

Proposition of New Protected Areas of the Northeast Atlantic Ocean

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Abstract

The United Nations has set a goal of conserving and managing 30% of land and sea by 2030. To aid in this effort, the distribution of nine different sedentary species in the Northeast Atlantic Ocean was modeled to identify regions of high biodiversity. These results, combined with data on the fishing activities in the region, were used to propose a set of regions to be protected to meet the United Nations' goal which protect these nine species while minimizing disruption to current fishing activities in the region.

1. Introduction

Coral reefs are typically associated with the shallow-water tropical regions. However, increases in commercial fishing in deep waters as well as advances in remote data collection have revealed a rich coral ecosystem in the cold, deep waters of the North Atlantic. (Freiwald 2002).

Along the European continental shelf, which is the focus of this paper, these rich coral ecosystems, and other sedentary species, boast a diverse range of coral and fish species. They have been a focus of study for ecologists in recent times as they seek to better understand these ecosystems and act to protect them (Frank et al., 2011).

Since as early as the 1920s trawlers and fishing boats were operating in deep waters previously unexplored. Their fishing nets became tangled in the coral resulting in a loss of economic profit. The increase of fishing activities in the region along the European continental shelf has resulted in habitat destruction of these ecosystems. As such many species have become vulnerable.

Recent efforts aim to increase conservation efforts towards vulnerable marine ecosystems (VMEs). The BBNJ Agreement under the United Nations sets a goal of conserving and managing 30% of land and sea by 2030 under the Kunming-Montreal Global Biodiversity Framework. To aid in these global conservation efforts, this paper aims to identify the best sites for protection in the Northeast Atlantic region based on nine different species common in the area. The nine different species, primarily focused on different coral species, chosen were: (1) chemosynthetic

species (seeps and vents), (2) cup coral, (3) generic sponge, (4) gorgonian, (5) lace coral, (6) sea pen, (7) stony coral, (8) anemone, and (9) black coral. These species were chosen due to their sedentary nature, which is easier to model than nomadic species, and the abundance of available occurrence data for these particular species.

2. Methodology

Species Distribution Modeling aims to combine environmental data and/or spatial data, often obtained through advances in GIS, with on-site location data. Observances of a species may be made by an ecologist on location. This information can be used with environmental and spatial data to predict species distribution across a larger landscape where available sample data may be sparse (Elith and Leathwick, 2009).

Systematic Conservation Planning aims to locate new locations for conservation to complement existing sites and achieve a given goal based on the biodiversity of the region (Margules and Pressey, 2000). This systematic approach can lead to designing new conservation areas that are better than current sites which may have been hampered by external factors, such as political or economic influences, or a lack of data in the region.

A database of VMEs and the environmental data of that area were used to create a separate species distribution model for nine species in the database using the MaxEnt algorithm (Phillips et al., 2006). MaxEnt is a method that specializes in modeling presence-only data and has been available since 2004, becoming a common method for ecologists around the world (Elith et al., 2011). Specifically, the R package maxnet (v. 0.1.4), which fits MaxEnt models using the glmnet R package, was used (Phillips et al., 2017).

Each model produces a prediction raster and a binary presence-absence raster is calculated by maximizing the specificity and sensitivity. The binary presence-absence rasters are combined to see which locations have a greater biodiversity, i.e. which areas contain most or all of the target species and which areas contain only a few of the target species. Areas of greater biodiversity are of more interest as these areas can be used for conservation efforts to protect multiple species while closing only a single area.

The R package prioritizr (v. 8.0.3) uses the environmental variables, the fishing pressure of the region (swept area ratio), and the binary presence-absence rasters previously calculated to define and solve a systematic conservation problem to target 30% conservation in the region (Hanson et al. 2023). All scripts used in this process are included in Appendix A and B.

3. Results

The MaxEnt models generated the ROC curves (Figure 1) with a minimum AUC of 0.88 (Anemone species), a maximum AUC of 0.992 (lace coral), and an average AUC of 0.919 across the nine different models. These scores are great across the board and aid in the high accuracy of the species distribution models.

