#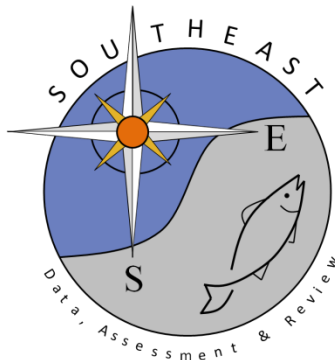 Relative abundance of scalloped hammerhead, *Sphyrna lewini*, and Carolina hammerhead, *Sphyrna gilberti*, along the southern U.S east coast.

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Relative abundance of scalloped hammerhead*, Sphyrna lewini*, and Carolina hammerhead, *Sphyrna gilberti*, along the southern U.S east coast.

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Barker et al. (2021) estimated the relative abundances of the sympatrically-distributed cryptic species pair; scalloped hammerhead, *Sphyrna lewini*, and Carolina hammerhead, *Sphyrna gilberti* in the U.S. south Atlantic (hereafter Atlantic) by genotyping individuals using diagnostic single nucleotide polymorphisms (Barker et al. 2021). A total of 927 animals were genotyped, and 251 were identified as Carolina hammerhead, 590 as scalloped hammerhead, 3 as great hammerhead, and the remaining 83 as admixed individuals. Discounting the admixed individuals and great hammerheads, 30% of the samples were Carolina hammerhead and 70% were scalloped hammerhead. However, sampling for that study was conducted largely in known nursery habitats, prompting concerns that the estimates might be biased. To account for this, we re-estimated the percentages of both species from the data in Barker et al. (2021) by 1) bootstrapping the data, 2) excluding samples in known nursery areas, and 3) comparing the genetic effective sizes (N_E) of both species in the Atlantic.

Bootstrap resampling: The geographic sampling area from Barker et al. (2021) was broken up into four even areas (Figure 1). All great hammerhead and admixed individuals were then removed from the data. The data were then resampled with replacement, with the number of samples equal to the number originally collected in each area. For each area 1,000 bootstrap replicates were run and an average percentage (and 95% CI) calculated for each species in each area and for the Atlantic as a whole.

Exclusion of nursery area samples: All individuals captured inside areas thought to be nursery habitat were excluded from the data (Figure 2). This resulted in a data set of only 172 individuals from which percentages of each species were calculated. Because nursery habitat designation is somewhat arbitrary, we also created a data set where all individuals caught inside a bay or estuary were excluded (Figure 3). This resulted in a data set of only 322 individuals from which percentages of each species were calculated.

Effective population size: For each species N_E was calculated using all samples collected in the Atlantic. Because the presence of siblings can downwardly bias N_E estimates but is also a characteristic of small populations (Waples & Anderson 2017), N_E was estimated using a dataset that excluded non-randomly sampled siblings, as well as a dataset that excluded all siblings. For this study non-randomly sampled siblings were defined as siblings caught in the same location in a period of 24 hours or less. The linkage disequilibrium method was used to estimate N_E, excluding alleles with a frequency of 0.02 or less and confidence intervals were estimated using the jackknife method (Do et al. 2014). Estimates of N_E cannot be directly related to census size (Frankham,1995; Luikart *et al.*, 2010) but if it is assumed that life history parameters of the two species are similar, they can be used to infer relative populations sizes of the two species.

Point estimates of relative abundance from bootstrapping ranged from 56.1% Carolina hammerhead in Area 2 to 7.5% Carolina hammerhead in Area 4, with a total estimate for the Atlantic of 29.8% Carolina hammerhead (Table 1). When data was constrained to individuals captured outside of proposed nurseries, Carolina hammerhead made up 24.4% of the individuals, but when data was constrained to individuals captured outside of bays or estuaries, Carolina hammerhead made up 18.8% of the individuals. Point estimates of N_E were smaller for Carolina hammerhead than scalloped hammerhead regardless of whether randomly sampled siblings were included or not (Table 2), and confidence intervals around the point estimates either barely overlapped (random siblings included) or did not overlap (no siblings). Relative abundance calculated from N_E was 33.5% (CI 30.3%-41.6%) when random siblings were included and 29.3% (CI 28.1%-33.3%) when no siblings were included.

