar Ecol Prog Ser. 391:153-163.

Trites AW, Donnelly CP. 2003. The decline of Steller sea lions Eumetopias jubatus in Alaska: a review of the nutritional stress hypothesis. Mammal Rev. 33(1):3-28.

Uhlmann S, Fletcher D, Moller H. 2005. Estimating incidental takes of shearwaters in driftnet fisheries: lessons for the conservation of seabirds. Biol Conserv. 123(2):151-163.

US Fish & Wildlife Service. FWS Deepwater Horizon Oil Spill Response. 2011. Bird impact data and consolidated wildlife reports. [accessed 2013 December 5]. http://www.fws.gov/home/dhoilspill/collectionreports.html .

Van Pelt TI, Piatt JF, Lance BK, Roby DD. 1997. Proximate composition and energy density of some North Pacific forage fishes. Comp Biochem Physiol B. 118(4):1393-1398.

Vandenabeele SP, Shepard EL, Grogan A, Wilson RP. 2012. When three per cent may not be three per cent; device-equipped seabirds experience variable flight constraints. Mar Biol. 159(1):1-14.

Vandenabeele SP, Wilson RP, Grogan A. 2011. Tags on seabirds: how seriously are instrument-induced behaviours considered? Animal Welfare. 20(4):559.

Vaughan DS, Shertzer KW, Smith JW. 2007. Gulf menhaden (Brevoortia patronus) in the US Gulf of Mexico: fishery characteristics and biological reference points for management. Fish Res. 83(2-3):263-275.

Velando A, Alvarez D, Mourino J, Arcos F, Barros Á. 2005. Population trends and reproductive success of the European shag Phalacrocorax aristotelis on the Iberian Peninsula following the Prestige oil spill. J Ornith. 146(2):116-120.

Villegas-Patraca R, Herrera-Alsina L. 2015. Migration of Franklin's Gull (Leucophaeus pipixcan) and its variable annual risk from wind power facilities across the Tehuantepec Isthmus. J Nat Conserv. 25:72-76.

Villegas-Patraca R, Cabrera-Cruz SA, Herrera-Alsina L. 2014. Soaring migratory birds avoid wind farm in the Isthmus of Tehuantepec, southern Mexico. PloS ONE. 9(3):e92462.

Wakefield ED, Bodey TW, Bearhop S, Blackburn J, Colhoun K, et al. 2013. Space partitioning without territoriality in gannets. Science. 341(6141):68-70.

Walker CH. 1990. Persistent pollutants in fish-eating sea birds—bioaccumulation, metabolism and effects. Aquat Toxicol 17(4):293-324.

Walter ST, Carloss MR, Hess TJ, Leberg PL. 2013. Hurricane, habitat degradation, and land loss effects on Brown Pelican nesting colonies. J Coast Res. 29(6a):187-195.

Walter ST, Leberg PL, Dindo JJ, Karubian JK. 2014. Factors influencing Brown Pelican (Pelecanus occidentalis) foraging movement patterns during the breeding season. Can J Zool. 92(10):885-891.

Wand MP, Jones MC. 1994. Multivariate plugin bandwidth selection. Comput Stat. 9(2):97–116.

Ward CH, Bender ME, Reish DJ, editors. 1979. The offshore ecology investigation: effects of oil drilling and production in a coastal environment. Houston (TX): Willian Marsh Rice University.

Weimerskirch H, Wilson RP. 2000. Oceanic respite for wandering albatrosses. Nature. 406(6799):955.

Weimerskirch H, Shaffer SA, Mabille G, Martin J, Boutard O, et al. 2002. Heart rate and energy expenditure of incubating wandering albatrosses: basal levels, natural variation, and the effects of human disturbance. J Exper Biol. 205(4):475-483.

Wessel P, Smith WH. 1996. A global, self-consistent, hierarchical, high-resolution shoreline database. J Geophys Res B: Solid Earth. 101(B4):8741-8743.

Whitehead A. 2013. Interactions between oil-spill pollutants and natural stressors can compound ecotoxicological effects. Integr Comp Biol. 53(4):635-647.

Wickliffe LC, Jodice PG. 2010. Seabird attendance at shrimp trawlers in nearshore waters of South Carolina. Mar Ornith. 38:31-39.

