Appendix A. R-script file for null model analysis.

```
# This program tests for heterogeneity in linear trend lines
of species abundances.

###########################################
# GLOBAL VARIABLES

ObservedMatrix <- as.matrix(read.csv("Grossman Streamfish Data.csv", header=TRUE, row.names=1))
# input has species as rows, columns as times, with labels in the first row and column


Time <- c(11, 21, 34, 35, 45, 47, 57, 59, 71, 81, 82, 93, 117, .94 Tm 0 Tc[( )] TETq0 -0.12 817.08 .86 539.14 Tm[817.08 .86
```

```
#
#
#########################################
# FUNCTION RandomSampler
# This function takes as input the SourcePool vector and the original data matrix
# It returns a single null matrix created by sampling individuals one at a time

RandomSampler <- function(FSourcePool, FMatrix) {

TimeProbs <- colSums(FMatrix)/sum(FMatrix)
PoissonN <- numeric(ncol(FMatrix))

for (j in 1:sum(FMatrix)) {
i <-sample(seq(1:length(PoissonN)),1,replace = TRUE,TimeProbs)
PoissonN[i] <- PoissonN[i] + 1
}


SampleMatrix <- matrix(0,length(FSourcePool),ncol(FMatrix))

for (j in 1:ncol(FMatrix)) {
      for (n in 1:PoissonN[j]) {
      i <- sample(seq(1:length(FSourcePool)),1,replace = TRUE,FSourcePool)
SampleMatrix[i,j] <- SampleMatrix[i,j] + 1
}
}
RandomSampler <- SampleMatrix
}
#########################################
#
#
#
#
#########################################
```

```
      Growth <- NULL #creates empty vector of unspecified length

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

      if (sum(FMatrix[i,]) > 0)
{
      model <- lm(FMatrix[i,]~FTime) #fits model for species that are present
      Growth[i] <- model$coefficients[2] #stores regression slope parameter

}

}


var(Growth, use = "complete") #species with 0 generate missing values that are ignored
}
#########################################
#
#
#
#
#########################################
# FUNCTION Chao2
# This function takes as input the observed matrix
# It calculated the bias corrected version of Chao2 (Equation 4 in EstimateS manual)
# Note that is this function is needed only once to get missing species for the simulation
# Results are rounded to the nearest whole integer

Chao2 <- function(FMatrix) {
Occurrences <- NULL
for (i in 1:nrow(FMatrix)) {
Occurrences[i] <- sum(FMatrix[i,] > 0)

 }
Uniques <- sum(Occurrences == 1)
Duplicates <- sum(Occurrences == 2)
m <- ncol(FMatrix)   # m = number of samples


Chao2 <- ((m - 1)/m)* ((Uniques*(Uniques - 1)))/(2*(Duplicates + 1))
Chao2 <- round(Chao2)

}
```

```
#########################################
#
#
#
#
#########################################
# PROGRAM Basic Simulation Loop

MissingSpecies <- Chao2(ObservedMatrix)
SourcePoolVector <- SourcePool(ObservedMatrix,MissingSpecies)
ObsVar <-GrowthVar(ObservedMatrix,Time)

for (i in 1:NRep) {
RandomMatrix <- RandomSampler(SourcePoolVector,ObservedMatrix)
SimVar[i] <-GrowthVar(RandomMatrix,Time)
}
ConfidenceInterval <- quantile(SimVar,c(0.025,0.975))
ConfidenceInterval
ObsVar
SES <- (ObsVar - mean(SimVar))/sqrt(var(SimVar))
SES
sum(ObsVar > SimVar)/NRep
summary(SimVar)
#######################################
```