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.

tourism-mpa-figure-plot.R – raw plot of results used in the paper. This uses the saved summarized data, load(here("scripts","03-figures","Figure\_data.RData"))

**Data**

Figure\_data.RData – Summarized results used for plotting

here("data","transformed\_stockdistrib.rds") – stock distribution

here("data","MegaData\_Sala.rds") – Fisheries data from Sala et al. 2021

here("data","homerange\_pld\_predictions","pld\_rf\_predictions\_final.csv") – PLD data used in the model

here("data","homerange\_pld\_predictions","homerange\_rf\_predictions\_10112022.csv")

* Home-range data used in our model

here("data","dive","tourism\_model\_input.RData") – tourism input data. This includes dive price, dive numbers etc. "ocean\_df\_with\_eezs" "dives\_input" "suitability\_input" "price\_constant\_input" "price\_country\_region\_input" "price\_interpolated\_input"

readRDS(file = here("data","collate\_biomass\_equi\_merged.rds")) – equi biomass

collate\_biomass\_equi\_merged\_dive <- readRDS(file = here("data","collate\_biomass\_equi\_merged\_dive.rds")) – equi biomass with dive sites all protected

readRDS(file = here("data","per\_pixel\_delta\_biodiv\_benefit.rds"))

#save(biomass\_data, land\_shp\_moll, explore\_user\_fee\_merged, effect\_name, effect\_biomass, effect\_biodiversity, average\_user\_fee,

# dives\_input, divepixels\_unprotected, cell\_id\_with\_country\_kat\_withregion, change\_consumer\_suplus, cell\_developmentstatus, file = here("scripts","figures","Figure\_data.RData"))

**Functions**

source(here("scripts", "functions","calculate\_relative\_bio\_benefit.R"))

source(here("scripts", "functions","func\_evaluateMPA\_explicit.R"))

#-- load data files necessary for biodiversity model

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

# set Z for biodiversity

z\_bio <- 0.25

source(here("scripts","functions","func\_evaluate\_divefee.R"))

xxxxxx

# 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)