Wiens JA, Crist TO, Day RH, Murphy SM, Hayward GD. 1996. Effects of the Exxon Valdez oil spill on marine bird communities in Prince William Sound, Alaska. Ecol Appl. 6(3):828-841.

Wiens JA, Ford RG, Heinemann D. 1984. Information needs and priorities for assessing the sensitivity of marine birds to oil spills. Biol Conserv. 28(1):21-49.

Wiese FK, Jones IL. 2001. Experimental support for a new drift block design to assess seabird mortality from oil pollution. The Auk: Ornithol Adv. 118(4):1062-1068.

Wilkinson PM, Nesbitt SA, Parnell JF. 1994. Recent history and status of the eastern brown pelican. Wildl Soc Bull. 22(3):420-430.

Will A, Watanuki Y, Kikuchi DM, Sato N, Ito M, et al. 2015. Feather corticosterone reveals stress associated with dietary changes in a breeding seabird. Ecol Evol. 5(19):4221-4232.

Williams CT, Kitaysky AS, Kettle AB, Buck CL. 2008. Corticosterone levels of tufted puffins vary with breeding stage, body condition index, and reproductive performance. Gen Comp Endocrin. 158(1):29-35.

Williams JC, Drummond BA, Buxton RT. 2010. Initial effects of the August 2008 volcanic eruption on breeding birds and marine mammals at Kasatochi Island, Alaska. Arct Antarct Alp Res. 42(3):306-314.

Wolf SH, Schreiber RW, Kahana L, Torres JJ. 1985. Seasonal, sexual and age-related variation in the blood composition of the brown pelican (Pelecanus occidentalis). Comp Biochem Physiol A. 82(4):837-846.

Wood DA, Gore JA, Nesbitt SA, Sasser MS. 1995. Dispersal of Brown Pelican from a natal site in Bay County, Florida, with an update on the Brown Pelican status in Florida. In: [n.e.]. Proceedings of the Annual Conference of the Southeastern Association of Fish and Wildlife Agencies, Vol. 49. Tallahassee (FL): Southeastern Association of Fish and Wildlife Agencies. p. 367-371.

Yaukey PH. 2012. Population changes of urban land birds in the three years following the hurricane Katrina flood. Nat Hazards. 61(3):1203-1217.

Yen PPW, Sydeman WJ, Bograd SJ, Hyrenbach KD. 2006. Spring-time distributions of migratory marine birds in the southern California Current: Oceanic eddy associations and coastal habitat hotspots over 17 years. Deep Sea Res Part II. 53(3-4): 399-418.

Yosef R, Gombobaatar S, Bortolotti GR. 2013. Sibling competition induces stress independent of nutritional status in broods of Upland Buzzards. J Raptor Res. 47(2):127-132.

Zaias J, Fox WP, Cray C, Altman NH. 2000. Hematologic, plasma protein, and biochemical profiles of brown pelicans (Pelecanus occidentalis). Am J Vet Res. 61(7):771-774.

Zamon JE, Phillips EM, Guy TJ. 2014. Marine bird aggregations associated with the tidally-driven plume and plume fronts of the Columbia River. Deep Sea Res Part II. 107:85-95.

Appendix A: Supplementary Methods for Analysis of Composition of Diet of Brown Pelican Chicks, 2013–2015

Processing: In the lab, we thawed samples in a hot water bath, separated and counted individual fish, and classified each fish according to its condition (Whole, W: completely intact; Partial-whole, PW: complete length, some skin and/or soft tissues and/or caudal fin missing; Partial, PA: incomplete length). We then identified each fish to species, individually weighed and measured (Total Length, TL and/or Standard Length, SL; in mm) all W and PW fish, and collected a full sample weight. For PA and PW samples that contained more than 10 fish of the same species, we randomly selected a sample of 10 to weigh and measure.

