Title 1: Movescapes and eco-evolutionary movement strategies in marine fish: assessing a connectivity hotspot

## By

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Running title: Fish movescapes


#### Abstract

We use data from the Integrated Tracking of Aquatic Animals in the Gulf of Mexico (iTAG) network, and sister networks, to evaluate fish movements in the Florida Keys - an extensive reef fish ecosystem just north of Cuba connecting the Atlantic Ocean and Gulf of Mexico. We analyzed $\sim 2$ million detections for 23 species, ranging from site-attached reef fish such as Nassau grouper, Epinephelus striatus, to migrant predators such as white sharks, Carcharodon carcharias. An eco-evolutionary movement strategy framework was developed to identify movement traits and their drivers, at multiple temporal scales, important to management. Detectability was species-specific and quantified with a detection potential index. Life stage use of the study area varied by species and residency varied with life stage. Hierarchical clustering identified four annual movement types: high site-fidelity residents, residents, seasonal migrants, and migrants. The greatest within-ecosystem connectivity was observed in the endangered smalltooth sawfish, Pristis pectinata - a seasonal migrant with strong stopover behavior. Siteattachment, stopover, and deep-water migration behaviors differed between individuals, species, and annual movement types. All apex predators were either migrants or seasonal migrants. Migrants were significantly larger than fish in the other movement types, suggesting a relationship between lower predation risk and spatial scale of movement. Movement to spawning sites was a common pattern in teleosts, regardless of annual movement type. As concerns grow over habitat and biodiversity loss, multi-species movescapes, such as presented here, are expected to play an increasingly important role in informing ecosystem-based and non-extractive management strategies.


Keywords: Acoustic telemetry, movement ecology, migration, migratory corridor, space use, network analysis, Florida Keys

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## 1. Introduction

It is well-known that species' movement patterns differ, affecting how species adapt to change. The movement ecology paradigm (Nathan, 2008) identifies mechanistic components affecting individual movement: external factors, internal state, and motion and navigation capacity. By linking lifetime movement to fitness, it sets the foundation for movement to be understood as part of a species' life history. However, to apply this paradigm to inform management and conservation, we need a movement framework that identifies measurable traits at the species, stock or population scale (Allen and Singh, 2016), and their ecological and evolutionary drivers. Ecological drivers include con-specific density and environmental conditions (temperature, habitat, currents, water quality, depth etc), spatially explicit stressors and habitat degradation (Tamario et al., 2019). At the evolutionary scale, movement patterns are selected for when they increase an animal's growth, survival or reproduction (Shaw, 2016). Ecological theory integrating these drivers focuses on growth and survival through optimal foraging theory (Gallagher et al., 2017; Wittemyer et al., 2019), the ideal free distribution (Fretwell and Lucas 1970) and the preemptive distribution, linking breeding site selection with reproductive success (Pulliam and Danielson 1991). For fish with the common small egg reproductive strategy (Andersen et al., 2016) — breeding and birth sites are the same and birth site selection affects offspring survival (Secor, 2002; Ciannelli et al., 2015; Lowerre-Barbieri et al., 2017). Animals also move due to physiological constraints defining favorable environmental conditions. In some species, this results in seasonal movements to overwintering grounds, or to specific spawning grounds, and in all species, this affects their distribution, with important implications for management (McGowan et al., 2017).

Research on animal movement has grown rapidly and is shifting from traditional site- and species-specific approaches (Holyoak et al., 2008; Crossin et al., 2017) to movescapes - the synthesis of many movement signatures (locations over time) from animals of various size, life stage, sex, and/or species (Lowerre-Barbieri et al., 2019a). Evaluating movement at this larger scale has numerous applications to conservation and management (Fraser et al., 2018; Hays et al., 2019), but in the marine realm, it has been primarily applied to data from pop-off satellite archival transmitting (PSAT) tags (Block et al., 2011; Harrison et al., 2018; Sequeira et al., 2018; Rooker et al., 2019), even though acoustic tagging is more common in aquatic animals (Hussey et al., 2015). This is because passive acoustic telemetry depends on the detection by fixed underwater receivers of a uniquely identified signal from an animal with a transmitter when it is in range. Detectability originally limited this approach to small spatial scale studies with speciesspecific objectives and receiver array designs (Heupel et al., 2006). However, telemetry networks - organized associations of researchers at regional to global scales - are facilitating sharing and the exchange of detection data across receiver arrays (Donaldson et al., 2014; Hussey et al., 2015). These integrated tracking data are increasingly used to assess large scale single-species (Griffin et al., 2018; Pratt et al., 2018; DeGroot et al., 2021; Graham et al., 2021; Rider et al., 2021) and multi-species (Brodie et al., 2018; Udyawer et al., 2018; Friess et al., 2021) movement patterns.

Spatial management, and our ability to predict how fish movements change with a changing ocean, are dependent on these larger scale tracking data. This is particularly true of high-connectivity ecosystems, such as the Florida Keys. These ecosystems may act as spatial bottlenecks, where changes in animal movement negatively affect not only the given ecosystem but a range of connected ecosystems. The Florida Keys ecosystem includes the world's third
largest barrier reef ( 580 km extent), expansive seagrass meadows, mangrove forests, and $>1000$ shipwrecks/artificial reef habitats, which are co-managed by the Florida Fish and Wildlife Conservation Commission and the Florida Keys National Marine Sanctuary (FKNMS; Montenero et al., 2020). These habitats are considered critical to supporting marine diversity in this ecosystem, as well as globally, but are increasingly affected by climate change (Graham et al., 2020), habitat degradation and high fishing pressure (Cinner et al., 2020). The Florida Keys region connects the Gulf of Mexico (GOM) and Atlantic Ocean and is just north of Cuba and the Caribbean (Figure 1). Multiple species such as king mackerel, Scomberomorus cavalla, and Spanish mackerel, Scomberomorus maculatus, migrate to this ecosystem to overwinter, providing seasonal prey pulses, which may attract larger predators (Johnson et al., 1994; Clardy et al., 2008). Due to these attributes, the Florida Keys was identified as a high priority site for collecting telemetry data for multiple species by the Integrated Tracking of Aquatic Animals in the Gulf of Mexico (iTAG) network in collaboration with the Ocean Tracking Network (OTN) a global aquatic tracking platform.

The Florida Keys ecosystem is also a high priority for biodiversity conservation through the $30 \%$ marine protected areas (MPAs) by 2030 initiative by the International Union for Conservation of Nature (Zhao et al., 2020). However, the ability for spatial management to protect biodiversity and ecosystem function is dependent on a better understanding of the space use and connectivity of species within the ecosystem - data currently lacking for the Florida Keys. To address this knowledge gap, we used integrated tracking data to assess multi-species movescapes and test hypotheses relevant to effective spatial management. We contextualize these hypotheses within an eco-evolutionary movement strategy framework with intra-annual, annual, and lifetime traits. Data from three arrays and 23 species collected over four years (Table

1) was used to assess how: (1) maturation affects immigration and emigration in the study area; (2) annual movement types affect multi-ecosystem and within-ecosystem connectivity; (3) species differ in site-attachment, stopover behavior, and use of a deep-water migratory corridor; and (4) relationships between annual movement type, body size, trophic niche, and spatial reproductive behavior (i.e., spawning migrations and aggregations) vary.

## 2. Methods

### 2.1 Movement strategy framework

We developed a conceptual model of eco-evolutionary movement strategies: their proximate and ultimate drivers (Riotte-Lampert \& Matthiopoulos, 2020) and measurable movement traits important to management, that can be evaluated at the stock, population, or species scale. This framework (Figure 2) builds on the movement ecology paradigm, which addresses the true movement path of an individual organism (Nathan et al., 2008). External drivers are the same for the movement ecology and movement strategy frameworks. However, the movement ecology framework (Nathan et al., 2008) focuses on the individual lifetime scale, whereas the temporal scale driving movement strategies is multi-generational with fitness and density-dependent feedback loops. An individual's genotype is part of its internal state, as is personality (Hertel et al., 2020) and these are shaped over multiple generations by ultimate drivers. Tracking data used to study true lifetime paths are affected by observation error, sample size, and the ratio of animal to tag longevity. Integrated tracking data from multiple studies (either PSAT tracks or shared detections) can increase sample size and spatio-temporal scale to that needed for management. Emerging analytical tools to assess this data include cluster and network analysis. Movescapes synthesize multiple movement signatures over life stage, sex, size, behavior type and/or species.

