

# **Marine Sensitivity**

## **Project Documentation**

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# Table of contents

<b>Preface</b>	<b>6</b>
Interactive Apps . . . . .	6
How to Cite . . . . .	7
Acknowledgments . . . . .	7
<b>1 Introduction</b>	<b>8</b>
1.1 Overview . . . . .	8
<b>I Science</b>	<b>11</b>
<b>2 Science</b>	<b>12</b>
2.1 Conceptual Framework . . . . .	12
2.2 Cell Vulnerability . . . . .	12
2.3 Sensitivity Components . . . . .	13
2.4 Ecoregional Rescaling . . . . .	13
<b>3 Data Sources</b>	<b>14</b>
3.1 Dataset Overview . . . . .	14
3.2 Source Datasets . . . . .	15
3.2.1 AquaMaps SDM ( <code>am_0.05</code> ) . . . . .	15
3.2.2 NMFS Core Area ( <code>ca_nmfs</code> ) . . . . .	15
3.2.3 NMFS Critical Habitat ( <code>ch_nmfs</code> ) . . . . .	15
3.2.4 FWS Critical Habitat ( <code>ch_fws</code> ) . . . . .	16
3.2.5 FWS Range ( <code>rng_fws</code> ) . . . . .	16
3.2.6 BirdLife Range ( <code>b1</code> ) . . . . .	16
3.2.7 IUCN Range ( <code>rng_iucn</code> ) . . . . .	16
3.3 Merged Model ( <code>ms_merge</code> ) . . . . .	17
3.4 Standard Grid . . . . .	17
3.5 Primary Productivity . . . . .	17
<b>4 Taxonomy</b>	<b>19</b>
4.1 Taxonomic Authorities . . . . .	19
4.2 ID Resolution Cascade . . . . .	20
4.3 Species Categories . . . . .	20

4.4	Data Quality . . . . .	21
4.4.1	Duplicate Resolution . . . . .	21
4.4.2	Synonym Handling . . . . .	21
4.4.3	Valid Species Filter ( <code>is_ok</code> ) . . . . .	21
4.5	Key Function . . . . .	21
<b>5</b>	<b>Extinction Risk</b>	<b>22</b>
5.1	Regulatory Framework . . . . .	22
5.1.1	Endangered Species Act (ESA) . . . . .	22
5.1.2	Marine Mammal Protection Act (MMPA) . . . . .	22
5.1.3	Migratory Bird Treaty Act (MBTA) . . . . .	23
5.1.4	IUCN Red List . . . . .	23
5.2	Scoring Methodology . . . . .	23
5.2.1	US-listed Species . . . . .	24
5.2.2	Species not federally listed (IUCN) . . . . .	24
5.2.3	Scale Note . . . . .	25
5.3	Implementation . . . . .	25
<b>6</b>	<b>Model Merging</b>	<b>26</b>
6.1	Pipeline Overview . . . . .	26
6.1.1	Step 1: Gather Source Models . . . . .	26
6.1.2	Step 2: MAX Across Datasets . . . . .	26
6.1.3	Step 3: Spatial Masking . . . . .	28
6.1.4	Step 4: MMPA Spatial Floor . . . . .	28
6.1.5	Step 5: MBTA Spatial Floor . . . . .	28
6.1.6	Step 6: Persist Results . . . . .	28
6.2	Valid Species Filter . . . . .	29
<b>7</b>	<b>Scoring</b>	<b>30</b>
7.1	Cell-Level Scoring . . . . .	30
7.2	Metric Keys . . . . .	30
7.3	Ecoregional Rescaling . . . . .	31
7.4	Primary Productivity Scoring . . . . .	31
7.5	Zone Aggregation . . . . .	31
7.6	Visualization . . . . .	32
7.6.1	Flower Plot . . . . .	32
7.6.2	Treemap . . . . .	34
7.6.3	Interactive Maps . . . . .	36
<b>8</b>	<b>Stressors</b>	<b>37</b>
8.1	Offshore Wind Energy . . . . .	37
8.2	Oil & Gas . . . . .	37

<b>II Software</b>	<b>39</b>
<b>9 Software</b>	<b>40</b>
9.0.1 Interactive Applications . . . . .	40
9.0.2 Overcoming Challenges with Large Spatial Data . . . . .	41
9.0.3 Github Repositories . . . . .	42
9.0.4 Software Components . . . . .	44
<b>10 Server</b>	<b>45</b>
10.1 Setup . . . . .	45
10.1.1 launch instance . . . . .	45
10.1.2 ssh to server . . . . .	46
10.1.3 install docker . . . . .	47
10.1.4 Backup /share with snapshots . . . . .	48
10.2 Docker compose . . . . .	49
10.3 DNS . . . . .	53
10.4 Caddyfile . . . . .	54
10.5 Services . . . . .	55
<b>11 Database</b>	<b>59</b>
11.1 Table and Column Naming Conventions . . . . .	59
11.2 Species Distribution Models . . . . .	59
<b>12 Workflows</b>	<b>60</b>
<b>13 APIs</b>	<b>61</b>
<b>14 Libraries</b>	<b>63</b>
<b>15 Apps</b>	<b>64</b>
15.1 Current Applications . . . . .	64
15.1.1 mapgl — Sensitivity Map . . . . .	64
15.1.2 mapsp — Species Distribution Viewer . . . . .	64
15.2 Legacy Applications . . . . .	65
<b>16 Docs</b>	<b>66</b>
<b>17 Summary</b>	<b>67</b>
17.1 Key Findings . . . . .	67
17.2 Future Directions . . . . .	67
<b>References</b>	<b>69</b>

<b>Appendices</b>	<b>70</b>
<b>Glossary</b>	<b>70</b>
<b>III Applications (Current)</b>	<b>72</b>
<b>A mapgl — Sensitivity Map</b>	<b>73</b>
A.1 Overview . . . . .	73
A.2 Features . . . . .	74
A.2.1 Map Display . . . . .	74
A.2.2 Sensitivity Metrics . . . . .	75
A.2.3 Flower Plot . . . . .	75
A.2.4 Species Table . . . . .	75
A.2.5 Data Export . . . . .	75
A.3 Generating Screenshots . . . . .	75
A.4 Source Code . . . . .	75
<b>B mapsp — Species Distribution Viewer</b>	<b>76</b>
B.1 Overview . . . . .	76
B.2 Features . . . . .	77
B.2.1 Species Selection . . . . .	77
B.2.2 Model Display . . . . .	77
B.2.3 Species Info Panel . . . . .	77
B.2.4 Deep-Linking . . . . .	77
B.3 Generating Screenshots . . . . .	78
B.4 Source Code . . . . .	78
<b>IV Applications (Legacy)</b>	<b>79</b>
<b>Areas of Interest</b>	<b>80</b>
<b>Bird Hotspots</b>	<b>81</b>
<b>Regional Map</b>	<b>82</b>
<b>Scores Explorer</b>	<b>83</b>
<b>Distributions, Vector</b>	<b>84</b>
<b>Distributions, Raster</b>	<b>85</b>
<b>Vulnerability Mapper</b>	<b>86</b>

# Preface

The **Marine Sensitivity Toolkit** (MST) is a cloud-native system developed for the Bureau of Ocean Energy Management (BOEM) to assess the sensitivity of marine ecosystems to off-shore energy development. It integrates 9,819 species distribution models with extinction risk assessments across 20 BOEM Program Areas spanning US waters.

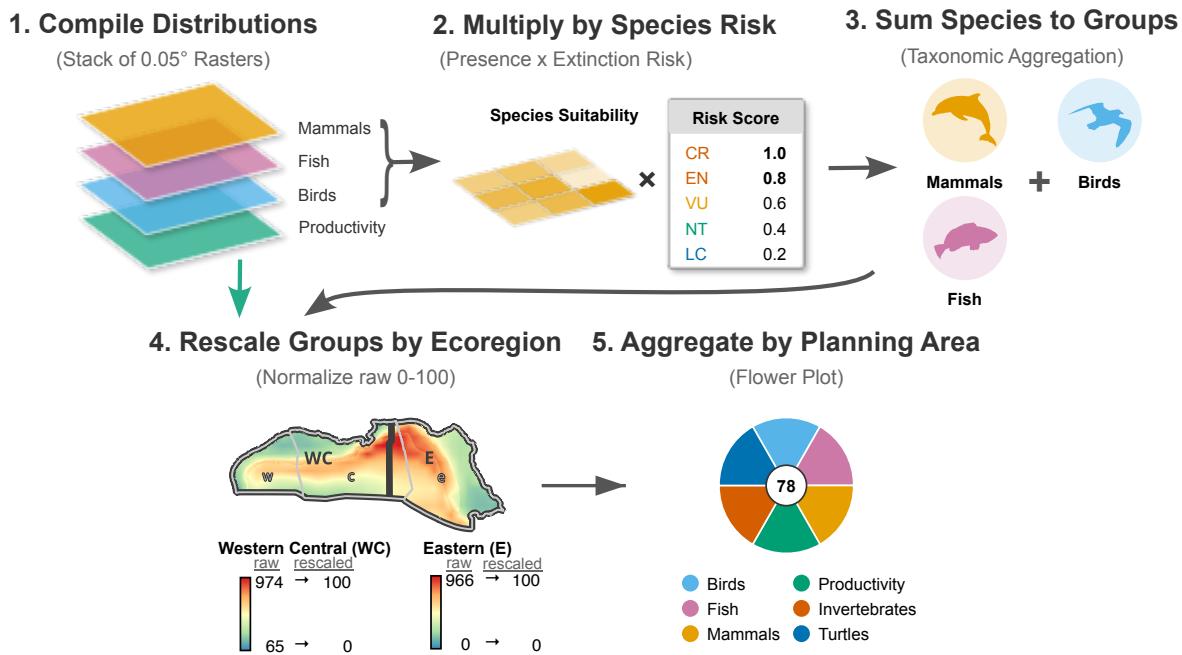


Figure 1: Overview of the MST methodology: species distribution models from 7 source datasets are merged, weighted by extinction risk scores (incorporating ESA, MMPA, MBTA, and IUCN protections), rescaled by ecoregion, and aggregated to management zones for visualization.

## Interactive Apps

- **Composite Scores** — explore sensitivity scores across BOEM Program Areas with flower plot summaries

- **Species Distribution** — view individual species distribution models and habitat suitability maps

This book documents the scientific methodology, software infrastructure, and interactive applications that comprise the MST. It is organized in two parts:

- **Science** (Chapter 2) — data sources, taxonomic integration, extinction risk scoring, model merging, and sensitivity scoring methodology
- **Software** — server architecture, databases, workflows, APIs, R libraries, and interactive applications

## How to Cite

Best, B.D. (2026). Marine Sensitivity Toolkit: Project Documentation. Bureau of Ocean Energy Management, Environmental Studies Program. <https://marinesensitivity.org/docs/>

## Acknowledgments

This work is funded by the [BOEM Environmental Studies Program](#) (BOEM-ESP). We thank the data providers whose open datasets make this work possible: [AquaMaps](#), [BirdLife International](#), [IUCN Red List](#), [NOAA Fisheries](#), and [U.S. Fish & Wildlife Service](#).

# 1 Introduction

The Marine Sensitivity Toolkit (MST) is a cloud-native system developed for [BOEM](#) (Bureau of Ocean Energy Management) to assess the sensitivity of marine species to offshore energy development, whether oil & gas or wind. The Outer Continental Shelf Lands Act (OCSLA), Section 18(a)(2)(G), mandates that BOEM consider “the relative environmental sensitivity and marine productivity of different areas of the OCS” when planning the timing and location of offshore energy activities. The MST operationalizes this mandate by combining the best available species distribution data with extinction risk assessments to map areas of the ocean that are most sensitive to human activities.

The MST marks a significant advancement over prior RESA methodologies (Morandi et al. 2018). Earlier approaches often relied on aggregated data from a limited set of broad species groups and surrogate species, lacking spatially explicit information for individual organisms. As a result, previous assessments were typically coarse and areawide, frequently missing critical ecological variation and fine-scale patterns across the OCS. In contrast, the MST uses a high-resolution  $0.05^{\circ}$  grid ( $\sim 4$  km per cell) on a species level to capture fine-scale conservation concerns and ecological patterns across US waters.

The current system integrates **9,819 valid marine species** across 7 source datasets, mapped at **0.05° resolution** ( $\sim 4$  km cells) across **20 BOEM Program Areas** spanning US waters. Species distributions are weighted by extinction risk scores that incorporate protections under the Endangered Species Act (ESA), Marine Mammal Protection Act (MMPA), and Migratory Bird Treaty Act (MBTA), as well as IUCN Red List assessments. The merged distribution of sensitivity per species is masked to expert ranges where available, so suitable habitat is not included outside known ranges.

This is a process, not a product. Information is imperfect, especially given the large expanse of US waters. Distributions and abundance of species change, modified increasingly by climate change and human activities. Knowledge on species sensitivities continues to expand with more research. Methods for both modeling and distributing this information continue to improve. In alignment with [Executive Order 14303](#), we aim to provide a transparent and reproducible process that can be regularly updated as new data and methods become available.

## 1.1 Overview

The MST analytical pipeline proceeds through the following stages (Figure 1.1):

- Data Sources:** 7 source datasets of species distributions (AquaMaps SDM, NMFS Core Area, NMFS Critical Habitat, FWS Critical Habitat, FWS Range, BirdLife Range, IUCN Range)
- Taxonomy Matching:** species names reconciled across WoRMS, GBIF, ITIS, IUCN, and BirdLife taxonomic authorities
- Model Merging:** per-species models merged by taking the MAX suitability across datasets, constrained by IUCN/Critical Habitat spatial masks, with MMPA/MBTA spatial floors
- Cell Scoring:** extinction risk weighted by species presence, summed by species category (bird, coral, fish, invertebrate, mammal, reptile/turtle)
- Ecoregional Rescaling:** scores normalized to [0–100%] within each BOEM ecoregion for meaningful cross-region comparison
- Zone Aggregation:** area-weighted averages to program areas, subregions, and ecoregions
- Visualization:** interactive flower plots, treemaps, and map applications

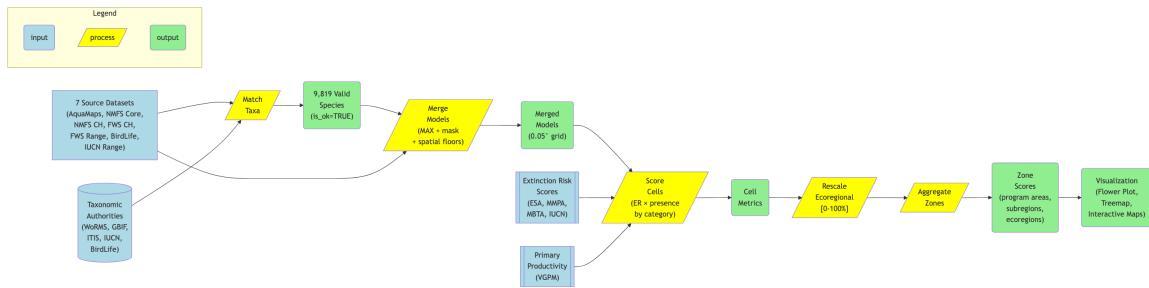


Figure 1.1: Flowchart of the MST analytical pipeline: from source datasets and taxonomic matching through model merging, scoring, and visualization.

Figure 1.2 illustrates the full methodology at a glance. On the left, species distribution data flows in from 7 source datasets and 5 taxonomic authorities. In the center, models are merged per species and weighted by extinction risk scores derived from ESA, MMPA, MBTA, and IUCN regulatory frameworks. On the right, cell-level scores are rescaled within BOEM ecoregions and aggregated to program areas for visualization in the interactive mapping applications.