Across methods a consistent pattern emerged, and the estimated percentage of Carolina hammerhead (19%-33%) was small relative to the estimated percentage of scalloped hammerhead. These results are consistent with what was reported by Barker et al. (2021) and suggest that a non-negligible percentage of individuals caught (either by scientists or fisheries) along the Atlantic will be Carolina hammerhead. It is important to note that the data used here are heavily skewed towards juveniles, with only 38 mature animals in the data set. Of those 38 animals, only three are Carolina hammerhead and more research is needed to understand the distribution of adult Carolina hammerhead. Furthermore, the percentage of Carolina hammerhead is greatest in South Carolina, and the probability of encountering them decreases greatly in the southern areas that were sampled. To date, none have been captured in the Gulf of Mexico.
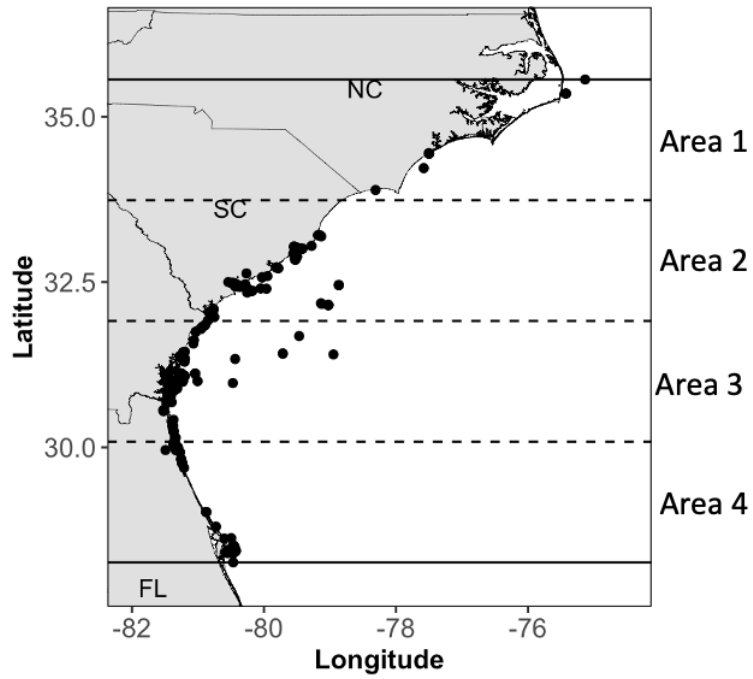
Figure 1. Map depicting the four evenly spaced geographic regions used for bootstrap resampling.
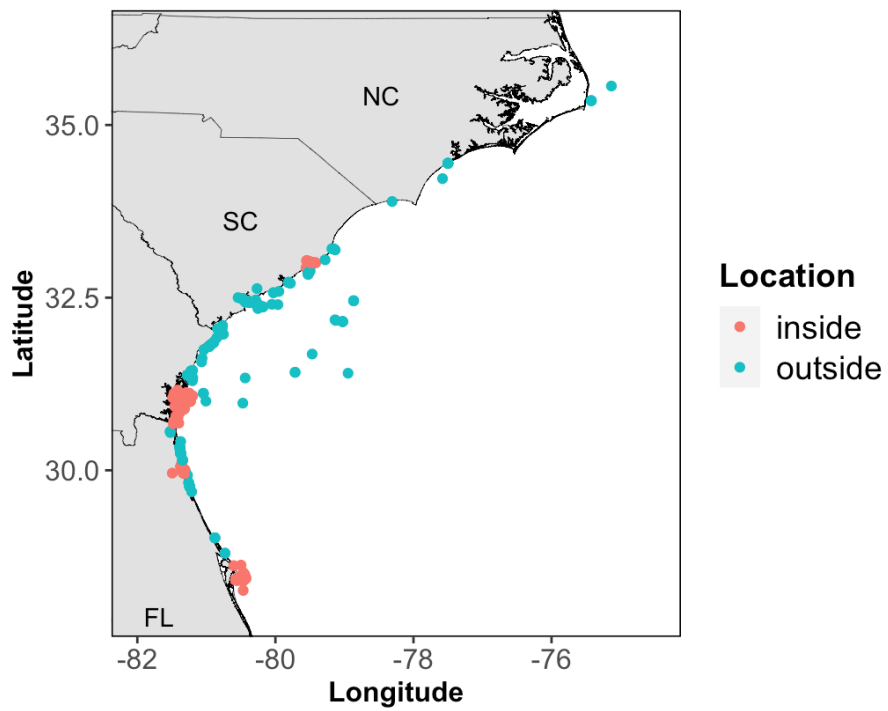

