

Marine and terrestrial Pseudosuchia macroevolution was independently affected by climate change

Abstract

Pseudosuchia makes up one half of the Archosauria. Once a rich, diverse reptilian clade, only 23 extant species remain with little morphological diversity. Here, correlational analysis is used to compare rates of speciation and extinction for both marine and terrestrial species from a fossil record. The results of the analysis show temperature as a driver for increases in speciation rates for both habitual clades. Results show decreases in sea level correlate to a rise in speciation. The analysis provides a potential indicator of the impacts of human induced climate change on carnivorous ectotherms.

Introduction

Pseudosuchia refers to an evolutionary diverse reptilian group that makes up one of the two groups of Archosauria. Pseudosuchia is composed of crocodiles and all extinct relatives that first appeared around 250 million years ago in the late lower Triassic period (Butler et al. 2011) (Nesbitt 2011). Pseudosuchia faced a mass decline in diversity around 201 million years ago (Triassic-Jurassic extinction) which was quickly followed by a large increase in evolutionary radiation (Toljagic and Butler 2013), occurring from crocodylomorphs. During this time, Pseudosuchia diversity was high with species occupying various ecological niches such as marine environments (Thalattosuchia) (DE ANDRADE et al. 2010) as well as terrestrial species that show varying amounts of morphological diversity (Buckley et al. 2000) (Sereno et al. 2001). Pseudosuchia diversity slowly began to fall leaving only 23 semi-aquatic species today. The reasons for the evolutionary decline of Pseudosuchia are likely due to climate change (Mannion et al. 2015) as Pseudosuchia are vulnerable to changes in environmental temperature, their only source of bodily heat. With current climate projections predicting global temperature increases as well as a rise in sea level, aridification and habitat loss (Knutti et al. 2013), Pseudosuchia face the threat of extinction. Usage of proxy data based on geological evidence allows for understanding of how climate can affect biodiversity of a wide variety of animal clades (Davis et al. 2016) (Tang et al. 2018). This allows for the development of clearer models for how future climate change may impact the natural world. This report will investigate how both temperature and sea level change has affected speciation and extinction rates of Pseudosuchia via correlational analysis.

Results and discussion

Marine and terrestrial phylogenetic tree construction

Phylogenetic trees were constructed for marine and terrestrial taxa separately using geological data (Payne et al., in prep). The data was created from morphological fossils records as well as sequence data for extant species. The terrestrial phylogenetic tree shown (fig.1.B) contains 206 taxa dating to around 282 million years ago. The marine phylogenetic tree shown (fig.1.A) contains 107 taxa dating to around 252 million years ago. Marine and terrestrial species were separated for both phylogenetic trees as well as analysis, this methodology was chosen as these two groups are likely to be affected by climate change differently as seen in similar studies (Mannion et al. 2015).