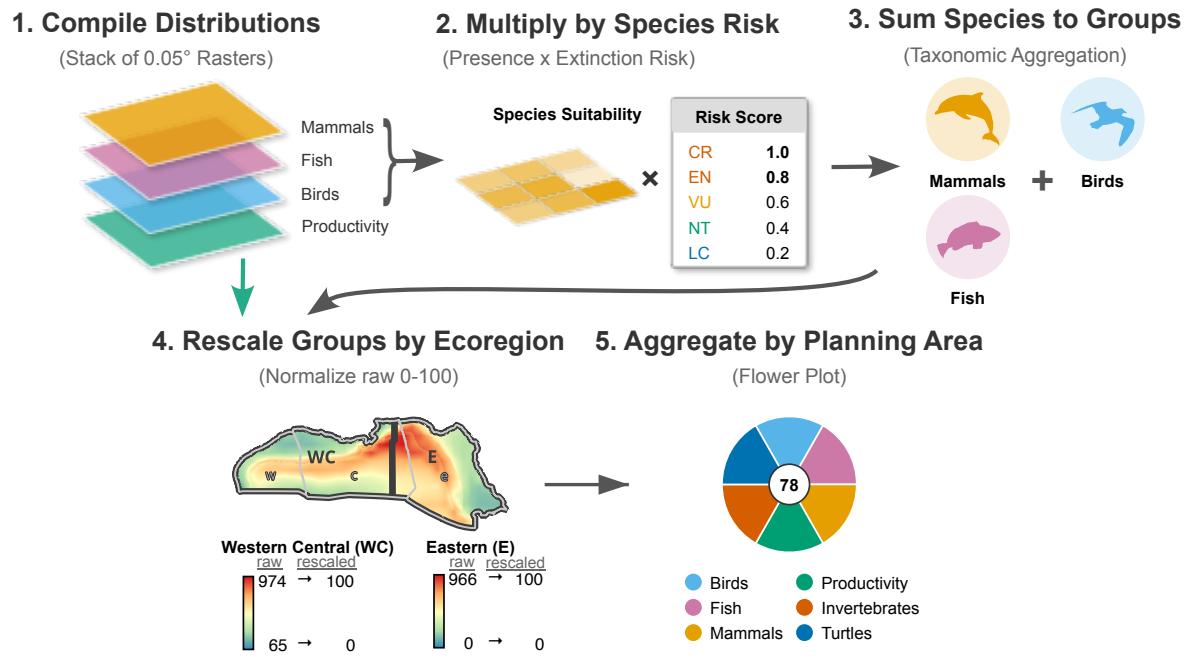


Figure 1.2: Overview of the Marine Sensitivity Toolkit methodology showing the integration of species distribution models, extinction risk scoring, ecoregional rescaling, and spatial aggregation into interactive visualizations.

# **Part I**

# **Science**

# 2 Science

## 2.1 Conceptual Framework

The term vulnerability ( $V$ ) is a function of exposure ( $E$ ), sensitivity ( $S$ ) and adaptive capacity ( $A$ ) (Equation 2.1).

$$V = f(E, S, A) \quad (2.1)$$

The more exposed and sensitive an area is—and the less able it is to recover—the more vulnerable it is to impacts from offshore human activities. The MST currently focuses on the **sensitivity** component, quantifying the intrinsic biological sensitivity of marine ecosystems based on the species present and their conservation status. Exposure and adaptive capacity components are planned for future phases (see Chapter 8).

## 2.2 Cell Vulnerability

For a given cell  $c$ , the vulnerability score for a species group  $g$  is the sum across all  $S_g$  species of the product of species presence probability  $p_{sc}$  and extinction risk weight  $w_s$  (Equation 2.2):

$$v_c = \sum_{s=1}^{S_g} p_{sc} \cdot w_s \quad (2.2)$$

where:

- $v_c$  = vulnerability score of cell  $c$  for species group  $g$
- $p_{sc}$  = probability of species  $s$  presence in cell  $c$  (0–1 scale, from merged species distribution models)
- $w_s$  = extinction risk weight for species  $s$  (0–1 scale, derived from ESA/MMPA/MBTA/IUCN status; see Chapter 5)
- $S_g$  = total number of species in taxonomic group  $g$  (e.g., bird, fish, mammal, coral, invertebrate, reptile/turtle)

In other words, if a cell has many species that are both likely to be present and at high risk of extinction, it gets a higher sensitivity score. This helps identify places where rare or threatened species are concentrated.

## 2.3 Sensitivity Components

The MST assesses sensitivity through three components:

1. **Species** — by taxonomic category (bird, coral, fish, invertebrate, mammal, reptile/turtle): extinction risk weighted species distribution models across 9,819 valid species (see Chapter 3, Chapter 5)
2. **Habitats** — benthic habitats such as coral reefs, seamounts, and hydrothermal vents (planned for future phases)
3. **Primary Productivity** — satellite-derived net primary productivity from the Vertically Generalized Production Model (VGPM), measured as metric tons C km<sup>-2</sup> yr<sup>-1</sup> (see Chapter 3)

## 2.4 Ecoregional Rescaling

Raw cell scores vary naturally across regions due to differences in species richness and oceanographic conditions. To enable meaningful cross-region comparison, scores are rescaled to a [0–100%] range within each BOEM ecoregion (Equation 2.3):

$$v'_c = \frac{v_c - v_{min}}{v_{max} - v_{min}} \times 100 \quad (2.3)$$

where  $v_{min}$  and  $v_{max}$  are the minimum and maximum cell scores within the ecoregion. This accounts for the natural gradient from species-rich tropical waters to less diverse polar regions, ensuring that a “high sensitivity” score has consistent meaning across all program areas.

Ecoregional rescaling makes it easy to compare areas within the same region, and Program Area aggregation gives an overall sensitivity score for each area, considering both the sensitivity of each part and how big each part is.

See subsequent chapters for detailed descriptions of: data sources (Chapter 3), taxonomic integration (Chapter 4), extinction risk scoring (Chapter 5), model merging (Chapter 6), and scoring methodology (Chapter 7).

# 3 Data Sources

The MST integrates species distribution data from 7 source datasets plus 1 derived merged dataset, all stored in a DuckDB database at 0.05° resolution (~4 km cells). Each dataset provides spatial predictions of species occurrence, ranging from continuous suitability models (AquaMaps) to binary range maps (NMFS, FWS, BirdLife, IUCN).

## 3.1 Dataset Overview

Table 3.1 summarizes all 8 datasets in the MST database.

Table 3.1: Summary of the 8 datasets in the MST database. Cell values represent species presence probability or suitability as a percentage (1–100%). Datasets marked `Is Mask = Yes` can also serve as spatial masks during model merging.

Dataset Key	Display Name	Cell Value Encoding	Is Mask	Sort
<code>am_0.05</code>	AquaMaps SDM	Continuous suitability 0–100%	No	1
<code>ca_nmfs</code>	NMFS Core Area	Core: 100%	Yes	2
<code>ch_nmfs</code>	NMFS Critical Habitat	EN: 100%, TN: 50%	Yes	3
<code>ch_fws</code>	FWS Critical Habitat	EN: 100%, TN: 50%	Yes	4
<code>rng_fws</code>	FWS Range	EN: 100%, TN: 50%, LC: 1%	Yes	5
<code>bl</code>	BirdLife Range	CR: 50%, EN: 25%, VU: 5%, NT: 2%, LC: 1%	Yes	6
<code>rng_iucn</code>	IUCN Range	CR: 50%, EN: 25%, VU: 5%, NT: 2%, LC: 1%	Yes	7
<code>ms_merge</code>	Merged Model	MAX across source datasets	No	0

The **sort order** determines priority during model merging: datasets with continuous predictions (AquaMaps) are considered first, followed by progressively coarser range maps. The

merged model (`ms_merge`) takes the MAX value across all available source datasets for each species in each cell.

## 3.2 Source Datasets

### 3.2.1 AquaMaps SDM (`am_0.05`)

[AquaMaps](#) provides standardized species distribution models (SDMs) for over 17,000 marine species based on environmental envelope models. Each species model defines habitat suitability as a function of depth, temperature, salinity, primary productivity, ice concentration, and distance from land.

- **Species count:** ~17,550 models
- **Native resolution:**  $0.5^\circ$  (c-squares), downscaled to  $0.05^\circ$  using bilinear interpolation
- **Cell values:** continuous suitability from 0–100%
- **Coverage:** global ocean

AquaMaps serves as the foundational dataset for most species, providing the highest spatial resolution and broadest taxonomic coverage.

### 3.2.2 NMFS Core Area (`ca_nmfs`)

Core areas delineated by the National Marine Fisheries Service (NMFS) identify regions of concentrated use for species under NMFS jurisdiction.

- **Species count:** limited to species with designated core areas
- **Cell values:** 100% within core area boundaries
- **Role:** contributes to merged model as a mask dataset

### 3.2.3 NMFS Critical Habitat (`ch_nmfs`)

Critical habitat designated under the Endangered Species Act (ESA) by NMFS for marine species.

- **Species count:** 34 species
- **Cell values:** Endangered species = 100%, Threatened species = 50%
- **Role:** dual function — contributes cell values AND forms part of the spatial mask for model merging

### **3.2.4 FWS Critical Habitat (ch\_fws)**

Critical habitat designated under the ESA by the U.S. Fish and Wildlife Service (FWS) for marine and coastal species.

- **Species count:** 29 species
- **Cell values:** Endangered species = 100%, Threatened species = 50%
- **Role:** dual function — contributes cell values AND forms part of the spatial mask

### **3.2.5 FWS Range (rng\_fws)**

Current range maps maintained by FWS for ESA-listed marine and coastal species.

- **Species count:** 106 species
- **Cell values:** Endangered = 100%, Threatened = 50%, Least Concern = 1%
- **Role:** mask dataset, providing spatial extent for species not covered by AquaMaps

### **3.2.6 BirdLife Range (b1)**

Expert-reviewed range maps from [BirdLife International's Birds of the World](#) (BOTW) dataset, representing the most authoritative global seabird distribution data.

- **Species count:** 573 seabird species
- **Cell values:** scaled by IUCN Red List category — CR: 50%, EN: 25%, VU: 5%, NT: 2%, LC: 1%
- **Role:** mask dataset, providing spatial constraints for seabird species
- **Note:** BirdLife range maps are expert-delineated polygons; cell values reflect conservation status rather than habitat suitability

### **3.2.7 IUCN Range (rng\_iucn)**

Range maps from the [IUCN Red List of Threatened Species](#) spatial data, covering a broad array of marine taxa.

- **Cell values:** scaled by IUCN Red List category — CR: 50%, EN: 25%, VU: 5%, NT: 2%, LC: 1%
- **Role:** mask dataset, providing spatial extent for species with IUCN range data

### 3.3 Merged Model (`ms_merge`)

The merged model is the derived output of the model merging pipeline (see Chapter 6). For each of the 9,819 valid species, cell values are computed as:

1. **MAX** across all source dataset values for that species in each cell
2. **Masked** to the spatial extent defined by IUCN, NMFS CH, and FWS CH ranges (when available)
3. **Floored** at minimum values for MMPA-protected species (20%) and MBTA-protected species (10%)

### 3.4 Standard Grid

All datasets are aligned to a standard **0.05° × 0.05°** latitude-longitude grid covering US waters within BOEM Program Areas. At mid-latitudes, each cell represents approximately 4 × 4 km (16 km<sup>2</sup>). The grid is stored as a reference raster with unique `cell_id` values, enabling efficient joins between spatial data and tabular attributes in DuckDB.

### 3.5 Primary Productivity

Primary productivity is specified in the explicit mandate for BOEM's management, per the Outer Continental Shelf Lands Act (OCSLA), Section 18(a)(2) of the OCSLA Amendments of 1978 specifying 8 factors the USDOI must consider in the timing and location of OCS oil and gas activities, including "the relative environmental sensitivity and marine productivity of different areas of the OCS."

We use satellite-derived net primary productivity (NPP) from the Vertically Generalized Production Model (VGPM) product from [Oregon State's Ocean Productivity Lab](#), based on VIIRS satellite data for 2014–2023. Values are converted to metric tons C km<sup>-2</sup> yr<sup>-1</sup> and averaged across the time period.

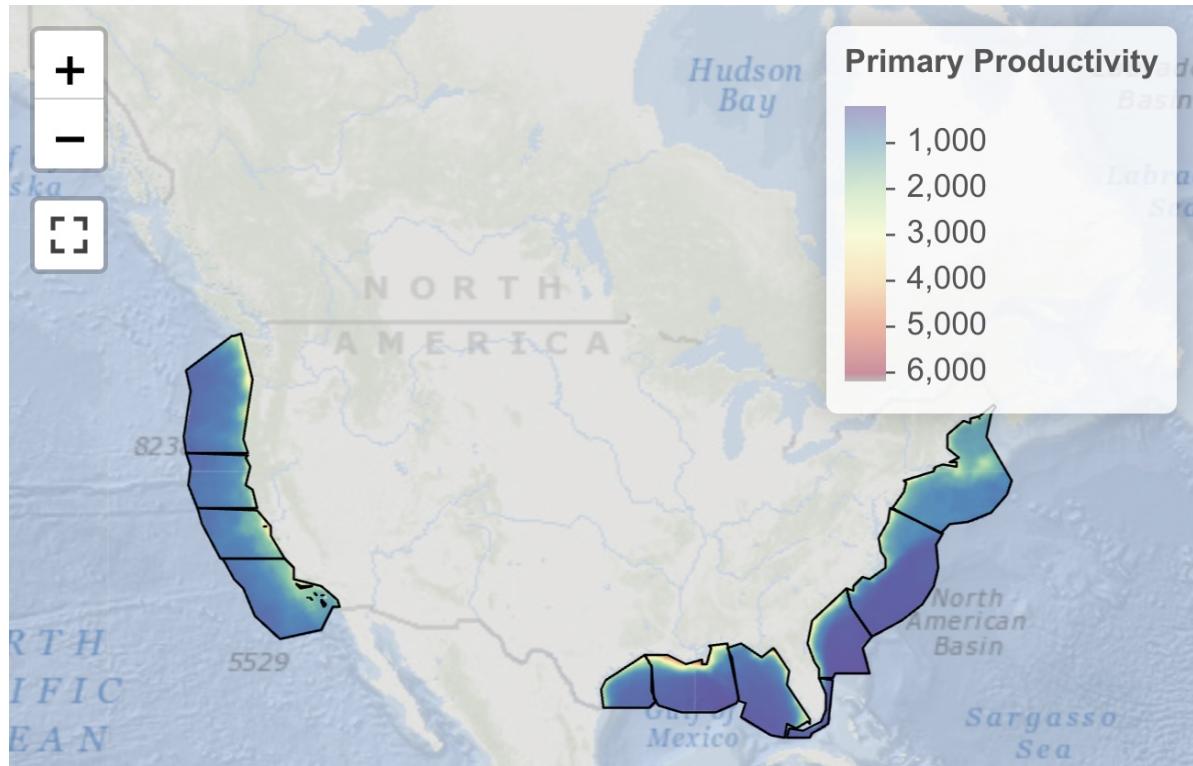


Figure 3.1: Primary productivity throughout the continental United States averaged across months of 2021, as measured by Oregon State's Vertically Generalized Production Model (VGPM). Expansion is anticipated across the entire US EEZ and for more recent years.

# 4 Taxonomy

Integrating species distribution data from 7 source datasets requires resolving taxonomic identities across multiple naming systems. The MST uses a multi-authority matching pipeline to ensure each species is uniquely identified, enabling accurate merging of models from different data providers.

## 4.1 Taxonomic Authorities

The following authorities are loaded into a reference database (`spp.duckdb`) for taxonomic reconciliation:

Table 4.1: Taxonomic authorities used in the MST for species name resolution.

Authority	Description	Key Identifier
<a href="#">WoRMS</a>	World Register of Marine Species — authoritative list for marine taxa	<code>worms_id</code> (AphiaID)
<a href="#">GBIF</a>	Global Biodiversity Information Facility Backbone Taxonomy (~6.3M taxa)	<code>gbif_id</code>
<a href="#">ITIS</a>	Integrated Taxonomic Information System — US federal standard	<code>itis_tsn</code>
<a href="#">IUCN Red List</a>	International Union for Conservation of Nature — conservation assessments	<code>iucn_id</code>
<a href="#">BirdLife BOTW</a>	Birds of the World — authoritative for seabird taxonomy	<code>botw_id</code>

## 4.2 ID Resolution Cascade

Species identifiers are resolved through a cascading lookup process:

1. **ITIS TSN match:** if the source dataset provides an ITIS Taxonomic Serial Number, use the ITIS-to-WoRMS crosswalk for direct matching
2. **WoRMS crosswalk:** look up accepted WoRMS AphiaID via the GBIF backbone, which integrates WoRMS as the marine taxonomy source
3. **Scientific name match:** for records without matching identifiers, attempt exact scientific name matching against WoRMS accepted names
4. **API lookup:** for remaining unresolved names, query the WoRMS REST API (`wm_records_name()`) for fuzzy matching

At each stage, deprecated names are resolved to their accepted synonyms, and the `taxonomicStatus` field is used to determine the preferred name.

