Aquaculture Suitability on the West Coast

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Where Can I Farm this Species?

EDS223, Homework Assignment 4

In the growing world of aquaculture, knowing where a species will thrive is vital. The subsequent analysis aims to determine which areas of the west coast of the United States are the best suited for a variety of aquaculture species. This is done through the utilization of spatial raster and vector data as well as species-specific requirements.

Setup

```
library(stars)
library(terra)
library(sf)
library(here)
library(tmap)
library(tidyverse)
```

Data

Sea Surface Temperature

This analysis will use average annual sea surface temperature (SST) from the years 2008 to 2012. The data was originally generated from NOAA's 5km Daily Global Satellite Sea Surface Temperature Anomaly v3.1.

```r
# There are 5 raster files of annual sst, each for a different year
# Their naming convention is the same, so we can use a for loop to load them all in at once

# Create a vector of the years we have rasters for (what we will iterate over)
years <- c(2008, 2009, 2010, 2011, 2012)

# Initialize empty vectors for for loop
raster_names <- c()
file_paths <- c()

# for loop follows the following steps:
#   - iterates over the sequence in years vector
#   - for each year, creates a variable name including the year
#   - for each year, creates a file path
#   - assigns the variable name to the raster, which is read in via the created file path
for (i in seq(years)){
  raster_names[i] <- paste0("sst_", years[i])
  file_paths[i] <- paste0("data/average_annual_sst_", years[i], ".tif")

  assign(raster_names[i], rast(here(file_paths[i])))
}

# Remove unnecessary objects from environment
rm(raster_names, file_paths, i, years)
```

Bathymetry

Bathymetry, or ocean depth data, is provided in meters from the General Bathymetric Chart of the Oceans (GEBCO)

```r
# Use terra package to load in raster
depth <- rast(here("data/depth.tif"))
```

Exclusive Economic Zones

An exclusive economic zone (eez) is "an area of coastal water and seabed within a certain distance of a country's coastline, to which the country claims exclusive rights for fishing, drilling, and other economic activities" (Oxford Languages).

Our eez data is specifically for the west coast of the United States and comes from Marineregions.org.

```
# Use stars package to load in shape data frame
# quiet = TRUE argument removes output/message
eez <- st_read(here("data/wc_regions_clean.shp"), quiet = TRUE)
```

Preparing Data

In order to proper perform analyses using all of data sets, we first need to ensure that they all
have matching CRSs.

First, we are going to stack our five SST rasters into one. As they all come from the same
source and only differ in year we can reasonably assume that they all have the same CRS, but
stacking would also throw an error if that was not the case.

```
# Create raster stack
sst <- c(sst_2008, sst_2009, sst_2010, sst_2011, sst_2012)
```

We can now compare our 3 data frames to see if they all have the same CRSs.

```
# sst and depth rasters
if (crs(sst)==crs(depth)){
  print("CRSs of sst and depth match!")
}else{
  print("CRSs of sst and depth do not match, transforming to CRS of sst")
  depth <- project(depth, crs(sst))
}
```

```
[1] "CRSs of sst and depth do not match, transforming to CRS of sst"

|---------|---------|---------|---------|
=========================================
```

```
# sst raster and eez object
if (crs(sst)==crs(eez)){
  print("CRSs of sst and eez match!")
}else{
  print("CRSs of sst and eez do not match, transforming to CRS of sst")
  eez <- st_transform(eez, crs(sst))
}
```

```
[1] "CRSs of sst and eez do not match, transforming to CRS of sst"
```

```
# We transfromed depth and eez to match the CRS of sst -- did it work?
if (crs(depth)==crs(eez)){
  print("CRSs of sst and eez match (transformations worked!)")
}else{
  print("Something went wrong...")
}
```

```
[1] "CRSs of sst and eez match (transformations worked!)"
```

Processing Data

Find mean SST over the years 2008-2012 (as our analysis will use the average temperature across 5 years).

```
# mean() operation on raster of multiple layers creates object with one raster layer
mean_sst <- mean(sst)
```

From preliminary exploration, we know that SST is stored in Kelvin instead of Celsius. In order to make our results more comprehensible, we will convert our data to Celsius.

```
# Subtract 273.15 (conversion from K to C) from all pixels
mean_sst_c <- mean_sst - 273.15
```

We want to combine our sst and depth data, but in order to do so, we have to ensure they have the same extent, resolution, and position.

```
# Is the extent the same?
ext(sst) == ext(depth)
```

```
[1] FALSE
```

```
# Is the resolution the same?
res(sst) == res(depth)
```

```
[1] FALSE FALSE
```

Our two datasets do not match.