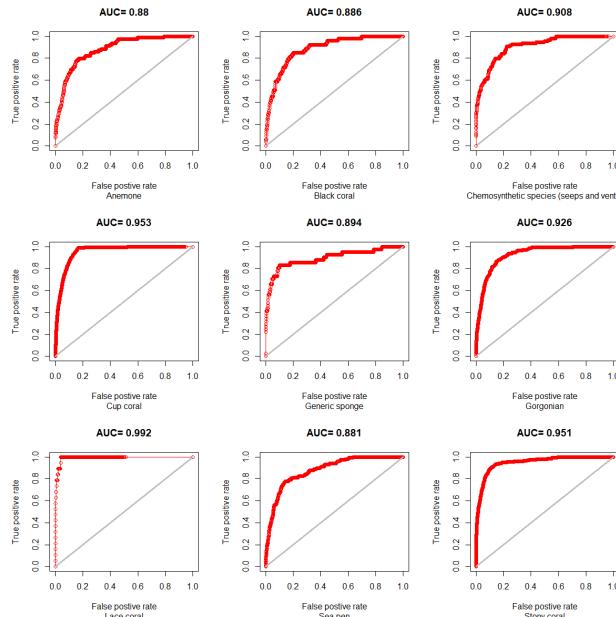


Figure 1. ROC Curves for Species Distribution Models

The one exception is the model of the lace coral. The lack of data on the lace coral, with only 19 occurrence points, suggests that the model may not be generalized very well. Visualizing the probability rasters generated by the MaxEnt models also shows that the data for the lace coral is far more sparse than for the other species, particularly compared to the generic sponge which had the second least number of occurrence points with 41 points (Figure 2).

The map in Figure 3 shows the result of combining the binary presence-absence rasters of the MaxEnt models for the nine species analyzed. Areas of high biodiversity, where most of the analyzed species are likely to be found, occur along the ridge of the continental shelf and the Porcupine Bank off the coast of Ireland.

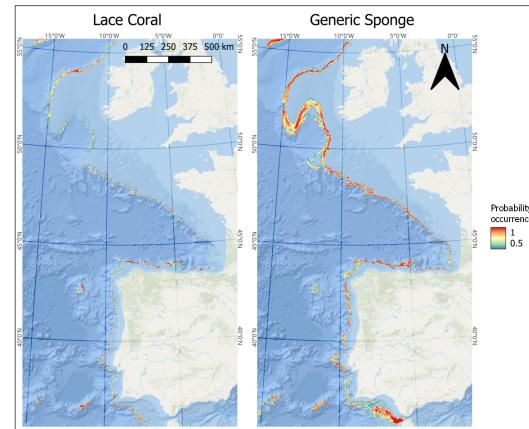


Figure 2. Lace Coral vs Generic Sponge Probability Rasters

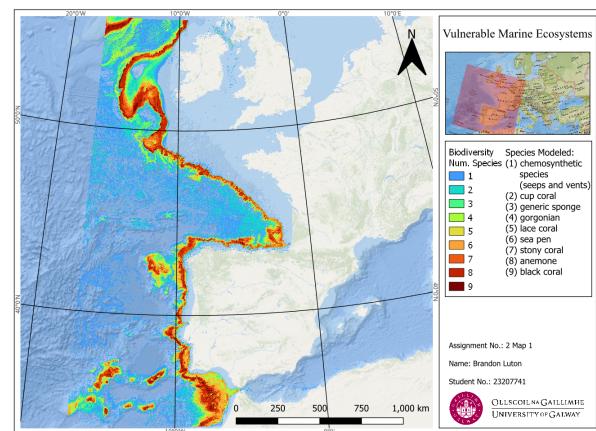


Figure 3. Biodiversity of NE Atlantic

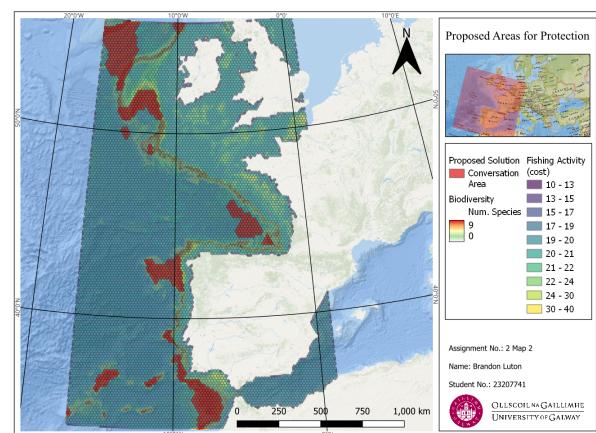


Figure 4. Proposed Conservation Sites

The map in Figure 4 shows a representation of fishing activities in the region. Fishing activities (cost) are highest

