**APPENDIX S1**

# Simple trace function

tr <- function(mat){

trace <- sum(diag(mat))

return(trace)

}

# three way unbalanced non-parametric MANOVA

threewaynpFtest <- function(sharks, Xr, Xf, a){

# TESTS FOR FACTOR A EFFECT

# sharks = MATRIX WHERE EACH ROW REPRESENTS A PROFILE OF A DIFFERENT INDIVIDUAL

# a = NUMBER OF FACTORS IN TREATMENT A BEING ANALYSED

# Xr = THE REDUCED DESIGN MATRIX EXCLUDING FACTOR A

# Xf = THE FULL DESIGN MATRIX

N <- nrow(sharks)

d <- matrix(0, nrow=N, ncol=N)

# USING AITCHISON'S DISTANCE MEASURE aDist, CALCULATING A DISTANCE MATRIX

for(i in 1:N){

for(j in 1:N){

d[i,j] <- aDist(sharks[i,],sharks[j,])

}

}

dsqr <- d^2

A <- (-1/2)\*dsqr

Hr <- Xr%\*%solve(t(Xr)%\*%Xr)%\*%t(Xr)

Hf <- Xf%\*%solve(t(Xf)%\*%Xf)%\*%t(Xf)

ones <- matrix(1,N,1)

I <- diag(N)

g <- (I - (1/N)\*ones%\*%t(ones))

G <- g%\*%A%\*%g

SSA <- tr(Hf%\*%G%\*%Hf)-tr(Hr%\*%G%\*%Hr)

SSR <- tr((I-Hf)%\*%G%\*%(I-Hf))

SST <- tr(G)

F <- ((tr(Hf%\*%G%\*%Hf)-tr(Hr%\*%G%\*%Hr))/(a-1))/(tr((I-Hf)%\*%G%\*%(I-Hf))/(N-ncol(Xf)))

return(F)

}

p.value3way <- function(sharks, Xa, Xb, Xc, Xf, a, b, c, nperm=1000){

# P-VALUE FOR THREE WAY MANOVA

# sharks = EACH ROW IS AN INDIVIDUAL SHARK FA SIGNATURE

# nperm = THE NUMBER OF PERMUTATIONS TO COMPUTE FOR THE P-VALUE

# Xa = THE REDUCED DESIGN MATRIX EXCLUDING FACTOR A

# Xb = THE REDUCED DESIGN MATRIX EXCLUDING FACTOR B

# Xc = THE REDUCED DESIGN MATRIX EXCLUDING FACTOR C

# a = THE NUMBER OF FACTORS IN TREATMENT A

# b = THE NUMBER OF FACTORS IN TREATMENT B

# c = THE NUMBER OF FACTORS IN TREATMENT C

Foriga <- threewaynpFtest(sharks, Xa, Xf, a)

Forigb <- threewaynpFtest(sharks, Xb, Xf, b)

Forigc <- threewaynpFtest(sharks, Xc, Xf, c)

# CALCULATING nperm RANDOM PERMUTATIONS AS DESCRIBED IN MARTI ANDERSON'S PAPER

# 1000 FOR 0.05 SIGNIFICANCE, 5000 FOR 0.01 SIGNIFICANCE

Fperma <- numeric(nperm)

Fpermb <- numeric(nperm)

Fpermc <- numeric(nperm)

for(i in 1:nperm){

ind <- c(1:nrow(sharks))

perm <- sample(ind)

sharks.perm <- sharks[perm,]

Fperma[i] <- threewaynpFtest(sharks.perm, Xa, Xf, a)

Fpermb[i] <- threewaynpFtest(sharks.perm, Xb, Xf, b)

Fpermc[i] <- threewaynpFtest(sharks.perm, Xc, Xf, c)

}

# HOW MANY PERMUTATIONS WERE GREATER THAN THE ORIGINAL Forig

p.valuea <- sum(Fperma > Foriga)/nperm

p.valueb <- sum(Fpermb > Forigb)/nperm

p.valuec <- sum(Fpermc > Forigc)/nperm

return(c(Foriga, p.valuea, Forigb, p.valueb, Forigc, p.valuec))

}