Movement strategy traits are categorized at the lifetime, annual, and intra-annual temporal scales (Figure 2). At the lifetime scale, important traits include natal dispersal although difficult to study with electronic tracking (Allen \& Singh, 2016), and ontogenetic habitat shifts (Gillanders et al., 2003; Grubbs, 2010), which are often associated with maturity (Hazen et al., 2012). Annual scale movement traits are the most commonly studied, with annual movement types often classified as resident, migrant, or nomad - although terms vary and there are sub-divisions (Mueller \& Fagan, 2008; Bastille-Rousseau et al., 2016; Abrahms et al., 2017; Allen \& Singh, 2016; Brodie et al., 2018, Berg et al., 2019). Resident typically refers to a rangeresident movement type, i.e., living year-round in a home range (Fagan \& Gurarie, 2020). In contrast, migrants make recurrent movements between non-overlapping activity spaces, exhibiting cross-ecosystem connectivity. Their impact on an ecosystem differs depending on whether they are seasonally resident in that ecosystem (seasonal migrants) or the ecosystem is simply part of their migratory route (migrant). Nomads occupy different activity spaces with low recurrence in annual movement paths (Mueller \& Fagan, 2008). Connectivity within and across ecosystems impacts ecosystem functioning. Behaviors affecting within-ecosystem space use relevant to spatial management include site attachment, stopover behavior, and the use of migratory corridors. Tracking data are also used at finer temporal scales to understand diel activity, core areas, water column and functional habitat use (Wittemyer et al., 2019). Individual variability in movement is an important trait - at all temporal scales (Hertel et al., 2020; Shaw 2020), as it affects the impact of habitat loss/degradation, availability to capture, and population resilience.

Movement strategies are shaped by multiple ultimate drivers including predation,
resource acquisition, birth-site-specific survivorship, and physiological functionality. For species
to persist, reproductive success rates must be adequate to keep abundance levels above those where depensation or the Allele effect occurs (Perälä \& Kuparinen, 2017). Reproductive success occurs when an individual produces offspring that survive to reproductive age, i.e., it survived long enough to develop the energy reserves and physiological capacity to reproduce offspring that can survive to maturity. Movement plays a critical role in this process, resulting in movement strategies that overcome predation risk, meet energetic needs, and support physiological functioning and offspring survival. Strategies can optimize one of these selection axes, but more commonly include tradeoffs between them. Here we use this framework to assess lifetime and annual movement traits and how they relate to ultimate drivers and life history components (e.g., size, trophic niche). Because we did not have data on activity spaces outside of the study area, we used as a proxy the number of basins (Atlantic, study area, Bahamas, GOM) a fish was detected in annually.

### 2.2. Application of the movement strategy framework

We implemented our movement strategy framework to explicitly test a series of hypotheses about movement traits important to spatial management: (1) within the study area, immature fish of multiple species exhibit greater residency than adults, and movement to the study area from outside nurseries is size-dependent; (2) annual movement type can be effectively assigned based on the number of basins used and temporal residence indices; (3) within-ecosystem space use and connectivity differ with annual movement type; (4) fine-scale behaviors - site attachment in residents, and stopover behavior and use of a deep-water migratory corridor in migrants (hereafter referred to as the migratory corridor) - vary across and within species; (5) size, trophic niche, and birth site selection are related to annual movement types.

### 2.2.1 Study area and receiver arrays

The study area encompassed most of the FKNMS as well as several seamounts to the south and artificial reefs to the north (Figure 1). Study area boundaries were $24.425^{\circ}$ to $25.250^{\circ}$ latitude and $-83.130^{\circ}$ to $-80.210^{\circ}$ longitude. Receivers (VR2W, VR2-Tx Innovasea, Halifax, Nova Scotia) were initially deployed to track reef fish ( $\mathrm{n}=39$; Keller et al., 2020), permit ( $\mathrm{n}=$ 123; Brownscombe et al., 2019), and multi-species migrations and stopover sites ( $\mathrm{n}=69$; iTAG).

Substrate types where receivers were deployed included: seamount, coral reef, reef rubble/scattered coral, seagrass, pavement, mangrove, and unconsolidated sediment (primarily sand). Receivers were grouped into nodes $(\mathrm{n}=40)$ based on proximity and habitat type, irrespective of original study array. Although receiver numbers increased over the study period from 176 in 2016 to 231 in 2018, Hurricane Irma in 2017 negatively affected receiver coverage, resulting in data gaps in 10 nodes. In 2018, lost receivers were replaced, and new nodes were established at the southernmost flats on the Gulf-side of the Florida Keys and at the northern wrecks (nodes 1 through 7; Figure 1C).

### 2.2.2 Tagging data

Transmitter codes $(\mathrm{n}=449)$ were assigned to tag owners and species based on iTAG, FACT (the Florida Atlantic Coast Telemetry network), and ACT (Atlantic Cooperative Tracking network) databases. Innovasea (formerly Vemco) contacted owners of unidentified tags (see Table 1 for list of species and scientific names). Research groups ( $n=22$ ) with $\geq$ five detected fish of a given species were invited co-authors and provided the following tag metadata: species, tagging date, location (Figure 3), number of fish tagged, tag expiration date, fish size and life stage at tagging, and annual detection basins by fish. The GOM and Atlantic basins were considered northwest and northeast of our study area, respectively, and The Bahamas refers to detections on Bimini Biological Field Station receivers deployed in and near Bimini, The Bahamas. Co-authors
reviewed the literature for their species' annual movement type and trophic niche (Supp., Table 1). Trophic niche was used to integrate predation risk into detection period calculation (section 2.3.1) and to assess potential relationships with annual movement type.

### 2.3 Data analysis

### 2.3.1 Detection potential

Detection potential drives the capacity of telemetry data to accurately reflect true movement paths. In single species studies, telemetry arrays are deployed to monitor habitat use of the target species, and detection potential is assumed to be driven by detection range. In this study, we used 200 m , a conservative estimate of known range for this area ( $<100 \mathrm{~m}$ to more than 500 m ; Brownscombe et al., 2019; Keller et al., 2020). However, in multi-species studies, detection potential is more complex, affected by species-specific monitoring and tracking power, where monitoring power (MP) is defined as characteristics of the observation system (e.g., receiver spatial coverage and density) and tracking power (TP) as species-specific sample size and potential detection periods (i.e., time within the study when a tagged fish is assumed to be alive and could be detected; hereafter referred to as detection period (DP). We calculated a detection potential index (DPI) for each species $i$ as the product of median MP and TP, scaled by median space use (based on standard deviation ellipses, SDEs; see section 2.3.5). Each factor was scaled by the maximum value observed across species:

$$
\begin{equation*}
D P_{i}=\frac{M P_{i}}{\max \left(M P_{i}\right)} * \frac{T P_{i}}{\max \left(T P_{i}\right)} * \frac{\max \left(\sqrt{S D E_{i}}\right)}{\sqrt{S D E_{i}}} \tag{1}
\end{equation*}
$$

Tracking power was calculated as the sum of individual detection periods ( $d p$ ):

$$
\begin{equation*}
T P_{i}=\sum_{j=1}^{n_{i}} d p_{j, i} \tag{2}
\end{equation*}
$$

where $n_{i}$ is the number of tagged individuals $j$ within species $i$. Theoretically, species-specific monitoring power is the sum of the proportion of habitats used ( $p h u$ ) multiplied by the proportion of those habitats monitored ( phm ) in the study area, with a maximum of one, if $100 \%$ of the habitats used by a species are monitored. We thus calculated individual MP as:

$$
\begin{equation*}
M P_{j, i}=\sum_{d=1} \sum_{g=1} p h m_{d, g} * p h u_{d, g, j, i} \tag{3}
\end{equation*}
$$

where $d=$ depth zone and $g=$ region. Species monitoring power $M P_{i}$ was obtained by calculating median MP across individuals within species. We used depth as a proxy for habitat, due to a lack of habitat information outside shallow-water zones. The spatial distribution of depth differs significantly on the Gulf versus Atlantic side of the Florida Keys, so those regions were treated separately. We used a border along the islands and just to the south of Marquesas Key to ensure no nodes were split between regions (Figure 1C). Four depth zones were categorized in each region: $0-10 \mathrm{~m}, 10.1-20 \mathrm{~m}, 20.1-40 \mathrm{~m}, 40.1-200 \mathrm{~m}$, resulting in eight cells. Proportion of habitat monitored was calculated as:

$$
\begin{equation*}
p h m_{d, g}=\frac{\pi 200^{2} n r e c_{d, g}}{A_{d, g}} \tag{4}
\end{equation*}
$$

where total area $A$ by depth and region was calculated in QGIS 3 (QGIS Development Team, 2021), 200 m is the detection radius for an individual receiver, and nrec is the number of receivers in a region and depth zone. Since $p h u$ was unknown, we had to estimate it from the data. We did this by scaling the total number of depth-and-region-specific detections per individual by the number of receivers in that depth zone and region:

$$
\begin{equation*}
r \operatorname{det}_{d, g, j, i}=\frac{n \operatorname{det}_{d, g, j, i}}{n r e c_{d, g}} \tag{5}
\end{equation*}
$$

