Ecography

Supplementary material
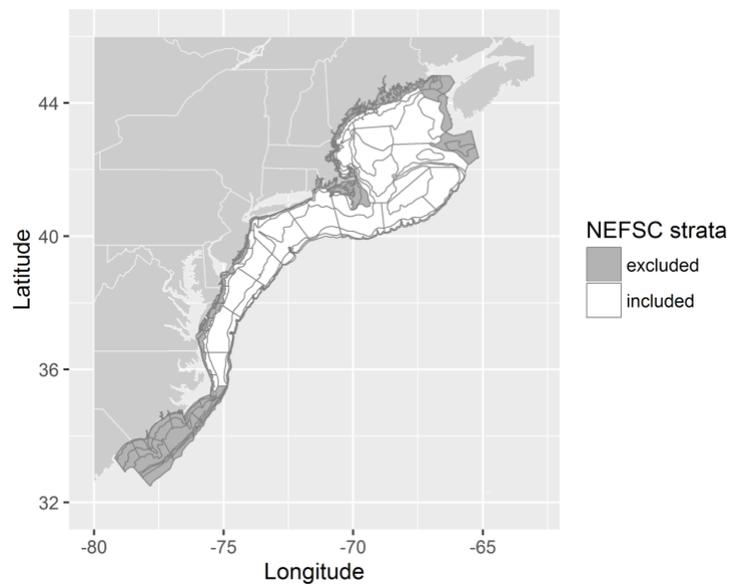
Appendix 1

Supplementary figures

Figure A1. Strata in Northeast Fisheries Science Center trawl survey.

Trawl data were only analyzed if they were collected from strata that were sampled in at least 90% of spring and fall surveys between 1982 and 2015, the years for which both trawl data and temperature data were available.
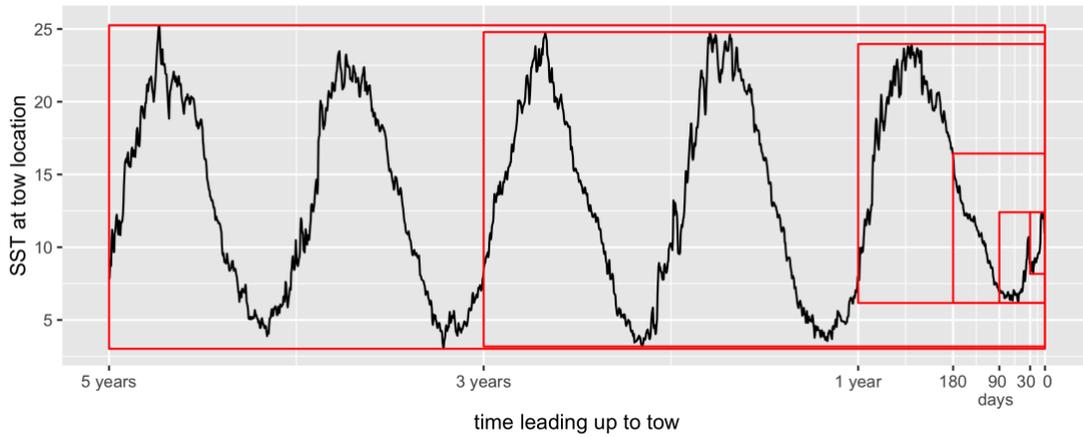
Figure A2. Temperature variables considered in analysis.

Temperature variables were generated for each tow by calculating four summary statistics (mean, minimum, maximum, variance) in each of six temporal windows (30 days, 90 days, 180 days, 1 year, 3 years, 5 years). In this example, the black line indicates daily SST values over the five years leading up to a tow conducted on April 24, 2012 at 41.864° N, 70.455° W. Red boxes bound the times and temperatures within which summary statistics were calculated.

	Used geographies	Available geographies	Regression plots
High Salience	AMERICAN LOBSTER (SPRING)	AMERICAN LOBSTER (SPRING)	AMERICAN LOBSTER (SPRING)
Moderate Salience	BLACKBELLY ROSEFISH (FALL)	BLACKBELLY ROSEFISH (FALL)	BLACKBELLY ROSEFISH (FALL)
Unknown Salience	ATLANTIC MACKEREL (SPRING)	ATLANTIC MACKEREL (SPRING)	ATLANTIC MACKEREL (SPRING)
Low Salience	ROUGHTAIL STINGRAY (FALL)	ROUGHTAIL STINGRAY (FALL)	ROUGHTAIL STINGRAY (FALL)
Very Low Salience	OFFSHORE HAKE (SPRING)	OFFSHORE HAKE (SPRING)	OFFSHORE HAKE (SPRING)

Figure A3. Thermal characteristics of used and available geographies and regression plots for sample taxa.