## 4.3 Species Categories

Valid species are classified into 7 categories based on their taxonomic position:

Table 4.2: Species categories used in the MST for scoring and visualization.

Category	Description	Examples
bird	Seabirds and shorebirds	albatross, petrel, tern, pelican
coral	Reef-building and deep-sea corals	stony coral, soft coral, black coral
fish	Bony and cartilaginous fishes	grouper, shark, ray, tuna
invertebrate	Non-coral marine invertebrates	crab, lobster, sea urchin, squid
mammal	Marine mammals	whale, dolphin, seal, manatee
reptile	Sea turtles	loggerhead, green, leatherback
other	Uncategorized marine organisms	worms, tunicates, and bryozoans

## 4.4 Data Quality

### 4.4.1 Duplicate Resolution

Multiple source datasets may provide models for the same species. The taxonomic matching step identifies duplicates by resolving all source names to canonical WoRMS or BirdLife identifiers. When a species appears in multiple datasets, the model merging pipeline (see Chapter 6) takes the MAX value across all sources rather than treating them as separate species.

### 4.4.2 Synonym Handling

Taxonomic names change over time as species are reclassified. The pipeline handles this by:

- resolving all names through `acceptedNameUsageID` in each authority
- tracking the original source name alongside the accepted name
- flagging deprecated WoRMS IDs and updating them to current accepted IDs

### 4.4.3 Valid Species Filter (`is_ok`)

Not all taxa in the database are included in the final analysis. A species is flagged as valid (`is_ok = TRUE`) when it meets all of the following criteria:

- has a merged model (i.e., at least one source dataset provides cell values)
- is classified as marine (based on WoRMS `isMarine` flag, or BirdLife seabird classification)
- is not extinct (WoRMS `isExtinct` or IUCN Red List EX status)
- has cells overlapping at least one BOEM Program Area

This filter yields **9,819 valid species** from approximately 17,333 total taxa across all datasets.

## 4.5 Key Function

The taxonomic matching is implemented in `msens::match_taxa()`, which orchestrates the ID resolution cascade and returns a unified taxon table with cross-referenced identifiers from all authorities.

# 5 Extinction Risk

Extinction risk scoring translates a species' conservation status into a numeric weight that reflects its vulnerability to population-level impacts. The MST integrates protections from three US federal regulatory frameworks and the international IUCN Red List to assign each species a score from 1 to 100.

## 5.1 Regulatory Framework

### 5.1.1 Endangered Species Act (ESA)

The [Endangered Species Act](#) (1973) provides protections for species listed as Endangered (EN) or Threatened (TN) by either NMFS (for marine species) or FWS (for terrestrial/coastal species).

- **Endangered (EN):** species in danger of extinction throughout all or a significant portion of its range
- **Threatened (TN):** species likely to become endangered within the foreseeable future

ESA listings are the primary driver of extinction risk scores for US-listed species, with Endangered receiving the maximum score (100) and Threatened receiving a score of 50.

### 5.1.2 Marine Mammal Protection Act (MMPA)

The [Marine Mammal Protection Act](#) (1972) protects **all marine mammals** in US waters regardless of their ESA status. This includes whales, dolphins, porpoises, seals, sea lions, walruses, sea otters, polar bears, and manatees.

Because MMPA provides blanket protection, all marine mammals receive a **minimum spatial floor score of 20** in cells where they are present — even species classified as Least Concern under IUCN. This ensures that the legal protection afforded to marine mammals is reflected in the sensitivity analysis.

The MMPA floor is intentionally higher than the MBTA floor because the MMPA imposes a stronger statutory standard: it affirmatively requires that all marine mammal populations be maintained at Optimum Sustainable Population levels and mandates active population

recovery, whereas the MBTA is primarily a prohibitive take statute. Marine mammals also tend to have lower reproductive rates and longer recovery times than most seabirds, making them intrinsically more sensitive to disturbance.

### 5.1.3 Migratory Bird Treaty Act (MBTA)

The [Migratory Bird Treaty Act](#) (1918) protects migratory birds, which includes most seabird species. Similar to MMPA, all migratory birds receive a **minimum spatial floor score of 10** in cells where they are present.

### 5.1.4 IUCN Red List

The [IUCN Red List of Threatened Species](#) provides internationally recognized conservation status assessments used for species not listed under US federal laws:

Table 5.1: IUCN Red List categories used in extinction risk scoring.

Category	Abbreviation	Description
Critically Endangered	CR	extremely high risk of extinction in the wild
Endangered	EN	very high risk of extinction in the wild
Vulnerable	VU	high risk of extinction in the wild
Near Threatened	NT	close to qualifying for a threatened category
Least Concern	LC	widespread and abundant
Data Deficient	DD	inadequate information to assess

## 5.2 Scoring Methodology

Extinction risk scores are computed by `msens::compute_er_score()`, which implements a two-track scoring system depending on whether the species is listed under US federal law.

### 5.2.1 US-listed Species

For species with NMFS or FWS ESA listings, the score is the **maximum** across three components:

$$\text{er\_score} = \max(\text{ESA base}, \text{MMPA floor}, \text{MBTA floor}) \quad (5.1)$$

Table 5.2: US-listed species scoring components. The final score is the MAX across applicable components.

Component	Score
ESA Endangered (EN)	100
ESA Threatened (TN)	50
ESA not listed (LC)	1
MMPA protected	20
MBTA protected	10

#### Examples:

- ESA Endangered whale (MMPA):  $\max(100, 20) = \mathbf{100}$
- ESA Threatened seabird (MMPA + MBTA):  $\max(50, 20, 10) = \mathbf{50}$
- Non-ESA marine mammal (MMPA only):  $\max(1, 20) = \mathbf{20}$
- Non-ESA migratory bird (MBTA only):  $\max(1, 10) = \mathbf{10}$

### 5.2.2 Species not federally listed (IUCN)

Species not federally listed or mentioned by NMFS ([Species Directory | NOAA Fisheries](#)) or FWS ([Species | U.S. Fish & Wildlife Service](#)) fall back to an extinction risk score based on their IUCN Red List category:

Table 5.3: IUCN-based extinction risk scores for US species not listed or mentioned by NMFS or FWS

IUCN Category	Score
Critically Endangered (CR)	50
Endangered (EN)	25
Vulnerable (VU)	5
Near Threatened (NT)	2
Least Concern / Data Deficient / other	1

Species with no matching extinction risk code (i.e., unmatched taxa) receive a default score of 1.

### 5.2.3 Scale Note

Scores range from 1 to 100, representing a percentage scale (1–100%). Integer storage is used for computational efficiency; conceptually the scale represents a 0–1 probability-like weight where 100 = 1.0 (maximum extinction risk) and 1 = 0.01 (minimum baseline).

## 5.3 Implementation

The scoring function is implemented in the `msens` R package:

```
msens::compute_er_score(  
  extrisk_code,           # e.g., "NMFS:EN", "FWS:TN", "IUCN:CR"  
  is_mmpa = FALSE,         # MMPA protection flag  
  is_mbta = FALSE          # MBTA protection flag  
)
```

The `extrisk_code` field follows the format AUTHORITY:STATUS where:

- **Authority:** NMFS, FWS, or IUCN
- **Status:** ESA codes (EN, TN, LC) or IUCN codes (CR, EN, VU, NT, LC, DD)

# 6 Model Merging

Each species may have distribution data in multiple source datasets (see Chapter 3). The model merging pipeline combines these into a single merged model per species, applying spatial masking and minimum floor values to reflect regulatory protections.

## 6.1 Pipeline Overview

The merge pipeline processes each of the 9,819 valid species through the following steps:

### 6.1.1 Step 1: Gather Source Models

For each species (identified by `taxa_id`), the pipeline queries all available models across the 7 source datasets. A species may have:

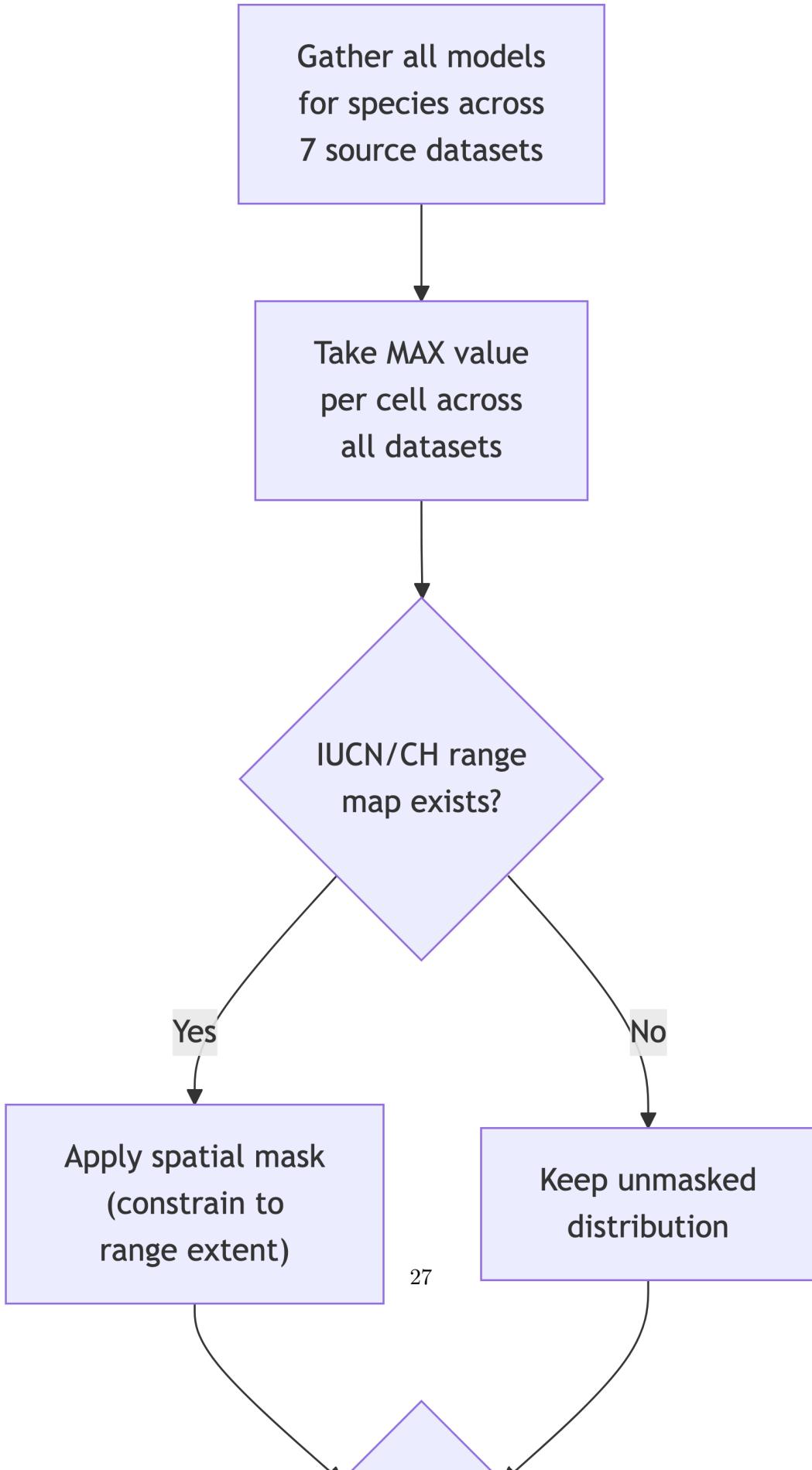
- an AquaMaps SDM (continuous suitability)
- one or more regulatory range/habitat designations (NMFS, FWS)
- a BirdLife or IUCN range map

### 6.1.2 Step 2: MAX Across Datasets

For each grid cell, the merged value is the **maximum** suitability across all source datasets:

$$v_{merged,c} = \max(v_{am,c}, v_{ca,c}, v_{ch,c}, v_{rng,c}, v_{bl,c}, v_{iucn,c}) \quad (6.1)$$

This ensures that the most informative (highest confidence) prediction is used. For example, if AquaMaps predicts 30% suitability but NMFS has designated the cell as critical habitat for an endangered species (100%), the merged value is 100%.



### 6.1.3 Step 3: Spatial Masking

When an IUCN range map, NMFS Critical Habitat, or FWS Critical Habitat exists for a species, the merged model is **constrained to the spatial extent** of these mask datasets. The mask is formed as the union of all available `is_mask = TRUE` datasets for that species.

This prevents the AquaMaps SDM (which often has broad environmental envelope predictions) from extending species presence far beyond their known range. Cells outside the mask are set to zero (species absent). This ensures that suitable habitat is not included outside known ranges, so that model predictions align with expert knowledge of where species actually occur.

### 6.1.4 Step 4: MMPA Spatial Floor

For species protected under the Marine Mammal Protection Act (all marine mammals), a spatial minimum floor is applied:

$$v_c = \max(v_{merged,c}, 20) \quad (6.2)$$

This ensures that every cell where a marine mammal is present has a minimum value of 20%, reflecting the legal protection that MMPA affords regardless of ESA status.

### 6.1.5 Step 5: MBTA Spatial Floor

Similarly, for species protected under the Migratory Bird Treaty Act (most seabirds), a spatial minimum floor of 10% is applied:

$$v_c = \max(v_{merged,c}, 10) \quad (6.3)$$

### 6.1.6 Step 6: Persist Results

The final merged model is stored in the DuckDB database as:

- **model table:** one row per species with metadata (dataset key `ms_merge`, taxa reference, model sequence)
- **model\_cell table:** one row per species × cell combination with the merged suitability value

## 6.2 Valid Species Filter

After merging, species are flagged as valid (`is_ok = TRUE`) based on the criteria described in Chapter 4. The filtering rules differ slightly between birds and other taxa:

**Birds** (from BirdLife BOTW):

- has a `botw_id` (BirdLife identifier)
- IUCN Red List code is not “EX” (Extinct)
- if also in WoRMS: must be marine and not extinct
- has cells overlapping at least one BOEM Program Area

**Other marine taxa** (from WoRMS):

- has a `taxa_id` and a merged model (`mdl_seq`)
- IUCN Red List code is not “EX”
- WoRMS `isMarine = TRUE` and `isExtinct != TRUE`
- species category is not “reptile” (except sea turtles, which are reclassified as category “reptile”)
- has cells overlapping at least one BOEM Program Area

This filtering yields **9,819 valid species** that contribute to the final sensitivity scores.

# 7 Scoring

The scoring methodology translates merged species distribution models and extinction risk weights into cell-level sensitivity metrics, which are then rescaled and aggregated to management zones for decision support.

## 7.1 Cell-Level Scoring

For each grid cell, sensitivity is computed as the extinction risk weighted sum of species presence within each species category (Equation 7.1):

$$\text{score}_{c,g} = \sum_{s=1}^{S_g} \frac{\text{er\_score}_s \times v_{s,c}}{100} \quad (7.1)$$

where:

- $\text{score}_{c,g}$  = sensitivity score for cell  $c$  and species category  $g$
- $\text{er\_score}_s$  = extinction risk score for species  $s$  (1–100; see Chapter 5)
- $v_{s,c}$  = merged model value for species  $s$  in cell  $c$  (0–100%; see Chapter 6)
- $S_g$  = number of valid species in category  $g$

Division by 100 converts the product from a 0–10,000 range back to a 0–100 scale.

In plain terms, for each cell in the ocean the MST adds up the sensitivity contributions of all species found there. If a cell has many species that are both likely to be present and at high risk of extinction, it gets a higher sensitivity score. This helps identify places where rare or threatened species are concentrated.

## 7.2 Metric Keys

Cell-level scores are stored as named metrics in the DuckDB database:

Table 7.1: Cell-level metric keys stored in the MST database.

