TECHNICAL DOCUMENTATION FOR MDAT SUMMARY PRODUCTS

The Marine-life Data and Analysis Team (MDAT) collectively produced a "reference library" of over 3,000 map products for models of individual avian and marine mammal species, and map products of biomass and distribution for many fish species. These data are summarized into synthetic maps of total abundance or biomass, species richness, diversity, and core abundance or biomass area for each taxonomic group and species group.

REGIONS OF INTEREST

Product assessment boundaries were decided with input from members of both the Northeast and Mid-Atlantic Regional Planning Bodies (RPBs), to reflect the commonality of species and habitat between the regions. As a result, the Northeast and Mid-Atlantic regions have an area of overlap off the coast of New York (Figure 1). Base layer products are not dependent on the extent or an area boundary. All avian and marine mammal base products exist at the full east coast scale, to the extent possible given the underlying data, while the fish data products vary in extent from spanning both regions, to local state waters in New England. Synthetic products were created specific to each regional spatial extent, and for some products the results differ between the regions. Model details, spatial and temporal coverage details, and data limitations specific to each marine-life component, are described below. Northeast RPB Marine Life Working group call summaries and final work plans are available online at http://neoceanplanning.org/projects/marine-life/.

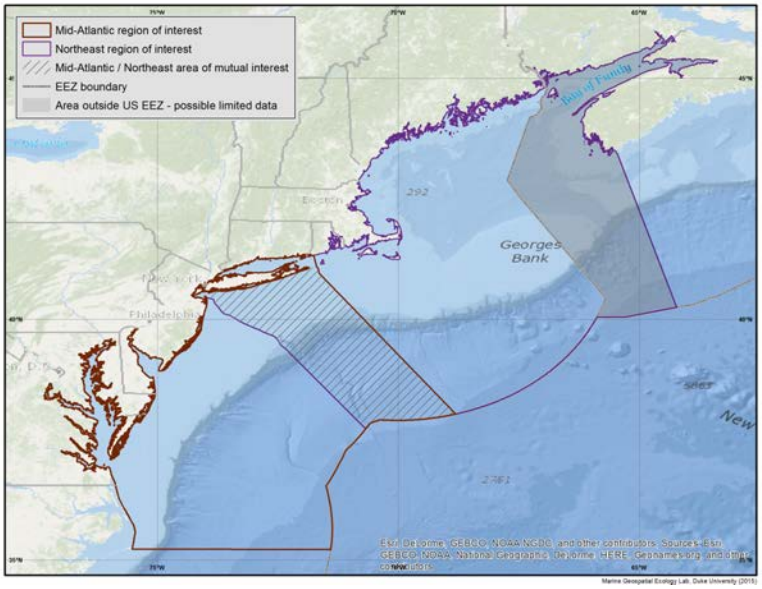

Figure 1. Geographic boundaries for marine life mapping. Data availability beyond the US EEZ (in Canadian waters) was limited, and some models did not predict into the gray area.

SUMMARY PRODUCTS

Marine-life data summary products are secondary or tertiary distillations of the abundance models or observation data. Summary products provide a means to distill hundreds of data layer and time period combinations into more simplified maps that supplement the base-layer reference library, with those data and models continuing to be fundamental to ocean planning and decision making. Higher-level, summary products are useful for revealing patterns in underlying data models and may not fully address the needs associated with answering species-level specific ecological or management questions. Targeted queries of species-specific products in the reference library are often the most reliable method for matching the data to specific questions.

Decisions made in the creation of the higher-level map products were discussed with the Northeast RPB, the taxa-specific expert work groups, the Ecosystem-Based Management work group and similar entities in the Mid-Atlantic region. Understanding the implication of applied thresholds and criteria is critical to appropriately interpret synthetic products.

Types of summary products include total abundance or biomass, species richness, diversity, and core abundance or biomass area richness (50%). Each type of product was created for various groups of species in each taxon, including an “all species” group.

All summary products were created at the scale of the underlying data sets. For avian and mammal model products this is the US east coast out to the Exclusive Economic Zone if possible, and for the NEFSC fish data the range is from Cape Hatteras NC to the Gulf of Maine out to the continental shelf break (approximately the 150m depth contour).

SUMMARY PRODUCT CAVEATS AND CONSIDERATIONS

There are four main caveats when considering use of the higher-level summary products created for species groups, and for all species within each taxon.

1. The species within these groups represent only those modeled or mapped by MDAT. As an example, there may be additional “migrant” bird species in the Northeast region not captured in this species group because there were insufficient observations available to develop an individual species model.
2. The groups are not exhaustive. There is potential for additional groups, but the data and information available at this time do not support their formation. In order to develop species membership lists for all groups, we relied on expert judgment and published sources of information.
3. Group level products for avian and marine mammals (abundance, richness, diversity, and core area richness) were created with the annual prediction models (vs monthly or seasonal models), and so should be interpreted accordingly.
4. Groups may be dominated by one (or few) species of very high abundance, which are often not species of particular concern.

