Impact of oceanographic connectivity on the future distribution of marine species

coastalNet Package

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Climate change is set to cause a major reshuffling of marine biodiversity, which will alter the structure of marine ecosystems and affect their performance and the benefits they deliver. Changes in the geographical distribution of marine species due to climate change are intricately linked to how ocean currents align with temperature gradients, underscoring the intricate nature of these distributional shifts. The interplay of climatic and other factors, including oceanic currents and species taxonomy, offers a deeper insight into the dynamics of climate-induced distributional changes in marine life.

This code investigates how a kelp species (Macrocystis pyrifera) might respond to climate change in terms of its ability to reach suitable habitats. It starts by loading maps showing the kelp's current distribution and a projection of where it could live in the future. The code then accesses an ocean connectivity database to figure out if kelp can move from its current range to those future areas. It pinpoints parts of the future range that might become isolated from the current population. Finally, the code creates maps visualizing the kelp's current and future distributions and highlights the areas that might become disconnected due to shifts in ocean currents.

By combining oceanographic connectivity information derived from coastalNet package withh empirical genetic data, this script demonstrates that intraspecific biodiversity can be highly structured by connectivity driven by oceanographic transport and barriers.

Here's a summary of the key steps and functionalities encapsulated in the code:

Environment Preparation and Package Loading

Cleans the R environment and forces garbage collection to ensure a clean workspace. Loads necessary R packages for the analysis, which include coastalNet package.

```r
# Clean environment and load packages
rm(list = ls())
gc(reset=TRUE)

library(coastalNet)

library(rnaturalearth)
library(viridis)
library(tidyterra)
library(ggplot2)
library(gridExtra)
library(sf)
sf_use_s2(FALSE)
```

Data Loading

Loading and cleaning raster data representing the current and projected future distributions of Macrocystis pyrifera. This step involves removing non-relevant cells (with a value of 0) to focus on areas of actual presence.

```
# Load raster layers with the present-day and projected (future, year 2100) distributions of the marine species Macrocystis pyrifera.
presentDayRangeRaster <- rast("https://raw.githubusercontent.com/jorgeassis/coastalNet/main/vignettes/data/presentDay.tif")
futureRangeRaster <- rast("https://raw.githubusercontent.com/jorgeassis/coastalNet/main/vignettes/data/Future.tif")

# Remove cells of no present-day distribution
presentDayRangeRaster[presentDayRangeRaster == 0] <- NA
futureRangeRaster[futureRangeRaster == 0] <- NA

# Transform raster layers information to data.frame
presentDayRange <- crds(presentDayRangeRaster, na.rm=TRUE, df=TRUE)
futureRange <- crds(futureRangeRaster, na.rm=TRUE, df=TRUE)
```

Connectivity Analysis

Initializes a local database for storing analysis results (if not already present). Establish the study's spatial extent based on the current range of Macrocystis pyrifera. It then identifies hexagon IDs representing both present-day locations and projected future sites, setting the stage for detailed connectivity analysis. Calculates oceanographic connectivity events within the defined study region, considering both present and future distributions. It assesses how well-connected present-day locations are with future potential habitats, using a 30-day period for event calculation.

```
# Load database
getDataBase(myFolder="Database", overwrite=FALSE)

# Get hexagon IDs that define the study region
combinedRange <- unique(rbind(presentDayRange,futureRange))
hexagonIDRegion <- getHexagonID(obj=combinedRange, level="extent", buffer=5, print=TRUE)
```

```
# Get hexagon IDs of the sampling sites
hexagonIDSitesFrom <- getHexagonID(obj=presentDayRange, level="site", buffer=0, print=FALSE)
hexagonIDSitesTo <- getHexagonID(obj=futureRange, level="site", buffer=0, print=FALSE)

# Get pairwise connectivity estimates between coordinate sites
pairwiseConnectivity <- getPairwiseConnectivity(connectivityEvents, hexagonIDFrom=hexagonIDSitesFrom, hexagonIDTo=hexagonIDSitesTo, connType="Forward", value="Probability", steppingStone=FALSE)
```

Pairwise Connectivity Estimates

By comparing hexagon IDs of current and future ranges, the script estimates the likelihood of connectivity between sites. This step is crucial for understanding potential migration paths and barriers under future oceanographic conditions.

```
# Find regions of probability zero
futureRangeConnected <- futureRange[which(apply(pairwiseConnectivity$connectivityMatrix,2,sum) != 0) ,]
futureRangeNotConnected <- futureRange[which(apply(pairwiseConnectivity$connectivityMatrix,2,sum) == 0),]
```