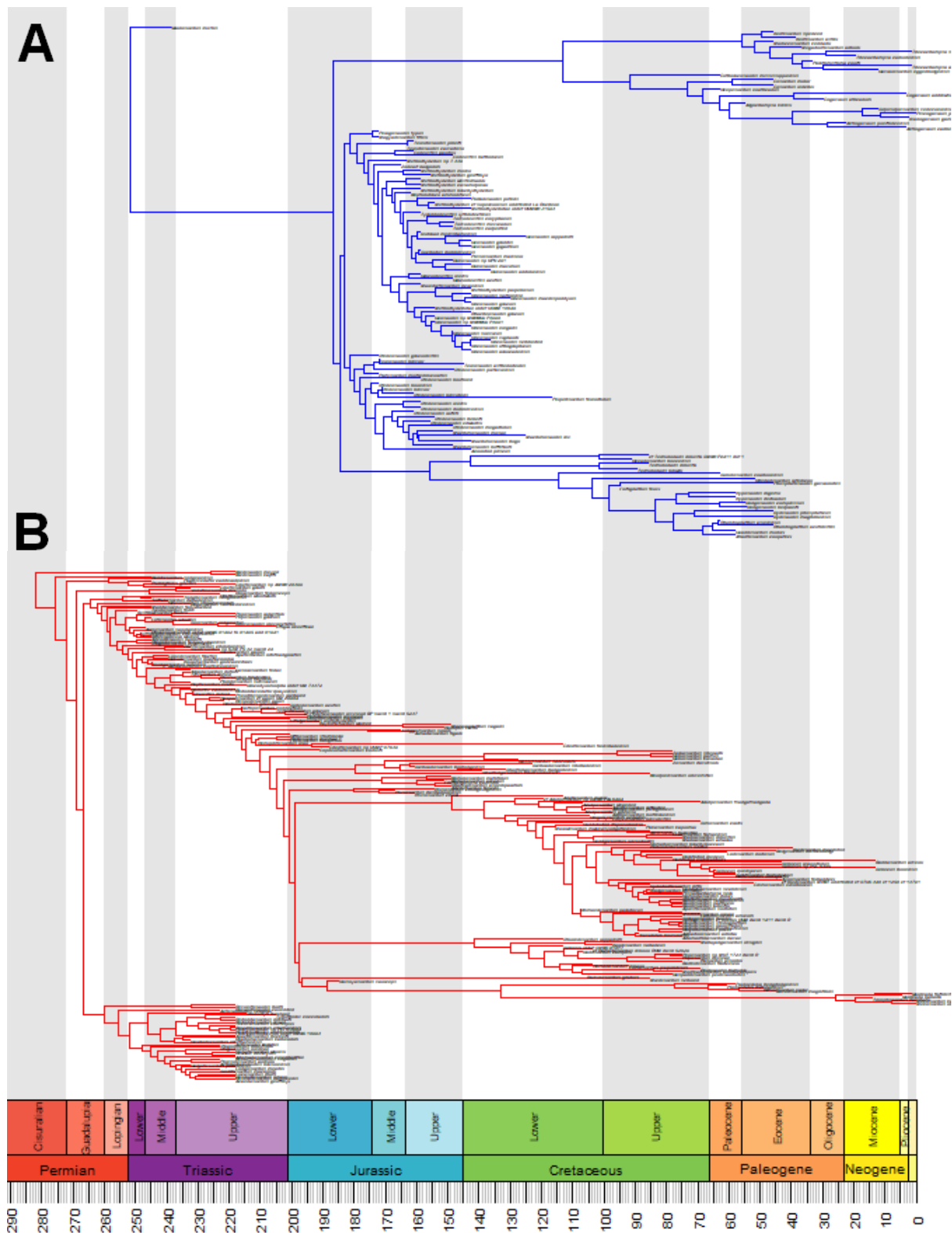


Fig 1.A/B The phylogeny of marine (blue) and terrestrial (red) taxa scaled against the geological timescale over 290 million years.

Terrestrial taxa speciation increased with temperature

Change in temperature is likely to have affected the evolution of Pseudosuchia due to their reliance on their environment for warmth. Thus, periods of cooling may have increased rates of extinction and speciation as organisms must rapidly adapt to colder environments, with those unable to dying out. To test this hypothesis, a Wilcoxon statistical test was carried out between two coefficients generated via a detrended cross correlation analysis (DCCA-based) test. The correlation coefficients were generated and tested in RStudio using the BMM package (Rabosky et al. 2014). This analysis was carried out for rates of speciation and extinction (Lloyd et al. n.d.) (Mitchell, Etienne, and Rabosky 2018) against temperature (Zachos et al. 2001), in terrestrial species. Temperature increase showed a significant correlation to speciation rate increase ($P = 0$), shown (fig.2.D). Temperature was also found to have a significant correlation to extinction rate increase ($P = 1.257953e-106$) (fig.2.E). The overall temperature change (fig.2.A) and extinction/speciation rates (fig.2.B/C) are shown. The results show a clear correlation between rise in both speciation and temperature. However, the correlation seen for extinction is less so due to the closeness of the mean to 0. Speciation is likely to be heavily affected by temperature change as it enables ectotherms to have elevated metabolism (Riemer et al. 2018). Higher metabolism likely heightened levels of reproduction leading to an increased rate of speciation. Extinction rate increase showed small unreliable correlation with temperature rise and therefore has limited reliability. Despite this significant temperature change is likely to have affected extinction rates but in the opposite direction than seen, as temperature decrease may have limited the metabolic activity of ectothermic Pseudosuchians.