Estimation of Total Length of Partial samples: In 2015, based on Whole (W: completely intact sample) regurgitates with recorded values for both TL and SL, we used a linear regression TL ~ SL to populate the missing values in both parameters. Regression equations were as follows (Table A.1):

Table A.1. Regression Values for Total Length of Main Prey Species Encountered in Diet Samples of Juvenile Brown Pelicans, Northern Gulf of Mexico 2013–2015

Species	Regression equation	R^2	P
Brevoortia patronus	TL = 1.251 SL + 0.547	0.986	< 0.005
Micropogonias undulatus	TL = 1.167 SL + 6.531	0.989	< 0.005
Leiostomus xanthurus	TL = 1.259 SL - 1.118	0.997	< 0.005
Lagodon rhomboides	TL = 1.118 SL + 12.029	0.956	< 0.005
Anchoa mitchilli	TL = 1.117 SL + 4.387	0.945	< 0.005
Anchoa lyolepis	TL = 1.192 SL + 0.203	0.958	< 0.005
Anchoa hepsetus	TL = 1.114 SL + 4.060	0.970	< 0.005
Opisthonema oglinum	TL = 1.284 SL - 2.198	0.997	< 0.005

Estimation of mass of Partial-whole samples: based on TL and mass (in g) of W regurgitates and fresh bait bought near the breeding colonies, we calculated linear regressions (log(mass) ~ log(TL)) for the main prey species of samples collected in 2014 and in 2015. We used the regression equations to correct the mass of PW samples. Regression equations were as follows (Table A.2).

Table A.2. Regression Values for Mass of Main Prey Species Encountered in Diet Samples of Juveniles Brown Pelicans, Northern Gulf of Mexico 2013–2015

Year	Species	Regression equation	R^2	P
2014	*Brevoortia patronus*	mass = $e^{-12.233} \times TL^{3.138}$	0.988	< 0.005
	Micropogonias undulatus	mass = $e^{-11.298} \times TL^{2.926}$	0.826	< 0.005
	Leiostomus xanthurus	mass = $e^{-11.324} \times TL^{2.976}$	0.982	< 0.005
	Opisthonema oglinum	mass = $e^{-16.051} \times TL^{3.278}$	0.972	< 0.005
2015	*Brevoortia patronus*	mass = $e^{-12.060} \times TL^{3.100}$	0.978	< 0.005
	Micropogonias undulatus	mass = $e^{-9.862} \times TL^{2.630}$	0.989	< 0.005
	Lagodon rhomboides	mass = $e^{-9.980} \times TL^{2.763}$	0.974	< 0.005
	Anchoa mitchilli	mass = $e^{-10.470} \times TL^{2.641}$	0.858	< 0.005
	Anchoa hepsetus	mass = $e^{-8.603} \times TL^{2.223}$	0.876	< 0.005
	Opisthonema oglinum	mass = $e^{-16.051} \times TL^{3.278}$	0.972	< 0.005

Estimation of mass of Partial samples: If there were W or PW samples of the same species in the regurgitate, we calculated TL of PA samples as the average of observed TL of W and PW samples for that species in the same regurgitate. We then used the linear regressions to estimate the initial mass (in g) of the sample. If there were no W or PW samples of the same species in the same regurgitate, or if the species was not one of the main species, the initial mass of the sample was kept as the corrected mass. For *Leiostomus xanthurus* and *Anchoa lyolepis* the sample sizes were too small and we used equations calculated from our 2014 samples.

Appendix B: Technical Summary

STUDY TITLE: Eastern brown pelicans: dispersal, seasonal movements, and monitoring of PAHs and other oil contaminants among breeding colonies in the Northern Gulf of Mexico

REPORT TITLE: Ecological drivers of brown pelican movement patterns, health, and reproductive success in the Gulf of Mexico

CONTRACT NUMBER: M12PG00014

SPONSORING OCS REGION: Gulf of Mexico

APPLICABLE PLANNING AREA(S): Western Gulf, Central Gulf, Eastern Gulf

FISCAL YEAR(S) OF PROJECT FUNDING: 2012–2019

COMPLETION DATE OF REPORT: May 2019

COSTS: $1.2M

PROJECT MANAGER(S): Dr. Patrick Jodice

AFFILIATION of Project manager: US Geological Survey South Carolina Cooperative Fish and Wildlife Research Unit

ADDRESS: 260 Lehotsky Hall, Clemson University, Clemson, SC, 29634

PRINCIPAL INVESTIGATOR(S)[3]: Dr. Patrick Jodice

KEY WORDS: brown pelican, diet, migration, nutritional stress, polycyclic aromatic hydrocarbons, risk exposure, spatial ecology, tracking

