

# Mantel Tests

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In this markdown I will:

1. Organize predictor and response variable dissimilarity matrices.
2. Run Mantel tests with different predictors.

## Transforming SRI similarity into distance

```
# Transforming SRI similarity into distance
year <- 5
dolp_dist = nxn[[year]] + 0.00001
dolp_dist <- 1-nxn[[year]]
## Remove the redundant cells and the diagonal
dolp_dist <- as.dist(dolp_dist)
```

## Organize data into foraging and HI frequency

```
# Select variables from the raw data
data <- list_years[[year]]
aux <- data[, c('Code', 'Behaviors', 'HumanInteraction', 'ConfHI')]

# Use 'Behaviors' variable to extract "Feed" and create another variable with two classes (Feed, Other)
aux$Foraging <- "Other"
aux$Foraging[grepl(pattern = 'Feed',
                    x = aux$Behaviors,
                    ignore.case = FALSE, perl = FALSE,
                    fixed = FALSE, useBytes = FALSE)] = "Feed"
#aux <- subset(aux, aux$Foraging == "Feed")
aux$ConfHI <- ifelse(aux$ConfHI == "0", 0, 1)

# Categorize ID to Foraging
IDbehav <- table(aux$Code, aux$Foraging)
IDbehav <- as.data.frame(IDbehav, stringsAsFactors = FALSE)
IDbehav <- IDbehav[,c(1,3)]
colnames(IDbehav) <- c("Code", "Forg_Freq")
# Group by the 'Code' column and sum the frequencies
IDbehav <- aggregate(. ~ Code, data = IDbehav, sum)
```

```

# Categorize ConfHI to IDs
rawHI <- as.matrix(table(aux$Code, aux$ConfHI))
rawHI <- as.data.frame(rawHI, stringsAsFactors = FALSE)
colnames(rawHI) <- c("Code", "ConfHI", "Freq")

## Add up the # of times each ID was seen in HI
IDbehav$HI <- rawHI$Freq[rawHI$ConfHI != 0]
IDdata <- IDbehav
colnames(IDdata) <- c("Code", "Foraging", "HI")

## Proportion of time Foraging spent in HI
IDdata$HIprop <- as.numeric(IDdata$HI)/as.numeric(IDdata$Foraging)
IDdata[is.na(IDdata)] <- 0

# Only ID to prop
HIprop_ID <- IDdata[,c(1, 4)]

```

## Create HI Dissimilarity Matrix using Euclidean Distance

```

# Dissimilarity of HI proportion among individual dolphins, using Euclidean distance
fake_HIprop <- HIprop_ID$HIprop
dissimilarity_HI <- as.matrix(dist(as.matrix(fake_HIprop), method = "euclidean"))
dissimilarity_HI[is.na(dissimilarity_HI)] <- 0