Metric Key	Description
<code>extrisk_bird</code>	extinction risk score for birds
<code>extrisk_coral</code>	extinction risk score for corals
<code>extrisk_fish</code>	extinction risk score for fishes
<code>extrisk_invertebrate</code>	extinction risk score for invertebrates
<code>extrisk_mammal</code>	extinction risk score for marine mammals
<code>extrisk_reptile</code>	extinction risk score for reptiles/turtles
<code>extrisk_other</code>	extinction risk score for other marine organisms
<code>primprod</code>	primary productivity (VGPM, metric tons C km <sup>-2</sup> yr <sup>-1</sup> )

### 7.3 Ecoregional Rescaling

Raw cell scores vary naturally across ecoregions due to differences in species richness, oceanographic conditions, and biogeographic patterns. To enable meaningful cross-region comparison, each metric is rescaled to a [0–100] range within each BOEM ecoregion:

$$\text{score}'_c = \frac{\text{score}_c - \text{score}_{min}}{\text{score}_{max} - \text{score}_{min}} \times 100 \quad (7.2)$$

where  $\text{score}_{min}$  and  $\text{score}_{max}$  are the minimum and maximum cell values for that metric within the ecoregion. This ensures that a score of 100 represents the most sensitive cell within each ecoregion, not globally.

### 7.4 Primary Productivity Scoring

Net primary productivity (NPP) from the VGPM satellite model is included as a separate metric (`primprod`) that does not undergo extinction risk weighting. Instead, the raw NPP values (metric tons C km<sup>-2</sup> yr<sup>-1</sup>) are directly rescaled within each ecoregion using the same [0–100] normalization.

### 7.5 Zone Aggregation

Rescaled cell scores are aggregated to three spatial levels using area-weighted averaging:

1. **Program Areas:** the 20 BOEM planning regions used for offshore energy management
2. **Subregions:** intermediate spatial groupings (e.g., Atlantic, Gulf of Mexico, Pacific, Alaska)
3. **Ecoregions:** BOEM-defined ecological regions used as the rescaling baseline

For each zone, the aggregated score is:

$$\text{score}_{\text{zone}} = \frac{\sum_{c \in \text{zone}} \text{score}'_c \times A_c}{\sum_{c \in \text{zone}} A_c} \quad (7.3)$$

where  $A_c$  is the area of cell  $c$  (accounting for latitude-dependent cell size in the  $0.05^\circ$  grid).

## 7.6 Visualization

### 7.6.1 Flower Plot

The flower plot provides an intuitive summary of sensitivity scores by species category, inspired by the Ocean Health Index (Halpern et al. 2012) visualization approach:

- **Petal length** represents the rescaled sensitivity score (0–100) for each species category — longer petals indicate higher sensitivity
- **Petal width** represents the weight of each category contributing to the overall score — wider petals have more influence on the center score
- **Center value** shows the weighted mean across all categories

Figure 7.1 shows flower plots for all 20 BOEM Program Areas, generated from the v3 scoring run. Each flower summarizes the sensitivity profile of one program area with petals for Bird, Coral, Fish, Invertebrate, Mammal, Other, Turtle, and Primary Production. Alaska program areas (e.g., HOP, COK, GOA) show dominant Fish and Mammal petals, while Gulf areas (GAB, CEC, MAT) show stronger Invertebrate and Coral contributions.

The flower plot lets decision-makers quickly spot which ecological elements drive sensitivity in an area, aiding better planning and impact assessment.

The flower plot is implemented as an interactive `ggiraph` visualization using polar coordinates in R (`ggplot2 + coord_polar()`), with tooltips showing detailed score breakdowns on hover. The `plot_flower()` function in `calc_scores.qmd` generates static versions for reports, while the `mapgl` web application implements an interactive JavaScript version for responsive rendering (see Figure A.2).

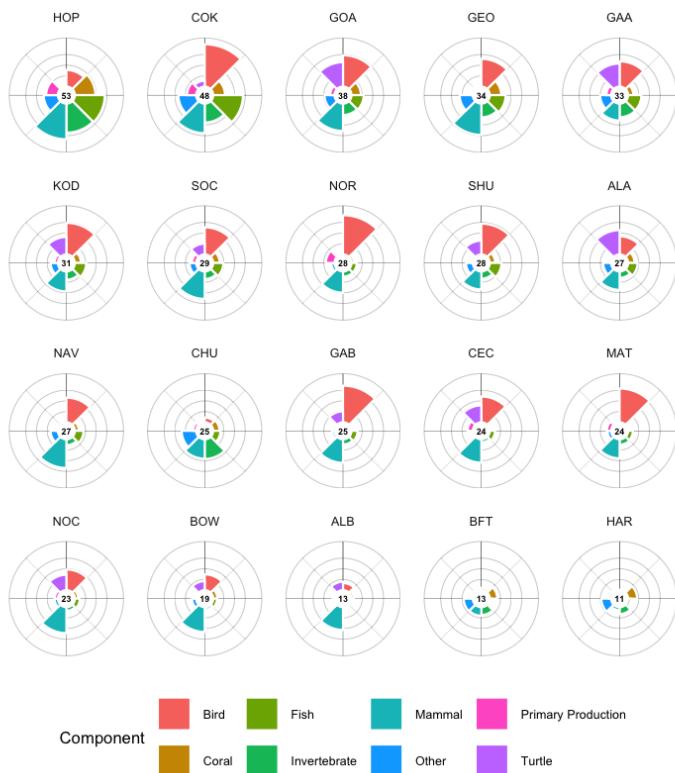


Figure 7.1: Flower plots for all 20 BOEM Program Areas showing ecoregionally rescaled sensitivity scores by species category. Petal length reflects the category score; petal width reflects its weight. Center values are the weighted mean across categories.

## 7.6.2 Treemap

The treemap provides a detailed, hierarchical view of species contributions to sensitivity scores (Figure 7.2):

- Audience: scientists and analysts
- Shows the contribution of each species to the overall score within a pixel or management zone
- Elements are hierarchical: first by extinction risk category, then by taxonomic classification
- Interactive zooming allows drilling down to individual species contributions

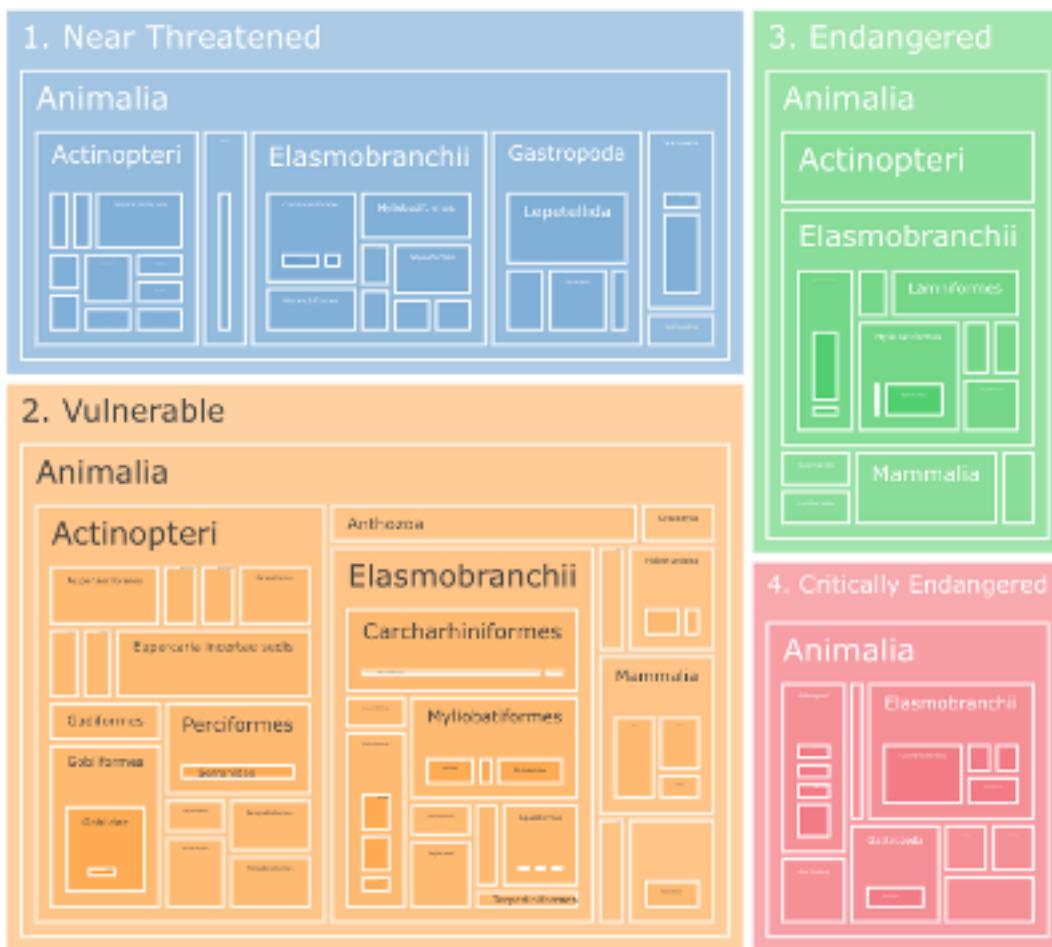


Figure 7.2: Treemap visualization showing species contributions to extinction risk scores, hierarchically organized by risk category and taxonomy.

Zooming into a specific category reveals individual species contributions:



Figure 7.3: Zoomed treemap showing individual species within a specific risk category and taxonomic group.

### 7.6.3 Interactive Maps

The primary visualization tools are two Shiny web applications:

- **mapgl**: general sensitivity mapping app showing composite scores by program area with flower plots and treemaps (see [Appendix: mapgl](#))
- **mapsp**: species distribution viewer showing individual and merged models with regulatory status information (see [Appendix: mapsp](#))

# **8 Stressors**

The stressor component of the vulnerability framework (see Chapter 2) addresses the human activities that may impact marine ecosystems. This section is a placeholder for future phases of the MST, which will incorporate stressor-receptor interaction matrices to complete the full vulnerability assessment.

## **8.1 Offshore Wind Energy**

Evaluation of stressors from the offshore wind industry needs to be evaluated based on human activities given the phase of development, whether pre-construction, construction, operation or decommissioning (Figure 8.1).

## **8.2 Oil & Gas**

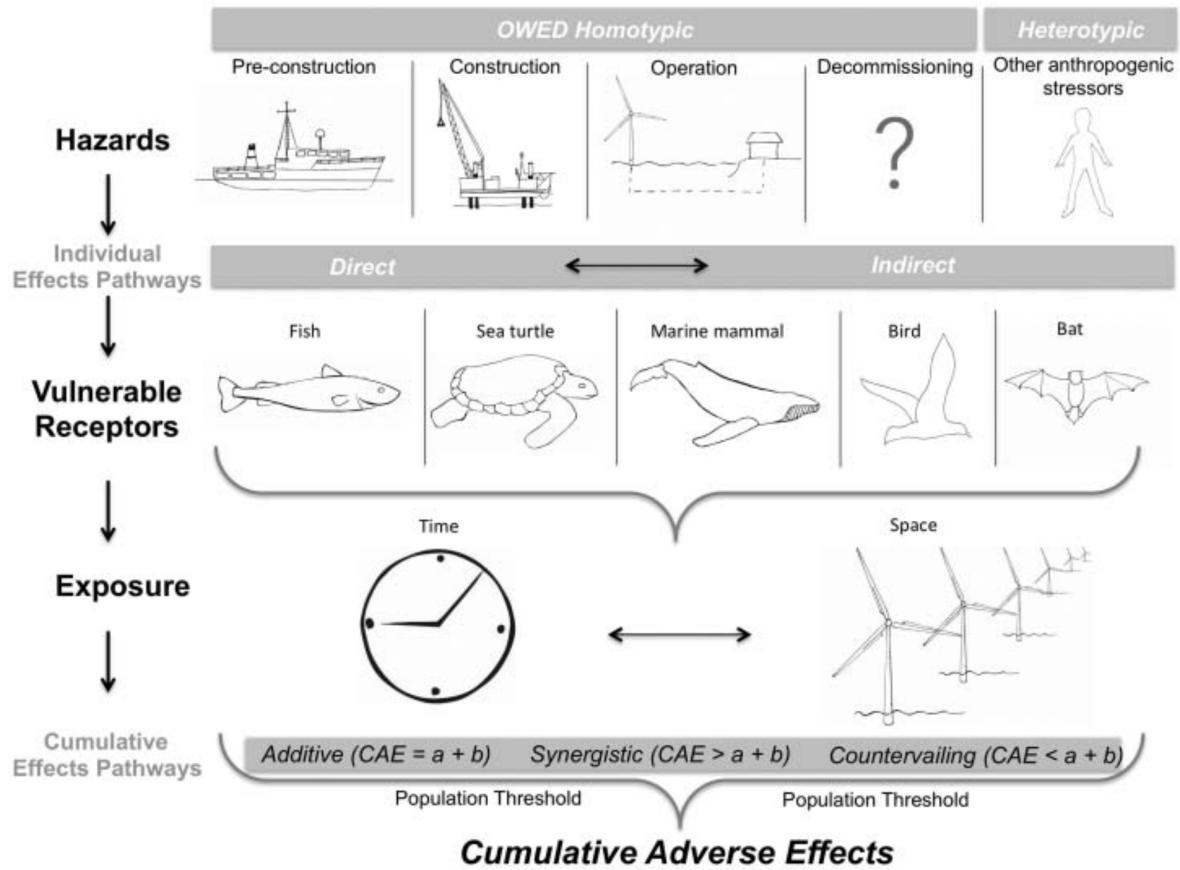


Figure 8.1: Cumulative adverse effects of offshore wind energy development on wildlife (Goodale and Milman 2016).

## **Part II**

# **Software**

# 9 Software

The **Marine Sensitivity Toolkit** (MST) is a stack of software components for reproducibly, interactively and hierarchically generating environmental vulnerability maps and scores. Tabular data is collated across studies evaluating sensitivity of species to oil & gas and offshore wind energy development. The best available species and benthic habitat distributions are being mosaicked across the US EEZ. Scores will be summarized according to subgroups within Species, Benthic Habitats and Primary Productivity. These scores will be averaged into an overall score and visualized as a flower plot, applicable to various levels of BOEM relevancy: regional, ecoregions, protraction diagrams, blocks and aliquots. The software components for achieving this interactively are: 1) server — a Docker configuration to spin up all the software; 2) database — a spatially enabled database (PostgreSQL with PostGIS extension); 3) workflows — scripts (as Quarto notebooks) to explore, ingest and update the database and output files; 4) APIs — application programming interfaces for rendering vector (using pg\_tileserv) or raster (using TiTiler) tile services for interactive mapping as well as a custom API (using R plumber); 5) libraries — re-usable documented functions as an R package for import, analysis and visualization using the APIs; 6) applications — interactive apps using the R Shiny framework for rendering vulnerability maps; and 7) documentation — as a Quarto notebook with figures, tables, glossary and references in interactive html or static docx/pdf output formats. This toolbox is intended to primarily serve BOEM needs internally, but by being open-source and fully reproducible the hope is to enlist buy-in and even contributions from external partners, whether from other government agencies, academia, NGOs or industry.

We ascribe to the philosophy of sharing all code for the sake of reproducibility, transparency and efficiency (Maitner et al. 2024; Lowndes et al. 2017); i.e. the FAIR principles of Findability, Accessibility, Interoperability, and Reusability (Wilkinson et al. 2016).

## 9.0.1 Interactive Applications

We have developed a series of interactive applications to explore the data and results of the MST project. These applications allow users to visualize the data, explore the results, and interact with the data in a more intuitive way. The applications are built using the `shiny` package in R (Chang et al. 2024), which allows us to easily create a user interface with complex reactivity for an interactive web application easily accessed through a web browser. The applications are designed to be user-friendly and intuitive, with interactive maps, charts, and tables that allow users to explore the data in a more dynamic way.

## 9.0.2 Overcoming Challenges with Large Spatial Data

The MS project incorporates many large spatial datasets that are problematic to render in a typical interactive application. For instance, the most common interactive mapping R package `leaflet` has a 4MB limitation for displaying rasters (see “Large Raster Warning” in [Raster Images • leaflet](#)). Vectors (i.e., points, lines and polygons) get smoothed when containing many vertices, but contiguity gets lost between polygons and rendering degrades to non-useable depending on the internet speed of the user’s connection.

To work around these limitations, we have implemented “cloud native” web services and formats (see also [Cloud-Optimized Geospatial Formats Guide](#)). Our implementations effectively reduce the size of any given spatial object based on the zoom level of the user’s browser. For rasters, we use cloud-optimized GeoTIFFs (COGs) and for vectors, we use Mapbox Vector Tiles (MVT). These formats are designed to be fast and efficient for web mapping applications, and they allow us to display large spatial datasets in an interactive web application without sacrificing performance or usability. Let’s take a closer look at implementation of each.

