

Investigating Exclusive Economic Zones (EEZ) for Marine Aquaculture

EDS-223 Assignment 4

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Assessing Potential Species for Marine Aquaculture in West Coast EEZs

README

marine-aquaculture

This repository's purpose is for assessing marine aquaculture in the West Coast of the United States for target species.

Assessing Potential Species for Marine Aquaculture in West Coast EEZs

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Contents

This repository contains the following file structure:

```
└── data
    └── images
        └── marine-aquaculture.qmd
        └── marine-aquaculture.Rproj
    └── README.md
```

How to access the data

Sea surface temperature data can be accessed through NOAA's Daily [Global 5km Satellite Sea Surface Temperature Anomaly](#) from 2008 to 2012. Bathymetry data can be accessed through the [General Bathymetric Chart of the Oceans \(GEBCO\)](#). Marine region designations for marine aquaculture are from [Marineregions.org](#).

Citations

SeaLifeBase. (n.d.). Summary for Species #47622 [Web page]. Retrieved November 29, 2025, from <https://www.sealifebase.ca/summary/47622>

Zagata, C., Young, C., Sountis, J., & Kuehl, M. (2008). *Mytilus edulis* [Web page]. Retrieved November 29, 2025, from https://animaldiversity.org/accounts/Mytilus_edulis/

GEBCO Compilation Group. (2022). GEBCO_2022 Grid [Data set]. <https://doi.org/10.5285/e0f0bb80-ab44-2739-e053-6c86abc0289c>

NOAA Coral Reef Watch. (n.d.). 5-km Sea Surface Temperature Anomaly (SSTA) product [Data set]. Retrieved November 29, 2025, from https://coralreefwatch.noaa.gov/product/5km/index_5km_ssta.php

Flanders Marine Institute. (2025). Maritime Boundaries Geodatabase: Exclusive Economic Zones (EEZ) [Data set]. Retrieved November 29, 2025, from <https://www.marineregions.org/eez.php>

"*Mytilus edulis*." MarLIN – The Marine Life Information Network, n.d., https://www.marlin.ac.uk/assets/images/marlin/species/web/o_mytedu.jpg. Accessed 29 Nov. 2025.

Acknowledgements

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Objectives:

Marine aquaculture has become popular for its use as a more suitable protein option than land-based meat production. In this project, I investigated where to prioritize marine aquaculture in the West Coast of the United States. I focused on two focal species: **oysters** and **blue mussels**.

My workflow outline is as follows:

1. Process sea surface temperature data
2. Process depth data
3. Reclassify sea surface temperature and depth data
4. Find suitable locations that satisfy temperature and depth specifications
5. Map suitable locations within West Coast EEZs
6. Generalizable function

Environment set-up

Load relevant libraries.

```
library(sf) # For vector data
library(stars) # For raster data
library(terra) # raster handling
library(tmap) # For static and interactive maps
library(here) # For importing data
library(tidyverse) # For data cleaning
library(dplyr) # For filtering data
library(paletteer) # For pretty colors
library(testthat) # For efficient workflows
library(kableExtra) # For pretty tables
library(patchwork) # For plotting
```

Data Import and Preparation

The data for this study includes a shapefile for the West Coast EEZ, bathymetry (depth) raster, and sea surface temperature raster.

Species data

The two focal species for this study are oysters and blue mussels (*Mytilus edulis*). Both of these bivalve species are found in the Pacific ocean and have the ability to serve as a great protein source for marine aquaculture.



Figure 2: Pacific Oyster



Figure 3: Blue Mussel

Table 1: Table 1. Species information

Species	Temperature Range	Depth Range
Oysters	11-30°C	0-70 m

Sea Surface Temperature Data

In this study, I will use average annual sea surface temperature (SST) from 2008 to 2012. The data is from NOAA's Daily Global Satellite Sea Surface Temperature anomaly. It contains the following data:

```
#.....Import Sea Surface Temperature Data.....  
  
# Read in SST rasters in a raster stack  
sst_fp <- list.files(here("data"), pattern = "average_annual_sst_", full.names = TRUE)  
# Stack  
sst <- rast(sst_fp) %>%  
  project("EPSG:4326") # project CRS  
  
# Clear working environment  
rm(list = 'sst_fp')
```

In this section, I will process the sea surface temperature (SST) data in order to combine it with the depth data. The SST data needs to be averaged and converted into celcius.

```
#.....Data Wrangling.....  
  
# Find the average sea surface temperature from 2008-2012  
avg_sst <- mean(sst)  
  
# Convert average SST from Kelvin to Celsius  
avg_sst_c <- avg_sst - 273.15  
  
# Clear working environment  
rm(list = 'avg_sst')
```