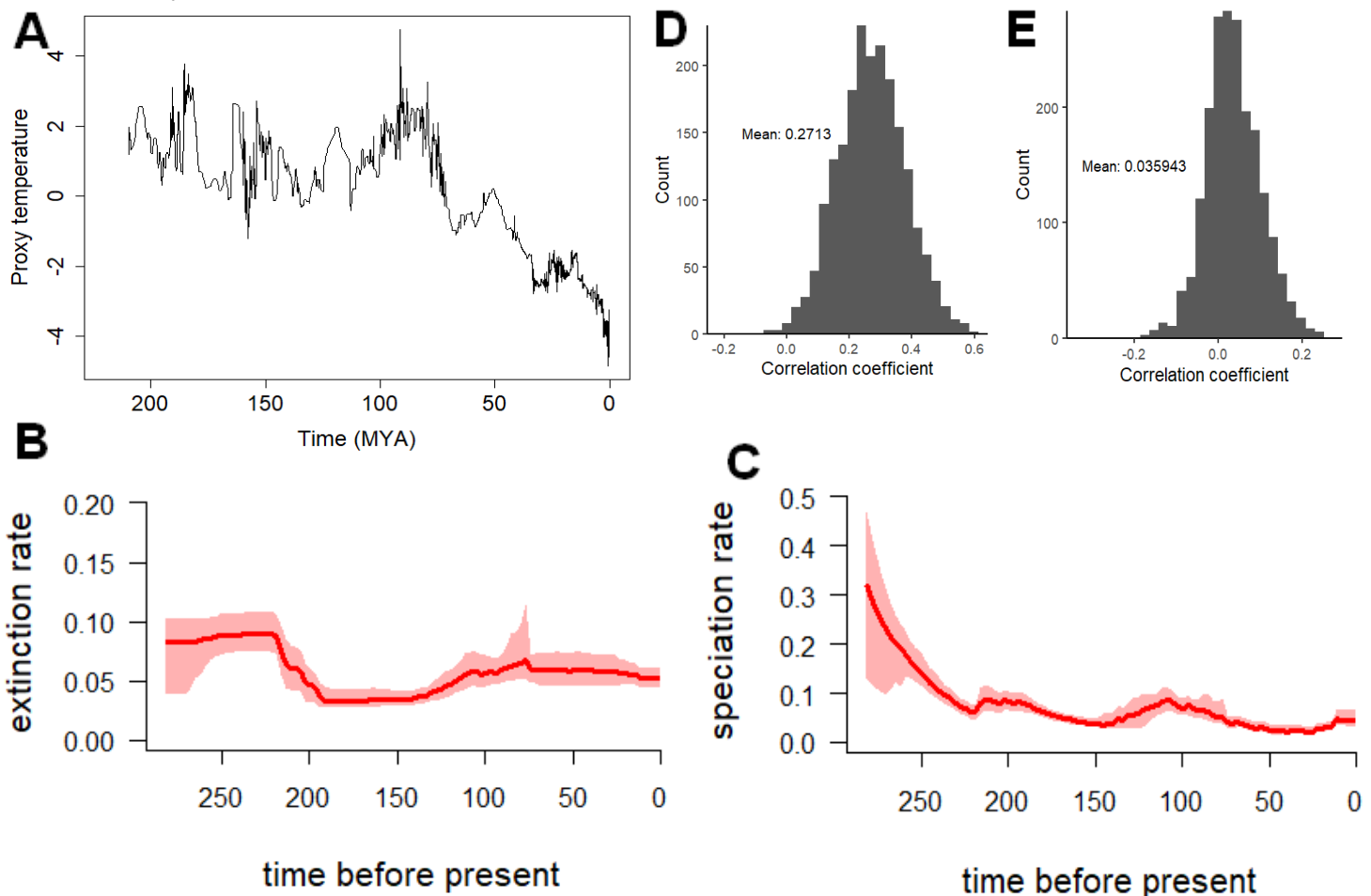


Fig 2: (A) Proxy temperature over ~280 million years, source: (Zachos et al. 2001). The two lower panels show the rates of extinction (B) and speciation (C) for terrestrial taxa. Histograms showing the correlation coefficients for speciation (D) and extinction (E) generated from a DCCA-based test.