This gave us relative detections ( $r d e t$ ) in which cells with fewer receivers were upweighted relative to those with more receivers. From rdet, we obtained the proportions of relative detections within each zone and region, which we used as a proxy for $p h u$ :

$$
\begin{equation*}
p h u_{d, g, j, i}=\frac{r \operatorname{det}_{d, g, j, i}}{\sum_{d=1} \sum_{r=1} r \operatorname{det}_{d, g, j, i}} \tag{6}
\end{equation*}
$$

Scaling MP and TP by space use was done to acknowledge that, all else being equal, greater space use increases the amount of time spent in unmonitored habitat and thereby reduces the DPI. The flipside of this is seen in reef fish with small activity spaces that were all tagged in the study area and had receivers deployed at tagging sites, dramatically increasing their DPI.

Tracking of multiple species that vary widely in size (Figure 4A) also necessitates addressing size effects on DP. This is due to the relationship between size and natural mortality (Lorenzen, 1996), trophic niche (Werner \& Gilliam, 1984), and often migratory scale (Putman, 2018), making it more likely that a terminal lack of detections in small fish is due to mortality while in large fish it is due to migration. To address this, we graphically identified 180 cm as a size threshold which did not overlap with the species' core $25 \%-75 \%$ size quantiles (Figure 4). Fish below or equal to this size were categorized as "small", with the remaining fish categorized as "large". According to the literature, all species categorized as "large" were migrants and either large meso- or apex predators. We then calculated size group-specific DP, where DP start date for all fish was tagging date or the first date of the study period, whichever came later. For "small" fish, subject to higher mortality, we followed the traditional method of using the date of last detection to determine the DP end date, and for "large" fish, we used end of study period or tag expiration date, whichever came first (with occasional extensions for tags detected after their expiration date).

### 2.3.2 Movement metrics

We calculated movement metrics to evaluate annual movement type and for subsequent hypothesis testing. To minimize the risk of false detections, we first removed duplicate detections of transmitter codes at a receiver in $<30 \mathrm{~s}$, and single detections that occurred in the study area within a 24 -hour period (Simpfendorfer et al., 2015). Only fish tagged a year or more before the study's end date (15 April 2019; $\mathrm{n}=295$ ) were used. We calculated two residence indices (RI) at differing temporal scales: (1) yearly RI (number of unique detection years/number of potential detection years); and (2) monthly RI (number of unique detection months/number of potential detection months). Because some species had low DPI, monthly RI was considered the best measure of time spent in the study area. We also calculated the mean maximum consecutive months each species was detected in the study period. Since none of the species-specific movement metrics were distributed normally based on the Shapiro-Wilk test, the nonparametric Kruskal-Wallis test was used to test for significant differences in metrics between annual movement types (section 2.3.4) and species. A Dwass, Steel, Critchlow-Fligner (DSCF) post hoc test was used to identify pairwise differences. To assess cross-ecosystem movements and identify migrants, we estimated the mean and maximum number of basins individuals were detected in annually, ranging from one (any basin) to four (a fish detected in the Atlantic, study area, Bahamas, and the GOM). All mean results are presented plus and minus one standard deviation (sd).

### 2.3.3 Ontogenetic habitat shifts

To evaluate how maturity affected immigration to and emigration from the study area, we tested whether residency differed with life stage within the study area. For immigration analysis, we analyzed species with $\geq$ five immature fish tagged outside and later detected within the study area. As maturation is size dependent, we tested if there was a significant linear relationship
between size at tagging and time elapsed (days) from tagging date to first detection in the study area. For emigration analysis, we selected species with both immature and mature fish detected within the Florida Keys with detection periods $\geq$ six months, then tested for significant differences in residency (as measured by monthly RI) with life stage using the Wilcoxon MannWhitney test.

### 2.3.4 Annual movement type

We hypothesized that annual detection basins and temporal detection patterns within the study area would be sufficient to identify the following annual movement types: residents, seasonal migrants, migrants, and nomads. Residents were defined as species that used only the study area year-round and thus would have been detected in only one basin and have a high monthly RI. Migrants and seasonal migrants were expected to use more than one basin, with seasonal migrants exhibiting greater residency in the study area than migrants. Both were expected to have multi-year detections. Nomads were expected to have both low monthly and annual RI due to low recurrence of movement paths.

Agglomerative hierarchical clustering was used to assign species to annual movement types based on the mean and maximum number of detection basins, maximum consecutive months detected, and monthly and annual RI. If not normally distributed, variables were logtransformed and standardized by scaling to a mean of zero and sd of 1 . Clustering was performed on the dissimilarity matrix computed using Euclidian distances, and the clustering method that resulted in the highest agglomerative coefficient was used. The resulting dendrogram was plotted and species were assigned to one of four annual movement types that were compared to movement types reported in the literature. Species-specific radar graphs were generated to visualize cluster analysis input data, with each movement metric standardized to one.

### 2.3.5 Within-ecosystem movement

Differences in connectivity and space use between annual movement types were tested to evaluate if within-ecosystem behavior differed. Connectivity was evaluated using network analysis (NA) metrics, and space use was estimated by calculating SDEs. To conduct NA, we calculated individual unipartite graphs (i.e., a movement graph constructed with a singular type of node [Jacoby et al., 2012], in this case representing the 40 receiver nodes) and estimated network metrics in the R package 'igraph' (Csardi \& Nepusz, 2006). Individuals' path numbers were calculated as the sum of edges at each node. These were averaged by species to compare species connectivity. SDEs for each individual were calculated using the R package 'aspace' (Bui, 2012) that estimates the standard deviation of x and y coordinates from the mean center using the equations outlined in the Crimestat IV Manual (Levine, 2010). Centers of activity (based on receivers rather than nodes) were first calculated by estimating average locations during one-hour windows, and these served as input for SDE analysis. Only tracks with three or more unique location points were used. Individuals with $\geq$ five detection days detected at only one or two receivers were assigned the expected area based on receiver range ( 0.13 or $0.25 \mathrm{~km}^{2}$ ). Individual space use was averaged by species. Neither mean path number nor SDE were normally distributed by species or group based on the Shapiro-Wilk test, resulting in the use of the nonparametric Kruskal-Wallis test to test for differences in space use between annual movement types and species and the DSCF post hoc test to identify movement groups and species that differed significantly.

Within-ecosystem movements were evaluated for individual variability at the receiver scale and three hypotheses were tested: (1) the prevalence of site-attachment varies between resident species; (2) all migrants primarily use the migratory corridor (from the reef tract to the
seamounts, nodes 22-40); and (3) stopover behavior varies in location and prevalence in migrant species. To assess individual site-attachment, we selected residents with $\geq 30$ detection days and a minimum DP of one year to ensure an appropriate temporal scale, as space use can increase with time (Carlisle et al., 2019). The selected residents had a mean of $219 \pm 170$ detection days. Individuals meeting these criteria were assigned as site attached if their space use was < 0.25 $\mathrm{km}^{2}$. To test if resident species differed in the proportion of individuals exhibiting site attachment we tested this against the null hypothesis of no difference with the Chi-square test. The same approach was applied to test for differences in stopover behavior in migrants (defined as fish with $\geq 3$ consecutive months of detection), and migratory corridor use by migrants. Corridor use was quantified based on the proportion of detections from receivers within the corridor versus outside of it.

### 2.3.6 Movement strategies and life history traits

We hypothesized that the annual movement type with the largest space use (based on detection basins) would also the lowest predation risk indicated by larger body size and their trophic niche. Size was distributed normally; however, variances were not homogenous across movement types. Thus, to test if size differed with annual movement type, we used Welsh's ANOVA and a Games-Howell post hoc test. We then evaluated the proportion of apex predators by movement type. We further hypothesized that birth site selection (i.e., spawning aggregations or spawning migrations based on the literature) would not differ significantly with annual movement type, given that it has been selected for to increase offspring survival. To better understand habitat associations with site-attachment behavior we assessed if all locations with this behavior had structure (i.e., artificial or natural reefs).

