Readme file for the tourism model

Important files

scripts/tourism-mpa.R - The main code for the dive tourism model

scripts/func\_evaluateMPA\_explicit.R – function for evaluating the biomass change from MPAs

prep\_stock\_geogrange.R – converts stock distribution to Mollweide

prep\_distance\_matrix.R – converts Juan’s distance matrices to the format we needed

prep\_biodiversity\_inputs.R – prepares the inputs for the biodiversity model

pld-params.R – this code is for preparing the PLD data

RUN\_MODEL\_example.R – sample code for running the biodiversity model

merged\_dist\_matrix.rds – distance matrix. Unit of values in meters.

# Path to the Pristine Seas tourism directory on the emLab Google Drive

this\_project\_dir <- "/Volumes/GoogleDrive/Shared drives/emlab/projects/current-projects/ps-tourism"

# Source functions

sapply(list.files(

pattern = "[.]R$",

path = here::here("scripts", "functions"),

full.names = TRUE

),

source)

# Load data files necessary for biodiversity model

load(file = file.path(this\_project\_dir, "data", "02-processed-data", "bio\_model\_input.RData"))

# set Z for biodiversity

z\_bio <- 0.25

# Vector of protected cell\_ids (starting) - this is just an example, this bit would likely be looped eventually such that pixels are iteratively added to the "is mpa" vector

is\_mpa\_vect <- ocean\_df$f\_highly\_mpa >= 0.5 # select pixels that are at least 50% highly protected

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### Section 4 - Run model ----------

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# Calculate biodiversity benefit from today's protected cells

calculate\_relative\_bio\_benefit(is\_mpa\_vect = is\_mpa\_vect,

v\_out\_matrix = v\_out\_matrix,

v\_in\_matrix = v\_in\_matrix,

weights = bio\_weights,

z\_bio = z\_bio,

bau\_benefit = bau\_benefit,

total\_benefit\_diff = total\_benefit\_diff)

# Just for fun (and to check), check maximum possible biodiversity benefit if the whole ocean was protected)

is\_mpa\_vect\_all <- is\_mpa\_vect

is\_mpa\_vect\_all[is\_mpa\_vect\_all==F] = T

calculate\_relative\_bio\_benefit(is\_mpa\_vect = is\_mpa\_vect\_all,

v\_out\_matrix = v\_out\_matrix,

v\_in\_matrix = v\_in\_matrix,

weights = bio\_weights,

z\_bio = z\_bio,

bau\_benefit = bau\_benefit,

total\_benefit\_diff = total\_benefit\_diff)