To ensure that depth and sst have the same extent, we crop depth to match sst.

```
# Crop depth raster to limits of sst raster
depth_cropped <- crop(depth, y = mean_sst_c)
```

To fix the issue of mismatched resolutions, we will resample the depth data to match the resolution of `sst`.

Resampling is the method by which we can compute values for new pixel locations in `depth` based on custom resolutions and origins. We will use the "nearest neighbor approach", a technique in which the value of each cell in the output raster (in this case, `depth_cropped`) is calculated using the value of the nearest cell in the input raster (`mean_sst`) (ESRI GIS Dictionary). This fills in the new cells that will be created in order for `depth` to match the resolution of `sst`.

```
# Resample depth data to match specifications of sst data, specifying nearest neighbor metho
depth_cropped_resampled <- resample(depth_cropped, y = mean_sst_c, method = "near")
```

A way to know if we have succeeded in matching the extent, resolution, and position of our two rasters is by seeing if they will stack or not. If they do not completely match, an error will be thrown and stacking will fail.

```
depth_sst <- c(depth_cropped_resampled, mean_sst_c)
```

We successfully stacked our two rasters!

Finding Areas with Suitable Growing Conditions: Oysters

Image Source: Pangea Shellfish Company

Research has shown that oysters need the following conditions for optimal growth:

- sea surface temperature: 11-30°C

- depth: 0-70 meters below sea level (or -70 in our data)

These specifications come from the EDS223 assignment description, but can also be retrieved from resources such as SeaLifeBase.

In order to find the areas with suitable growing conditions for oysters, we will assign a value of 1 to each pixel that is within the suitable range and 0 otherwise, for both of our separate raster layers.

```r
# Change layer names to be more indicative ("mean" --> "sst_mean")
names(depth_sst) <- c("depth", "sst_mean_c")

# Create copy of data frame to serve as mask
depth_sst_mask <- depth_sst
```

```r
# Create suitability matrix based on min and max sst
sst_suitability <- matrix(c(-Inf, 11, 0,   # Will return 0 for values (-Inf, 11)
                             11, 30, 1,      # Will return 1 for values (11, 30)
                             30, Inf, 0),    # Will return 0 for values (30, Inf)
                           nrow = 3, byrow = TRUE)

# Classify sst layers using matrix
depth_sst_mask[["sst_mean_c"]] <- classify(depth_sst_mask[["sst_mean_c"]], rcl = sst_suitabil

# Create suitability matrix based on min and max sst
depth_suitability <- matrix(c(-Inf, -70, 0,
                               -70, 0, 1,
                               0, Inf, 0),
                             nrow = 3, byrow = TRUE)

# Classify depth layers using matrix
depth_sst_mask[["depth"]] <- classify(depth_sst_mask[["depth"]], rcl = depth_suitability)
```

To create one suitability layer that contains suitability based on *both* variables, we will multiply the two layers, obtaining the following results:

- if a cell = 1, it is suitable based on both conditions
- if a cell = 0, it is not suitable (either based on one of or both conditions)

This can be true because anything multiplied by 0 (not suitable in this case), will equal 0. If at least one of our layers contains 0, our new suitability layer will also contain the value 0. Cells that are suitable for both sst and depth will be the only ones that contain 1 as their value.

```r
# Multiple two layers and save as a new raster
oyster_suitability <- depth_sst_mask[["depth"]] * depth_sst_mask[["sst_mean_c"]]

# Rename raster layer to be more indicative ("depth" --> "suitable")
names(oyster_suitability) <- c("suitable")
```

Determining the Most Suitable EEZ

We want to determine the total suitable area within each EEZ in order to rank zones by priority.