Depth Data

In this study, I will use bathymetry data from the General Bathymetric Chart of the Oceans.

```
#.....Import Depth Data.....  
depth <- rast(here("data/depth.tif")) %>%  
  project("EPSG:4326") # project CRS
```

In this section, I matched the resolution (number and size of pixels) of depth to match avg_sst_c.

```
#.....Crop depth raster.....  
  
# Create extent of 'avg_sst_c'  
ext_sst <- ext(avg_sst_c)  
  
# Crop depth raster to match the extent of the SST raster  
depth_cropped <- crop(depth, ext_sst)  
  
# Ensure data was cropped  
if(ncell(depth) == ncell(depth_cropped)) {  
  warning("data did not crop!")  
} else {  
  message("data cropped!")  
}  
  
#.....Resample.....  
  
# Resample to match resolutions  
depth <- resample(depth_cropped, avg_sst_c, method = "bilinear") # method bilinear  
  
# Check that the resolutions match  
if (all(res(depth) == res(avg_sst_c))) {  
  message("Resolutions match!")  
} else {  
  warning("Resolutions do not match")  
}  
  
# Remove 'depth_cropped' from environment  
rm(list = 'depth_cropped')  
  
#.....CRS check.....  
  
# Check that CRSSs match  
if (crs(depth) != crs(avg_sst_c)) {  
  warning("Coordinate refrence systems DO NOT match!")  
} else {  
  message("Coordinate refrence systems match!")  
}
```

Find suitable locations

In this section I will find suitable locations (area in km) that satisfy the specific sea surface temperature and depth range for oysters.

Reclassification Matrix

In order to find suitable locations for the oyster, I need to reclassify `avg_sst_c` and `depth` data into locations that are suitable for oysters. This process returns the cells in the raster that satisfy the criteria.

- 1: suitable locations
- 0: unsuitable locations

```
#.....Reclassification matrix: sea surface temperature.....  
  
sst_matrix <- matrix(c(-Inf, 11, 0, # values -Inf to 11 = 0  
                      11, 30, 1, # values 11 to 30 = 1  
                      30, Inf, 0), # values 30 to Inf = 0  
                      ncol = 3, byrow = TRUE)  
  
# Apply the matrix to reclassify the raster, making all cells 0 or 1  
sst_rcl <- terra::classify(avg_sst_c, rcl = sst_matrix)  
  
# Assign Nan values as NA  
values(sst_rcl)[is.nan(values(sst_rcl))] <- NA  
  
# Check output of sst_rcl  
kable(unique(values(sst_rcl)))
```

mean
0
NA
1

```
# Check sst values after reclassification  
sum(values(sst_rcl), na.rm = TRUE)
```

```
[1] 105016
```

```

# Ensure SST was reclassified
if (identical(values(avg_sst_c), values(sst_rcl))) {
  warning("SST not reclassified!")
} else {
  message("SST reclassified!")
}

#.....Reclassification matrix: Depth..... 

depth_matrix <- matrix(c(-Inf, -70, 0, # values -Inf to 70 = 0
                         -70, 0, 1, # values 70 to 0 = 1
                         0, Inf, 0), # values
                         ncol = 3, byrow = TRUE)

# Apply the matrix to reclassify the raster, making all cells 0 or 1
depth_rcl <- terra::classify(depth, rcl = depth_matrix)

# Check output of dept_rcl
kable(unique(values(depth_rcl)))

```

depth
0
1

```

# Check out values of depth_rcl
sum(values(depth_rcl), na.rm = TRUE)

```

[1] 2480

```

# Ensure depth was reclassified
if (identical(values(depth), values(depth_rcl))) {
  warning("Depth not reclassified!")
} else {
  message("Depth reclassified!")
}

```

I now have suitable locations for the specific sea surface temperature and depth specifications for oysters.

```
#.....Find suitable locations.....  
  
# Multiply reclassification matrices to find suitable locations  
suitable_locations <- sst_rcl * depth_rcl  
  
# Convert all zeros to NA values  
suitable_locations[suitable_locations == 0] <- NA  
  
# View the cells left  
sum(values(suitable_locations), na.rm = TRUE)
```

[1] 856

```
# Find the area of suitable locations for oysters  
suitable_area <- expanse(suitable_locations, unit = "km")  
  
print(paste("The total suitable area for oysters is", round(suitable_area$area, 2), "km"))
```

[1] "The total suitable area for oysters is 14216.68 km"