## 3. Results

### 3.1 Detections

Approximately two million detections were recorded from 15 June 2015 to 15 April 2019 for 23 fish species. Based on the literature, these species were mostly migrants (44\%) or year-long residents (39\%; Suppl Table 1; Table 1). Four species were considered seasonal migrants, either over-wintering in the study area (i.e., blacktip shark, crevalle jack, spotted eagle ray, hereafter eagle ray) or moving to the area to spawn during March through May (i.e., greater amberjack). Slightly more than half of the detected fish were tagged outside the study area, with some tagged as far away as Canada, the west coast of Florida, and The Bahamas (Table 2, Figure 3A \& B). All sharks - except four great hammerheads - were tagged outside the study area, as were cobia and eagle rays. Mean size of tagged fish (Figure 4) ranged from 38.3 cm total length (TL; grey snapper) to 367.6 cm TL (white sharks). Eight species had both immature and adult fish tagged within the study period (Table 2).

### 3.1.1. Detection potential

Species had uneven TP, with the number of tagged fish per species ranging from 1 to 189 and mean DP ranging from 39 d to over 1,000 d (Figure 5, Table 2). This resulted in TP of $<1,000$ days for crevalle jack and most reef fish (excluding black and Nassau groupers); > 20,000 days for Atlantic tarpon (hereafter tarpon), smalltooth sawfish (hereafter sawfish), great hammerheads, white sharks and permit; and > 40,000 days for bull sharks. The study area was $\sim 21,153 \mathrm{~km}^{2}$, with a receiver density of 0.011 receivers $/ \mathrm{km}^{2}$. Receiver coverage was not homogenous across region or depth zones (Table 3). The greatest receiver density (0.05 receivers $/ \mathrm{km}^{2}$ ) occurred in the 20 to 40 m depth zone in the Atlantic (Table 3), which also detected the highest number of unique fish. However, the highest number of fish detected per receiver (12.4) was in the deepest Atlantic depth zone (with receivers at an artificial reef and the
seamounts). Species-specific DPI was lowest in eagle rays and greatest in black grouper (Table 2; Figure 3C).

### 3.2 Ontogenetic habitat shifts

Multiple species moved to the study area after leaving nursery habitat, but size-dependence was not uniform, nor was within-study area residency with life stage. Sawfish, blacktip sharks, and white sharks had immature fish tagged outside the study area. Immature sawfish (156 to 364 cm TL) were tagged in the Charlotte Harbor estuarine system ( $\sim 200 \mathrm{~km}$ away, $\mathrm{n}=11$, elapsed time: 25-275 d; Figure 3A) and Everglades National Park ( $\sim 53 \mathrm{~km}$ away, n=12, elapsed time: 6 to 587 d; Figure 3B). Time elapsed between tag date and first detection of sawfish in the study area decreased significantly (F-test, $\mathrm{n}=23, \mathrm{p}<0.0001$ ) with size. No significant relationship between elapsed time and size was found for blacktip sharks (F-test, $n=7, p=0.19$ ) or white sharks (Ftest, $\mathrm{n}=19, \mathrm{p}=0.59$ ). Immature blacktip sharks ( 59 to 87 cm TL ) were tagged $\sim 322 \mathrm{~km}$ away and elapsed time varied from 82 to 984 d. Similarly, immature white sharks tagged $\sim 2,200 \mathrm{~km}$ away ( 250 to 450 cm TL) exhibited a wide range of elapsed times ( 141 d to 803 d ). DPIs for blacktip sharks (0.15) and white sharks (0.54) were lower than in sawfish (0.68) and may have affected results. Permit (resident) and tarpon (seasonal migrant) had immatures and adults tagged in the study area. Each species exhibited changes in residency with life stage, but in permit adults showed greater residency. Immature permit had a lower mean monthly RI of $0.49 \pm 0.20(\mathrm{n}=5)$ than adults $(0.71 \pm 0.25, \mathrm{n}=64)$, and these differences were significant (Mann Whitney Wilcoxon, $n=69 ; p=0.05$ ). In contrast, immature tarpon had significantly higher (Mann Whitney Wilcoxon, $\mathrm{n}=26 ; \mathrm{p}=0.006$ ) mean monthly $\mathrm{RI}(0.94 \pm 0.82, \mathrm{n}=3)$ than adults $(0.36 \pm$ $0.28, n=23)$.

### 3.3 Annual movement type

Although common annual movement types include residents, seasonal migrants, migrants, and nomads, hierarchical clustering resulted in the following four annual movement types: high site fidelity residents, residents, seasonal migrants, and migrants (Figure 6). These movement types agreed well with the literature for all but two species (Table 1). Both migrant movement types exhibited between ecosystem connectivity but differed in their mean number of detection basins and residency. Seasonal migrants included three species detected in two basins: blacktip shark, nurse shark, and eagle ray; and both blacktips and eagle rays were identified a priori as seasonal migrants, while nurse sharks were assigned as migratory. However, tarpon and sawfish - also in this group - were often detected in three basins, while also exhibiting high seasonal use of the study area. Tarpon and sawfish had significantly greater (Mann Whitney Wilcoxon, $\mathrm{n}=217$; p $<0.0001$ ) monthly RIs $(0.40 \pm 0.30)$ than other migrants of both types $(0.13 \pm 0.12)$. All migrant species were identified a priori as migratory. These species had low residence patterns and a maximum detection basin of $\geq$ three, except for bluefin tuna. Bluefin tuna were only detected in two basins and never in the GOM, although they are known to migrate there. No individual bluefin tuna were detected in more than one year, suggestive of nomads, but small sample size $(\mathrm{n}=9)$ and low DPI (0.20) precludes assigning this.

Resident species (both movement types) were tagged in the study area and had low sample sizes $(\mathrm{n}=1-12)$, with the exception of permit $(\mathrm{n}=102)$. They also had low to no betweenecosystem connectivity, again with the exception of permit. Six permit were detected outside the study area. Most ( $83 \%$ ) were detected $<50 \mathrm{~km}$ from study borders but one travelled > 200 km along the east coast of Florida. Although overall measures of residency were greater in high site fidelity residents than residents, monthly RIs overlapped between these movement types ranging from 0.60 (scamp) to 0.83 (yellowfin grouper), except for gag and greater amberjack which had
much lower monthly RIs ( 0.38 and $0.27 \pm 0.41$, respectively). The literature indicates female gag are migratory and male gag are resident and greater amberjack are seasonal migrants (Table 1).

### 3.4 Within-ecosystem movement

Within-ecosystem connectivity, measured by NA path number, differed significantly between annual movement types (Kruskal-Wallis, $\chi^{2}=25.1591, \mathrm{p}<0.0001$ ). Mean path numbers fell along a continuum from seasonal migrants ( $11.57 \pm 13.15$ ), migrants ( $8.63 \pm 11.46$ ), residents ( $5.6 \pm 6.57$ ) to high site fidelity residents $(1.17 \pm 1.20)$. Connectivity between the Atlantic and GOM sides of the study area also differed (Figure 7). With the exception of permit, no resident species (both types) were detected in the GOM. Two seasonal migrants had the majority of their detections in the GOM: blacktip sharks and eagle rays ( $97 \%$ and $95 \%$, respectively). Tarpon and bull sharks had $\sim 20 \%$ of their detections in the GOM and sawfish had $\sim 10 \%$. Detections in the GOM were low to none in the rest of the migrant species: 2-3\% (great hammerhead, lemon shark, nurse shark, and tiger shark), $0.13 \%$ (white shark), $0 \%$ (bluefin tuna, cobia).