This requires three distinct steps:

1. Find the number of cells within each zone that are deemed suitable (based on previous analysis).

2. Find the physical area that each cell represents (in km^2).

3. Multiply number of cells by area that cells represent to get actual suitable area, by zone.

```
# Create a raster of species suitability only within the EEZ boundaries
suitable_westcoast <- mask(oyster_suitability, eez)

# Rasterize EEZ (will allow for zonal operations)
eez_rast <- rasterize(eez, suitable_westcoast,
                      field = "rgn")      # Set region as the value we want populating the e
```

We can find the number of suitable *cells* in each EEZ region by using the `terra::zonal` function. It summarizes values of one SpatRaster based on the zones provided by another. In our case, we will be summing the values of our suitable cells grouped by eez.

Summation works to provide the number of suitable cells in this case because we had populated suitable with "1"s and unsuitable with "0"s.

```
# Find the number of suitable cells per EEZ region
suitable_per_region <- zonal(suitable_westcoast, eez_rast, fun = "sum", na.rm = TRUE)
```

EEZ Region	# of Suitable Cells
Central California	238
Northern California	11
Oregon	71
Southern California	211
Washington	162

Find area of each cell in square km.

```
# cellSize() returns a SpatRaster object of information, we want to extract just cell area
cell_area <- cellSize(suitable_westcoast, unit="km")[1]
```

Multiply cell area by number of cells.

```
# Multiplying by each region by adding and specifying columns to data frame
suitable_per_region <- suitable_per_region %>%
  mutate(cell_area = cell_area,
         area_suitable = suitable * cell_area) %>%
  relocate(cell_area, .after = suitable)
```

In order to produce a map of West Coast EEZs colored by amount of suitable species area in each region, we need to join our EEZ geometries to our `suitable_per_region` data frame.

```
# Join eez data frame (with goemetries) to data frame with suitable area by region
eez_suitability_geom <- left_join(eez, suitable_per_region, by = "rgn")
```

The `eez_suitability_geom` now contains the five West Coast region polygons with their corresponding suitable areas for oysters.

The final step of our oyster analysis is to create a map of EEZ regions colored by amount of suitable area. For this, we use our original depth raster to provide a background image (and general outlines of the California coast), overlayed with the 5 West Coast EEZs, colored by amount of suitable area.

```
# Turn off autoscale -- messes with font size
tmap_options(component.autoscale = FALSE)

# Create map using tmap
tm_shape(depth) +                                     # Plot depth raster as first layer
  tm_raster(col.scale  = tm_scale(values = c("#1d3891", "#84d18d")),
            col.legend = tm_legend(show = FALSE)) +   # Hide depth legend because not of in
tm_shape(eez_suitability_geom) +                      # Plot EEZ polygons
  tm_polygons(fill = "area_suitable",                 # Fill by suitable area
              fill.scale = tm_scale(values = "brewer.yl_or_rd"),
              fill.legend = tm_legend(title = "Suitable Area (km^2)"),
              fill_alpha = 0.8,
              lwd = 1.5) +
  tm_text(text = "rgn",                               # Add EEZ zone labels
          size = 0.3,
          xmod = -2.35,
          bgcol = "white",
          bgcol_alpha = 0.5,
          fontface = "bold")+
tm_grid(alpha = 0.5) +
```

```
tm_title("Suitability of West Coast EEZs for Oyster Aquaculture",
         size = 1)
```

