# Load required libraries

library(ape)

library(paco)

# Input: Host-Parasite association data

data <- data.frame(

Host = c("fish2", "fish3", "fish4", "fish6", "fish8", "fish9", "fish10",

"fish11", "fish13", "fish14", "fish15", "fish16", "fish18",

"fish19", "fish20", "fish21", "fish23", "fish24", "fish25",

"fish26", "fish27", "fish28", "fish30", "fish31", "fish32",

"fish33", "fish34", "fish35", "fish36", "fish38", "fish39",

"fish43"),

Parasite = c("Co2", "Co3", "Co4", "Co6", "Co8", "Co9", "Co10", "Co11",

"Co13", "Co14", "Co15", "Co16", "Co18", "Co19", "Co20",

"Co21", "Co23", "Co24", "Co25", "Co26", "Co27", "Co28",

"Co30", "Co31", "Co32", "Co33", "Co34", "Co35", "Co36",

"Co38", "Co39", "Co43")

)

# Create a list of unique hosts and parasites

hosts <- unique(data$Host)

parasites <- unique(data$Parasite)

# Initialize a binary association matrix

association\_matrix <- matrix(0, nrow = length(hosts), ncol = length(parasites),

dimnames = list(hosts, parasites))

# Fill the matrix based on the associations

for (i in 1:nrow(data)) {

association\_matrix[data$Host[i], data$Parasite[i]] <- 1

}

# View the association matrix

print(association\_matrix)

# Compute cophenetic distance matrices

D\_host <- cophenetic(host\_tree)

D\_parasite <- cophenetic(parasite\_tree)

# Prepare PACo data

paco\_data <- prepare\_paco\_data(D\_host, D\_parasite, association\_matrix)

# Continue with the PACo workflow...

paco\_data <- add\_pcoord(paco\_data)

paco\_result <- PACo(paco\_data, nperm = 999, method = "r0")

summary(paco\_result)

str(paco\_result)

# Extract first two axes for host and parasite

host\_pcoord <- paco\_result$H\_PCo[, 1:2] # First two principal coordinates of hosts

parasite\_pcoord <- paco\_result$P\_PCo[, 1:2] # First two principal coordinates of parasites

# Plotting

plot(host\_pcoord[, 1], host\_pcoord[, 2], col = "blue", pch = 19, xlab = "PCo1", ylab = "PCo2",

main = "PACo: Host vs Parasite Principal Coordinates", xlim = range(c(host\_pcoord[, 1], parasite\_pcoord[, 1])),

ylim = range(c(host\_pcoord[, 2], parasite\_pcoord[, 2])))

points(parasite\_pcoord[, 1], parasite\_pcoord[, 2], col = "red", pch = 19)

# Adding legend

legend("topright", legend = c("Host", "Parasite"), col = c("blue", "red"), pch = 19)

# Extract Procrustes coordinates for host and parasite

host\_procrustes <- paco\_result$proc$X[, 1:2]

parasite\_procrustes <- paco\_result$proc$Yrot[, 1:2]

# Plot Procrustes transformation

plot(host\_procrustes[, 1], host\_procrustes[, 2], col = "blue", pch = 19, xlab = "PCo1", ylab = "PCo2",

main = "PACo Procrustes: Host vs Parasite", xlim = range(c(host\_procrustes[, 1], parasite\_procrustes[, 1])),

ylim = range(c(host\_procrustes[, 2], parasite\_procrustes[, 2])))

points(parasite\_procrustes[, 1], parasite\_procrustes[, 2], col = "red", pch = 19)

# Adding legend

legend("topright", legend = c("Host", "Parasite"), col = c("blue", "red"), pch = 19)

# Plot the PCoA or Procrustes results

plot(paco\_result)

# Add labels to the points (for both hosts and parasites)

# Assuming the data is stored in the variables 'H' for hosts and 'P' for parasites

# Plot host points (blue) with labels

text(paco\_result$H[, 1], paco\_result$H[, 2], labels = rownames(paco\_result$H), col = "blue", cex = 0.7)

# Plot parasite points (red) with labels

text(paco\_result$P[, 1], paco\_result$P[, 2], labels = rownames(paco\_result$P), col = "red", cex = 0.7)

# Extract the host and parasite coordinates from the PACo result

host\_coords <- paco\_result$H\_PCo # Coordinates for hosts

parasite\_coords <- paco\_result$P\_PCo # Coordinates for parasites

# Create an empty plot (this will create the axes and space for the plot)

plot(host\_coords[, 1], host\_coords[, 2],

xlab = "PCoA Axis 1", ylab = "PCoA Axis 2",

pch = 19, col = "blue", xlim = range(c(host\_coords[, 1], parasite\_coords[, 1])),

ylim = range(c(host\_coords[, 2], parasite\_coords[, 2])))

# Add parasite points to the plot (in red)

points(parasite\_coords[, 1], parasite\_coords[, 2], pch = 19, col = "red")

# Add labels to the host points (blue)

text(host\_coords[, 1], host\_coords[, 2], labels = rownames(host\_coords), col = "blue", cex = 0.7)

# Add labels to the parasite points (red)

text(parasite\_coords[, 1], parasite\_coords[, 2], labels = rownames(parasite\_coords), col = "red", cex = 0.7)