BRIEF ABSTRACT: We investigated spatial, reproductive, and physiological ecology of brown pelicans (Pelecanus occidentalis) throughout the Northern Gulf of Mexico (GOM). Home range size and the probability and distance of migration were positively correlated with colony size. Pelicans from all colonies overlapped in space use in the Mississippi River Delta region of Louisiana during the nonbreeding season. Diet was primarily of menhaden in the eastern and central planning areas but was more GOM in the western planning area. Risk of exposure to contaminants was often higher in the west and central Gulf compared to the eastern Gulf, although factors other than planning area also contributed to exposure risk.

BACKGROUND: The GOM contains a high density of oil infrastructure. It also supports a rich assemblage of seabirds. Understanding the effects of oil and gas activity on seabirds in the region requires a thorough understanding of reproductive ecology, foraging ecology, physiology, and habitat use. Because of its distribution patterns, behavior, and known sensitivity to contaminants, the brown pelican is a good indicator of species-level effects of interaction with coastal and marine development.

[3]P.I.'s affiliation may be different than that listed for Project Manager(s).

OBJECTIVES: Our objectives were to assess reproductive ecology, movement patterns, habitat use, diet, physiology, and exposure to polycyclic aromatic hydrocarbons.

DESCRIPTION: Research was conducted at seven pelican colonies throughout the Northern GOM between 83° and 98° W and 27° and 31° N. We deployed 85 GPS satellite tags on breeding adults to measure and describe home ranges, migration strategies, and risk exposure to oil and gas development and other surface pollutants. We also collected data on colonies (e.g., reproductive success, diet, contaminants).

SIGNIFICANT CONCLUSIONS: Most of the response variables we measured or modeled varied substantially among colonies and planning areas, although individual characteristics also were significant. Therefore, the effects of environmental or anthropogenic stressors on pelicans may differ based on a combination of environmental, individual, and colony-based attributes and may not be strictly “region-based”. The use of the Mississippi River Delta region of Louisiana during migration by individuals from all planning areas suggests this is a hot spot for pelicans and risk exposure.

STUDY RESULTS: Colony size was positively related to home range size, and to distance and probability of migration. Individuals from different colonies and planning areas overlapped spatially and temporally during breeding, staging, and migration. These overlap areas (e.g., the Mississippi River Delta region of Louisiana) represent 'hot spots for pelicans at specific times of year such as staging and migration. Menhaden comprised 60–85% of the diet of pelican chicks at colonies within the summer range of menhaden, but < 40% at colonies outside of the core summer range of menhaden (i.e., Texas). Reproductive success was positively related to meal provisioning rates, which in turn were lowest at colonies in Texas. Fledging success was positively related to stress levels and body condition of chicks. Exposure to oil and gas activity, surface pollutants, and shipping lanes was least in the eastern planning area and higher but similar between the central and western planning areas. The similarity in exposure between the central and western planning areas is due to inclusion of multiple sources of risk. Hot spots of risk were located in the Mississippi River Delta (Louisiana) and Galveston Bay (Texas). The PAH profile of brown pelicans in the Northern GOM was diverse and comprised predominantly of alkylated PAHs. The level of oil and gas development in a planning area was not consistently the best predictor of PAH levels or individual health, and other factors (e.g. body condition, sex) also were influential.

STUDY PRODUCT(S): Primary products noted, complete list available in Final Report.

Lamb JS. 2016. Ecological drivers of brown pelican movement patterns and reproductive success in the Gulf of Mexico [dissertation]. Clemson (SC): Clemson University.

Lamb JS, O’Reilly KM, Jodice PGR. 2016. Physical condition and stress levels during early development reflect feeding rates and predict pre- and post-fledging survival in a nearshore seabird. Conserv Physiol. 4 (1): cow060.

Lamb JS, Satgé YG, Fiorello CV, Jodice PGR. 2016. Behavioral and reproductive effects of bird-borne data logger attachment on Brown Pelicans on three temporal scales. J Ornith. 158: 617-627.