Path numbers, SDEs, and contiguous use of the study area varied by species and were affected by DPI (Figure 8). Although mean path number did not differ significantly between migrant types (Mann Whitney Wilcoxon, $\mathrm{n}=217 ; \mathrm{p}=0.2258$ ), it did between species within these types (both groups; Kruskal-Wallis, $\chi^{2}=60.5938, p<0.0001$ ). Significant within-group differences also occurred for residents (Kruskal-Wallis, $\chi^{2}=25.6568, \mathrm{p}=0.0023$ ). Permit had a mean path number of $7.0 \pm 6.8$, while all other residents had $\leq 2$ (Figure 8A). Similarly, SDEs differed significantly by annual movement type (Kruskal-Wallis, $\chi^{2}=95.9491, \mathrm{p}<0.0001$ ), although not between seasonal migrants and migrants (post hoc DSCF test, p=0.0057). For migrant species (both types) there was not a significant correlation between path number and SDE (Pearson's correlation coefficient $=0.14351, \mathrm{p}=0.0553, \mathrm{n}=179$ ) due to individual
variability in space use and MP of those spaces. Path number correlated highly with space use only in species with high site fidelity. Nassau and black grouper exhibited small activity spaces and the highest maximum consecutive months of detections. Seasonal migrants exhibiting strong contiguous use of the study area included nurse shark, tarpon, and sawfish.

Use of the migratory corridor, based on detections at receivers deployed in the corridor, varied among migrant species (both types) and these differences were significant $\left(\chi^{2}=36311, \mathrm{n}\right.$ $=80,317, p<0.0001)$. Blacktip sharks and eagle rays, although commonly detected in the GOM, were rarely detected in the corridor ( $0 \%$ and $2 \%$ of detections, respectively). Corridor detections were highly variable for the other seasonal migrants: $95 \%$ in nurse sharks, $58 \%$ in sawfish and only $4 \%$ in tarpon. Bull sharks were similar to sawfish with $55 \%$ of detections in the corridor. The remaining migrant species had GOM detections ranging from 85\% (great hammerheads), > $90 \%$ (cobia, lemon shark, tiger shark) to $\sim 100 \%$ (bluefin tuna and white sharks).

Individual variability in movement occurred in most species and across movement types (Figure 9). Species with relatively consistent movement signatures included: bluefin tuna, which exhibited vertical lines representing rapid longitudinal movements; cobia, which exhibited a zigzag pattern, indicative of rapid longitudinal movements from east to west, a gap in detections of $\sim$ one year and then the same rapid longitudinal movements from east to west again; and reef fish species exhibiting horizontal, almost-daily detections at either the same station or stations in close proximity. Some individual black grouper, gag, Nassau grouper, permit, rock hind, scamp, and yellowfin grouper exhibited site-attached behavior (detection period $\geq$ one year, detection days $\geq 30$, and space use $\leq 0.25 \mathrm{~km}^{2}$ ). The sites supporting this behavior were all near or on natural or artificial reefs. However, the proportion of fish showing this behavior differed significantly by species $\left(\chi^{2}=16.48, n=50, p=0.0114\right)$. Discounting species with only one
tagged fish, permit had the lowest proportion of site-attached individuals (6 out of 32), Nassau grouper were intermediate (1 out of 3 ), and black grouper had the highest (8 out of 11).

Stopover behavior and location also varied, with the proportion of fish exhibiting stopover behavior varying significantly among migrant species ( $\chi^{2}=65.52, n=217, p<0.0001$ ). No stopover behavior (defined as $\geq$ three consecutive detection months) was observed in bluefin tuna, white sharks, or cobia. Those fish detected in more than two basins but assigned as seasonal migrant species had the greatest stopover behavior: sawfish ( $67 \%, \mathrm{n}=27$ ), tarpon ( $52 \%$, $\mathrm{n}=29)$, and nurse sharks $(40 \%, \mathrm{n}=5)$. Nurse sharks and three additional migrant species exhibited stopover behavior within the corridor (Figure 10): tiger sharks ( $25 \%, \mathrm{n}=12$ ), great hammerheads $(17 \%, \mathrm{n}=23)$, and lemon sharks $(13 \%, \mathrm{n}=8)$. Eagle rays $(20 \%, \mathrm{n}=10)$, and bull sharks $(12 \%, \mathrm{n}=41)$ exhibited stopover behavior outside the corridor.

### 3.5 Movement strategies and life history traits

We hypothesized that size, trophic niche, and birth site selection were related to annual movement type and our results supported this. Size differed significantly with annual movement type (Welch's ANOVA, $\mathrm{n}=294, \mathrm{p}<0.0001$ ). Migrants were significantly larger ( $260 \mathrm{~cm} \pm 92$ cm TL; $\mathrm{p}<0.0001$ ) than seasonal migrants ( $202 \pm 111 \mathrm{~cm} \mathrm{TL}$ ), residents $(71 \pm 20 \mathrm{~cm} \mathrm{TL}$ ), and high site fidelity residents ( $61 \pm 15 \mathrm{~cm}$ TL). Trophic level also varied significantly with annual movement type $\left(\chi^{2}=20.1, \mathrm{n}=22, \mathrm{p}=0.0026\right.$ ). No residents (both groups) were apex predators. Most migrant species ( $86 \%$ ) and some seasonal migrants ( $20 \%$ ) were apex predators. These relationships with migratory scale suggest a link between decreased predation risk and increased migratory scale and, presumably, consumption to support the larger body mass. These findings highlight how size plays a role in the evolution of movement strategies to address tradeoffs between predation and resource acquisition. Teleost species tracked in this study were all
reported to exhibit movements associated with birth site selection (Suppl, Table 1), regardless of annual movement type or size.

## 4. Discussion

### 4.1 Movement strategy framework

Multiple frameworks have been proposed to help understand drivers of individual movements (Nathan et al., 2008), scaling those drivers to population dynamics (Doherty \& Driscoll, 2018), and applying the concepts of movement ecology to understanding biodiversity (Jeltsch et al., 2013) and wildlife management (Allen \& Singh, 2016; Fraser et al., 2018). How movements affect fisheries management from single species to ecosystem based has also been outlined (Lowerre-Barbieri et al., 2019a). However, we could find no literature that provided a movement strategy framework integrating a species' movement traits and drivers over temporal scales - a framework needed to compare species' movement ecology and how it affects resilience to stressors such as fishing, habitat degradation and climate change. The movement strategy framework presented here is intended to fill this gap and begin the process of standardizing terms that often vary across studies, species, and realms (Allen and Singh 2016; Bastille-Rousseau et al., 2016; Brodie et al., 2018; Berg et al., 2019). The intent is to be universally applicable, although water column use would need to be changed to altitude in terrestrial and avian species and depth for burrowing species. To fully evaluate this framework will necessitate asking scientists studying movement in other realms and species to test it and provide feedback.

The advantage of framing movement strategies in a fashion similar to life history strategies is two-fold: (1) it integrates the concept of movement strategies evolving over evolutionary time under conditions potentially quite different from those they currently exist in; and (2) identifies measurable traits, providing a foundation for future trait-based analyses
(Beukhof et al., 2019). Fisheries science-to-date has focused mainly on changes in movements/distributions due to ecological context (Morley et al., 2018; Pinsky et al., 2020) or density dependence (MacCall, 1990; Thorson et al., 2016). However, inherited components of species-specific movement strategies will mediate how these strategies respond to changing conditions. Drawing from the fast-slow continuum of life history strategies (Promislow and Harvey, 1990), we hope this framework will provide a similar foundation to assess speciesspecific movement strategies, although an understanding of how movement strategies relate to population resilience is still emerging. Adult movement strategies fall along a continuum from site attached to highly migratory (although they both often move to specific birth sites). Longterm site attachment is only possible in environments where energetic and survival needs can be met in one location. Advantages of site attachment include the "resident advantage" against competitors for prime habitat, increased efficiency in extracting resources from "well-known" habitats, and effective predator avoidance (Gerber et al., 2019). In migration and nomadism, animals move to optimal locations for feeding, offspring survival, and physiological functioning (Shaw 2016), but in consequence giving up the advantages of site attachment.

Birth site selection is a common driver of movement in marine ecosystems, occurring in marine mammals, teleosts and elasmobranchs (Shaw 2016). Most teleosts in this study exhibited birth site selection and it occurred across a wide range of sizes, trophic niches and in all annual movement types. Resident species in this study all formed spawning aggregations, with the possible exception of gag (Lowerre-Barbieri et al., 2020). Given that many of them also were highly site-attached, this suggests tradeoffs in movement choices to meet adult and offspring survival needs. The only seasonal migrant which was a teleost was tarpon. They form prespawning aggregations prior to migrating to presumed deep-water spawning sites (Luo et al.,
2019). Cobia and bluefin tuna are migrants and both undertake movements associated with birth site selection. Cobia migrate from south Florida to the northern GOM, where they spawn in aggregations (Perkinson et al., 2019). Bluefin tuna are known to migrate between northern foraging grounds to spawning grounds in the Caribbean and GOM, although they do not form spawning aggregations (Block et al., 2005; Hazen et al., 2016). Although spawning site selection remains poorly understood in marine fish, it will affect how a species adapts to a changing ocean, with concern for phenological disconnects negatively affecting productivity. This has been observed in multiple bird species for which cues to initiate migration no longer result in arriving at fixed breeding grounds at the optimal time (Møller et al., 2008).