Thermal characteristics of used geographies are calculated by matching each year of tow data with its corresponding year of temperature data. Thermal characteristics of available geographies are calculated across all years of tow data and temperature data. Regression plots show temperature trajectories within available geographies (defined by each year of tow data) and in the geographies actually used by a species through time. A) Variance in SST (5-year window) for American lobster (*Homarus americanus*). B) Maximum SST (90-day window) for blackbelly rosefish (*Helicolenus dactylopterus*). C) Maximum SST (30-day window) for Atlantic mackerel (*Scomber scombrus*). D) Mean SST (30-day window) for roughtail stingray (*Dasyatis centroura*). E) Minimum SST (1-year window) for offshore hake (*Merluccius albidus*).
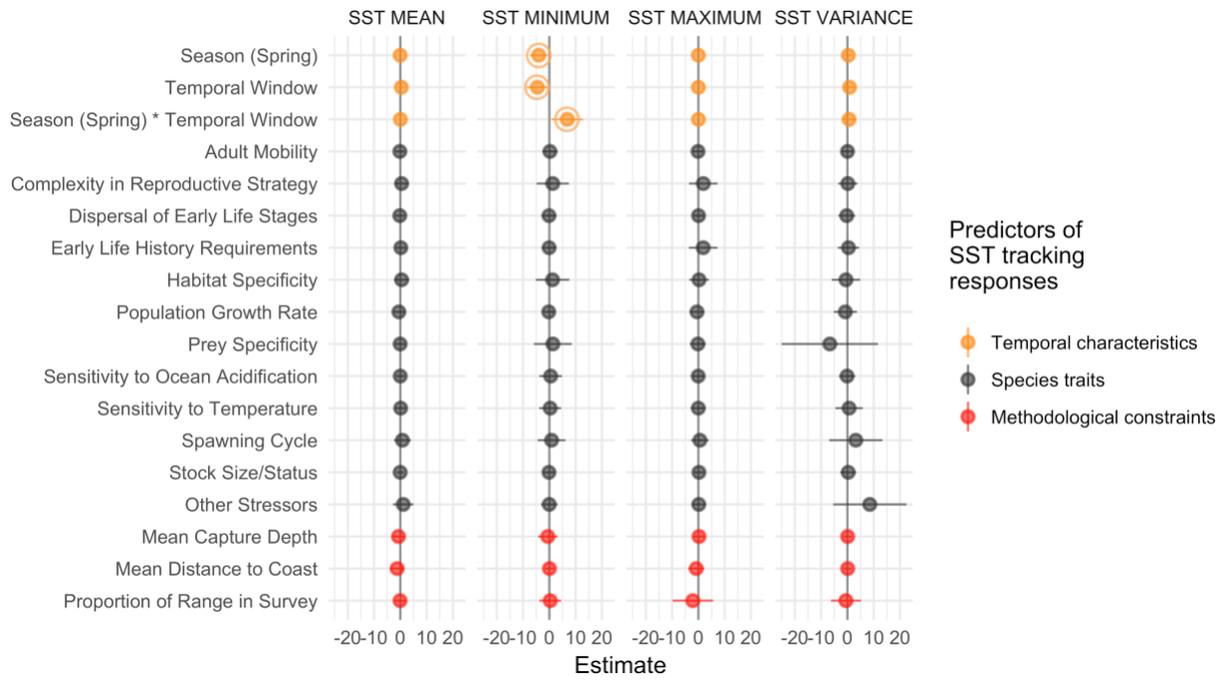
Figure A4. Predictors of SST tracking responses across species sampled in at least 90% of survey years.