Lamb JS, Satgé YG, Jodice PGR. 2017. Diet composition and provisioning rates of nestlings determine reproductive success in a subtropical seabird. Mar Ecol Prog Ser. 581:149-164.

Lamb JS, Satgé YG, Jodice PGR. 2017. Influence of density-dependent competition on foraging and migratory behavior of a subtropical colonial seabird. Ecol Evol. 7(16):6469-6481.

Streker R. 2019. Reproductive ecology and diet of brown pelicans in the Gulf of Mexico [thesis]. Clemson (SC): Clemson University.

Lamb JS, Satgé YG, Jodice PGR. 2020. Environmental and behavioral drivers of annual-cycle habitat selection in a nearshore seabird, the Brown Pelican. Divers Distrib. 26(2):254–266.

Appendix C: Publications, Data, and Other Materials Resulting from Data Collected Under This Study

C.1 Published peer-reviewed publications

Lamb JS, O'Reilly KM, Jodice PGR. 2016. Physical condition and stress levels during early development reflect feeding rates and predict pre- and post-fledging survival in a nearshore seabird. Conserv Physiol. 4 (1):cow060. https://doi.org/10.1093/conphys/cow060

Lamb JS, Satgé YG, Fiorello CV, Jodice PGR. 2016. Behavioral and reproductive effects of bird-borne data logger attachment on Brown Pelicans on three temporal scales. J Ornith. 158:617-627.

Haney JC, Jodice PGR, Montevecchi WA, Evers DC. 2017. Challenges to oil spill assessment for seabirds in the deep ocean. Arch Environ Contam Toxicol. 73:33-39.

Lamb JS, Satgé YG, Jodice PGR. 2017. Diet composition and provisioning rates of nestlings determine reproductive success in a subtropical seabird. Mar Ecol Prog Ser. 581:149-164.

Lamb JS, Satgé YG, Jodice PGR. 2017. Influence of density-dependent competition on foraging and migratory behavior of a subtropical colonial seabird. Ecol Evol. 7(16):6469-6481. https://doi.org/10.1002/ece3.3216

Lamb JS, Newstead DJ, Koczur LM, Ballard BM, Green CM, et al. 2018. A bridge between oceans: Overland migration of marine birds in a wind energy corridor. J Avian Biol. (2018):e01474. https://doi.org/10.1111/jav.01474

Lamb JS, Satgé YG, Jodice PGR. 2019. Seasonal variation in environmental and behavioural drivers of annual-cycle habitat selection in a nearshore seabird. Divers Distrib. 00:1-13. https://doi.org/10.1111/ddi.13015

C.2 Peer-reviewed publications in review

Streker RA, Lamb JS, Jodice PGR. Submitted. Local weather as an ecological driver of reproductive success in the Brown Pelican. Waterbirds.

C.3 Peer-reviewed publications in preparation

Lamb JS, Satgé YG, Jodice PGR. Individual movement patterns inform exposure to surface pollutants in a nearshore seabird, the Brown Pelican.

C.4 Theses

Lamb JS. 2016. Ecological drivers of brown pelican movement patterns and reproductive success in the Gulf of Mexico [dissertation]. Clemson (SC): Clemson University.

Streker R. 2019. Reproductive ecology and diet of brown pelicans in the Gulf of Mexico [thesis]. Clemson (SC): Clemson University.

C.5 Conference presentations

Jodice PGR, Lamb JS, Satgé YG, Poli CR. 2017. Spatial ecology of seabirds in the Gulf of Mexico. Bureau of Ocean Energy Management Information Transfer Meeting; 22–24 August 2017; New Orleans, LA.

Jodice PGR, Lamb JS, Satgé YG. 2019. Health assessments of brown pelicans from the Gulf of Mexico. Paper presented at: 5th World Seabird Twitter Conference; 9–11 April 2019.

Jodice PGR, Mackin W, Harrison A-L, Ronconi R, Lamb JS, et al. 2015. Tracking Atlantic and Caribbean seabirds. Paper presented at: 2nd World Seabird Conference; 26–30 October 2015; Cape Town, South Africa.

Jodice PGR, Woodrey MS, Fournier A. Paper presented at: 2018. Movement ecology of seabirds: multi-scale and multi-taxa approaches to addressing conservation needs in the Gulf of Mexico. Paper presented at: 72nd Conference of the Southeastern Association of Fish and Wildlife Agencies; 21–24 October 2018; Mobile, AL.