Speciation rates fell with sea level rise in terrestrial taxa

Sea level change has shown much variation over the past 250 million years and is likely to have affected terrestrial Pseudosuchia. Sea level rise beginning around 200 MYA and peaking around 90 MYA (fig 3.A) is known to have led to many habitat adaptations with many terrestrial species transitioning to marine or semi-aquatic environments (Wilberg, Turner, and Brochu 2019). It is therefore likely that increased sea levels may lead to extinction of many terrestrial species due to habitat loss and increased competition. To test the effects of changing sea levels on terrestrial speciation and extinction, the same correlation previously described was run for sea level change (Haq, Hardenbol, and Vail 1987). The results from the speciation-sea level analysis show a significant correlation between a decrease in sea level and a rise in the rate of speciation ($P = 0$) (fig 3.B). Extinction-sea level analysis showed a significant correlation ($P = 0$) (fig 3.C) between rise in sea level and rise in extinction. The results described clearly fit the hypothesis, sea level rise led to a significant increase in extinction of terrestrial species likely due to destruction of habitats and competition. The decline of terrestrial species and their replacement with semi-aquatic taxa found today also supports this and is seen in adaptations that support the terrestrial-semi aquatic transition (Schwab et al. 2020). Speciation rate increase strongly correlated with the decrease in sea levels. This result also seems to fit the hypothesis as lower sea levels may have provided new terrestrial habitats allowing for further speciation of terrestrial Pseudosuchia.

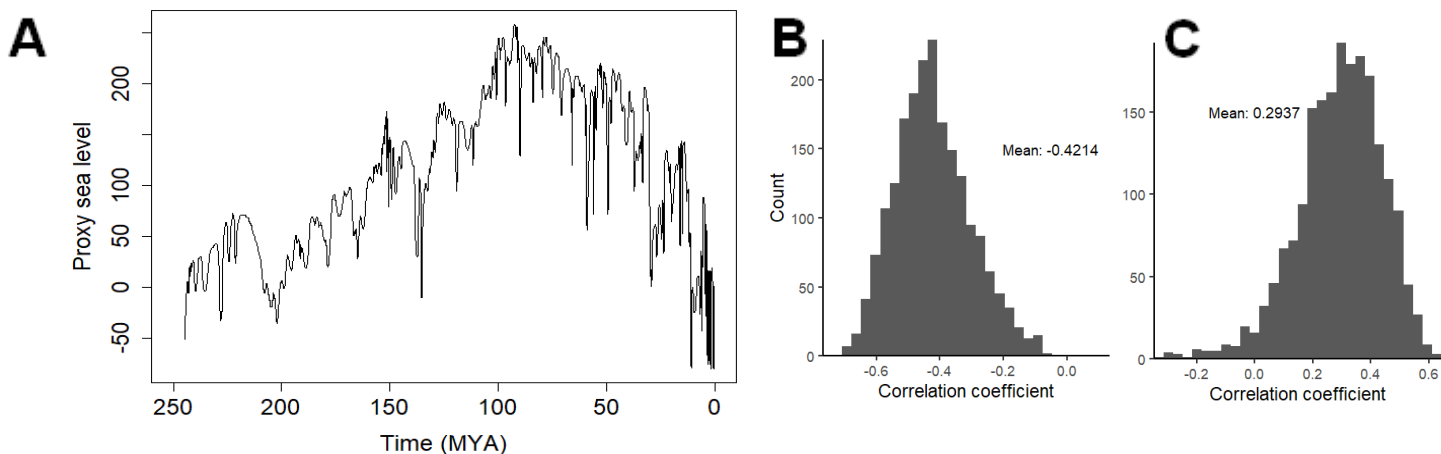


Fig 3: (A) Proxy sea level over ~240 million years, source: (Haq, Hardenbol, and Vail 1987). Histograms for speciation (B) and extinction (C) correlation coefficients generated by a DCCA-based test.

Temperature increase drives speciation rate increase in marine taxa

Temperature change may have had a small impact on the speciation and extinction of marine taxa compared to terrestrial due to the off set of temperature changes in marine environments. Despite this, temperature fall following the K-Pg asteroid was shown to cause a major extinction in both marine and terrestrial taxa for non-Pseudosuchian species (Robertson et al. 2013). Temperature change (fig 4.A) was correlated for marine taxa speciation and extinction rates. A significant correlation was found between increase in temperature and increase in speciation ($P = 0$) (fig 4.D). A significant correlation was also found between a decrease in temperature and a rise in extinction ($P = 0$) (fig 4.E). The extinction and speciation rates for marine taxa are also shown (fig 4.B/C). The results show that temperature increase leads to speciation like that seen for the analysis of terrestrial taxa. This trend seen for marine taxa is also likely due to increase in ectotherm metabolism

for both Pseudosuchia and their prey which may allowing for higher reproductive levels and thus greater speciation. Warmer waters in the poles may have allowed for the increase spread of marine Pseudosuchia opening new habitats increasing speciation. The results from this analysis match those seen in similar investigations (Martin et al. 2014).