Suitability of West Coast EEZs for Oyster Aquaculture
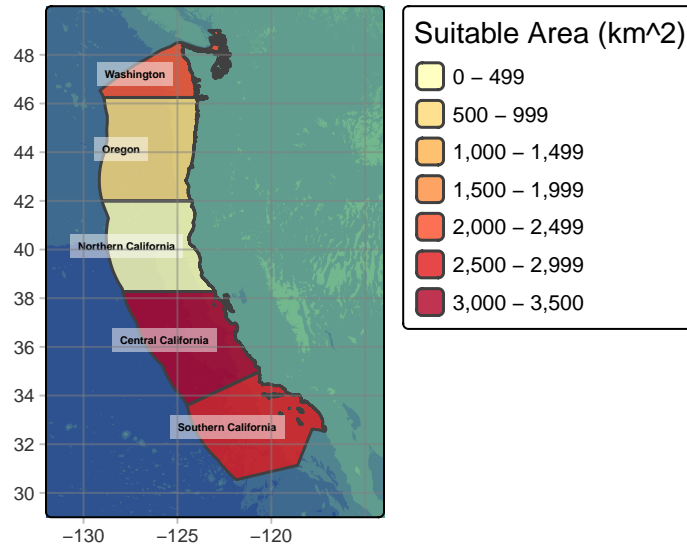
From this visualization, we can see that – based on suitable depth and sst – Central and Southern California are the best suited for oyster aquaculture compared to the other EEZs of the US West Coast.

Finding Most Suitable EEZs for Any Species

In the code above, we developed a method of extracting the most suitable regions for marine aquaculture based on just a few parameters: temperature range and depth range. By making our workflow generalizable, we can create a function that takes a handle of arguments and produces a map of suitable West Coast EEZs for any marine species.

Generalizing Workflow

Our function will assume that the datasets/rasters `sst` (single layer), `depth`, and `eez` are pre-loaded and contain the correct attributes.

The other thing to note is that when inputting minimum and maximum depth, we will input the absolute value of depth (so, no negatives), with the larger number being maximum depth. For example, a depth of 70 meters, or 70 meters below sea level, should be entered as 70.

```r
# Initialize function
west_coast_suitability_map <- function(species, min_sst, max_sst, min_depth, max_depth){

# Creating depth and sst mask based on min and max values
depth_sst_mask <- depth_sst

# sst matrix and classification, using function arguments
sst_suitability <- matrix(c(-Inf, min_sst, 0,
                            min_sst, max_sst, 1,
                            max_sst, Inf, 0),
                            nrow = 3, byrow = TRUE)

depth_sst_mask[["sst_mean_c"]] <- classify(depth_sst_mask[["sst_mean_c"]], rcl = sst_suitabil

# depth matrix and classification
depth_suitability <- matrix(c(-Inf, -max_depth, 0,
                              -max_depth, min_depth, 1,
                              min_depth, Inf, 0),
                              nrow = 3, byrow = TRUE)

depth_sst_mask[["depth"]] <- classify(depth_sst_mask[["depth"]], rcl = depth_suitability)

# Creating suitability raster
suitability_raster <- depth_sst_mask[["depth"]] * depth_sst_mask[["sst_mean_c"]]

# Renaming raster layer value to be more accurate
names(suitability_raster) <- c("suitable")

# Create a raster of species suitability only within the EEZ boundaries
suitable_westcoast <- mask(suitability_raster, eez)

# Rasterize EEZ (will allow for zonal operations)
eez_rast <- rasterize(eez, suitable_westcoast,
                      field = "rgn")      # Set region as the value we want populating the ee

# Find the number of suitable cells per EEZ region
suitable_per_region <- zonal(suitable_westcoast, eez_rast, fun = "sum", na.rm = TRUE)

# cellSize() returns a SpatRaster object of information, we want to extract just area
cell_area <- cellSize(suitable_westcoast, unit="km")[1]

# Multiplying by each region by adding and specifying columns to data frame
```

```r
suitable_per_region <- suitable_per_region %>%
  mutate(cell_area = cell_area,
         area_suitable = suitable * cell_area) %>%
  relocate(cell_area, .after = suitable)

# Join eez data frame (with goemetries) to data frame with suitable area by region
eez_suitability_geom <- left_join(eez, suitable_per_region, by = "rgn")

# Turn off autoscale -- messes with font size
tmap_options(component.autoscale = FALSE)

# Create map using tmap
tm_shape(depth) +                                      # Plot depth raster as first layer
  tm_raster(col.scale  = tm_scale(values = c("#1d3891", "#84d18d")),
            col.legend = tm_legend(show = FALSE)) +    # Hide depth legend because not of int
tm_shape(eez_suitability_geom) +                       # Plot EEZ polygons
  tm_polygons(fill = "area_suitable",                  # Fill by suitable area
              fill.scale = tm_scale(values = "brewer.yl_or_rd"),
              fill.legend = tm_legend(title = "Suitable Area (km^2)"),
              fill_alpha = 0.8,
              lwd = 1.5) +
  tm_text(text = "rgn",                                # Add EEZ zone labels
          size = 0.3,
          xmod = -2.35,
          bgcol = "white",
          bgcol_alpha = 0.5,
          fontface = "bold")+
tm_grid(alpha = 0.5) +
tm_title(paste("Suitability of West Coast EEZs for", species, "Aquaculture"),
         size = 1)
}
```