closest to shore, particularly in the regions west of France, south of Portugal, and south of the UK and Ireland. Trends of higher fishing activities seem to generally follow the ridge, but there is not a strong correlation. Overlayed on top of the fishing activities is the solution, denoted in red color, found by the prioritizr program. This solution protects all nine species modeled and hits the 30% conservation goal by protecting large areas with high biodiversity while minimizing the impact of fishing activities. Most of the major fishing locations are either unaffected or minimally impacted by the proposed protected sites.

4. Conclusion

From the environmental data and the occurrence data of nine different sedentary species, a species distribution model was developed for each species using the MaxEnt program. The results of these models are generally very good except for the lace coral model (and possibly the generic sponge model) likely due to the lack of occurrence data for these species in the Northeast Atlantic. Using these models, a prediction of the likely locations of these species could be determined. Overlaying the results of all the models resulted in a general representation of the biodiversity of the region to locate regions where multiple species are likely to be found.

These models, along with data denoting the fishing activity of the region, allowed the identification of potential conservation sites through the use of systematic conservation planning. These potential sites aim to maximize the conservation effort by protecting as many species in as few distinct areas as possible while achieving the United Nation's goal of 30% protection. Additionally, these sites aim to minimize the impact these new protection zones would have on the current fishing activities in the region.

References

- Elith, J. and Leathwick, J.R., 2009. Species distribution models: ecological explanation and prediction across space and time. *Annual review of ecology, evolution, and systematics*, 40, pp.677-697.
- Elith, J., Phillips, S.J., Hastie, T., Dudík, M., Chee, Y.E. and Yates, C.J., 2011. A statistical explanation of MaxEnt for ecologists. *Diversity and distributions*, 17(1), pp.43-57.
- Frank, N., Freiwald, A., Correa, M.L., Wienberg, C., Eisele, M., Hebbeln, D., Van Rooij, D., Henriet, J.P., Colin, C., Van Weering, T. and de Haas, H., 2011. Northeastern Atlantic cold-water coral reefs and climate. *Geology*, 39(8), pp.743-746.
- Freiwald, A., 2002. Reef-forming cold-water corals. *Ocean margin systems*, pp.365-385.
- Hanson JO, Schuster R, Morrell N, Strimas-Mackey M, Edwards BPM, Watts ME, Arcese P, Bennett J, Possingham HP (2023). prioritizr: Systematic Conservation Prioritization in R. R package version 8.0.3, <https://github.com/prioritizr/prioritizr>, <https://prioritizr.net>.
- Kunming-Montreal Global Biodiversity Framework (CBD/COP15/L.25) (Convention on Biological Diversity, 2022). Available from: <https://prod.drupal.www.infra.cbd.int/sites/default/files/2022-12/221222-CBD-PressRelease-COP15-Final.pdf>
- Margules, C.R. and Pressey, R.L., 2000. Systematic conservation planning. *Nature*, 405(6783), pp.243-253.
- Phillips, S.J., Anderson, R.P., Dudík, M., Schapire, R.E. and Blair, M.E., 2017. Opening the black box: An open-source release of Maxent. *Ecography*, 40(7), pp.887-893.
- Phillips, S.J., Anderson, R.P. and Schapire, R.E., 2006. Maximum entropy modeling of species geographic distributions. *Ecological modelling*, 190(3-4), pp.231-259.