Determine the most suitable EEZ

Exclusive Economic Zones are regions of the ocean that are open for a country to explore. The U.S. West coast has five regions. In this section, I will determine the total suitable area within each EEZ for oysters. This data is from [Marineregions.org](#).

```
#.....Import Data and Check CRS.....  
  
# Import data  
eez <- st_read(here("data", "wc_regions_clean.shp"))  
  
# Check if CRS match  
if (st_crs(eez) == st_crs(4326)) {  
  message("CRS match with depth and average sea surface temperature")  
} else {  
  warning("CRS does not match! Transforming required.")  
}
```

Find suitable areas within West Coast EEZs

In this section I will find the suitable areas within West Coast EEZs

```
#.....Apply mask ......

# Mask suitable locations to eez habitat
eez_cells <- mask(suitable_locations, eez)

if (ncell(suitable_locations) == ncell(eez_cells)) {
  message("Mask worked!")
} else {
  warning("Mask did not work")
}

#.....Calculate total area ......

# Calculate cell size area of each raster cell
eez_cells_area <- cellSize(eez_cells, unit = "km")

#.....Find total area......

# Extract raster values per polygon, sum within each polygon
# Result is a data frame
area_by_eez <- terra::extract(eez_cells_area, eez, fun = sum, na.rm = TRUE)

kable(area_by_eez)
```

ID	area
1	179848.50
2	163746.32
3	202760.09
4	206587.81
5	67827.38

```
#.....Join data.....



# Add polygon IDs to eez
eez <- eez %>%
  rename(ID = rgn_id)
```

```
# Join the raster summaries back to eez polygons df
eez_area <- eez %>%
  left_join(area_by_eez, by = "ID")
```

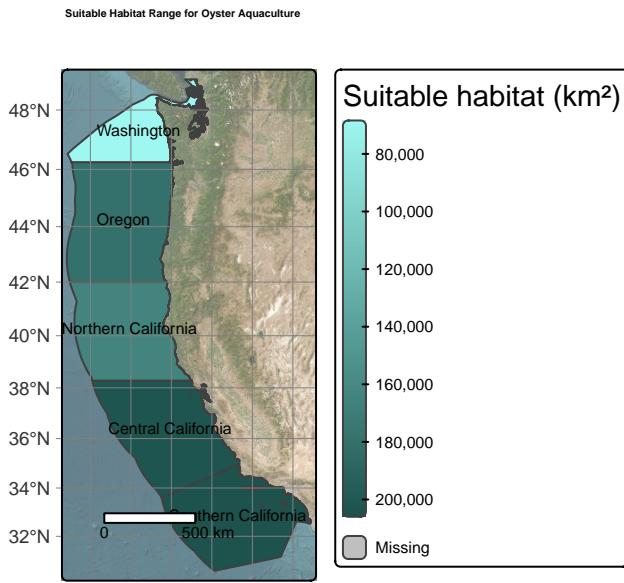
Table 5: Table 2. Suitable Area for Oysters

Regions	Suitable Habitat (km)
Oregon	179848.50
Northern California	163746.32
Central California	202760.09
Southern California	206587.81
Washington	67827.38

Map: Oyster Suitable Area

```
#| label: oyster map
oyster_map <- tm_tiles("Esri.WorldImagery", alpha = 0.6) + # basemap with tm_tiles()
tm_shape(eez_area) +
  tm_polygons(fill = "area" , # fill polygons based on suitable area
              style = "cont", # continuous value scale
              palette = c("#9ef7f0", "#1d524d"), # palette of colors
              title = "Suitable habitat (km2)", size = 0.8) + # legend title
  tm_layout(legend.outside = TRUE,
            legend.text.size = 0.5) + # legend position and size
  tm_title("Suitable Habitat Range for Oyster Aquaculture", fontface = "bold", size = 1) +
  tm_graticules(lwd = 0.2) + # gridlines
  tm_scalebar(position = c("left", "bottom"), text.size = 0.5) + #scalebar
  tm_text("rgn", # overlay text for region
         size = 0.5,
         xmod = 0.2,
         ymod = 0.2)

# View map
oyster_map
```



