A STACKED SPECIES DISTRIBUTION MODEL (S-SDM) FOR BERING SEA KRILL & THEIR TROPHIC INTERACTORS

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RESEARCH QUESTION & RATIONALE

Research Questions:

1. Where are euphausiids often found in the Southeastern Bering Sea?

2. What environmental conditions serve as strong predictors of euphausiid presence?

3. How does euphausiid distribution compare to:

- Predator distributions (walleye pollock)

- Prey distributions (phytoplankton and zooplankton)

- Competitors (different species of euphausiid)

Rationale: SEBS krill indices parameters may need revision.

image credit: Norkrill, Creative Commons
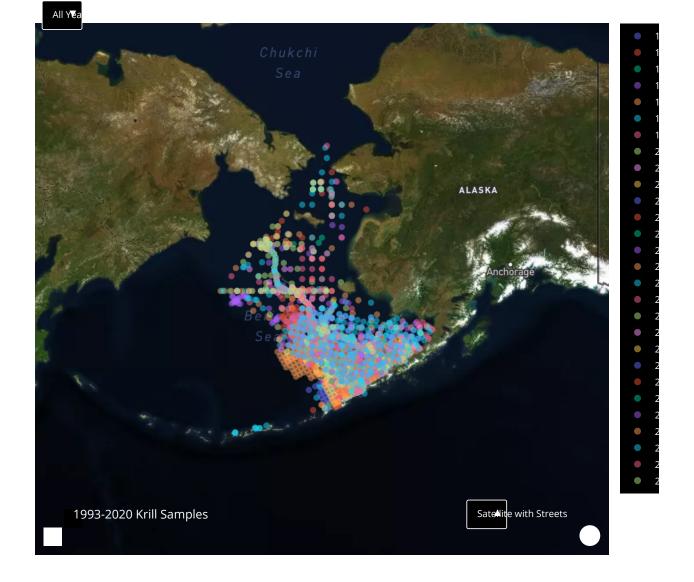
STUDY SYSTEM & SPECIES

BIOTIC DATA:

- Krill bongo net tows
- Pollock and their stomach contents
- Zooplankton biomass
- Chlorophyll A concentration as proxy for phytoplankton productivity

ABIOTIC DATA:

- Sea surface temperature
- Salinity
- Bathymetry
- Proximity to shelf-incising canyon
- Currents?
- Precipitation?

STUDY SYSTEM & SPECIES

1993-2020 Krill Samples

Satellite with Streets

EDIT CHART

ANTICIPATED DATA REQUIREMENTS

For the stacked species distribution model (s-SDM):

Category	Procured	Metric	Time
Krill	Yes	presence/absence	1993-2020
Pollock	Yes	presence/absence, stomach content	1981-2020
Zooplankton	Yes	total biomass	1981-2013
SST	Yes	0.1 degrees resolution	1990-2020
Bathymetry	Yes	1.0 degrees resolution	static
Salinity	Yes	25km resolution	static
Canyon	Yes	region (categorical variable)	static
Currents	No		
Precipitation	No		

POTENTIAL ANALYSES & TECHNIQUES

The R SSDM package could be used to create the s-SDM:

1) Fit individual taxa SDMs on environmental predictor variables using a single algorithm. 2) Create an ensemble SDM (ESDM) that combines the outputs of the above SDMs and their unique algorithms. 3) Create the SSDM by combining the ESDM and SDM outputs to model assemblages (ie. predator/prey, competitors).

```
1  library(SSDM)
2  library(raster)
3  Env <- load_var(system.file('extdata',  package = 'SSDM'), categorical = 'SUBSTRATE', verbose = FALSE)
4  Env
5  Occ <- load_occ(path = system.file('extdata',  package = 'SSDM'), Env,
6        Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
7        file = 'Occurrences.csv', sep = ',', verbose = FALSE)
8  head(Occ)
9  SDM <- modelling('GLM', subset(Occurrences, Occurrences$SPECIES == 'elliptica'),
10               Env, Xcol = 'LONGITUDE', Ycol = 'LATITUDE', verbose = FALSE)
11 plot(SDM@projection, main = 'SDM for Taxa Name with Generalized Linear Model (GLM) algorithm')
12 ESDM <- ensemble_modelling(c('CTA', 'MARS'), subset(Occurrences, Occurrences$SPECIES == 'taxa'),
13                        Env, rep = 1, Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
14                        ensemble.thresh = 0, verbose = FALSE)
15 plot(ESDM@projection, main = 'ESDM for Taxa with Classification tree analysis (CTA) and Multivariate Adaptive Regression Splines (MARS) al
16 SSDM <- stack_modelling(c('CTA', 'SVM'), Occurrences, Env, rep = 1, ensemble.thresh = 0,
17                  Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
18                  Spcol = 'SPECIES', method = "pSSDM", verbose = FALSE)
19 plot(SSDM@diversity.map, main = 'SSDM for Taxa with CTA and Support Vector Machine (SVM) algorithms')
```

Error ✕