Separate regression analyses were performed for each type of SST variable (i.e., mean, minimum, maximum, variance) across 67 species. Multi-model inference approaches were used to obtain model-averaged parameter estimates and standard errors. Points indicate parameter estimates and error bars indicate ± 2 SE. Statistically significant predictors of tracking responses are circled. Some variables were rescaled to aid model fitting and display of effect sizes (Temporal Window, Mean Capture Depth, Mean Distance to Coast, Number of Years in Survey). We distinguished three different types of variables that may influence tracking responses, or our ability to detect them: variables related to time (seasonality and scale), life history characteristics, and study methodology.
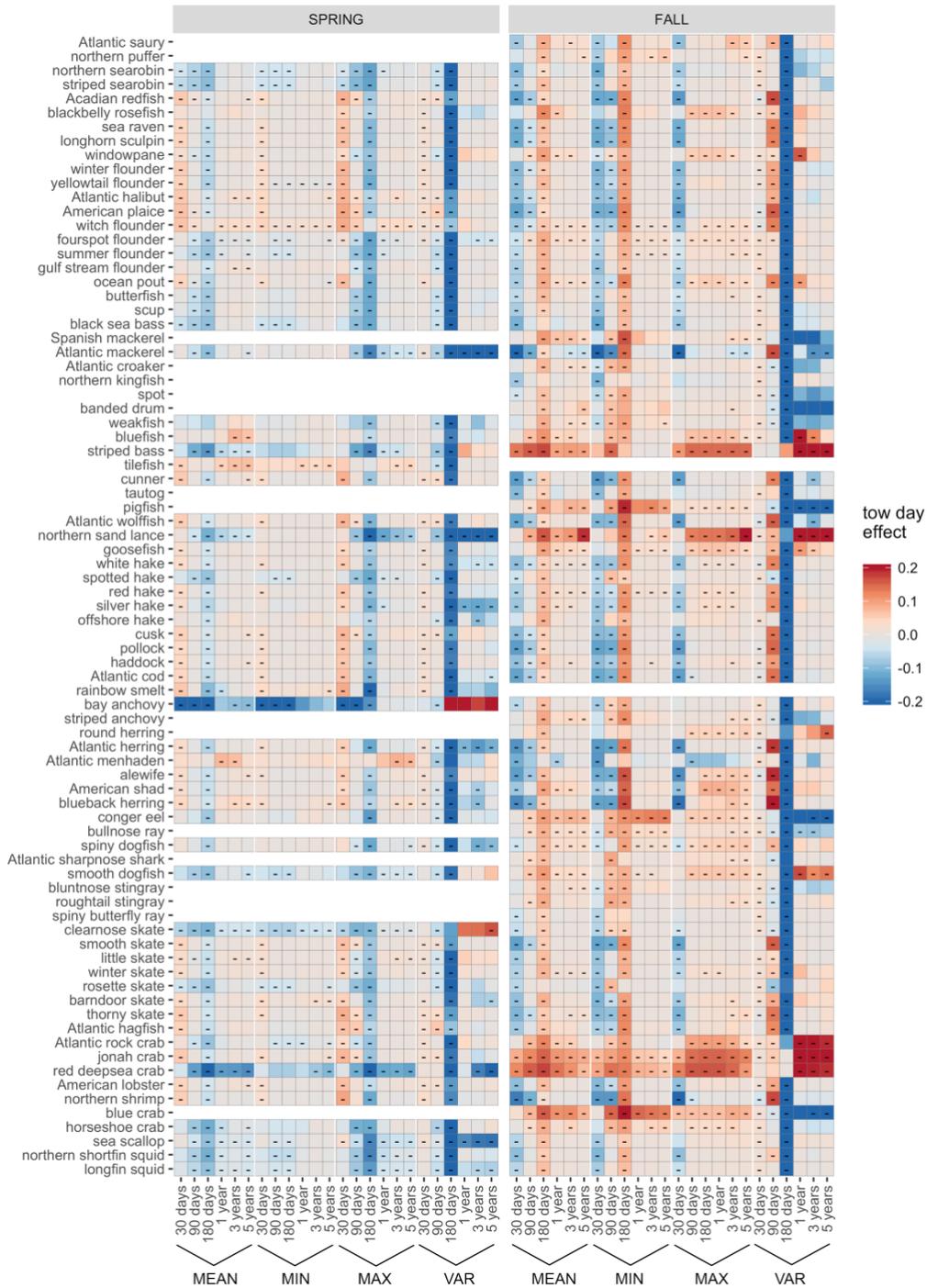
Figure A5. Effect of tow day on biomass-weighted SST estimates.

Positive effects (red) indicate higher sea surface temperature values at later tow days. Negative effects (blue) indicate lower sea surface temperature values at later tow days. Cells containing a dash indicate statistically significant effects.

Supplementary Methods

Cluster Analysis

We used hierarchical agglomerative cluster analysis to group taxa based on the similarity of their responses to 24 temperature variables. Separate analyses were performed for each season using "pvclust" (Suzuki and Shimodaira 2015), an R package that implements bootstrap resampling to estimate uncertainty in hierarchical cluster analyses (Shimodaira 2004). Manhattan distances were used to characterize the dissimilarity of species' tracking responses and clusters were formed using Ward's method. Ten thousand bootstrap samples were used to generate approximately unbiased p-values for each cluster in the resulting dendrogram. We only utilized clusters for subsequent analyses if they were supported by p-values smaller than 0.05.

Join-count Analysis

To assess whether species belonging to the same cluster occupied similar geographies, we implemented join-count analyses for each season using the "spdep" package in R (Bivand et al. 2013, Bivand and Piras 2015). Biomass-weighted centers of species distributions were "colored" by cluster membership. Species that did not group with any other taxa in cluster analyses were removed from the join-count analysis because they did not share a "color" with any other taxa. A spatial weights matrix was generated among all remaining species (i.e., points) using inverse distance weighting. We then used a permutation test, which randomizes "colors" across the given point locations, to assess whether same "colors" were spatially autocorrelated. We tested for positive spatial autocorrelation (i.e., species of the same "color" closer than expected by

chance) and negative spatial autocorrelation (i.e., species of the same "color" further from each other than expected by chance) using 10000 simulated distributions of "colors".

References

Bivand, R. and Piras, G. 2015. Comparing implementations of estimation methods for spatial econometrics. – J. Stat. Software 63: 1–36.

Bivand, R. et al. 2013. Computing the Jacobian in Gaussian spatial autoregressive models: an illustrated comparison of available methods. – Geogr. Anal. 45: 150–179.

Shimodaira, H. 2004. Approximately unbiased tests of regions using multistep-multiscale bootstrap resampling. – Ann. Stat. 32: 2616–2641.

Suzuki, R. and Shimodaira, H. 2015. pvclust: hierarchical clustering with p-values via multiscale bootstrap resampling. – <https://cran.r-project.org/web/packages/pvclust/index.html>.