Appendix

A: R Script - Species Distribution Modeling

```

1 #install.packages('maxnet')
2 #install.packages('terra')
3 #install.packages('predicts')
4 #install.packages("SDMtune")
5
6 library(maxnet)
7 library(terra)
8 library(predicts)
9 library(SDMtune)
10
11 set.seed(123)
12
13 # file path to the folder with the env_vars
14 inputFolder = ""
15 # file path to the VMEs_database CSV file
16 vme_path = ""
17
18 env_vars = rast(list.files(inputFolder, pattern=".asc", full.names = TRUE))
19 background = spatsample(env_vars, n=10000, "random", na.rm=TRUE,
20 as.points=TRUE)
21 backvals = values(background)
22
23
24 VME_data = read.csv(vme_path)
25
26 # take a look at the structure
27 str(VME_data)
28
29 # convert it to spatial points to facilitate spatial operations
30 VME_data = vect(VME_data, geom=c("MiddleLongitude", "MiddleLatitude"),
31 crs="epsg:4326", keepgeom=TRUE)
32 crs(env_vars) = "epsg:32629"
33
34 # clip the occurrence data to the extent of the environmental raster data
35 VME_data = crop(VME_data, project(ext(env_vars), from="epsg:32629",
36 to="epsg:4326"))
37 VME_data = values(VME_data)
38
39 str(VME_data)
40
41 summary_vme = table(VME_data$VME_Indicator, useNA="ifany")
42 summary_vme
43
44 # get rid of NA cases
45 VME_data = VME_data[complete.cases(VME_data[, 'VME_Indicator']), ]
46 VME_data$VME_Indicator = gsub("Black Coral", "Black coral",
47 VME_data$VME_Indicator)
48
49 summary_vme = table(VME_data$VME_Indicator, useNA="ifany")
50 summary_vme
51
52 # specify some minimum cut-off value for the number of records that's acceptable
53 cutoff = 100
54 categories_over_100 = names(summary_vme[summary_vme > cutoff])
55 categories_over_100
56
57 occ_points = list()
58 MX_mods = list()
59 raster_predictions = list()
60 PA_predictions = list()
61 Evaluations = list()
62
63 for (category in categories_over_100)
64 {
65   species = na.omit(VME_data[VME_data$VME_Indicator==category,
66     c("VME_Indicator", "MiddleLongitude",
67     "MiddleLatitude")])
68   species = vect(species, geom=c("MiddleLongitude", "MiddleLatitude"),
69   crs="epsg:4326", keepgeom=FALSE)
70   species = project(species, "epsg:32629")
71
72   species = thinData(as.data.frame(species, geom='XY'), env=env_vars)
73
74   Occ_points[[category]] = species
75
76   presvals = extract(env_vars, species[,-1])
77   presvals = presvals[,1]
78
79   # create presence-background column
80   pb = c(rep(1, nrow(presvals)), rep(0, nrow(backvals)))
81
82   sdadata = data.frame(cbind(pb, rbind(presvals, backvals)))
83   sdadata = na.omit(sdadata)
84
85   mod = maxnet(sdadata[,1], sdadata[,-1])
86   MX_mods[[category]] = mod
87
88   prediction = predict(env_vars, mod, clamp=FALSE, type="cloglog", na.rm=TRUE)
89   raster_predictions[[category]] = prediction
90
91   e = pa_evaluate(sdadata[sdadata==1,], sdadata[sdadata==0,], mod,

```

```

92   type="cloglog")
93   Evaluations[[category]] = e
94
95   # create a binary presence-absence raster based on the determined maximum
96   # specificity and sensitivity there
97   presence_absence_raster = prediction
98   presence_absence_raster[presence_absence_raster>threshold(e$max_spec_sens)]= 1
99   presence_absence_raster[presence_absence_raster!=1] = 0
100
101 PA_predictions[[category]] = presence_absence_raster
102 gc() # free memory
103 }
104
105 # example plots
106 category = categories_over_100[1]
107 dev.off()
108 par(mfrow=c(2,2))
109 plot(raster_predictions[[category]])
110 points(Occ_points[[category]][,2:3])
111 plot(Evaluations[[category]], "ROC")
112
113 # Plot all ROC curves
114 #dev.off()
115 par(mfrow=c(3,3))
116 for (category in categories_over_100)
117 {
118   plot(Evaluations[[category]], "ROC", sub=category)
119
120 }
121
122 plot(PA_predictions[[category]])
123 barplot(as.matrix(threshold(Evaluations[[category]])), beside=TRUE,
124 legend.text=TRUE)
125
126 # write outputs to folders
127 pa_path = ""
128 prob_path = ""
129
130 Pa_pred_rast = rast(PA_predictions)
131 setwd(pa_path)
132 writeRaster(Pa_pred_rast, paste0(names(Pa_pred_rast), ".tif"), overwrite=TRUE)
133
134 prob_rast = rast(raster_predictions)
135 setwd(prob_path)
136 writeRaster(prob_rast, paste0(names(prob_rast), ".tif"), overwrite=TRUE)