Generalizable function

The purpose of this section is to define a function that can be used with any marine species of interest for marine aquaculture.

```
# Define function name and arguments
suitability_fun <- function(sst_min, sst_max, depth_min, depth_max, species) {

  # Ensure avg_sst_c and depth are new
  avg_sst_c <- rast(avg_sst_c)
  depth <- rast(depth)

  # 1. Reclassification matrices

  # Define SST reclassification matrix
  sst_matrix <- matrix(
    c(
      -Inf, sst_min, 0,   # below min sst = 0/unsuitable
      sst_min, sst_max, 1, # range of sst = 1/suitable
      sst_max, Inf, 0     # above max sst = 0/unsuitable
    ),
    ncol = 3, byrow = TRUE
  )
}
```

```

)

# Define Depth reclassification matrix
depth_matrix <- matrix(
  c(-Inf, depth_min, 0, # below min depth = 0/unsuitable
    depth_min, depth_max, 1, # range of depth = 1/suitable
    depth_max, Inf, 0        # range of depth = 1/suitable
  ),
  ncol = 3, byrow = TRUE
)
# 2. Reclassify SST and Depth data

# Reclassify SST
sst_rcl <- terra::classify(avg_sst_c, rcl = sst_matrix)
# Fill NAN values with NAs
values(sst_rcl)[is.nan(values(sst_rcl))] <- NA

# Reclassify depth
depth_rcl <- terra::classify(depth, rcl = depth_matrix)

# 3. Find suitable locations
# Find suitable locations
suitable_locations <- sst_rcl * depth_rcl

# Convert zeros to NAs
suitable_locations[suitable_locations == 0] <- NA

# Apply mask to keep only suitable raster cells in eez
eez_cells <- mask(suitable_locations, eez)

# Find cell area
eez_cells_area <- cellSize(eez_cells, unit = "km")

# 4. Summarize and create df

# Summarize area within eez
area_by_eez <- terra::extract(eez_cells_area, eez, fun = sum, na.rm = TRUE)

# Add ID
#eez <- eez %>% rename(ID = rgn_id)

# Join area back into polygons

```

```

eez_area <- eez %>%
  left_join(area_by_eez, by = "ID")

# 5. Make table of suitable area per eez

rgns <- c("Oregon", "Northern California", "Central California",
         "Southern California", "Washington")

rgn_table <- data.frame(
  rgn = rgns,
  area_km2 = eez_area$area[1:5]
)

rgn_table %>%
  kable(col.names = c("Region", "Suitable Habitat (km2)"),
        caption = paste("Table 2. Suitable Area for", species)) %>%
  kable_styling(bootstrap_options = "striped", full_width = FALSE)

# Create map

species_map <- tm_tiles("Esri.WorldImagery", alpha = 0.7) + # basemap with tm_tiles()
tm_shape(eez_area) +
  tm_polygons(fill = "area" , # fill polygons based on suitable area
              style = "cont", # continuous value scale
              palette = c("#9ef7f0", "#1d524d"), # palette of colors
              title = "Suitable habitat (km2)", size = 0.8) + # legend title
  tm_layout(legend.outside = TRUE,
            legend.text.size = 0.5) + # legend position and size
  tm_title(
    paste0("Suitable Habitat Range for ", species, " Aquaculture"),
    fontface = "bold",
    size = 1
  )+ # title
  tm_graticules(lwd = 0.2) + # gridlines
  tm_scalebar(position = c("left", "bottom"), text.size = 0.5) + #scalebar
  tm_text("rgn", # overlay text for region
          size = 0.5,
          xmod = 0.3,
          ymod = 0.2)

# return species map and table of eez suitable area

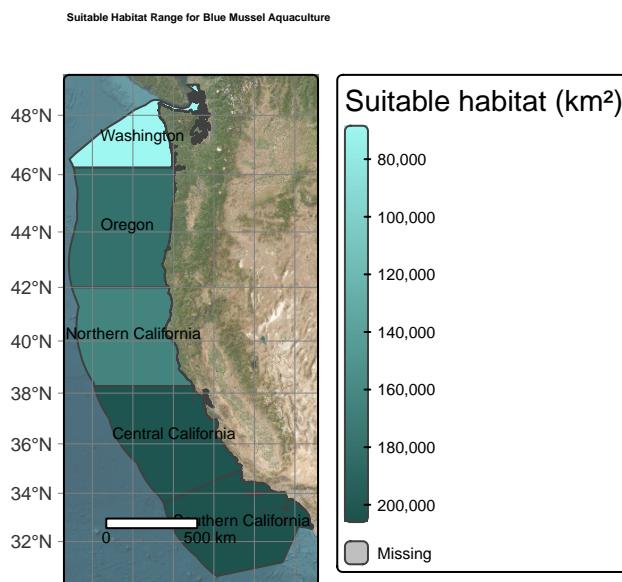
```

```
    return(species_map)
}
```

Apply function: Blue Mussels

In this section I will apply the `suitability_fun` function to my second focal species **blue mussels**. I will then *reproduce* my `oyster_map` with my function.

```
suitability_fun(
  sst_min = 5, # define min stt value
  sst_max = 20, # define max sst value
  depth_min = 0, # define min depth value
  depth_max = 60, # define max depth value
  species = "Blue Mussel" # define species name
)
```



```
suitability_fun(
  sst_min = 11, # define min stt value
  sst_max = 30, # define max sst value
  depth_min = 0, # define min depth value
```

```
depth_max = 70, # define max depth value
species = "Oyster" # define species name
)
```