Running Suitable Region Function on Species of Choice: Bull Kelp

Image Source: aquaculturenorthamerica.com

Bull kelp farming is a niche sector of seaweed aquaculture, especially small compared to the large seaweed operations taking place in Asia. Currently, there are only a few active, albeit experimental, bull kelp farms in Alaska and BC.

This lack of development is partially due to the fact that bull kelp is not necessarily a commercial commodity in the same way other species of seaweed, such as sugar kelp (Sacharrina latissima) or ribbon kelp (Alaria marginata), are. Despite its challenges, bull kelp is essential for ocean health and biodiversity, so farming more of it could help with restoration efforts, as well as help fill knowledge gaps in its cultivation.
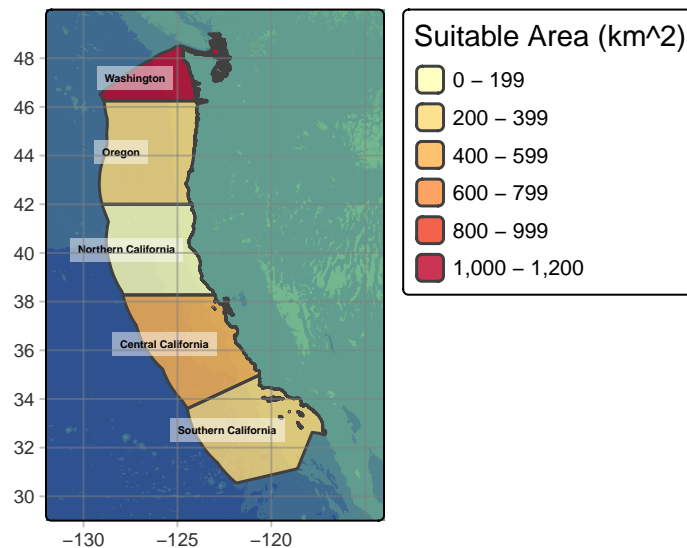
Bull kelp's suitability conditions are as follows:

- depth: 17 to 40 meters

- sst: 10 to 16 degrees Celsius

```
# Use function to plot regions with highest suitability
west_coast_suitability_map(species = "Bull Kelp" ,
                           min_sst = 10,
                           max_sst = 16,
                           min_depth = 40,
                           max_depth = 17)
```

Suitability of West Coast EEZs for Bull Kelp Aquaculture

From this visualization, we can see that – based on suitable depth and sst – the Washington region is by far the best suited for bull kelp aquaculture compared to the other EEZs of the US West Coast. This agrees with our previous research: if successful bull kelp farms are mostly in Alaska and Canada, it would make sense that the northernmost region would be the most suitable.

Sources:

CA.gov Marine Species Portal

bullkelp.info

Weigel, B. L., Small, S. L., Berry, H. D., & Dethier, M. N. (2023). Effects of temperature and nutrients on microscopic stages of the bull kelp (Nereocystis luetkeana, Phaeophyceae). Journal of phycology, 59(5), 893–907. https://doi.org/10.1111/jpy.13366