```

B: R Script - Systematic Conservation Planning

```

1 # Systematic Conservation Planning
2
3 #install.packages("Rtools")
4 #install.packages("prioritizr")
5 #install.packages("Rsymphony")
6 #install.packages("sf")
7
8 library(terra)
9 library(sf)
10 library(prioritizr)
11 library(Rsymphony)
12
13 # path to the folder containing the env_vars
14 inputFolder = ""
15
16 env_vars = rast(list.files(inputFolder, full.names=T, pattern=".asc"))
17
18 # make a hexagonal grid based on the extent of the environmental vars
19 cellarea = 2.5e8
20 PU_Layer = st_make_grid(st_multipart(matrix(ext(env_vars), ncol=2)),
21   cellsize=sqrt(2*(cellarea)/sqrt(3))), square=FALSE)
22
23 st_crs(PU_Layer) = 32629
24
25 plot(PU_Layer)
26 plot(env_vars)
27
28 # Get only water areas
29 Marine_area = env_vars[[4]]
30 crs(Marine_area) = "epsg:32629"
31 Marine_area[!is.na(Marine_area)] = 1
32
33 plot(Marine_area)
34
35 # convert to a vector polygon file
36 Marine_area = as.polygons(Marine_area)
37 Marine_area = st_as_sf(Marine_area)
38
39 plot(Marine_area)
40
41 # clip the Planning unit layer to the Marine area only
42 PU_Layer = st_intersection(PU_Layer, Marine_area)
43 PU_Layer = st_sf(PU_Layer)
44
45 PU_Layer$area = st_area(PU_Layer) # add area column
46
47 hist(PU_Layer$area)
48
49 PU_Layer$area = as.numeric(PU_Layer$area)
50 # discard small cells
51 PU_Layer = PU_Layer[PU_Layer$area>1.25e8]
52
53 plot(env_vars[[4]])
54 plot(PU_Layer, add=T)
55
56 # raster of fishing pressure (as swept area ratio)
57 sar_path = ""
58 SAR = rast(sar_path)
59 plot(SAR, add=T)
60
61 # extract mean SAR in each cell

```

```

62 PU_Layer$SAR = fast_extract(SAR, PU_Layer)
63 PU_Layer$SAR[is.na(PU_Layer$SAR)] = 0
64
65 # scale fishing effort to be between 0 and 1
66 normalize = function(x, na.rm=TRUE)
67 {
68   return((x-min(x))/(max(x)-min(x)))
69 }
70 PU_Layer$SAR = normalize(PU_Layer$SAR)
71 PU_Layer$SAR = PU_Layer$SAR + 1
72
73 PU_Layer$area = normalize(PU_Layer$area)
74 PU_Layer$area = PU_Layer$area + 1
75
76 PU_Layer$cost = 10^(PU_Layer$SAR * PU_Layer$area)
77 PU_Layer$cost = ceiling(PU_Layer$cost)
78 PU_Layer$cost = as.integer(PU_Layer$cost)
79
80 # path to the presence-absence rasters
81 pa_path = ""
82 PA_pred_rast = rast(list.files(pa_path, full.names=T, pattern=".tif"))
83
84 # define a systematic conservation problem
85 p1 =
86   problem(PU_Layer, PA_pred_rast, cost_column="cost") %>%
87   add_min_set_objective() %>%
88   add_boundary_penalties(penalty=0.00025) %>%
89   add_relative_targets(0.3) %>%
90   add_binary_decisions()
91
92 print(p1)
93
94 s1 = solve(p1)
95
96 par(mfrow=c(1,1))
97 plot(st_as_sf(s1[, "solution_1"]), main="Prioritization",
98      pal = cm.colors(2, alpha=1))
99 #setwd(" ")
100 st_write(s1, "s1.shp")

```