Figure 1: Hexagon IDs (in black) defining the study region

Visualization of Results

The outcomes are visualized on a map, highlighting the present-day range, future range locations connected by oceanographic pathways, and those not connected. This visualization uses different colors to distinguish between currently occupied sites, future sites with potential connectivity, and future sites likely isolated due to lack of connectivity.

```
worldMap <- ne_countries(scale = "medium", returnclass = "sf")
worldMap <- st_crop(worldMap,presentDayRangeRaster)

plot1 <- ggplot() +
  geom_sf(data = worldMap , fill="#CDCDCD", colour = "#9E9E9E" , size=0.25) +
  geom_point(data = presentDayRange, aes(x = x, y = y), colour = "#000000",size=2.5) +
  geom_point(data = presentDayRange, aes(x = x, y = y), colour = "#FFFFFF",size=1) +
  theme_minimal() + theme(axis.title.x=element_blank(),
                          axis.ticks.x=element_blank(),
                          axis.title.y=element_blank(),
                          axis.ticks.y=element_blank(), legend.position = "none") +
  coord_sf()

plot2 <- ggplot() +
  geom_sf(data = worldMap , fill="#CDCDCD", colour = "#9E9E9E" , size=0.25) +
  geom_point(data = futureRange, aes(x = x, y = y), colour = "#000000",size=2.5) +
  geom_point(data = futureRange, aes(x = x, y = y), colour = "#FFFFFF",size=1) +
  theme_minimal() + theme(axis.title.x=element_blank(),
                          axis.ticks.x=element_blank(),
                          axis.title.y=element_blank(),
                          axis.ticks.y=element_blank(), legend.position = "none") +
  coord_sf()

plot3 <- ggplot() +
  geom_sf(data = worldMap , fill="#CDCDCD", colour = "#9E9E9E" , size=0.25) +
  geom_point(data = futureRangeNotConnected, aes(x = x, y = y), colour = "#000000",size=2.5)
     +
  geom_point(data = futureRangeNotConnected, aes(x = x, y = y), colour = "red",size=1) +
  geom_point(data = futureRangeConnected, aes(x = x, y = y), colour = "#000000",size=2.5) +
  geom_point(data = futureRangeConnected, aes(x = x, y = y), colour = "#6067f3",size=1) +
```

```r
  geom_point(data = presentDayRange, aes(x = x, y = y), colour = "#000000",size=2.5) +
  geom_point(data = presentDayRange, aes(x = x, y = y), colour = "#FFFFFF",size=1) +
  theme_minimal() + theme(axis.title.x=element_blank(),
                          axis.ticks.x=element_blank(),
                          axis.title.y=element_blank(),
                          axis.ticks.y=element_blank(), legend.position = "none") +
  coord_sf()

grid.arrange(plot1, plot2, plot3, ncol = 3)
```

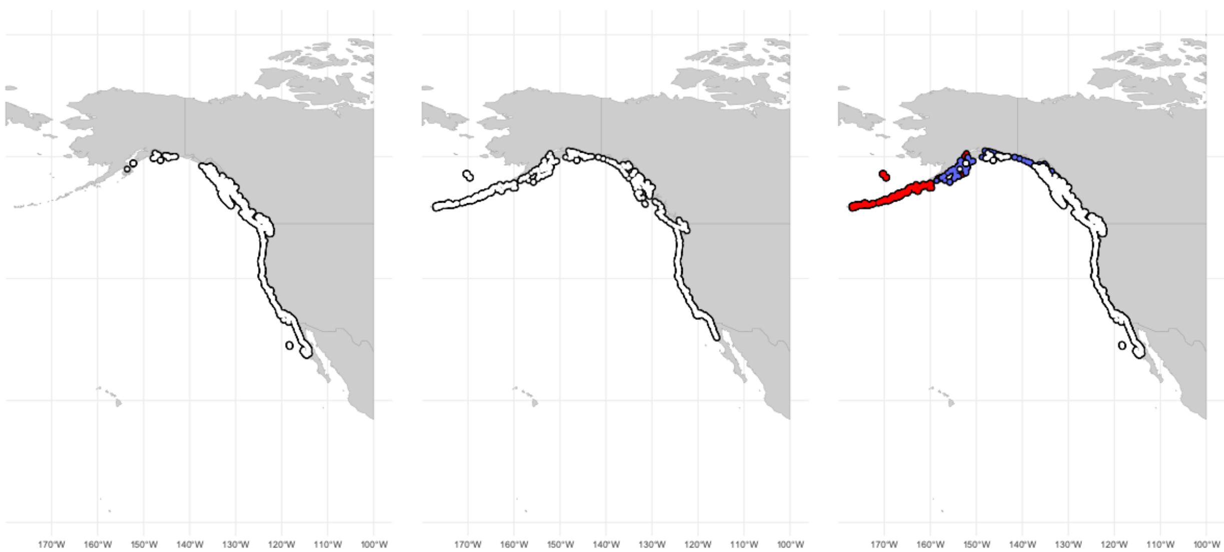

Figure 2: Future range expansions. While: Present range; Blue future range expansion; Red restricted future range expansion driven by oceanographic connectivity