

Appendix 2.

Goal: Mantel test for Migratory Connectivity Analysis

Input: 2_Connectivity_Data.csv

Input includes: Breeding location (b_lat and b_lon), wintering location (w_lat and w_lon)

Ocean crossing location in fall (o_lat_f and o_lon_f), and Ocean crossing location in

spring (o_lat_s and o_lon_s)

Output: Table 2

Load required libraries

library(dplyr)

library(vegan)

library(geosphere)

library(ade4)

Set working directory and load data

data <- read.csv("2_Connectivity_Data.csv")

Function to create distance matrix in ade4-compatible format

create_ade4_dist <- function(coords) {

dist_matrix <- distm(coords, fun = distHaversine) / 1000 # Convert to km

as.dist(dist_matrix) # Convert to distance object

}

###---- Section 1: Define all distance matrices ----

```
# Breeding locations distance matrix
```

```
breeding_coords <- data[, c("b_lon", "b_lat")]
```

```
breeding_dist <- create_ade4_dist(breeding_coords)
```

```
# Wintering locations distance matrix
```

```
wintering_coords <- data[, c("w_lon", "w_lat")]
```

```
wintering_dist <- create_ade4_dist(wintering_coords)
```

```
# Fall ocean crossing distance matrix
```

```
fall_ocean_coords <- data[, c("o_lon_f", "o_lat_f")]
```

```
fall_ocean_dist <- create_ade4_dist(fall_ocean_coords)
```

```
# Spring ocean crossing distance matrix
```

```
spring_ocean_coords <- data[, c("o_lon_s", "o_lat_s")]
```

```
spring_ocean_dist <- create_ade4_dist(spring_ocean_coords)
```

```
###---- Section 2: Run all pairwise Mantel tests (6 pairs) ----
```

```
# Test 1: Breeding Locations vs. Wintering Locations
```

```
mantel_result_1 <- mantel.rtest(breeding_dist, wintering_dist, nrepet = 999)
```

```
cat("\n1. Breeding vs Wintering:\n")
```

```
print(mantel_result_1)
```

```
# Test 2: Breeding Locations vs. Fall Ocean Crossing Locations
```

```
mantel_result_2 <- mantel.rtest(breeding_dist, fall_ocean_dist, nrepet = 999)
```

```
cat("\n2. Breeding vs Fall Ocean Crossing:\n")
```

```
print(mantel_result_2)
```

```
# Test 3: Breeding Locations vs. Spring Ocean Crossing Locations
```

```
mantel_result_3 <- mantel.rtest(breeding_dist, spring_ocean_dist, nrepet = 999)
```

```
cat("\n3. Breeding vs Spring Ocean Crossing:\n")
```

```
print(mantel_result_3)
```

```
# Test 4: Wintering Locations vs. Fall Ocean Crossing Locations
```

```
mantel_result_4 <- mantel.rtest(wintering_dist, fall_ocean_dist, nrepet = 999)
```

```
cat("\n4. Wintering vs Fall Ocean Crossing:\n")
```

```
print(mantel_result_4)
```

```
# Test 5: Wintering Locations vs. Spring Ocean Crossing Locations
```

```
mantel_result_5 <- mantel.rtest(wintering_dist, spring_ocean_dist, nrepet = 999)
```

```
cat("\n5. Wintering vs Spring Ocean Crossing:\n")
```

```
print(mantel_result_5)
```

```
# Test 6: Fall Ocean Crossing vs. Spring Ocean Crossing Locations
```

```
mantel_result_6 <- mantel.rtest(fall_ocean_dist, spring_ocean_dist, nrepet = 999)
```

```
cat("\n6. Fall Ocean Crossing vs Spring Ocean Crossing:\n")
```

```
print(mantel_result_6)
```

```
### --- Section 3: Summary of results ----
```

```
results_summary <- data.frame(
```

```
  Comparison = c("Breeding vs Wintering",
```

```

    "Breeding vs Fall Ocean",
    "Breeding vs Spring Ocean",
    "Wintering vs Fall Ocean",
    "Wintering vs Spring Ocean",
    "Fall Ocean vs Spring Ocean"),
Correlation = c(mantel_result_1$obs,
    mantel_result_2$obs,
    mantel_result_3$obs,
    mantel_result_4$obs,
    mantel_result_5$obs,
    mantel_result_6$obs),
P_value = c(mantel_result_1$pvalue,
    mantel_result_2$pvalue,
    mantel_result_3$pvalue,
    mantel_result_4$pvalue,
    mantel_result_5$pvalue,
    mantel_result_6$pvalue)
)

# Order by correlation strength
results_summary <- results_summary[order(results_summary$Correlation, decreasing = TRUE),
]

cat("\nSummary of Mantel test results (ordered by correlation strength):\n")
print(results_summary)

```