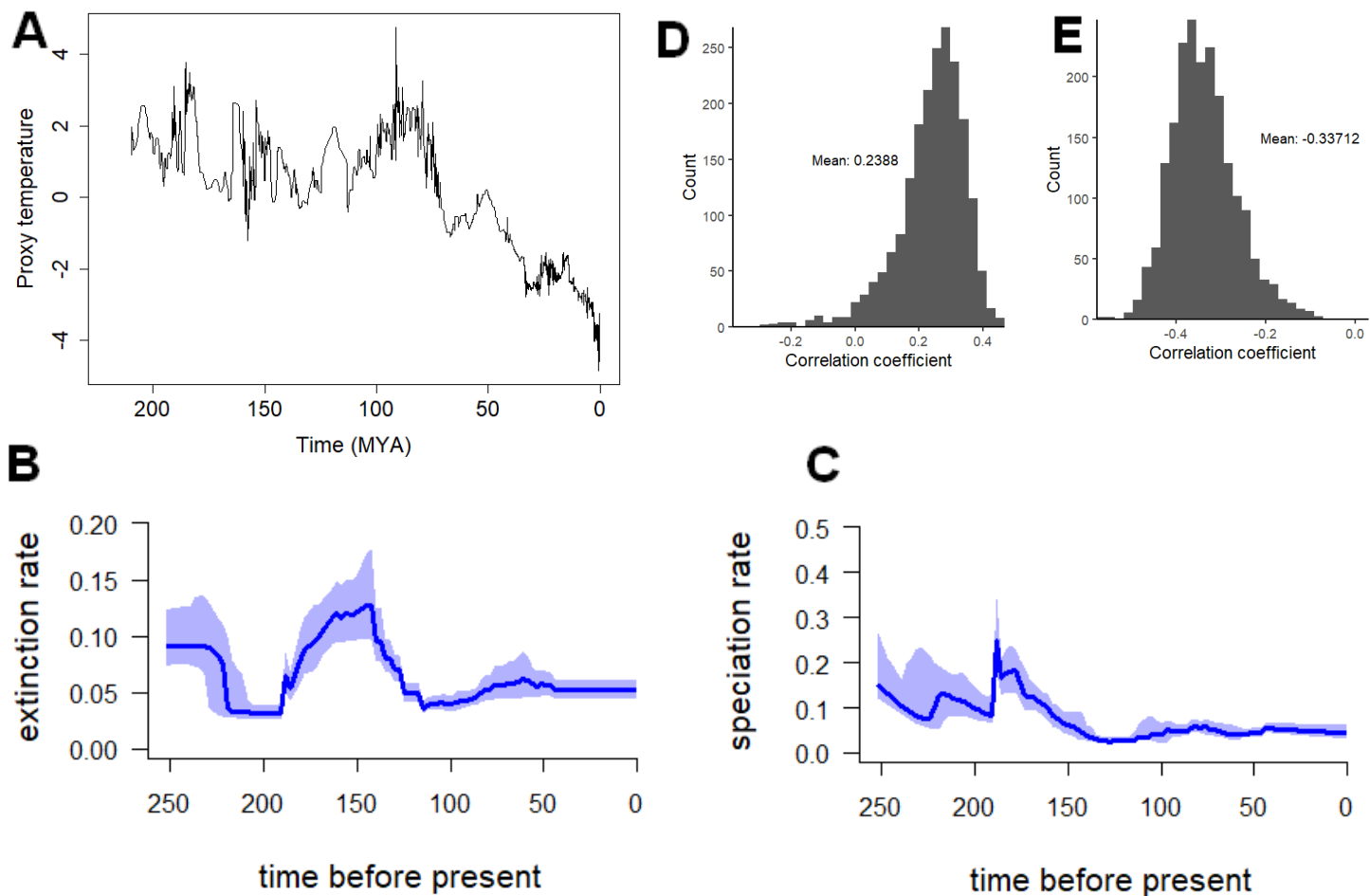


Fig 4: (A) Proxy temperature over ~280 million years, source: (Zachos et al. 2001). Lower panels indicate the extinction (B) and speciation (C) rates for marine taxa. Histograms for speciation (D) and extinction (E) correlation coefficients generated via a DCCA-based test.