### 9.0.2.1 Raster: Cloud-Optimized GeoTIFFs (COGs) and Titiler

Historically, to read a raster, such as a GeoTIFF, from the web, the client software would have to read the entire file before rendering. Cloud Optimized GeoTIFFs ([COGs](#)) take advantage of [HTTP GET range requests](#) to read only the part of the file needed for rendering. So a COG stores quadtree simplifications of the original raster at multiple zoom levels and metadata for accessing their byte ranges in the file in the metadata header. This allows the client software to request only the parts of the file needed for rendering, which can greatly reduce the amount of data transferred and speed up rendering. This is for accessing the raw data in pixel values, e.g., for a raster of species distribution then the abundance of a species in each cell. We would want to also apply a color ramp to visualize the data. The open-source ([TiTiler](#)) software is a lightweight web service that serves up these color ramped tiles on the fly. So COGs can be stored on a simple file server (like Amazon S3 or Azure Blob Storage) and served up as interactive web maps with TiTiler as an intermediary between the COG files and the client accessing the interactive Shiny mapping app (Figure 9.1).

### 9.0.2.2 Vector: Mapbox Vector Tiles (MVTs) and pg\_tileserv

Although “cloud native” vector formats exist for simple file storage (see [Cloud-Optimized Geospatial Formats Guide](#)), none of these allow for flexible filtering and manipulation. Instead, we use PostgreSQL with the spatial extension ([PostGIS](#)) to store the vector data and serve it as Mapbox Vector Tiles ([MVTs](#)) using the [pg\\_tileserv](#) web service written in the language Go, which is very fast. This means that we don’t have to pre-render the MVTs (such as you might do with [tippecanoe](#)), but can instead serve the raw vector data directly from the database and let [pg\\_tileserv](#) handle the rendering on the fly. Filters (in the form of [CQL](#)) can be applied

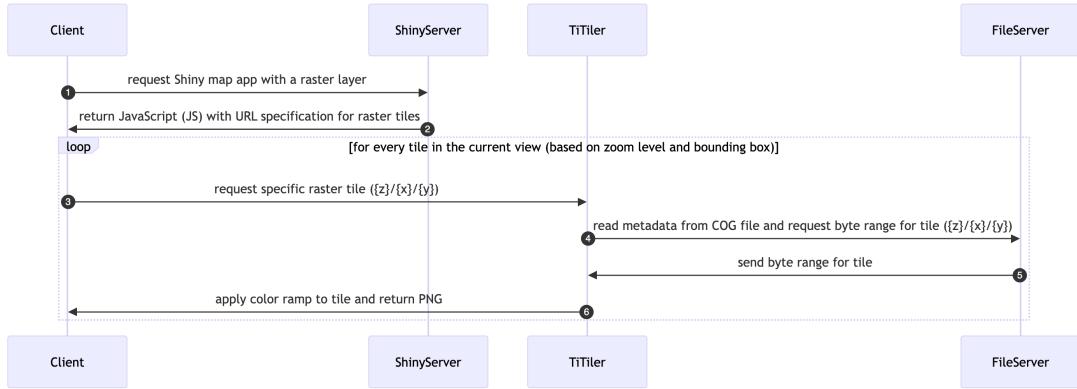


Figure 9.1: Sequence diagram implementing large raster interactive display using Cloud-Optimized Geotiffs (COGs) and Titiler in a Shiny mapping app.

to the request. Symbology is rendered client-side via JavaScript, which allows for interactive hover and click events on vector objects (e.g., BOEM aliquot). Some speed-up is enabled by implementing a Varnish cache service in between. We can even write our own database functions for customized rendering, such as H3 hexagonal summaries. This allows us to serve vector data as web maps with minimal configuration and setup, and it provides a fast and efficient way to display large vector datasets in an interactive web application (Figure 9.2).

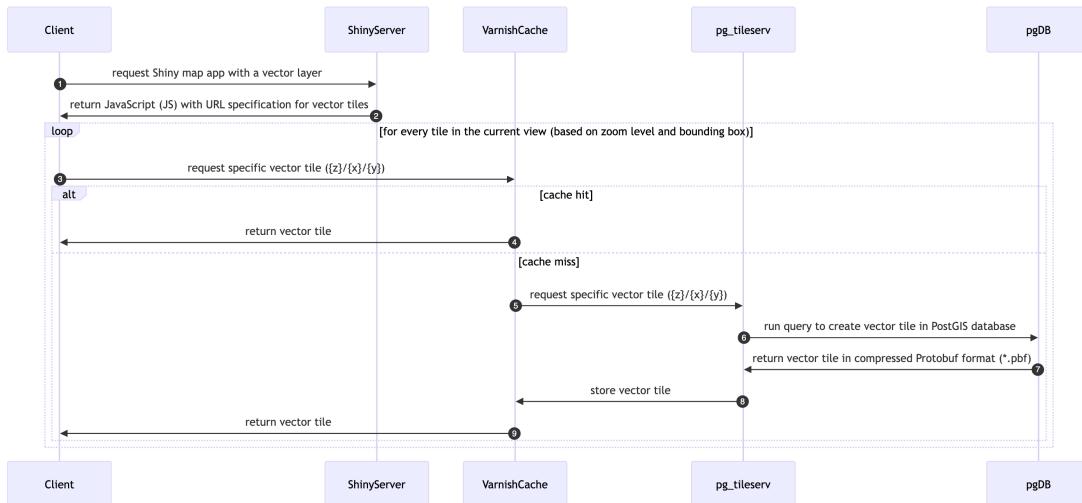
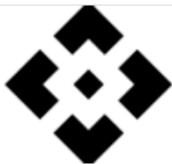


Figure 9.2: Sequence diagram implementing large vector interactive display using Mapbox Vector Tiles (MVTs) and pg\_tileserv in a Shiny mapping app.

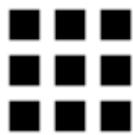
### 9.0.3 Github Repositories

repo	description
<a href="#">github</a>	organization README
<a href="#">api</a>	application programming interface (API) using R Plumber package
<a href="#">apps</a>	Shiny applications
<a href="#">docs</a>	documentation for BOEM's offshore environmental sensitivity index products
<a href="#">manuscripts</a>	Manuscripts with review of sensitivities by industry and receptors (species, habitats, human uses)
<a href="#">MarineSensitivity.github.io</a>	default website
<a href="#">msens</a>	R library of functions for mapping marine sensitivities, sponsored by BOEM
<a href="#">objectives</a>	repository for issues spanning multiple repositories and doing big picture roadmapping
<a href="#">server</a>	server setup for R Shiny apps, RStudio IDE, R Plumber API, PostGIS database, pg_tileserv
<a href="#">workflows</a>	scripts for testing data analytics and visualization as well as production workflows

#### 9.0.4 Software Components



APIs  
application programming  
interfaces (APIs)



Apps  
interactive applications using  
Shiny



Database  
PostgreSQL database  
extended spatially with  
PostGIS



Docs  
technical documentation



Libraries  
documented functions as an R  
package



Server  
server software configuration  
using Docker



Workflows  
scripts for exploring plus  
production workflows

# 10 Server

The server is for serving up any web services outside those of Github (e.g., [website](#), [docs](#) and R package [msens](#)) using [Docker](#) (see the [docker-compose.yml](#); with reverse proxying from subdomains to ports by [Caddy](#)).

## 10.1 Setup

For the latest instructions on launching an Amazon instance and installing the server software, see [Server Setup · MarineSensitivity/server Wiki](#), which is pasted below for convenience...

*on AWS as EC2 instance using Docker*

### 10.1.1 launch instance

name: **msens1**:

- Software Image (AMI)  
Canonical, **Ubuntu**, 22.04 LTS, amd64 jammy image build on 2023-09-19 ami-0fc5d935ebf8bc3bc
- Virtual server type (instance type)  
**t2.xlarge** (4 vCPU, 16 GB memory)
- Firewall (security group)  
New security group
- Storage (volumes)  
2 volume(s)
  - **20 GB**  
/ server software, disposable
  - **60 GB**  
/share for all data, persistent and to be backed up

### 10.1.1.1 allocate IP address

- [Elastic IP addresses | EC2 | us-east-1](#) for persistent IP address
- Allocated IPv4 address: 100.25.173.0
- Associate Elastic IP address

### 10.1.2 ssh to server

```
pem='/Users/bbest/My Drive/private/msens_key_pair.pem'  
ssh -i $pem ubuntu@msens1.marinesensitivity.org
```

#### 10.1.2.1 set hostname

- Change the hostname of your Amazon Linux instance - [Amazon Elastic Compute Cloud](#)

```
sudo vi /etc/cloud/cloud.cfg  
# preserve_hostname: true  
sudo hostnamectl set-hostname msens1.marinesensitivity.org  
sudo reboot
```

#### 10.1.2.2 mount volume

The extra volume (60 GB for `/share`) was added during EC2 launch instance wizard, but needs to be mounted before available for use.

- Make an Amazon EBS volume available for use on Linux - [Amazon Elastic Compute Cloud](#)

```
df -H
```

Filesystem	Size	Used	Avail	Use%	Mounted on
/dev/root	21G	2.3G	19G	11%	/
tmpfs	8.4G	0	8.4G	0%	/dev/shm
tmpfs	3.4G	898k	3.4G	1%	/run
tmpfs	5.3M	0	5.3M	0%	/run/lock
/dev/xvda15	110M	6.4M	104M	6%	/boot/efi
tmpfs	1.7G	4.1k	1.7G	1%	/run/user/1000

```
lsblk
```

NAME	MAJ:MIN	RM	SIZE	RO	TYPE	MOUNTPOINTS
loop0	7:0	0	24.6M	1	loop	/snap/amazon-ssm-agent/7528
loop1	7:1	0	55.7M	1	loop	/snap/core18/2790
loop2	7:2	0	63.5M	1	loop	/snap/core20/2015
loop3	7:3	0	111.9M	1	loop	/snap/lxd/24322
loop4	7:4	0	40.8M	1	loop	/snap/snapd/20092
xvda	202:0	0	20G	0	disk	
xvda1	202:1	0	19.9G	0	part	/
xvda14	202:14	0	4M	0	part	
xvda15	202:15	0	106M	0	part	/boot/efi
xvdb	202:16	0	60G	0	disk	

```
sudo file -s /dev/xvdb
# /dev/xvdb: data
```

So no file system on `/dev/xvdb` yet.

```
sudo mkfs -t xfs /dev/xvdb
sudo mkdir /share
sudo mount /dev/xvdb /share
```

```
sudo cp /etc/fstab /etc/fstab.orig
sudo blkid
# /dev/xvdb: UUID="bc766dfb-1c42-49cf-9320-2242a2d48a2e" BLOCK_SIZE="512" TYPE="xfs"
sudo vim /etc/fstab
# UUID=bc766dfb-1c42-49cf-9320-2242a2d48a2e /share xfs defaults,nofail 0 2

df -h
sudo umount /share ; df -h
sudo mount -a ; df -h
```

### 10.1.3 install docker

Following:

- Step-by-Step Guide to Install Docker on Ubuntu in AWS | by Srija Anaparthys | Medium

```
sudo apt-get update
#OLD: sudo apt-get install docker.io -y
```

NEW: [[Migrate to docker compose]]

```
sudo systemctl start docker
sudo docker run hello-world
sudo systemctl enable docker
docker --version
# Docker version 24.0.6, build ed223bc
sudo usermod -a -G docker $(whoami)
```

#### 10.1.3.1 run docker compose

- /Users/bbest/My Drive/private/[msens\\_server\\_env-password.txt](#)

```
sudo chown -R ubuntu:ubuntu /share
mkdir -p /share/github/MarineSensitivity
cd /share/github/MarineSensitivity
# clone server repo
git clone https://github.com/MarineSensitivity/server.git
cd server

# add password, used as $PASSWORD in docker-compose.yml
echo 'PASSWORD=*****' > .env

# launch docker instances
sudo docker-compose up -d
```

#### 10.1.4 Backup /share with snapshots

Per [Automate snapshot lifecycles - Amazon Elastic Compute Cloud](#), created two policies:

- [bkup\\_msens-share\\_daily](#) every 24 hrs at 09:00 UTC, max of 7
- [bkup\\_msens-share\\_weekly](#) every Monday 09:00 UTC, max of 8

## 10.2 Docker compose

The Docker compose file is used to define and run multi-container Docker applications. Here is the [docker-compose.yml](#) file for the server pasted for convenience ...

```
version: "3.9"

services:
  caddy:
    container_name: caddy
    image: caddy:latest
    ports:
      - 80:80
      - 443:443
    restart: unless-stopped
    volumes:
      - ./caddy/Caddyfile:/etc/caddy/Caddyfile
      - /share:/share
      - /share/caddy/data:/data
      - /share/caddy/config:/config

  rstudio:
    container_name: rstudio
    build: ./rstudio
    environment:
      ROOT: 'true'
      USER: admin
      PASSWORD: ${PASSWORD}
      ADD: shiny
    ports:
      - 8787:8787 # rstudio
      - 3838:3838 # shiny
    restart: unless-stopped
    volumes:
      - /share:/share
      - /share/shiny_apps:/srv/shiny-server

  plumber:
    container_name: plumber
    build: ./plumber
    ports:
      - 8888:8888 # api
```

```

restart: unless-stopped
volumes:
  - /share:/share
depends_on:
  - postgis

postgis:
  container_name: postgis
  image: postgis/postgis:latest
  environment:
    POSTGRES_DB: msens
    POSTGRES_USER: admin
    POSTGRES_PASSWORD: ${PASSWORD}
    ANON_PASSWORD: ${ANON_PASSWORD}
    PGDATA: /share/postgis/data
  volumes:
    # all files in /docker-entrypoint-initdb.dare automatically executed
    # in alphabetical order on container creation
    - ./postgis/init.sh:/docker-entrypoint-initdb.d/init.sh # add user anon
    - /share:/share
    - /share/postgis:/var/lib/postgresql
  restart: unless-stopped
  healthcheck:
    test: 'exit 0'
  ports:
    - 5432:5432

pgadmin:
  container_name: pgadmin
  image: dpage/pgadmin4:8.14
  restart: always
  environment:
    PGADMIN_DEFAULT_EMAIL: ben@ecoquants.com
    PGADMIN_DEFAULT_PASSWORD: ${PASSWORD}
    PGADMIN_LISTEN_PORT: 8088
    # PGADMIN_CONFIG_CONFIG_DATABASE_URI: "'postgresql://admin:$PASSWORD@postgis:5432/msens"
  ports:
    - 8088:8088
  volumes:
    - /share/pgadmin:/var/lib/pgadmin
depends_on:
  - postgis

```

```

pgbkups:
  container_name: pgbkups
  image: prodriegestivill/postgres-backup-local
  restart: always
  user: postgres:postgres # Optional: see below
  volumes:
    - /share/postgis_backups:/backups
      # sudo mkdir /share/postgis_backups; sudo chown -R 999:999 /share/postgis_backups
  links:
    - postgis
  depends_on:
    - postgis
  environment:
    - POSTGRES_HOST=postgis
    - POSTGRES_DB=msens
    - POSTGRES_USER=admin
    - POSTGRES_PASSWORD=${PASSWORD}
    - POSTGRES_EXTRA_OPTS=-Z6 --blobs
    - SCHEDULE=@daily
    - HEALTHCHECK_PORT=8088
    - BACKUP_KEEP_DAYS=2
    - BACKUP_KEEP_WEEKS=2
    - BACKUP_KEEP_MONTHS=4

tile:
  container_name: tile
  environment:
    DATABASE_URL: 'postgresql://admin:${PASSWORD}@postgis:5432/msens'
  image: pramsey/pg_tileserv:latest
  depends_on:
    - postgis
  ports:
    - 7800:7800

tilecache:
  container_name: tilecache
  image: varnish:latest # 7.4.2 # last updated: 2023-12-26
  volumes:
    - /share:/share
      # - "./varnish/default.vcl:/etc/varnish/default.vcl"
  ports:
    - 6081:6081

```

```

environment:
  # VARNISH_SIZE: '2G'
  # VARNISH_BACKEND_HOST: tile # .marinesensitivity.org
  # VARNISH_BACKEND_PORT: 7800
  # VARNISH_HTTP_PORT: 6081 # VARNISH_PROXY_PORT: '6081'
#command: "-p default_keep=43200" # 60*60*12 = 43200 sec = 12 hrs
restart: always
depends_on:
  - "tile"

# rest:
#   container_name: rest
#   environment:
#     PGRST_DB_URI: 'postgresql://anon:${ANON_PASSWORD}@postgis:5432/msens'
#     PGRST_OPENAPI_SERVER_PROXY_URI: http://127.0.0.1:3000
#     PGRST_DB_ANON_ROLE: anon # db-anon-role
#   image: postgrest/postgrest
#   depends_on:
#     - postgis
#   ports:
#     - "3000:3000"

# swagger:
#   container_name: swagger
#   image: swaggerapi/swagger-ui
#   depends_on:
#     - rest
#   ports:
#     - "8080:8080"
#   expose:
#     - "8080"
#   environment:
#     API_URL: https://rest.MarineSensitivity.org/

titiler:
  container_name: titiler
  image: ghcr.io/developmentseed/titiler:latest
  environment:
    PORT: 8000
    # WORKERS_PER_CORE: 1
  ports:
    - "8000:8000"

```

```

titilecache:
  container_name: titilecache
  image: varnish:latest # 7.4.2 # last updated: 2023-12-26
  volumes:
    - /share:/share
    # - "./varnish/default.vcl:/etc/varnish/default.vcl"
  ports:
    - 6082:6082 # which ports?
  environment:
    # VARNSH_SIZE: '2G'
    VARNSH_BACKEND_HOST: titiler # .marinesensitivity.org
    VARNSH_BACKEND_PORT: 8000
    VARNSH_HTTP_PORT: 6082 # VARNSH_PROXY_PORT: '6081'
#command: "-p default_keep=43200" # 60*60*12 = 43200 sec = 12 hrs
  restart: always
  depends_on:
    - "titiler"

```

## 10.3 DNS

The domain name server (DNS) records are managed by [SquareSpace](#). The subdomains point to the server on Amazon at 100.25.173.0, whereas the main website is hosted by Github servers, per [Managing a custom domain for your GitHub Pages site - GitHub Docs](#).