Jodice, PGR, Lamb JS. 2019. An overview of research and conservation on Pelicans in the 21st century: data gaps and data strengths. Paper presented at: 43rd Annual Conference of the Waterbird Society, Salisbury, MD.

Jodice, PGR, Lamb JS, Satgé YG. 2019. Exposure of Brown Pelicans to polycyclic aromatic hydrocarbons in the northern Gulf of Mexico. Paper presented at: 43rd Annual Conference of the Waterbird Society, Salisbury, MD.

Lamb JS Jodice PGR. 2014. Gradients in breeding Brown Pelican foraging radius, chick condition, and diet across the Northern Gulf of Mexico. Paper presented at: 41st Pacific Seabird Group Annual Meeting; 19–22 February Juneau, AK.

Lamb JS, Jodice PGR. 2014. Comparative performance of cellular and satellite transmitters deployed on Brown pelicans in the Northern Gulf of Mexico. Poster presented at: 41st Pacific Seabird Group Annual Meeting; 19–22 February Juneau, AK.

Lamb JS, Jodice PGR. 2014. Year-round spatial overlap between energy infrastructure and brown pelican movements in the Gulf of Mexico. Paper presented at: 3rd International Marine Conservation Congress; 14–18 August 2014; Glasgow, Scotland.

Lamb JS, Jodice PGR. 2015. Brown pelican fledging success and diet in the northwestern Gulf of Mexico: potential drivers of changing regional distribution. Poster presented at: 42nd Pacific Seabird Group Annual Meeting; 18–21 February 2015; San Jose, CA.

Lamb JS, Jodice PGR. 2015. Physiology and geography predict individual migratory strategies in the Brown Pelican. Paper presented at: Texas Bays and Estuaries Meeting; 8–9 April 2015; Port Aransas, TX.

Lamb JS, Jodice PGR. 2015. Sex, death, and oil: Conservation implications of individual variation in Brown Pelican movement patterns. Paper presented at: 2nd World Seabird Conference; 26–30 October 2015; Cape Town, South Africa.

Lamb JS, Jodice PGR. 2015. Should I stay or should I go? Physiology and geography predict individual migratory strategies in the brown pelican. Paper presented at: 42nd Pacific Seabird Group Annual Meeting; 18–21 February 2015; San Jose, CA.

Lamb JS, Jodice PGR. 2016. Spatial distribution and behavior mediate surface pollutant exposure risk in a nearshore seabird, the Brown Pelican. Paper presented at: 4th International Marine Conservation Congress;30 July – 3 August 2016; St. John's, Canada.

Lamb JS, Jodice PGR. 2017. Movement patterns and habitat selection of Brown Pelicans in the Gulf of Mexico. Paper presented at: 41st Waterbird Society Annual Meeting; 8–11 August 2017; Reykjavik, Iceland.

Lamb JS, Newstead D, Ballard B, Koczur L, Jodice PGR, et al. 2014. Paper presented at: A bridge between oceans: evidence for use of the Tehuantepec Isthmus by waterbirds during dispersal and migration. 38th Waterbird Society Annual Meeting; 4–7 November 2014; La Paz, Mexico.

Lamb JS, O'Reilly K, Jodice PGR. 2016. Feather corticosterone as possible index of developmental conditions and probability of post-fledging survival in Brown pelicans. Paper presented at: 43rd Pacific Seabird Group Annual Meeting; 10–11 February 2016; O'ahu, HA.

Lamb JS, O'Reilly K, Jodice PGR. 2016. Long-term physiological responses of nestling seabirds to variation in prey availability and nest conditions. Paper presented at: Society for Integrative and Comparative Biology; 3–7 January 2016; Portland OR.

Lamb JS, O'Reilly KM, Jodice PGR. 2016. Long-term physiological responses of nestling seabirds to variation in prey availability and nest site characteristics. Paper presented at: 40th Waterbird Society Annual Meeting; 21–23 September 2016; New Bern, NC.