### 4.2 Detection potential

Large scale and long-term movement data is needed to better understand movement strategies.
Current solutions to collecting this data marine fish are: (1) synthesizing tracks of many animals from archival tags (including satellite); or (2) sharing detection data through acoustic telemetry networks (Hussey et al., 2015; Lennox et al., 2019; Lowerre-Barbieri et al., 2019a; Bangley et al., 2020). Integrated tracking data has greatly improved the scale of inferences we can make from acoustic telemetry but also presents new challenges in terms of separating process from observation effects (Friess et al., 2021) and a need to develop new methods to address issues such as varying detection periods and the varying efficacy of receiver coverage to detect different species. To begin to address this, we quantified TP and MP, and developed the DPI to quantify disparate observation capacity by species. However, in an ideal world DPI would be determined from independent space use data or prior information about species habitat preferences and integrate variability in range with habitat and over time. The opportunistic nature of the networked data requires a temporal threshold considered representative of annual
movements. Here we used a year. Crevalle jack exemplify this need. Within the study period they had a mean detection period of 39 days and were detected only within the study area. However, consequent detections (after the study ended) of Crevalle jack were made in the Gulf of Mexico and in the Atlantic basin (Gervasi pers. comm.). Tagging location and numbers tagged also affects accurate representation of within-species variability at the contingent and individual scales. For example, resident and migrant contingents of blacktip shark use the study area (Grubbs, pers. comm.), but because the fish tracked in this study were all tagged in the GOM only the migratory contingent is represented in these data.

### 4.3 Life cycle space use

Although we can rarely track an animal over its lifetime, using tracking to help inform life cycle space use has important implications for management. Spatial population structure, natal homing, and biocomplexity affect a species' resilience to environmental and anthropogenetic perturbations (Goethel et al., 2020) and ontogenetic habitat shifts are common, affecting availability to capture and harvest control rules (Carruthers et al., 2015). Components of space use at this scale typically differ between teleosts and elasmobranchs due to different reproductive strategies. In teleosts, mating and birthing grounds are usually the same, with models needed to predict birth site and nursery ground connectivity (Swearer et al., 2019). In contrast, most elasmobranchs have separate mating and birthing sites and the overlap between birth and nursery grounds is species-specific, with some species not using nursery grounds (Heupel et al., 2007). Immature blacktip sharks, sawfish, and white sharks tagged outside the study area were detected, but only sawfish showed the hypothesized size dependence in arrival time. This appears to be due to varying life cycle space use and DPIs (Table 2). In west-central Florida, blacktip sharks use estuarine nursery grounds and exhibit homing to these grounds after
seasonal migrations to the Florida Keys (Hueter et al., 2004), tropical storm-induced movements (Heupel et al., 2003), and experimental displacement (Gardiner et al., 2015). Sawfish nursery grounds are also estuarine and documented in the Charlotte Harbor system and Everglades National Park (Norton et al., 2012). Large juvenile sawfish tagged in Charlotte Harbor commonly move to the study area, later returning to the tagging area (Graham et al., 2021). However, it is not yet known if this is due to seasonal changes in temperature, changing foraging opportunities, or mating site selection. The white shark migratory scale is much larger, including transoceanic, as well as long distance coastal migrations (Bonfil et al., 2005; Skomal et al., 2017). White sharks tracked in this study were primarily tagged off Massachusetts, a known foraging ground, south of the New York Bight, which acts as a nursery area (Curtis et al., 2018). The birth site of these white sharks remains unknown.

Shifts in habitat use and annual movement type with maturity are common in fish (Lowerre-Barbieri et al., 2016) as well as many other species - especially those with major changes in body size or morphology with life stage, such as amphibians and insects (Werner \& Gilliam, 1984). These shifts have been traditionally thought to be driven by the size to predation risk relationship, with animals leaving their nursery grounds when the benefits of increased growth outweigh those of increased mortality. However, shifts in habitat use and/or annual movement type can be driven by any trait that takes time to develop and affects foraging, survival, or reproduction, including the development in birds of salt glands or muscular gizzards (Fokkema et al., 2020), or in some fish, the ability to successfully defend a territory (Gruss et al., 2011). Given the need to reach an energetics threshold both to mature and to migrate, reproductive development and ontogenetic habitat shifts are linked to an animal's condition (Goossens et al., 2020), potentially driving the individual variability observed in the timing of
emigration from nursery grounds (Walters Burnsed et al., 2020). We hypothesized adults would exhibit lower residency than immature fish, a common pattern, which was observed in tarpon but not permit. However, most permit appear to spend their full life cycle within the study area, whereas adult tarpon are seasonal migrants that undertake long migrations (Griffin et al., 2018; Luo et al., 2019).

### 4.4 Annual movement type

We hypothesized that basin use and temporal detection patterns could effectively categorize species' annual movement types and our results supported this and agreed well with the literature (Table 1). However, sample size, number of clusters, and variable DPI affected results. Five species had only one tagged fish, and cannot be considered representative of the species, but were retained because their movement type agreed with the literature. In our cluster analysis, we chose four clusters a priori to represent the four major types of annual movement (residents, seasonal migrants, migrants, and nomads). However, results grouped species into two resident types (high site fidelity versus range resident), seasonal migrants, and migrants.

Our results support those of Brodie et al. (2018) and Friess et al. (2021) that acoustic telemetry, with appropriate monitoring power, can determine annual movement types. For gag and greater amberjack, our movement type results differed from the literature, in large part due to the range of species in the study and the constraint of four movement types. Greater amberjack demonstrate both the importance of adequate monitoring power and within-species annual movement type analysis to identify partial migration. Greater amberjack form large spawning aggregations at the Islamorada and Marathon seamounts (Figure 1C, nodes 38 and 40; Hargrove et al., 2018) and, based on conventional tag recaptures, are believed to make long, coastal migrations to these sites (Harris et al., 2011). None of our fish were detected outside the study
area and virtually all detections occurred at the seamounts, suggesting there could be partial migration. However, greater amberjack has low MP and DPI and this was underscored by the recapture of one fish $\sim 600 \mathrm{~km}$ north of the study area.

### 4.5 Within-ecosystem behavior

Our results are a first step towards providing the movement data needed for future spatial management and multi-species dynamic ocean management (Hazen et al., 2018) in the study area. MPAs are often created to protect spawning aggregations for resident species. In the study area, spawning aggregation sites have been documented for mutton snapper, grey snapper (Keller et al., 2020), permit (Brownscombe et al. 2020) and greater amberjack (Harris et al., 2011). However, it is also important to design MPAs to protect key areas for migrating species such as foraging and reproductive habitats (Runge et al., 2014; Hays et al., 2019), migratory corridors, and stopover sites. For ecosystem-based management (EBM), it is especially important to protect these habitats for migratory meso- and apex predators, given their importance to ecosystem health (Heithaus et al., 2010; Speed et al., 2010; Hammerschlag et al., 2019). The UN's target to increase MPAs by 2030 provides an opportunity to support additional studies like this to identify and protect these habitats (Sequeira et al., 2019).

Species' movement strategies evolved in habitats unaltered by humans but now have to adapt to the available habitat mosaic - habitat contiguity and quality (e.g., Section 2.1.2.1 in Adams, 2017). Connectivity will be affected by these factors and our ability to accurately measure it depends on the overlap between movement routes and receiver coverage (i.e., MP). Low connectivity occurred in residents of both movement types (other than permit), blacktip sharks, eagle rays, bluefin tuna and white sharks - but not for the same reasons. Residents exhibited little horizontal movement and were well-tracked at their tagging sites. However, it is
often assumed that site attached species leave the array primarily due to predation, recently documented by Bohaboy et al. (2020). But fish also leave due to natural triggers, such as tropical storms (Secor et al., 2019), but their probability of being detected at other arrays is often low. This was the case for red snapper off the west coast of Florida (Friess et al., 2021), presumably due to high site fidelity at the new location.