```

## Calculate Mantel test

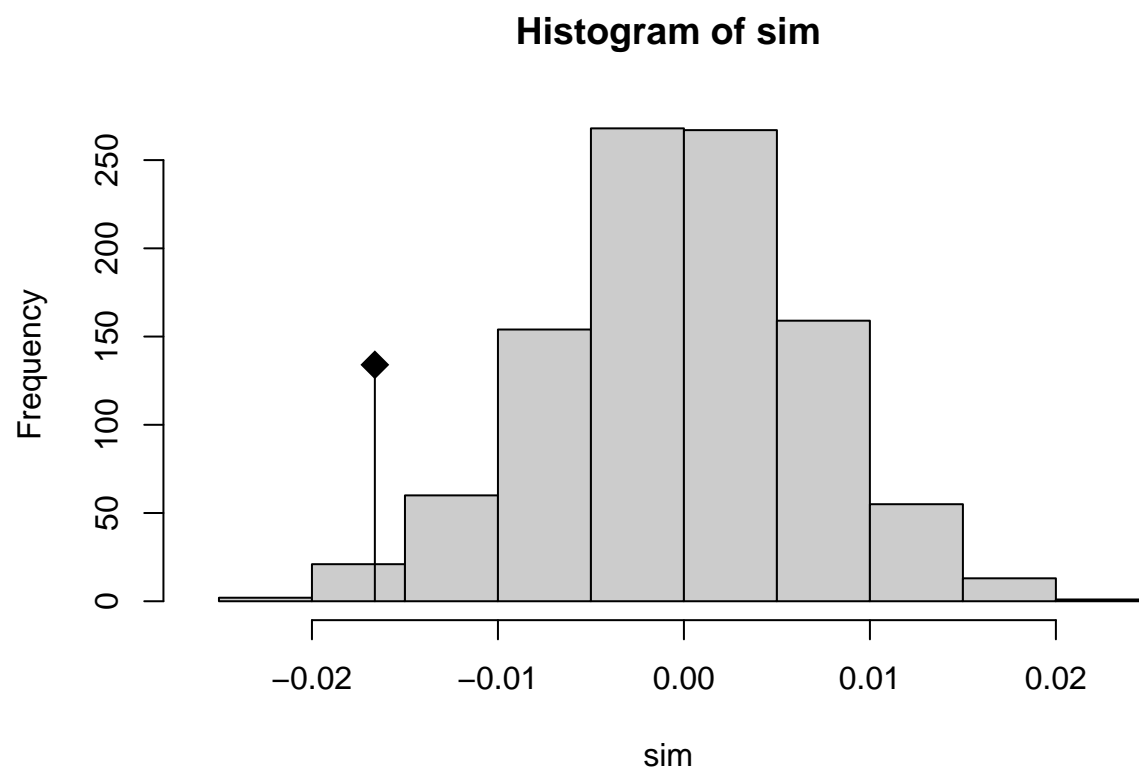
```

dissimilarity_HI <- as.dist(dissimilarity_HI) # HI dissimilarity
kov <- as.dist(kov) # Home range overlap

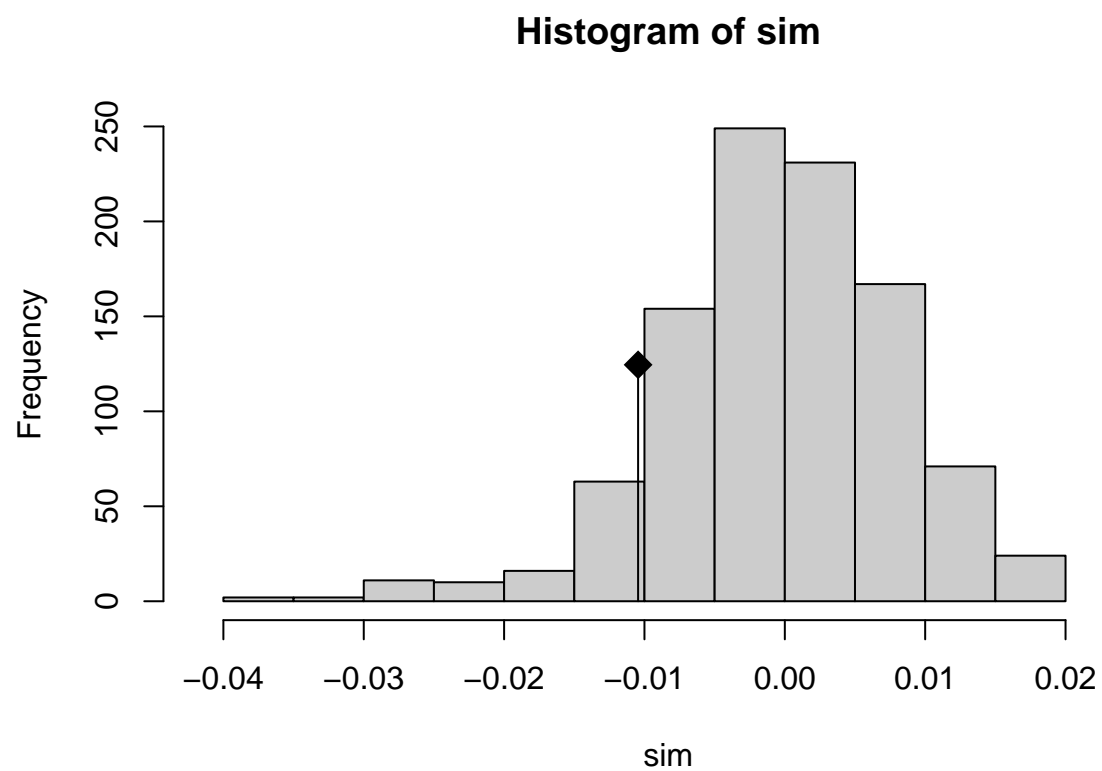
# Dissimilarity matrices
## HRO
hro_test <- mantel.rtest(dolp_dist, kov, nrepet = 1000)

plot(hro_test)

```



```
## HI  
HI_test <- mantel.rtest(dolp_dist, dissimilarity_HI, nrepet = 1000)  
  
plot(HI_test)
```



So far there are no correlation with HI engagement and associations.