Lamb JS, Satgé Y, Jodice N, Jodice PGR. 2017. Should I stay or should I go? Physiology and geography predict individual migratory strategies in the Brown pelican. Paper presented at: 3rd World Seabird Twitter Conference; 12–14 April 2017. (Special Achievement in Scientific Communication)

Lamb JS, Satgé YG, Jodice PGR. 2015. Brown pelican fledging success and diet in the Western Gulf of Mexico: potential drivers of changing regional distribution. Paper presented at: 1st World Seabird Twitter Conference; 19–21 March 2015.

Lamb JS, Satgé YG, Jodice PGR. 2015. Conservation implications of individual variation in Brown Pelican migration strategies. Poster presented at: 27th International Congress for Conservation Biology; 2–6 August 2015; Montpellier, France.

Lamb JS, Satgé YG, Jodice PGR. 2015. Variation in Brown Pelican energy provisioning rates across a range of juvenile forage fish availability. Paper presented at: 39th Waterbird Society Annual Meeting; 11 – 15 August 2015; Bar Harbor, ME.

Lamb JS, Satgé YG, Jodice PGR. 2017. Movement patterns and habitat selection of Brown Pelicans in the Gulf of Mexico. Paper presented at: 44th Pacific Seabird Group Annual Meeting; 22–25 February 2017; Tacoma, WA.

Lamb JS, Satgé YG, Jodice PGR. 2018. A bridge between oceans: overland migration of brown pelicans increases exposure to terrestrial wind energy. Paper presented at: 4th World Seabird Twitter Conference; 17–19 April 2018.

Satgé YG, Lamb JS, Jodice PGR. 2015. Brown pelican fledgling success and diet: potential drivers of changing regional distribution in the Texas coast. Paper presented at: Texas Bays and Estuaries Meeting 8–9 April 2015; Port Aransas, TX.

Satgé YG, Lamb JS, Jodice PGR. 2016. Diet composition and provisioning rates determine reproductive success in a nearshore seabird. Paper presented at: 2nd World Seabird Twitter Conference; 13–15 April 2016.

Satgé YG, Lamb JS, Jodice PGR. 2017. Using a novel way to communicate seabird research: Physiology and geography predict individual migratory strategies in the Brown Pelican. Paper presented at: 1st British Ornithology Union Twitter Conference; 28–29 November 2017.

Streker RA, Jodice PGR, Lamb JS. 2018. Daily survival rates of Brown Pelican (Pelecanus occidentalis carolinensis) nests and chicks and their relationships with nest habitat. Poster presented at: Association of Field Ornithologists and Wilson Ornithological Society Joint Meeting; 6–9 June 2018; Chattanooga, TN.

Streker RA, Lamb JS, Dindo J., Jodice PGR. 2019. Diet of maturing Brown Pelican chicks in Coastal Alabama. Poster presented at: 43rd Annual Conference of the Waterbird Society, Salisbury, MD.

C.6 Invited seminars

Jodice PGR. 2014. Seabird ecology and conservation in the Northwest Atlantic and Gulf of Mexico: insights from individual tracking. Invited seminar at: Department of Biology, Wake Forest University; September 2014; Winston-Salem, NC.

Jodice PGR. 2015. Examining the movement ecology of seabirds across a range of spatial and temporal scales. Invited seminar at: Department of Wildlife Ecology and Conservation, University Florida; January 2015; Gainesville, FL.

Jodice PGR. 2019. Multi-scale movement and risk in seabirds. Invited seminar at: Duke Marine Lab, Duke University; March 2019; Beaufort, NC.

Lamb, J.S. 2018. Using individual movements to evaluate risk factors for brown pelicans in the Gulf of Mexico. Invited seminar at: University of Florida; February 2018; Gainesville, FL.

Lamb, J.S. 2017. Developing ecologically-motivated risk assessments for marine birds in the Gulf of Mexico. Invited seminar at: University of Georgia; March 2017; Athens, GA.

Lamb, J.S. 2017. Evaluating year-round seabird habitat needs in the Gulf of Mexico to improve oil pollution risk assessment and mitigation. Invited seminar at: Queen’s University; January 2017; Kingston, Ontario.