Blacktip sharks and eagle rays migrated to the GOM to over-winter. They had low DPIs, due to lower receiver coverage along migratory routes from the GOM compared to the Atlantic. In contrast, bluefin tuna and white sharks appear to exhibit rapid migrations through the study area within the migratory corridor, although much remains unknown about use of the corridor, seamounts, and deeper waters. Only two receivers were deployed in waters 50 m to 400 m . Given these conditions, the detection of approximately a third of the white sharks tagged off Massachusetts suggests this is a common migratory route for this population. However, to understand movements within the corridor, the range of species using it, and whether species will change movements due to climate change and anthropogenic stressors requires additional tracking studies and synthesis of PSAT tracks from prior studies with catch-based data.

Stopover (or staging) sites are commonly studied in birds, but less so in fish. The term refers to intermediary sites used during migration that provide resources and environmental conditions supporting effective migration (Warnock 2010). Here we defined stopover behavior based on three or more consecutive months of detection but is certainly possible at shorter durations. Again, our ability to assess it will be affected by species-specific DPIs. Seasonal migrants, not surprisingly, had the most individuals exhibiting stopover behavior: sawfish (67\%, $n=27)$, tarpon $(52 \%, n=29)$, and nurse sharks $(40 \%, n=5)$. Stopover sites for these species ranged from within the corridor (nurse sharks), only in shallower waters (tarpon) or in both
(sawfish). The mechanistic driver of this behavior is unknown, with the exception of tarpon which form pre-spawning aggregations, an increasingly acknowledged form of stopover behavior, where fish feed and increase their energy reserves prior to undertaking spawning migrations. In terms of spatial protection, stopover sites in shallow water are expected to be the most impacted by anthropogenic stressors and thus should be prioritized.

## 5 Conclusions

Given that movement links habitat with life history processes important to population dynamics, conservation, and management (Hays et al., 2019; Wittemyer et al., 2019), there is a clear need to integrate spatial processes into fisheries management (Berger et al., 2017;

Cumming et al., 2017; Lowerre-Barbieri et al., 2019b; Link et al., 2020). Roadblocks to doing so (for tracking data) are both methodological and conceptual. Acoustic telemetry networks have greatly increased the biological and spatial scale over which marine fish can be tracked, but also present new challenges including data standardization (Sequeira et al., 2021) and the need to move from opportunistic data to designed network studies to monitor multi-species movements. This, of course, necessitates funding. Such an approach would address the issues we encountered in terms of varying TP, MP, and DPI. However, there is also a need to invest in long-term arrays that can track changes in movements over time.

While, conceptually, the linkage between movement strategies and management is clear, how to incorporate movement strategies into management is less so, given the current management paradigm. Within a traditional stock assessment framework, there is increased integration of tracking results into stock identification (Cadrin 2020) and interest in developing spatially explicit stock assessment models (Goethel et al., 2020). We would like to also encourage the integration of movement into management strategy evaluations to assess how
movement affects catchability. Specifically, we suggest simulations which address: (1) spatiotemporal patterns of effort and life cycle space use to identify vulnerability bottlenecks; (2) how movement affects availability to capture and thus catch-based estimates of abundance; and (3) at the multi-species scale, how movement affects by-catch. We also suggest that water depths and annual movement types be used to refine definitions of stock complexes, recognizing their importance to more than just highly migratory and coastal migratory species.

Within- and cross-ecosystem movements (space use, connectivity, migratory routes, stopover sites, and functional use of habitats) are also important to productivity and ecosystem functioning. However, traditional management is extraction-based, using life history parameters and catch data (fisheries-dependent and fisheries-independent) to manage stocks in terms of the optimal catches they can sustain. However, management is shifting from optimizing single species yield to managing ocean use and ecosystem health (Halpern et al., 2015), with the following management approaches not predicated on single species biomass optimization: spatial management, dynamic ocean management (DOM; Lewison et al., 2015), and EBM (Dolan et al., 2016). These new management paradigms will necessitate new data streams and the funding to provide them. Similar to the investment in surveys to estimate relative abundance for the current management paradigm, spatial management, DOM, and EBM will need data on movements and how they change with climate and habitat degradation (Lotze et al., 2006). To effectively collect these data, we need to identify globally important connectivity hot spots under stress from the Anthropocene, like the Florida Keys, and provide long-term funding for infrastructure, technological innovation, and personnel who can bridge the gap between traditional and emerging ocean management.

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DATA AVAILABILITY STATEMENT: The data that support the results in this study were shared through iTAG and are archived through the Ocean Tracking Network (OTN), whose data system is an Associate Data Unit of the Intergovernmental Oceanographic Commission's International Oceanographic Data and Information Exchange. Access to the data on the OTN system is guided by the public data policies of OTN and the member nodes who participate in the system. There is no fee to access the data from the system, and OTN staff are available to assist with data requests. A citation format crediting the owners of the data is available from the OTN publication data repository https://members.oceantrack.org/data/pblctn_data/publication-data-repository\#10\<ucode\>\<ucodep\>\·\</

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| Common name | Scientific name | Movement <br> (literature) | Movement (cluster) |
| :--- | :--- | :--- | :--- |
| Spotted Eagle Ray | Aetobatus narinari | Seasonal | Seasonal migrant |
| Bull Shark | Carcharhinus leucas | Migratory | Migrant |
| Blacktip Shark | Carcharhinus limbatus | Seasonal | Seasonal migrant |
| White Shark | Carcharodon carcharias | Migratory | Migrant |
| Tiger Shark | Galeocerdo cuvier | Migratory | Migrant |
| Nurse Shark | Ginglymostoma cirratum | Migratory | Seasonal migrant |
| Lemon Shark | Negaprion brevirostris | Migratory | Migrant |
| Smalltooth Sawfish | Pristis pectinata | Migratory | Seasonal migrant |
| Great Hammerhead | Sphyrna mokarran | Migratory | Migrant |
| Rock Hind | Epinephelus adscensionis | Resident | Resident |
| Nassau Grouper | Epinephelus striatus | Resident | High site fidelity resident |
| Mutton Snapper | Lutjanus analis | Resident | Resident |
| Gray Snapper | Lutjanus griseus | Resident | Resident |
| Black Grouper | Mycteroperca bonaci | Resident | High site fidelity resident |
| Gag grouper | Mycteroperca microlepis | Resident males/ | migrant females |

TABLE 2 Species detected, trophic niche, maximum distance travelled from tagging site in either the Atlantic (A), Gulf of Mexico (G) or Bahamas (B), mean detection period, number of tagged fish by life stage ( $\mathrm{I}=$ immature; $\mathrm{A}=$ adult; $\mathrm{U}=$ unknown ), maximum detection basins (Atlantic, Keys, Bahamas, and Gulf), tags detected, proportion tagged in the Keys, and detection potential index (DPI)

| Common name | Trophic niche | Max. distance from tag $\qquad$ | Mean detection period (d) | Life stage | Max \# basins | Tags | Keys tag ratio | DPI |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Atlantic bluefin tuna | Apex | 2,976 (A) | 699 | A | 2 | 9 | 0 | 0.20 |
| Atlantic tarpon | Meso | $\begin{gathered} 953 \text { (A); } \\ 631(\mathrm{G}) \end{gathered}$ | 433 | $11 \mathrm{I}, 42 \mathrm{~A}$ | 3 | 53 | 0.79 | 0.60 |
| Black grouper | Meso |  | 449 | $7 \mathrm{I}, 5 \mathrm{~A}$ | 1 | 12 | 1 | 14.40 |
| Blacktip shark | Meso | 322 (G) | 343 | I | 2 | 7 | 0 | 0.15 |
| Bull shark | Apex | 310 (B) | 1082 | $3 \mathrm{I}, 38 \mathrm{~A}$ | 4 | 41 | 0 | 0.69 |
| Cobia | Apex | 434 (A) | 396 | A | 3 | 20 | 0 | 0.17 |
| jack | Meso |  | 39 | A | 1 | 24 | 1 |  |
| Gag grouper | Meso |  | 448 | A | 1 | 1 | 1 | 1.15 |
| Gray snapper | Meso |  | 84 | A | 1 | 4 | 1 | 0.23 |
| Great hammerhead | Apex | $\begin{aligned} & 214 \text { (A) } \\ & 310 \text { (B) } \end{aligned}$ | 935 | $1 \mathrm{I}, 27 \mathrm{~A}$ | 3 | 28 | 0.14 | 0.50 |
| Greater amberjack | Meso |  | 472 | A | 1 | 5 | 1 | 0.02 |
| Lemon shark | Meso | 310 (B) | 1268 | A | 3 | 8 | 0 | 0.21 |
| Mutton snapper | Meso |  | 348 | A | 1 | 1 | 1 | 0.30 |
| Nassau grouper | Meso |  | 375 | A | 1 | 5 | 1 | 3.07 |
| Nurse shark | Meso | $\begin{gathered} 208 \text { (A), } \\ 278 \text { (B) } \end{gathered}$ | 1090 | A | 2 | 6 | 0 | 0.47 |
| Permit | Meso |  | 284 | $9 \mathrm{I}, 93 \mathrm{~A}$ | 2 | 102 | 1 | 2.78 |
| Rock hind | Meso |  | 163 | A | 1 | 1 | 1 | 0.42 |
| Scamp | Meso |  | 110 | A | 1 | 1 | 1 | 0.40 |
| Smalltooth sawfish | Apex | 190 (G) | 733 | $23 \mathrm{I}, 11 \mathrm{~A}$ | 3 | 34 | 0.29 | 0.68 |