Host	Type	Data
@	A	185.199.111.153
@	A	185.199.110.153
@	A	185.199.109.153
@	A	185.199.108.153
api	A	100.25.173.0
file	A	100.25.173.0
msens1	A	100.25.173.0
pgadmin	A	100.25.173.0
rest	A	100.25.173.0
rstudio	A	100.25.173.0
shiny	A	100.25.173.0
swagger	A	100.25.173.0
tile	A	100.25.173.0
tilecache	A	100.25.173.0
titiler	A	100.25.173.0

Host	Type	Data
www	CNAME	marinesensitivity.org

## 10.4 Caddyfile

The Caddyfile parameterizes the reverse proxying between the external subdomains and the Docker's internal ports. Here is the [Caddyfile](#) pasted for convenience ...

```
(cors) {
    @origin header Origin *
    header @origin {
        Access-Control-Allow-Origin "*"
        Access-Control-Request-Method GET
    }
}

api.marinesensitivity.org {
    reverse_proxy plumber:8888
}

file.marinesensitivity.org {
    import cors
    root * /share/public
    file_server browse {
        # serve *.zst, *.br or *.gz if file exists and client supports precompressed files
        precompressed zstd br gzip
    }
}

pgadmin.marinesensitivity.org {
    reverse_proxy pgadmin:8088
}

# rest.marinesensitivity.org {
#     reverse_proxy rest:3000
# }

rstudio.marinesensitivity.org {
    reverse_proxy rstudio:8787
}
```

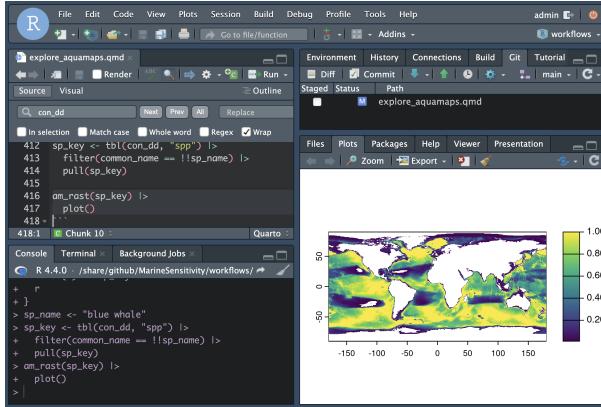
```
shiny.marinesensitivity.org {  
    reverse_proxy rstudio:3838  
}  
  
app.marinesensitivity.org {  
    reverse_proxy rstudio:3838  
}  
  
shiny.oceanmetrics.io {  
    reverse_proxy rstudio:3838  
}  
  
# swagger.marinesensitivity.org {  
#     reverse_proxy swagger:8080  
# }  
  
tile.marinesensitivity.org {  
    reverse_proxy tile:7800  
}  
  
tilecache.marinesensitivity.org {  
    reverse_proxy tilecache:6081  
}  
  
titiler.marinesensitivity.org {  
    reverse_proxy titiler:8000  
}  
  
titilecache.marinesensitivity.org {  
    reverse_proxy titilecache:6082  
}
```

## 10.5 Services

The server is running the following services:

- **RStudio**

*integrated development environment (IDE) to code and debug directly on the server*

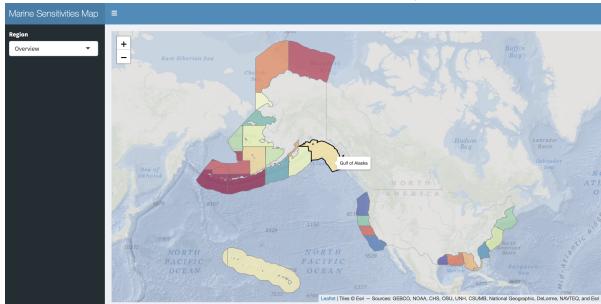


[More info..](#)

- **Shiny**

*interactive applications*

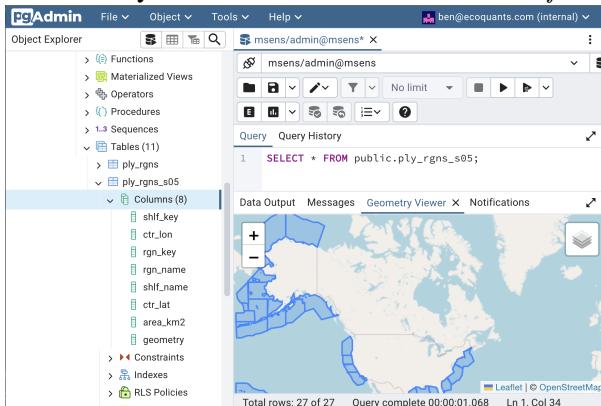
e.g., [shiny.marinesensitivity.org/map](http://shiny.marinesensitivity.org/map)



[More info..](#)

- **PGadmin**

*PostGreSQL database administration interface*



[More info..](#)

- **api**

*custom API: using R plumber*

The screenshot shows the MarineSensitivities Custom API documentation generated by Swagger. At the top, it displays the URL <https://api.marinesensitivities.org/openapi.json> and an 'Explore' button. Below this, the title 'MarineSensitivities Custom API 1.0.0 (OAS3)' is shown, along with a link to the API Description. A 'Servers' dropdown is set to <https://api.marinesensitivities.org/>. The main content area shows a 'default' server configuration with four endpoints:

- GET /echo**: Echo back the input.
- GET /plot**: Plot a histogram.
- POST /sum**: Return the sum of two numbers.
- GET /**: redirect to the swagger interface.

[More info..](#)

- **swagger**

*generic database API: using PostGREST*

The screenshot shows the standard public schema PostGREST Documentation generated by Swagger. At the top, it displays the URL <https://rest.MarineSensitivities.org/> and an 'Explore' button. Below this, the title 'standard public schema 1.0.0 (OAS3)' is shown, along with a link to the PostGREST Documentation. A 'Schemes' dropdown is set to 'HTTP'. The main content area shows the following endpoints:

- Introspection** (under 'OpenAPI description (this document)'):
  - GET /**: OpenAPI description (this document).
- geography\_columns**:
  - GET /geography\_columns**
- geometry\_columns**:
  - GET /geometry\_columns**
  - POST /geometry\_columns**
  - DELETE /geometry\_columns**
  - PATCH /geometry\_columns**

[More info..](#)

- **tile**

*spatial database API: using pg\_tileserv for serving vector tiles*

## pg\_tileserv

### Service Metadata

- [index.json](#) for layer list

### Table Layers

- aquamaps.cells ([preview](#) | [json](#))
- public.ply\_rgn ([preview](#) | [json](#))
- public.ply\_rgn\_s05 ([preview](#) | [json](#))
- public.ply\_shfs ([preview](#) | [json](#))
- public.ply\_shfs\_s05 ([preview](#) | [json](#))
- public.sdm\_geometries ([preview](#) | [json](#))
- raw.boem\_ak\_blk\_clip ([preview](#) | [json](#))
- raw.boem\_ak\_prot\_clip ([preview](#) | [json](#))
- raw.boem\_atl\_atl ([preview](#) | [json](#))
- raw.boem\_atl\_blk\_clip ([preview](#) | [json](#))
- raw.boem\_atl\_prot\_clip ([preview](#) | [json](#))
- raw.boem\_gom\_blk\_clip ([preview](#) | [json](#))
- raw.boem\_gom\_prot\_clip ([preview](#) | [json](#))
- raw.boem\_pc\_atl ([preview](#) | [json](#))
- raw.boem\_pc\_blk\_clip ([preview](#) | [json](#))
- raw.boem\_pc\_prot\_clip ([preview](#) | [json](#))
- raw.boem\_usa\_mhk\_plan ([preview](#) | [json](#))
- raw.boem\_usa\_wind\_lease ([preview](#) | [json](#))
- raw.boem\_usa\_wind\_plan ([preview](#) | [json](#))
- raw.mr\_eez ([preview](#) | [json](#))

### Function Layers

- public.sdm\_spatial ([preview](#) | [json](#))

Serves the Species Distribution Model given parameters: dataset\_key, species\_key, popn, time\_interval, variable.

[More info..](#)

•••

# 11 Database

## 11.1 Table and Column Naming Conventions

- Table names are plural and use all lower case.
- Unique identifiers are suffixed with:
  - \*\_id for unique integer keys;
  - \*\_key for unique string keys;
  - \*\_seq for auto-incrementing sequence integer keys.
- Column names are singular and use snake\_case.
- Foreign keys are named with the singular form of the table they reference, followed by \_id.
- Primary keys are named id.

## 11.2 Species Distribution Models

See entity relationship diagram (ERD) for the species distribution models (SDM) database tables in this workflow:

- [Create SDM Tables](#)

And example of ingesting SDM outputs into the database in this workflow:

- [Ingest GoMex cetacean & sea turtle SDMs](#)

## 12 Workflows

Workflows are scripts for testing data analytics and visualization as well as production workflows for ingesting data. See:

- [marinesensitivity.org/workflows](https://marinesensitivity.org/workflows)  
rendered html pages from the scripts (as Quarto notebooks)
- [github.com/MarineSensitivity/workflows](https://github.com/MarineSensitivity/workflows)  
source code in the Github repository

# 13 APIs

There three APIs, each used for different purposes:

## 1. api

*custom API: using R plumber*  
source: [MarineSensitivity/api](#)

The screenshot shows the MarineSensitivity Custom API documentation generated by Swagger. At the top, there's a navigation bar with the title "MarineSensitivity Custom API 1.0.0 OAS3", the URL "https://api.marinesensitivities.org/openapi.json", and an "Explore" button. Below the navigation, there's a section for "API Description" and a "Servers" dropdown set to "https://api.marinesensitivities.org/". The main content area displays a list of endpoints under the "default" server. The endpoints are color-coded: blue for GET methods and green for POST methods. The endpoints listed are: /echo (blue), /plot (blue), /sum (green, highlighted with a green background), and / (blue). Each endpoint has a brief description below it.

## 2. swagger

*generic database API: using PostGREST*  
source: Postgres database, non-spatial

The screenshot shows the standard public schema documentation for PostGREST. At the top, there's a navigation bar with the title "standard public schema 1.0.0 OAS3", the URL "https://rest.MarineSensitivity.org/", and an "Explore" button. Below the navigation, there's a "Schemes" dropdown set to "HTTP". The main content area displays an "Introspection" section. It lists two main entities: "geography\_columns" and "geometry\_columns". Each entity has its own expandable section showing various HTTP methods (GET, POST, DELETE, PATCH) and their corresponding URLs. The "geometry\_columns" section is expanded, showing endpoints like /geometry\_columns (GET), /geometry\_columns (POST), /geometry\_columns (DELETE), and /geometry\_columns (PATCH).

## 3. tile

*spatial database API: using pg\_tileserv for serving vector tiles*

source: Postgres database, spatial

## pg\_tileserv

### Service Metadata

- [index.json](#) for layer list

### Table Layers

- aquamaps.cells ([preview](#) | [json](#))
- public.ply\_rgns ([preview](#) | [json](#))
- public.ply\_rgns\_s05 ([preview](#) | [json](#))
- public.ply\_shfts ([preview](#) | [json](#))
- public.ply\_shfts\_s05 ([preview](#) | [json](#))
- public.sdm\_geometries ([preview](#) | [json](#))
- raw.boem\_ak\_blk\_clip ([preview](#) | [json](#))
- raw.boem\_ak\_prot\_clip ([preview](#) | [json](#))
- raw.boem\_atl\_atlq ([preview](#) | [json](#))
- raw.boem\_atl\_blk\_clip ([preview](#) | [json](#))
- raw.boem\_atl\_prot\_clip ([preview](#) | [json](#))
- raw.boem\_gom\_blk\_clip ([preview](#) | [json](#))
- raw.boem\_gom\_prot\_clip ([preview](#) | [json](#))
- raw.boem\_pc\_atlq ([preview](#) | [json](#))
- raw.boem\_pc\_blk\_clip ([preview](#) | [json](#))
- raw.boem\_pc\_prot\_clip ([preview](#) | [json](#))
- raw.boem\_usa\_mnh\_plan ([preview](#) | [json](#))
- raw.boem\_usa\_wind\_lease ([preview](#) | [json](#))
- raw.boem\_usa\_wind\_plan ([preview](#) | [json](#))
- raw.mr\_eez ([preview](#) | [json](#))

### Function Layers

- [public.sdm\\_spatial](#) ([preview](#) | [json](#))

Serves the Species Distribution Model given parameters: dataset\_key, species\_key, popn, time\_interval, variable.

## 14 Libraries

By creating an R package, we can document functions and make them easily available to other users.

- [msens](#)

R library of functions for mapping marine sensitivities, sponsored by BOEM

Functions can *read* data from the one [APIs](#) (which communicate with the [Database](#)), *analyze* the data, *visualize* the results and store some smaller *data*.

# 15 Apps

The MST provides two primary interactive web applications for exploring sensitivity data, plus several legacy applications from earlier development phases.

These tools allow stakeholders, scientists, and decision-makers to understand the underlying components contributing to an area's sensitivity to offshore energy development, supporting better planning and impact assessment.

## 15.1 Current Applications

### 15.1.1 mapgl — Sensitivity Map

The [mapgl](#) application is the primary tool for exploring composite sensitivity scores across BOEM Program Areas. Key features include:

- **Multi-resolution viewing:** toggle between cell-level ( $0.05^\circ$  grid) and program area aggregations
- **Study area selection:** focus on specific program areas or subregions
- **Layer selection:** view individual species category scores or composite metrics
- **Flower plot:** interactive summary showing scores by species category with weighted center value
- **Species table:** sortable table of species present in selected area with extinction risk details
- **Treemap:** hierarchical view of species contributions to sensitivity
- **CSV export:** download data for selected area or species

See [Appendix: mapgl](#) for details.

### 15.1.2 mapsp — Species Distribution Viewer

The [mapsp](#) application enables exploration of individual species distribution models. Key features include:

- **Species selection:** search by common or scientific name, filter by species category
- **Model display:** view merged models or individual source dataset layers

- **IUCN masking toggle:** compare masked vs. unmasked distributions
- **Species info panel:** ESA listing, IUCN Red List category, MMPA/MBTA protection flags, extinction risk score
- **Deep-linking:** URL parameters support direct links to specific species

See [Appendix: mapsp](#) for details.