Figure 2. Map of sampled individuals inside and outside designated nursery areas.
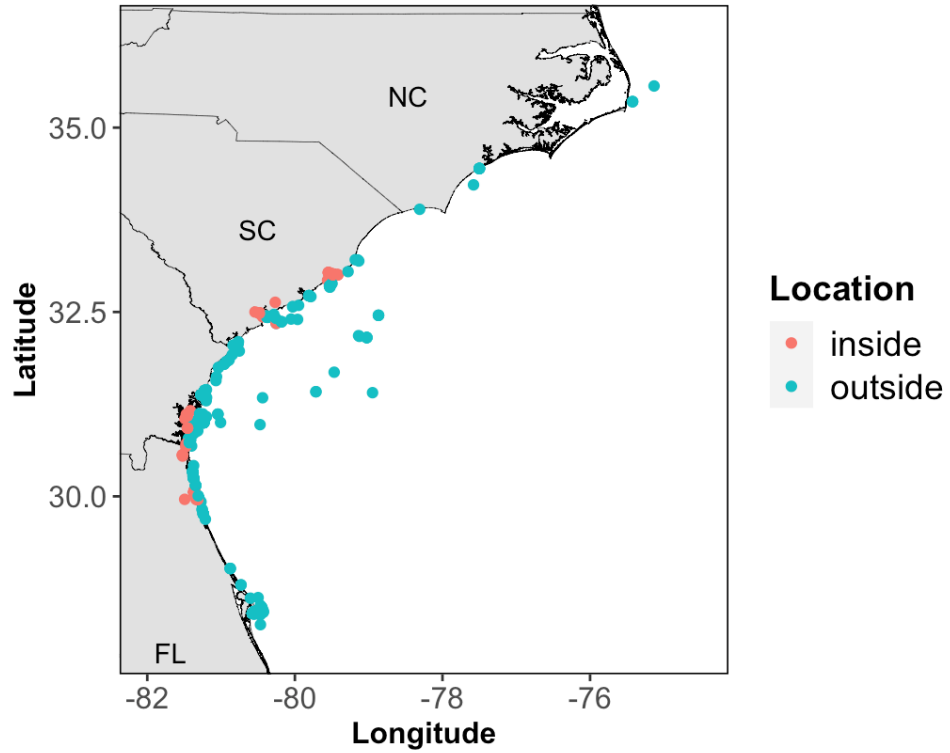
Figure 3. Map of sampled individuals inside and outside bays and estuaries.

Table 1. Mean relative abundance of Carolina hammerhead across four evenly spaced geographic areas (Figure 1) estimated with bootstrap resampling and 95% confidence intervals.

Area	Relative Abundance	Min	Max
1	33.70%	8.30%	58.30%
2	56.20%	51.40%	60.90%
3	16.90%	9.70%	23.90%
4	7.60%	4.70%	10.10%

Table 2. Effective population size for scalloped and Carolina hammerhead in the U.S. south Atlantic estimated with randomly sampled siblings included (Included) and with no siblings included (Excluded)

Species	N	Min	Mode	Max	Siblings
Scalloped	431	4204.6	5521.4	7996.0	Included
Carolina	204	1828.3	2781.6	5696.7	Included
Scalloped	385	10519.1	15795.6	31502.4	Excluded
Carolina	189	4120.9	6549.3	15754.0	Excluded

N, number of individuals used to calculate estimates; min, lower bound of 95% CI; mode, point estimate of N_E; max, upper bound of 95% CI.

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