Sea level rise increased extinction of marine taxa

A significant rise in the sea level from 200 MYA to 90 MYA is likely to have acted as a major driver in the speciation of marine taxa which would have opened new habitats for marine species. Similarly, a fall in the sea level seen following this period is likely to have contributed to the extinction of marine taxa leaving only 23 semi-aquatic species remaining. To test these hypotheses a final correlation analysis was carried out between sea level change (fig 5.A) and speciation/extinction rates. A significant correlation for a sea level fall and rise in speciation ($P = 9.770145e-259$) was observed as well as a significant rise in sea level and a rise in extinction ($P = 0$). The results from the analysis of sea level-speciation (fig 5.B) do not match the hypothesis. The closeness of the mean to 0 combined with the large distribution of coefficient values for this analysis indicates a weak correlation between sea-level fall and speciation increase, indicates unreliability in the result. The correlation between rise in sea level and extinction (fig 5.C) may be down to greater selection pressures as a higher sea level may lead to more species and thus greater competition for resources. It may be hypothesised that sea level fluctuations, rather than a direct rise or fall, cause variation in

speciation/extinction rates as seen in similar investigations (Tennant, Mannion, and Upchurch 2016).

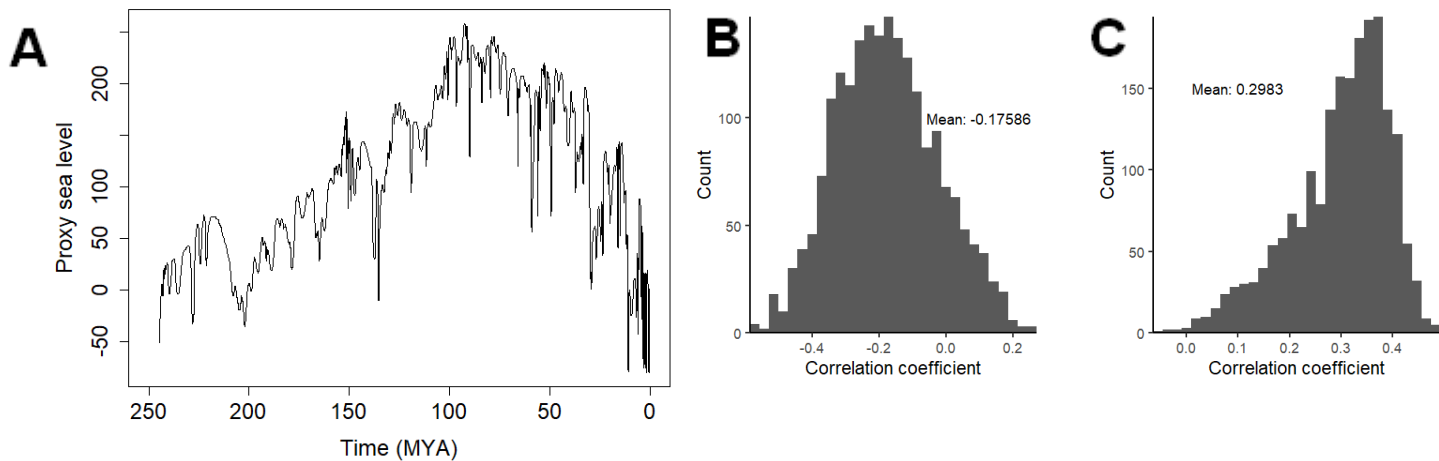


Fig 5: (A) Proxy sea level change starting around 240 million years ago, source: (Haq, Hardenbol, and Vail 1987). Histograms for speciation (B) and extinction (C) correlation coefficients generated by a DCCA-based test.

Conclusion

The results from the analysis generally fit the hypothesis described based on similar literature. The investigation may be limited by a lack of inclusion of other abiotic factors such as carbon and sulfur cycles that may contribute to Pseudosuchian macroevolution (Tennant, Mannion, and Upchurch 2016). The results of this investigation may be further explained via analysis of Pseudosuchian prey extinction in response to the environmental changes studied. To clearly understand the macroevolution of Pseudosuchia it is vital that all factors, both abiotic and biotic are considered. This knowledge is vital in understanding how anthropological induced climate change may affect the future of Pseudosuchia.