Caveats specific to the marine mammal summary products:

Marine mammal summary products do not include seals.

Caveats specific to the avian summary products:

Avian summary products do not include four species for which actual numerical values of predicted relative abundance were very high or highly skewed and thus unduly influenced the summary products. The species not included in avian summary products are:

- Audubon's shearwater
- Black guillemot
- Black-capped petrel
- Common eider

Avian summary products are based on normalized individual species annual relative abundance distributions. The mean value of the relative distribution was used to normalize the distribution values. This normalization helps reduce the impact of very large predicted populations in the subsequent synthetic product development.

Avian summary products were developed using the masked model results. This means that model results beyond 100 km from a minimum-distance path connecting the raw sighting location data for each species (which are masked out at the individual species model level) were not included in the summary products.

Caveats specific to the fish summary products:

Only the NEFSC trawl data sources were used to create the fish summary products. There is currently no defined process for combining each of the four sources of individual species products.

Fish group species richness, group diversity, and core biomass area richness products represent the expected richness or diversity of a tow if done in that area, and are not necessarily representative of the true fish species richness or diversity in that location. These products represent the expected richness and diversity for the gear type used in NEFSC fall trawls, and considering each species' catchability. These data are not meant to be used to determine absolute fish biomass hotspots.

SPECIES GROUPS

Regulatory groups depict the distribution and densities or biomass of marine life species that have been formally protected, designated as a species of concern, or are managed through a specific state or federal program or partnership. Membership lists for regulatory species groups were developed from the published documentation associated with each regulatory authority.

Ecological/Biological groups portray the distribution and abundance or biomass of species with similar characteristics or life history requirements. Membership lists for ecologically based species groups were developed by taxa experts within MDAT with guidance and input from expert work group members and RPB members.

Stressor-sensitivity groups enable a better understanding of specific interactions between marine life and human activities and the potential effects of ecosystem changes. We sought to develop groups based on existing and quantified relationships between species and stressors, and as a result the development of stressor sensitivity-based species groups has been limited at present. The species membership of stressor sensitivity based groups was determined using peer-reviewed literature and federal agency research.

GROUP ABUNDANCE OR BIOMASS

Summed abundance or biomass products were created for every defined group including an “all species” group in each taxon. There are slight differences in interpretation among the avian, fish and mammal products, summarized below. Grid cell sizes for each summary product are the same as the individual species products from which they are composed. Marine mammals and fish summary products have a grid cell size of 10km x 10km, whereas avian summary products have a grid cell size of 2km x 2km.

Individual abundance for mammals and biomass for fish are not normalized. Therefore, patterns in some group products for mammals and fish may be driven by particularly abundant species, which may not be species of concern or interest. While individual avian species relative abundances are normalized by the mean of the species’ distribution for inclusion in the group summary products, patterns in some group products may still be driven by particularly abundance species, which may not be species of concern or interest.

Marine Mammal (Cetacean) Total Abundance

MDAT total abundance products for marine mammals do not include seals. For all cetacean species together, and for each species group, total abundance maps are calculated in a Geographic Information System (GIS) by stacking each individual species’ predicted annual abundance layers and summing the values of the pixels in each resulting “column”. The result is the total predicted abundance of all individuals (of the included species) in that cell. Each map cell is 10km x 10km.

Avian Total Relative Abundance

For all avian species together, and for each species group, total relative abundance maps are calculated in a GIS by stacking each individual species’ predicted annual long-term average relative abundance layers and summing the values of the cells in each resulting “column”. The result is the total predicted long-term average relative abundance of all individuals (of the included species in the group) in that cell. Each map cell is 2km x 2km. It is important to note these products represent and reflect **relative** abundance, not predicted absolute abundance. This caveat is based on the properties of the base-layer products being aggregated, i.e., the base-layer avian products do not predict absolute abundance. In addition, individual species base-layers were normalized to their mean prior to summation.

Fish Total Biomass

For all fish species together, and for each species group, total biomass maps are calculated in a GIS by stacking each individual species' Inverse Distance Weighted (IDW) interpolation layers and summing the values of the pixels in each resulting "column". The result is the total interpolated biomass of all individuals (of the included species) in that cell. Each map cell is 10km x 10km. Note that individual fish species IDW maps calculate biomass on a natural logarithm scale, and these aggregate maps are raw biomass, in kilograms.