C.7 Data releases

Lamb JS, Satgé YG, Jodice PGR. 2017. Foraging ecology of Brown Pelican in the northern Gulf of Mexico (2013–2015) [datasets]. US Geological Survey data release. Washington (DC): US Department of the Interior, US Geological Survey. https://doi.org/10.5066/F7R78D6J.
- Composition of diet of juvenile Brown Pelican in the northern Gulf of Mexico (2013-2015)
- Productivity of Brown Pelican in the northern Gulf of Mexico (2014-2015)
- Provisioning rate of Brown Pelican in the northern Gulf of Mexico (2014-2015)
- Proximate Composition and Energy Density of Brown Pelican Prey in the Northern Gulf of Mexico (2014-2015)
- Reference_Brown pelican foraging ecology in the northern Gulf of Mexico (2013-2015)_Colonies
- Reference_Taxonomical identification of Brown Pelican prey in the northern Gulf of Mexico (2013-2015)

Lamb JS, Satgé YG, Jodice PGR. 2017. Data from: Influence of density-dependent competition on foraging and migratory behavior of a subtropical colonial seabird [datasets]. Movebank Data Repository. https://doi.org/10.5441/001/1.7856r086.
- GPS tracking of Brown Pelican in the northern Gulf of Mexico (2013-2016) - Location data
- GPS tracking of Brown Pelican in the northern Gulf of Mexico (2013-2016) - Reference data

Lamb JS, Satgé YG, Jodice PGR. 2019. Brown Pelican Utilization Distribution, Breeding Season, Northern Gulf of Mexico, 2013-2015 [datasets]. South Carolina Cooperative Fish and Wildlife Research Unit data release. Clemson (SC). https://doi.org/10.5066/P9K0HK27.
- BRPE_GoM_20132015_AL_RastUD_NAD83
- BRPE_GoM_20132015_AL_RastUD_WGS84
- BRPE_GoM_20132015_FL_RastUD_NAD83
- BRPE_GoM_20132015_FL_RastUD_WGS84
- BRPE_GoM_20132015_LA_RastUD_NAD83
- BRPE_GoM_20132015_LA_RastUD_WGS84
- BRPE_GoM_20132015_TX_RastUD_NAD83
- BRPE_GoM_20132015_TX_RastUD_WGS84

C.8 Data releases in preparation

Lamb JS, Satgé YG, Jodice PGR. 2019. Physiological ecology of Brown Pelican in the Gulf of Mexico, 2013-2016 [datasets]. US Geological Survey data release. Washington (DC): US Department of the Interior, US Geological Survey. Reserved DOI: 10.5066/P94GBJ4G.
- Blood Analytes in Brown Pelican in the Northern Gulf of Mexico (2013-2015)
- Polycyclic Aromatic Hydrocarbons in Brown Pelican in the Northern Gulf of Mexico (2013-2015)

Streker R, Lamb JS, Satgé YG, Jodice PGR. Reproductive physiology of Brown Pelican along the coast of Alabama, 2017-2018 [datasets]. U.S. Geological Survey data release. Washington (DC): US Department of the Interior, US Geological Survey. Reserved DOI: 10.5066/P9AB53QZ .
- Physiology of Reproduction of Brown Pelican Along the Coast of Alabama, 2017-2018_Nest - monitoring
- Physiology of Reproduction of Brown Pelican Along the Coast of Alabama, 2017-2018_Nest monitoring-temperature

Department of the Interior (DOI)

The Department of the Interior protects and manages the Nation's natural resources and cultural heritage; provides scientific and other information about those resources; and honors the Nation’s trust responsibilities or special commitments to American Indians, Alaska Natives, and affiliated island communities.

Bureau of Ocean Energy Management (BOEM)

The mission of the Bureau of Ocean Energy Management is to manage development of U.S. Outer Continental Shelf energy and mineral resources in an environmentally and economically responsible way.

BOEM Environmental Studies Program

The mission of the Environmental Studies Program is to provide the information needed to predict, assess, and manage impacts from offshore energy and marine mineral exploration, development, and production activities on human, marine, and coastal environments. The proposal, selection, research, review, collaboration, production, and dissemination of each of BOEM’s Environmental Studies follows the DOI Code of Scientific and Scholarly Conduct, in support of a culture of scientific and professional integrity, as set out in the DOI Departmental Manual (305 DM 3).