## 15.2 Legacy Applications

Earlier versions of the MST included several prototype applications developed during the research phase. These are documented in the Appendix under [Applications \(Legacy\)](#) for reference.

# 16 Docs

Technical documentation is principally in this book:

- [marinesensitivity.org/docs](http://marinesensitivity.org/docs)  
the main documentation site
- [github.com/MarineSensitivity/docs](https://github.com/MarineSensitivity/docs)  
source code in the Github repository

But there are also some other self-documenting resources:

- [marinesensitivity.org/msens](http://marinesensitivity.org/msens)  
documented R functions

# 17 Summary

The Marine Sensitivity Toolkit (MST) provides a comprehensive, reproducible system for assessing the sensitivity of marine ecosystems to offshore energy development across US waters.

## 17.1 Key Findings

- **9,819 valid marine species** mapped at 0.05° resolution (~4 km cells) across **20 BOEM Program Areas**, integrating data from 7 source datasets including AquaMaps SDMs, NMFS and FWS regulatory designations, BirdLife seabird ranges, and IUCN range maps
- **Extinction risk scoring** (1–100 scale) incorporates protections under the Endangered Species Act (ESA), Marine Mammal Protection Act (MMPA), and Migratory Bird Treaty Act (MBTA), ensuring that federally protected species are properly weighted in the sensitivity analysis
- **Model merging** combines multiple distribution datasets per species using a MAX-value approach, constrained by spatial masks from IUCN/Critical Habitat ranges and enhanced with MMPA (floor=20) and MBTA (floor=10) spatial minimums
- **Ecoregional rescaling** normalizes sensitivity scores to a [0–100%] range within each BOEM ecoregion, enabling meaningful cross-region comparison despite natural differences in species richness between tropical and polar waters
- **Interactive tools** (mapgl and mapsp applications) provide decision makers and scientists with accessible interfaces for exploring sensitivity patterns, individual species distributions, and score breakdowns at multiple spatial scales

## 17.2 Future Directions

Several enhancements are planned for future phases of the MST:

- **OBIS/GBIF validation:** refine species distributions using occurrence data from the Ocean Biodiversity Information System and Global Biodiversity Information Facility with temporal filters

- **H3 hexagonal grid:** explore Uber’s H3 hierarchical hexagonal indexing system for multi-resolution spatial analysis, replacing the current latitude-longitude grid
- **Cloud-Optimized GeoTIFFs (COGs) and STAC catalogs:** export raster data as COGs with SpatioTemporal Asset Catalog metadata for interoperability with geospatial platforms
- **DAG pipeline:** implement a formal directed acyclic graph (DAG) workflow using the `targets` R package for automated, reproducible data processing
- **Stressor-receptor matrices:** expand from sensitivity-only assessment to full vulnerability analysis by integrating exposure data for offshore wind, oil & gas, and other marine activities (see Chapter 8)
- **Enhanced applications:** arbitrary area selection tools, taxonomic tree browsing, automatic high-quality static figure generation, and story-map/scrollytelling explainer interfaces
- **Infrastructure transfer:** support transition of data and applications to BOEM server infrastructure for long-term operational deployment

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# Glossary

- acclimatisation** the adjustment of an organism to environmental conditions in the field or environment rather than the laboratory without an adjustment in their genetics. Acclimation has been used to describe phenotypically plastic responses in natural conditions. Source: Ross et al. (2023).
- adaptation** the evolutionary mechanism where natural selection of traits is genetically passed on, typically over many generations, to create an organism suited to the environment. Source: [rossRoss et al. (2023)]
- adaptive capacity** the capacity of the ecosystem or organism to improve and reorganise in response to stress such as climate change through phenotypic plasticity (acclimation, acclimatisation) or adaptation, distributional shifts, and rapid evolution of traits suited to new conditions. Source: Ross et al. (2023).
- BOEM** Bureau of Ocean Energy Management — US federal agency responsible for managing offshore energy and mineral resources on the Outer Continental Shelf.
- COG** Cloud-Optimized GeoTIFF — a raster file format optimized for efficient access over HTTP, enabling range requests for partial reads.
- DuckDB** an embedded analytical database engine used for storing and querying species distribution models, extinction risk scores, and sensitivity metrics.
- ecoregion** a BOEM-defined ecological region used as the spatial unit for rescaling sensitivity scores to enable meaningful cross-region comparison.
- epigenetics** the modification of phenotype plasticity of an organism through altered gene expression without an alteration to the DNA sequence. ‘Epi’ means above the DNA and includes DNA methylation, modification of histones, and non-coding RNA. Source: Ross et al. (2023).
- ESA** Endangered Species Act (1973) — US federal law providing protections for species listed as Endangered or Threatened by NMFS or FWS.
- exposure** the magnitude of the change in the environment
- fecundity** the maximum physiological potential reproductive output of an organism to produce offspring (reproductive output). This differs from fertility, which is the number of offspring born. Source: Ross et al. (2023)
- MBON** Marine Biodiversity Observation Network; see [MarineBON.org](#)
- MBTA** Migratory Bird Treaty Act (1918) — US federal law protecting migratory birds, including most seabird species. MBTA-protected species receive a minimum spatial floor score of 10.
- MMPA** Marine Mammal Protection Act (1972) — US federal law protecting all marine mammals in US waters. MMPA-protected species receive a minimum spatial floor score of

20.

**MST** Marine Sensitivity Toolkit — the cloud-native system developed for BOEM to assess marine ecosystem sensitivity to offshore energy development.

**OCSLA** Outer Continental Shelf Lands Act — US federal law governing the management of offshore resources, including the mandate to consider environmental sensitivity and marine productivity.

**resilience** the capacity of an ecosystem, society, or organism to absorb disturbance and reorganise while undergoing change so as to retain essentially the same function, structure, identity, and feedbacks. Resilience reflects the degree to which a complex adaptive system is determined by its capacity to reorganise and adapt in order to avoid being disturbed again. Source: Ross et al. (2023).

**SDM** Species Distribution Model — a statistical or environmental envelope model predicting the spatial distribution of a species based on environmental variables.

**sensitivity** the magnitude of response to the change

**stressor** the stimulus that causes stress to an organism

**vulnerability** combination of exposure and sensitivity

## **Part III**

# **Applications (Current)**

# A mapgl — Sensitivity Map

## A.1 Overview

The **mapgl** application ([shiny.marinesensitivity.org/mapgl](http://shiny.marinesensitivity.org/mapgl)) is the primary interactive tool for exploring composite marine sensitivity scores across BOEM Program Areas. It enables users to visualize extinction risk weighted species presence at multiple spatial resolutions, with integrated flower plot and treemap summaries.

Figure A.1 shows the global view of cell-level sensitivity scores across all US waters. The sidebar provides controls for study area, spatial units (raster cells or program areas), and layer selection.

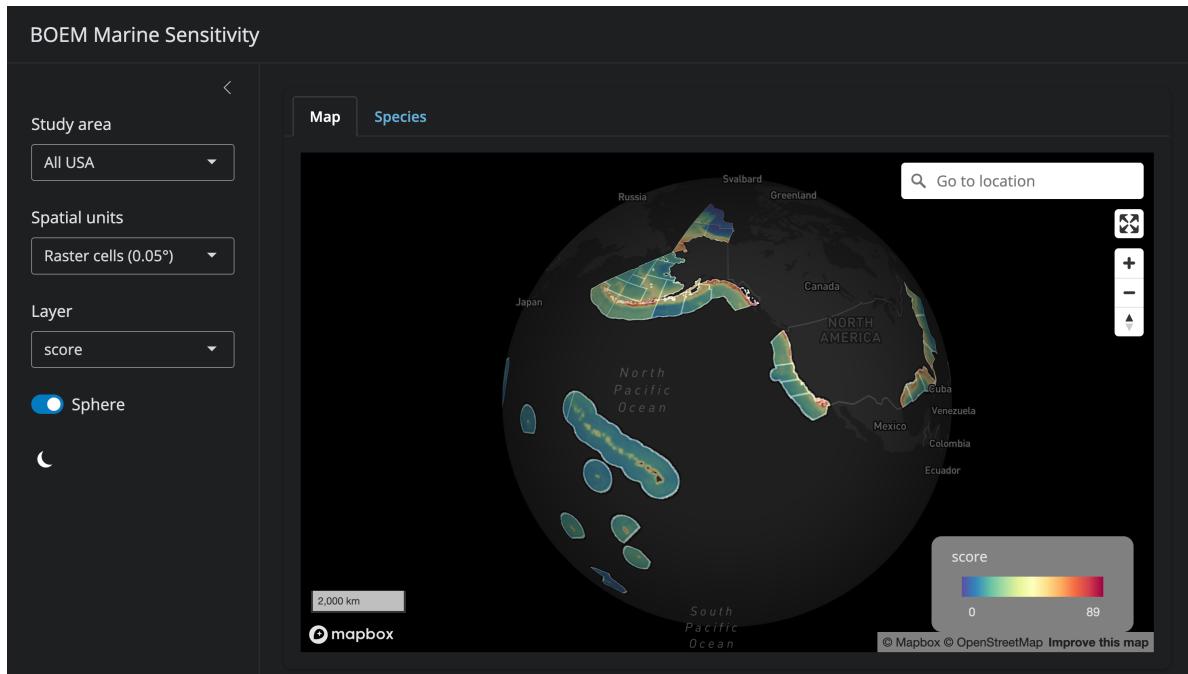


Figure A.1: The mapgl application displaying cell-level sensitivity scores across US waters. The sidebar provides controls for study area selection, spatial resolution (raster cells vs. program areas), and layer choice. The globe view shows scores from 0 (blue) to 89 (red) with MapBox basemap.

Figure A.2 shows the flower plot panel that appears when a program area is selected. Here, the Southern California program area displays a weighted mean score of 29, with petals representing species categories (bird, coral, fish, invertebrate, mammal, other, turtle) and primary productivity.

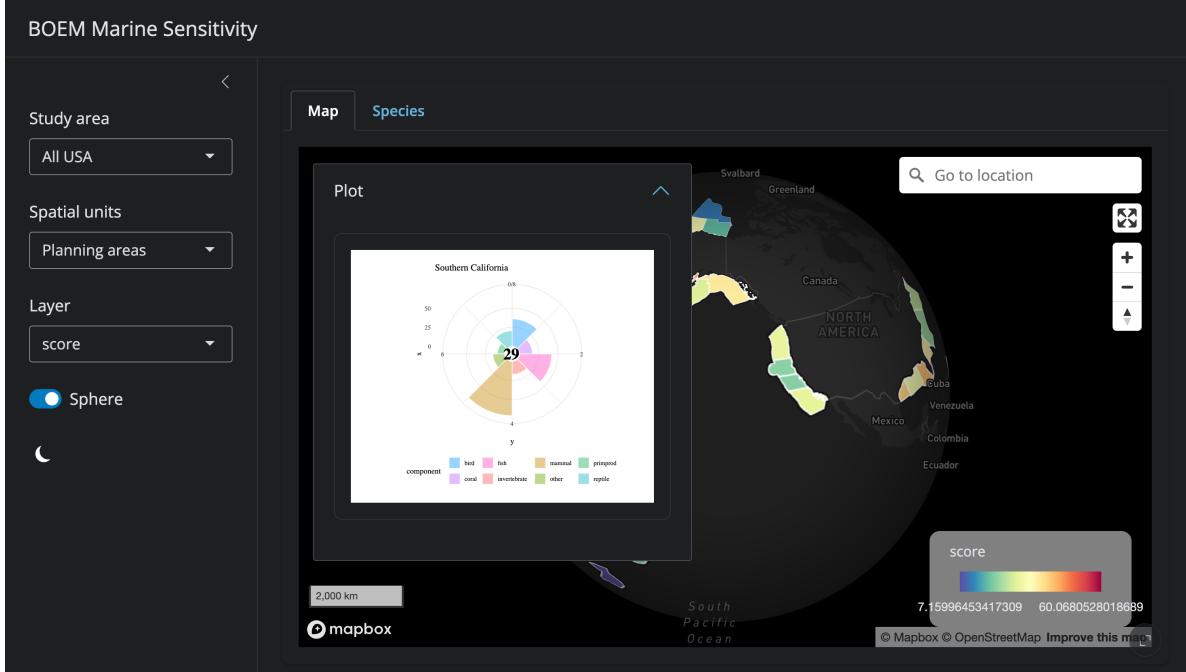


Figure A.2: The mapgl application showing the flower plot panel for Southern California. Petal length represents each category's rescaled sensitivity score; petal width represents its weight. The center value (29) is the weighted mean across all categories.

## A.2 Features

### A.2.1 Map Display

- **Cell-level view:**  $0.05^\circ$  grid cells colored by sensitivity score for the selected metric
- **Program area view:** aggregated scores by BOEM Program Area, with boundaries overlaid
- **Base maps:** multiple MapBox base layers (satellite, streets, light, dark)
- **Study area selection:** click a program area to focus the view and update summary panels

### A.2.2 Sensitivity Metrics

The map can display any of the following layers:

- Composite extinction risk (weighted sum across all species categories)
- Individual category scores: bird, coral, fish, invertebrate, mammal, reptile/turtle
- Primary productivity

All scores are ecoregionally rescaled to [0–100] for meaningful cross-region comparison (see Chapter 7).

### A.2.3 Flower Plot

Selecting a program area displays a flower plot summarizing the sensitivity profile:

- Each petal represents a species category
- Petal length = rescaled sensitivity score (0–100)
- Petal width = category weight
- Center value = weighted mean across categories

### A.2.4 Species Table

A sortable table of all valid species present in the selected area, showing:

- Scientific and common name
- Species category
- ESA listing, IUCN Red List status
- MMPA/MBTA protection flags
- Extinction risk score

### A.2.5 Data Export

Users can download CSV files of scores and species lists for the selected program area or custom area of interest.

## A.3 Generating Screenshots

## A.4 Source Code

The application source code is at: [apps/mapgl/app.R](#)

# B mapsp — Species Distribution Viewer

## B.1 Overview

The **mapsp** application ([shiny.marinesensitivity.org/mapsp](http://shiny.marinesensitivity.org/mapsp)) enables exploration of individual species distribution models within the MST database. Users can view merged and source-level models, compare masked vs. unmasked distributions, and access detailed species regulatory status information.

Figure B.1 shows the merged distribution model for the blue whale (*Balaenoptera musculus*). The map displays cell values from 1 (low suitability, blue) to 100 (high suitability, red) across all US program areas where the species occurs.

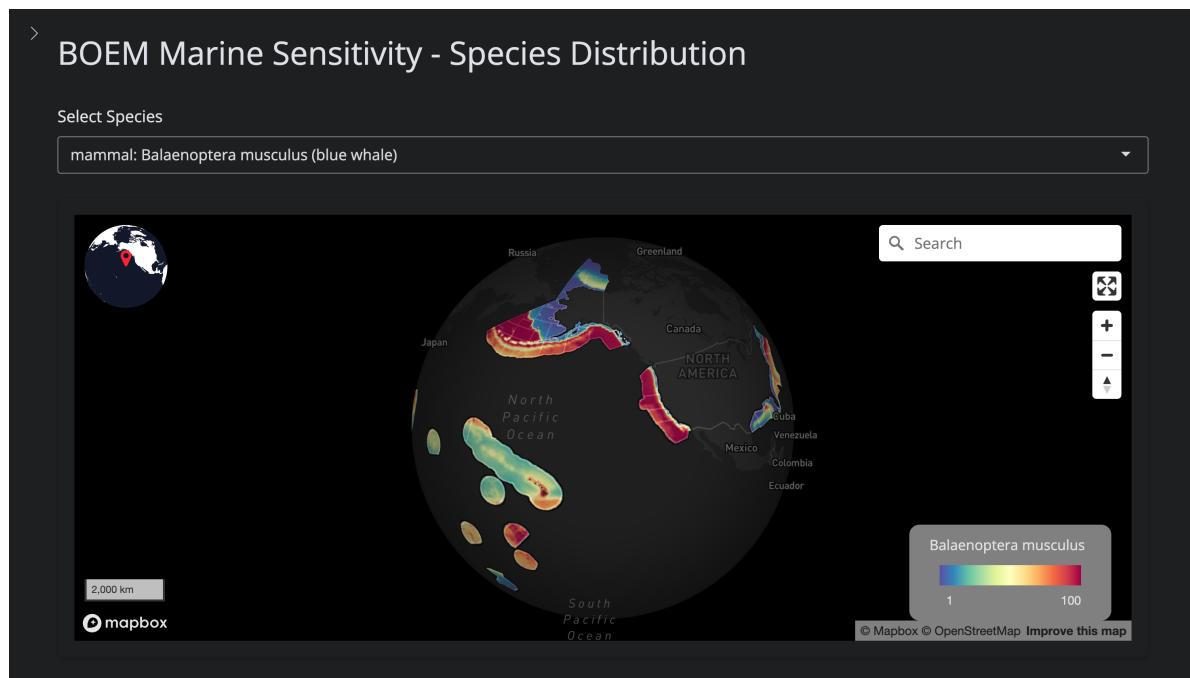


Figure B.1: The mapsp application showing the merged distribution model for blue whale (*Balaenoptera musculus*). Cell values range from 1 (low suitability) to 100 (high suitability). The species selector dropdown allows searching by common or scientific name with category prefix.