| Spotted eagle ray | Meso | 322 (G) | 715 | A | 2 | 11 | 0 | 0.01 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | 831 (A), |  |  |  |  |  |  |
| Tiger shark | Apex | 310 (B) | 1004 | $6 \mathrm{I}, 8 \mathrm{~A}$ | 4 | 14 | 0 | 0.30 |
|  |  |  |  | $19 \mathrm{I}, 11 \mathrm{~A}$, |  |  |  |  |
| White shark | Apex | 2,201 (A) | 909 | 1 U | 3 | 31 | 0 | 0.54 |
| Yellowfin grouper | Meso |  | 324 | A | 1 | 1 | 1 | 0.52 |

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| Region | Depth zone | Nodes | Total \# receiver s | Total area ( $\mathbf{k m}^{2}$ ) | \# Fish | \# <br> Fish/ <br> re- <br> ceiver | Total area ( $\mathbf{k m}^{2}$ ) | Receiver density (\#/km ${ }^{2}$ ) | Receiver <br> depth $\pm$ <br> SD (m) |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Gulf | 20-40 | -- | 0 | 5583 | 0 | 0 | 0 | 0 |  |
| Gulf | $\begin{aligned} & 40- \\ & \hline \end{aligned}$ | -- | 0 | 2581 | 0 | 0 | 0 | 0 |  |
| Gulf | 10-20 | 1,2,3 | 5 | 3749 | 25 | 5 | 0.63 | 0.001 | $\begin{aligned} & 18.2 \pm \\ & 1.60 \end{aligned}$ |
| Atlantic | $\begin{aligned} & 40- \\ & 200 \end{aligned}$ | $\begin{aligned} & \text { 26,37,38,3 } \\ & 9,40 \end{aligned}$ | 5 | 3524 | 62 | 12.4 | 0.63 | 0.001 | $\begin{aligned} & 105.0 \pm \\ & 44.49 \end{aligned}$ |
| Gulf | 0-10 | $\begin{aligned} & 4,5,6,7,8,9 \\ & 12,11,13,1 \\ & 4,16,17,20 \end{aligned}$ | 76 | 7048 | 126 | 1.7 | 9.55 | 0.011 | $3.1 \pm 1.17$ |
| Atlantic | 10-20 | $\begin{aligned} & 10,22,23,2 \\ & 4,25,27,29 \\ & 33,36 \end{aligned}$ | 31 | 1060 | 185 | 6 | 3.9 | 0.029 | $\begin{aligned} & 14.3 \pm \\ & 2.89 \end{aligned}$ |
| Atlantic | 0-10 | $\begin{aligned} & 10,15,21,2 \\ & 2,24,29,31, \\ & 36 \end{aligned}$ | 65 | 1975 | 153 | 2.4 | 8.17 | 0.033 | $6.1 \pm 2.15$ |
| Atlantic | 20-40 | $\begin{aligned} & 22,23,24,2 \\ & 5,27,28,29, \\ & 30,31,32,3 \\ & 3,34,35,36 \\ & \hline \end{aligned}$ | 49 | 979 | 213 | 4.4 | 6.16 | 0.05 | $\begin{aligned} & 31.9 \pm \\ & 5.57 \end{aligned}$ |

TABLE 3. Measures of monitoring power within categories defined by region and depth zone: nodes, number of receivers, total area, number of unique fish detected in that area, number of unique fish detected per receiver, total monitored area, receiver density, and mean receiver depth. Receivers in nodes often were distributed across multiple depth zones.

FIGURE 1 Geographic location of the study area, arrows indicate Tampa Bay (to the north) and below that Charlotte Harbor (A); boundaries of the Florida Keys National Marine Sanctuary (black lines), underlying habitat, and deployed receiver sites, with red markers denoting seamount sites and black artificial reef sites (B). Habitat types were obtained from Florida Unified Reef Tract data; (C) nodes plotted by depth zone, colored by deployment year and scaled by number of receivers in each node. The black line along the islands and just south of Marquesas Key denotes the boundary used to separate depth on the Atlantic versus Gulf side. Nodes 37 through 40 are seamounts, 38=Islamorada and 40=Marathon.


FIGURE 2 A conceptual model of the proposed movement strategy framework addressing how well tracking data reflect true movement paths, and thus the accuracy of our movement metrics and analysis to inform species' eco-evolutionary movement strategies. These strategies are made up of movement traits which occur at the lifetime, annual, and intra-annual time scales, exhibiting varying levels of intra-specific variability. These characteristics are mediated by inherited optimization end points and ecological context, with behavioral choices resulting in both density-dependent and fitness feedback loops.


FIGURE 3 The spatial distribution of tagging sites for species detected in the study area (A) The relative number of fish detected in this study from each tagging site is represented by marker diameter. Fish tagged within or near the study area (B); log-scaled species-specific detection potential (C).


FIGURE 4 Individual (A) and summary statistics (B) for size in cm (disc width for rays; total length for others) for species tracked in this study and dashed lines indicate the 180 cm size threshold. In A. fish tagged within the study site are indicated by filled markers.


FIGURE 5 Dates of detection by individual and species, exhibiting variable detection periods, sample sizes, and temporal patterns.


FIGURE 6 Results of the agglomerative hierarchical clustering based on maximum and mean number of basins of detection, maximum consecutive detection months and yearly and monthly residence indices. Also shown are species-specific radar graphs depicting the relative value of the variables used for the cluster analysis (i.e., each variable was standardized by its maximum for the radar plots).


FIGURE 7 Species-specific network analysis graphs, which are grouped by annual movement type. Sample sizes for fish with detection periods of a year or greater are indicated above each network. Colors indicate individuals' paths. Marker size is scaled to indicate nodes with the greatest paths for each species.


FIGURE 8 Species space use based on standard deviation ellipses (A); maximum consecutive detection months (B); and dates of detection (C). Annual movement types are colored similarly (reds/pinks=seasonal migrants; greens=migrants; blues=high-site fidelity residents, aquas=resident). Crevalle jack are not represented due to their short detection periods.


FIGURE 9 Station numbers were assigned to each receiver based on longitude, with the lowest number representing the western-most station. This allowed us to calculate and plot mean daily station (circles) of detection over the study period. January 1 of each year is noted on the x axis. All detection days are connected (dashed and colored lines) to make it easier to see shifts in location, but do not necessarily indicate a direct movement from one location to another. Site fidelity results in horizontal lines, while rapid movement along a longitudinal gradient results in vertical lines. Different color and line patterns were used to distinguish individual fish. Cluster analysis movement types are indicated in parenthesis after species names $\left(\mathrm{M}=\right.$ migrant, $\mathrm{M}_{\mathrm{S}}=$ seasonal migrant, $\mathrm{R}_{\mathrm{H}}=$ high site fidelity resident, $\mathrm{R}=$ resident $)$ and colored-coded.


FIGURE 10 Movement signatures of individual migrants exhibiting stopover behavior (left) versus those rapidly migrating through the study area (right). Station numbers were assigned to each receiver based on longitude, with the lowest number representing the western-most station. Mean daily station is indicated with markers, which are connected (dashed and colored lines) to make it easier to see shifts in location, but do not necessarily indicate a direct movement from one location to another. Cluster analysis movement types are indicated in parenthesis after species names $(\mathrm{M}=$ migrant, $\mathrm{MS}=$ seasonal migrant, $\mathrm{RH}=$ high site fidelity resident, $\mathrm{R}=$ resident) and colored-coded.


Date