SPECIES RICHNESS

Marine Mammal (Cetacean) Species Richness

MDAT species richness products do not include seals. For all cetacean species together, and for each group of species, total richness maps are calculated in a GIS by stacking each individual species' predicted presence or absence and counting the total number of species present in each cell. A species is considered present in a cell if that cell is included in the top 99% of total predicted abundance for the species.

Some of the individual models for mammal species were species guilds. For example, the beaked whale model is based on data from five beaked whale species (Blainville's beaked whale, Cuvier's beaked whale, Gervais' beaked whale, Sowerby's beaked whale, and True's beaked whale). This was done to create the best available model at the guild level when not enough data were available to create robust models at the individual species level. To better reflect true species counts in the richness map products, these guild density maps were counted as multiple species. Each beaked whale cell counted as five species (listed previously). Each map cell is 10km x 10km.

Avian Species Richness

For all avian species together, and for each species group, total richness maps are calculated in a GIS by stacking each individual species' predicted presence or absence and counting the total number of species present in each cell. A species is considered present in a cell if that cell is included in the top 95% of total predicted relative abundance for the species. Each map cell is 2km x 2km.

Fish Species Richness

For all fish species together, and for each species group, total richness maps are calculated in a GIS by stacking each individual species' predicted presence or absence and counting the total number of species present in each cell. A species was considered present in a cell if its biomass (from the IDW product) in that cell was greater than 1.5kg. Each map cell is 10km x 10km.

DIVERSITY

The Shannon diversity index (Shannon & Weaver, 1949) was used to create maps showing areas of high and low biodiversity. The Shannon index considers both abundance and evenness of species in an area in its calculation of diversity. Grid cells with high Shannon index scores have a high number of species (relative to the total number of species being considered in the area), as well as overall similar abundances (or biomass for fish) of these species. Areas that have a large number of species, but are dominated in abundance or biomass by only a few species, will not score as high on the Shannon index. The index approaches zero if the abundance is dominated by one species, regardless of how many other rare species occur in the area. The index is maximized when all the species evaluated have equal abundances, at which point the index equals the natural log of the species richness value (the number of species).

For avian diversity products, no cells were excluded.

For fish diversity products, cells with less than 2kg of biomass were excluded.

For mammal diversity products, cells with density values less than 0.001 were excluded.

CORE ABUNDANCE OR BIOMASS AREA RICHNESS

It is clear from examining MDAT individual species products that animals are not evenly distributed in the study area. The Northeast RPB and work group members indicated that it would be useful for ocean planning purposes to visualize areas where species or groups were concentrated. To do this, the concept of a “core abundance area” or “core biomass area” was defined. After exploring several options for statistically defining a “core area”, a method was chosen that would be easily explained to a wide audience with varying levels of statistical and technical backgrounds.

A threshold of 50% visually conveys two areas, each of which contains half the predicted population. This threshold is easy to understand: half of the population falls within the identified core area, and half of the population occurs outside of it.

The core abundance/biomass area is calculated by ranking cells by their abundance/biomass value from greatest to least, selecting the cells with the highest values, and then summing those values until the total is equal to or greater than 50% of the total predicted abundance/biomass.

Core abundance/biomass area *richness* refers to the fact that many core abundance/biomass areas are stacked in a GIS for the relevant taxa or species group. The values of the grid cells in these products represent the number of overlapping core abundance/biomass areas for species in that taxa/group.

As with all summary products, the annual marine mammal and avian individual species model results were used to calculate core abundance areas. The IDW products for fish species were used to calculate core biomass areas.

Core Area Caveats and Considerations

- Extent matters. Because core abundance/biomass areas are calculated using a proportion of the total abundance/biomass, the total extent of the study area will influence the results. For this effort, core abundance/biomass areas were created for Northeast region and the Atlantic Coast scale (Northeast Shelf scale for fish) to highlight the importance/lack of importance of the Northeast region to a group/taxa.
- Avian core relative abundance area richness was calculated using annual individual species products that were normalized by the mean of their distribution.
- Calculations for marine mammal core abundance area considered only the top 99% of total predicted abundance for each species.
- Calculations for marine mammal core abundance area richness did not include species with uniformly distributed models. So-called stratified models showing uniform density were created when there were not enough sightings to create a habitat-based density model. These species include:
    - Clymene dolphin
    - Fraser’s dolphin
    - Pantropical spotted dolphin
    - Rough-toothed dolphin
    - Spinner dolphin
    - White-beaked dolphin
    - False killer whale
    - Killer whale
    - Melon-headed whale
    - *Kogia* whales
    - Northern bottlenose whale
    - Blue whale
    - Bryde’s whale
- Calculations for avian core relative abundance area richness did not include brown pelican.