## B.2 Features

### B.2.1 Species Selection

- **Search:** find species by common name or scientific name
- **Category filter:** narrow results by species category (bird, coral, fish, invertebrate, mammal, reptile/turtle)
- **Alphabetical browsing:** scroll through species lists within each category

### B.2.2 Model Display

- **Merged model:** the final merged distribution showing MAX values across all source datasets, with masking and spatial floors applied
- **Source datasets:** toggle individual source layers (AquaMaps, NMFS CH, FWS CH, FWS Range, BirdLife, IUCN Range) to see each dataset's contribution
- **IUCN masking toggle:** compare the unmasked AquaMaps SDM with the masked merged model to visualize the effect of range constraints

### B.2.3 Species Info Panel

Detailed information for the selected species:

- Scientific name and common name
- Species category (bird, fish, mammal, etc.)
- ESA listing status (Endangered, Threatened, or not listed)
- IUCN Red List category
- MMPA protection flag
- MBTA protection flag
- Computed extinction risk score (1–100)
- Number of source datasets contributing to the merged model

### B.2.4 Deep-Linking

The application supports URL parameters for direct linking to specific species, enabling bookmarking and sharing of specific views:

`https://shiny.marinesensitivity.org/mapsp/?species=Balaenoptera+musculus`

## **B.3 Generating Screenshots**

## **B.4 Source Code**

The application source code is at: [apps/mapsp/app.R](#)

## **Part IV**

# **Applications (Legacy)**

# Areas of Interest

Map high resolution Areas of Interest (using vector tiles) for visualization (and later summarization).

- [website](#)
- [code](#)

Area Explorer

The screenshot shows the 'Area Explorer' interface. On the left, there's a sidebar titled 'Areas of Interest' with a dropdown menu set to 'Regions'. Below it, a code snippet shows the coordinates of a polygon:

```
last edited: POLYGON((-141.0639 46.55907, -136.6324 42.0423, -132.0404 48.99068, -135.5994 49.97881, -141.0639 46.55907))
```

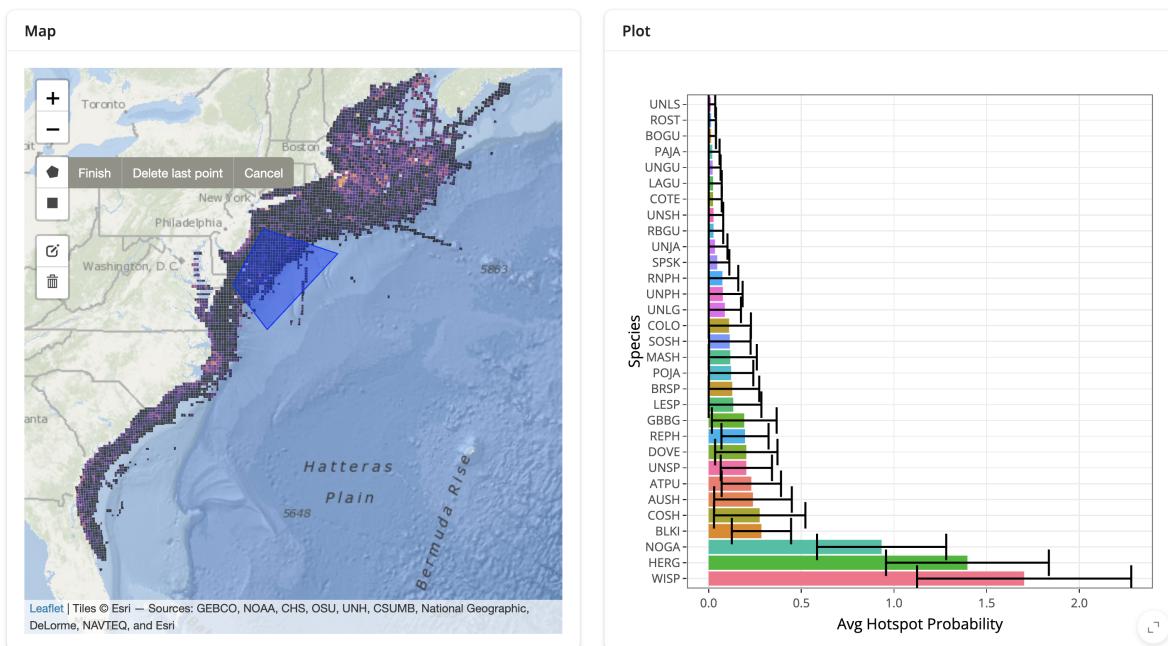
The main area is a map of North America with a blue polygon highlighting the Aleutian Arc region off the coast of Alaska. A tooltip provides detailed information about this area:

aoi	shlf_key	shlf_name	rgn_key	rgn_name	ctr_lon	ctr_lat	area_km2	geometry
			AK	Alaska	-178.56252307137368	51.149538291898025	860518.1237176519	null
			ALA	Aleutian Arc				

# Bird Hotspots

Bird hotspots application showing hotspot probability for species present given drawn Area of Interest.

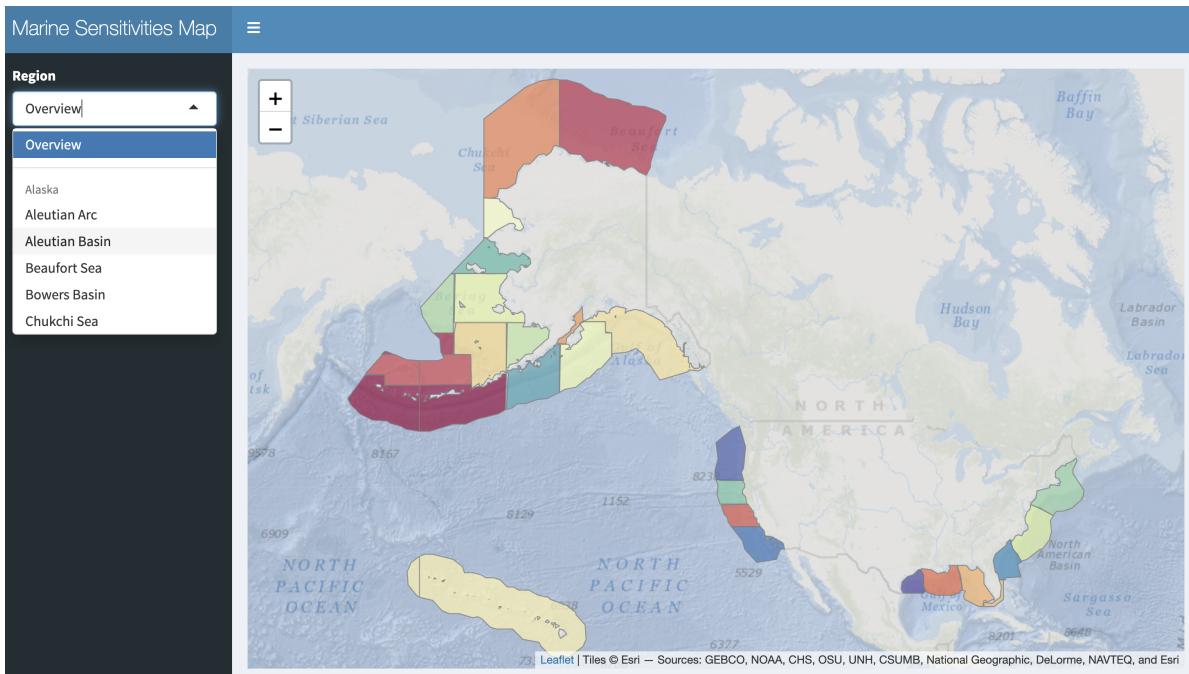
- [🌐 website](#)
- [💻 code](#)



# Regional Map

Basic interactive map of BOEM regions.

- [🌐 website](#)
- [🔗 code](#)

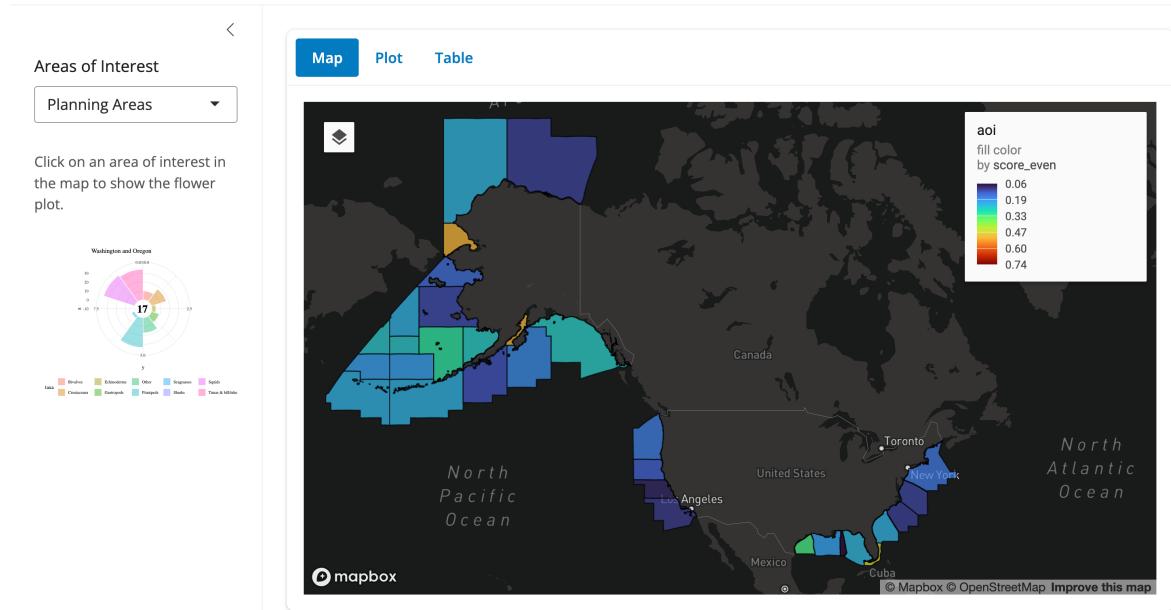


# Scores Explorer

Calculate scores based on sensitivity metric – for now, extinction risk across taxonomic groups.

-  website
-  code

Scores Explorer

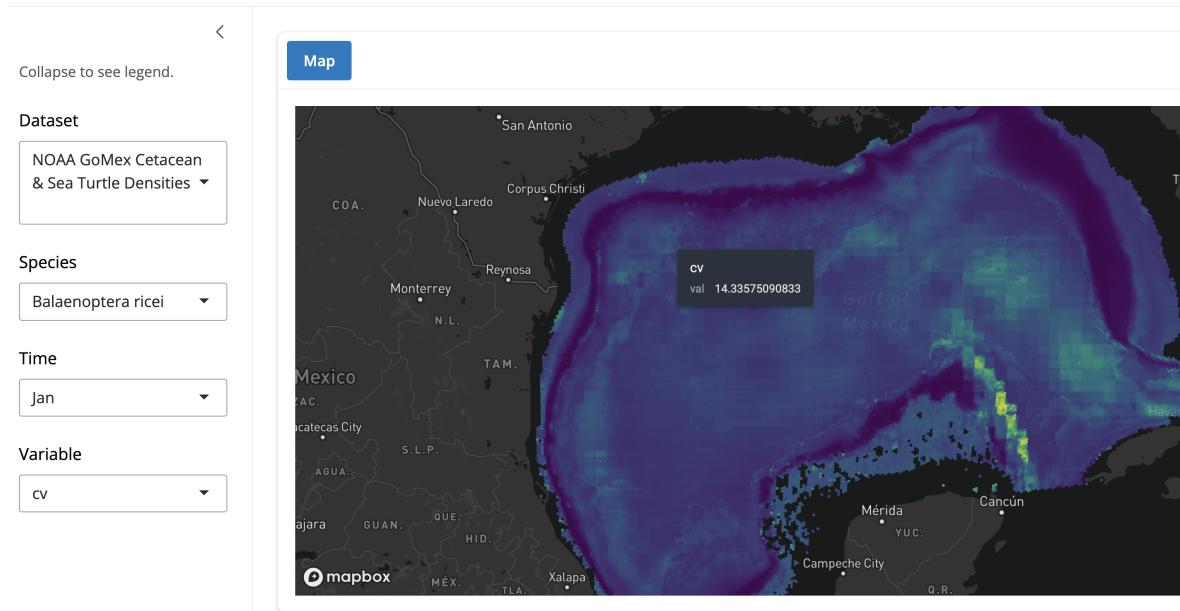


# Distributions, Vector

Show species distributions with high resolution vectors (as vector tiles).

- [website](#)
- [code](#)

SDM Explorer

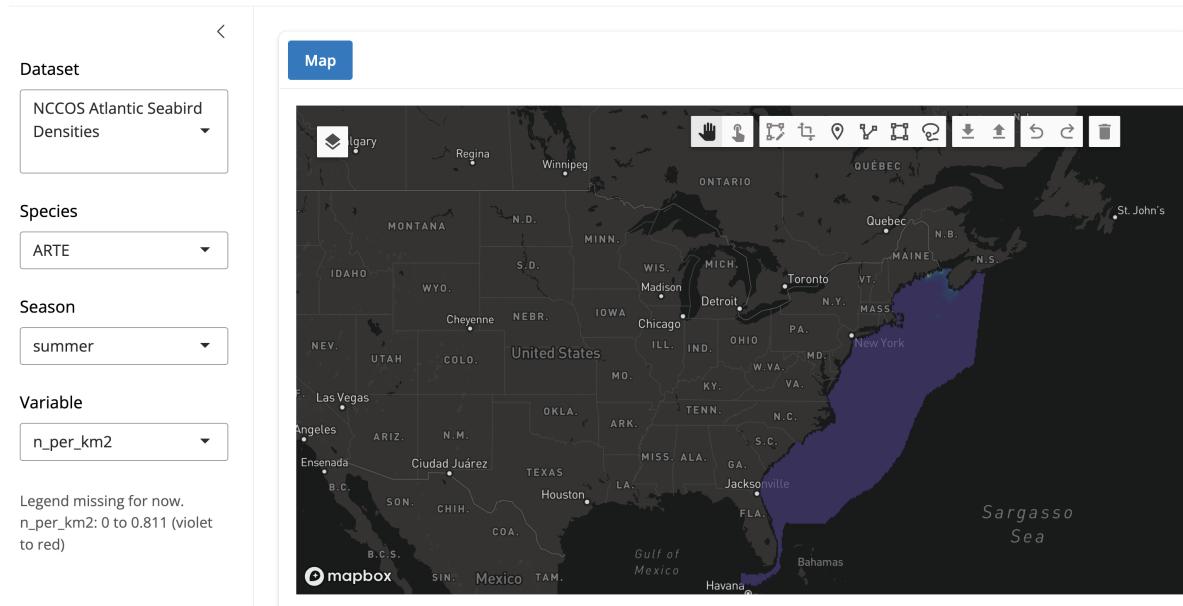


# Distributions, Raster

Show species distributions with high resolution rasters as cloud-optimized GeoTIFFs (COGs).

- [🌐 website](#)
- [📄 code](#)

SDM Raster Explorer



# Vulnerability Mapper

Combine species distribution models (raster) and vulnerability metrics (tables) to identify areas of high conservation concern.

- [🌐 website](#)
- [💬 code](#)