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Supplementary methods

#Load packages

```
library(ggplot2)
```

```
library(strap)
```

```
library(BAMMtools)
```

```
library(tidyverse)
```

```
library(phylotools)
```

```
#####
```

#Load in temperature data

```
temperature <- read.csv("temperatureTimeSeries.csv", header = F)
```

#Smooth temperature data

```
finaltemp <- smooth(smooth(temperature$V2))
```

#Plot temperature over time

```
plot(temperature$V1,finaltemp, xlab='Time (MYA)', xlim=c(220,0), type = 'l', ylab = "Proxy temperature", lwd = 1.8, cex.lab=1.5, cex.axis=1.5)
```

#Load in sea level data

```
seaLevel <- read.csv("seaLevelTimeSeries.csv",header=TRUE)
```

#Plot sea level over time

```
plot(seaLevel, xlim=c(250,0), type = 'l', lwd = 1.8, cex.lab=1.5, cex.axis=1.5, xlab="Time (MYA)", ylab="Proxy sea level")
```

```
#####
```

#Creating a tree for the Pseudosuchia

```
tree <- read.tree("fossilCrocPhylogeny.tre")
```


#Creating a data set for the terrestrial species

```
habitatdata <- read.csv("HabitatData.csv", header=T, stringsAsFactors = F)
TerrestrialTaxa <- subset(habitatdata, habitatdata$Habitat=='Terrestrial')$Taxon
```

#Creating a terrestrial tree

```
treeT <- keep.tip(tree, TerrestrialTaxa)
plot(treeT, cex=0.2)
```

#Creating a data set for marine species

```
MarineTaxa <- subset(habitatdata, habitatdata$Habitat=='Marine')$Taxon
```

#Creating a marine tree

```
treeM <- keep.tip(tree, MarineTaxa)
```

#Creating a geoscalePhylo tree for terrestrial species

```
Tlengths <- nodeHeights(treeT)
Troot.time <- max(Tlengths)
treeT$root.time <- Troot.time
Tall_otus <- treeT$tip.label
Tall_otudates <- matrix(0, nrow = length(Tall_otus), ncol = 2)
Tall_otudates <- data.frame(Tall_otudates)
row.names(Tall_otudates) <- Tall_otus
colnames(Tall_otudates) <- c('FAD', 'LAD')
par(mar = c(5, 2, 2, 2))
geoscalePhylo(treeT, ages = Tall_otudates, cex.tip = 0.2, lwd=1, quat.rm = T, units =
c("Period", "Epoch", "Era"), boxes = "Epoch", cex.ts = 0.6, cex.age = 0.6, font = 4, x.lim =
c(280,0), col="red")
```

#Creating a geoscalePhylo tree for marine species

```
Mlengths <- nodeHeights(treeM)
Mroot.time <- max(Mlengths)
treeM$root.time <- Mroot.time
Mall_otus <- treeM$tip.label
Mall_otudates <- matrix(0, nrow = length(Mall_otus), ncol = 2)
Mall_otudates <- data.frame(Mall_otudates)
row.names(Mall_otudates) <- Mall_otus
colnames(Mall_otudates) <- c('FAD', 'LAD')
geoscalePhylo(treeM, ages = Mall_otudates, cex.tip = 0.2, lwd=1, quat.rm = T, units =
c("Period", "Epoch", "Era"), boxes = "Epoch", cex.ts = 0.6, cex.age = 0.6, font=4,
x.lim=c(280,0), col="blue")
```

```
#####
```

```
#Load in Pseudosuchia species data
```

```
edata <- getEventData(tree, eventdata = 'fossilCrocDiversificationData.txt', burnin=0.1)
```

```
#Create terrestrial taxa sub-tree
```

```
streeTerrestrial <- subtreeBAMM(edata, tips=TerrestrialTaxa)
```

```
#Create terrestrial through-time matrix
```

```
rtt_T <- getRateThroughTimeMatrix(streeTerrestrial)
```

```
#Plot terrestrial speciation through time
```

```
plotRateThroughTime(streeTerrestrial, ratetype='speciation', avgCol="red", ylim=c(0,0.5),  
cex.axis=1, intervalCol='red', intervals=c(0.05, 0.95), opacity=0.3)
```

```
#Plot terrestrial extinction through time
```

```
plotRateThroughTime(streeTerrestrial, ratetype = 'extinction', avgCol = "red", cex.axis = 1,  
intervalCol = "red", intervals = c(0.05, 0.95), opacity = 0.3, ylim = c(0,0.2))
```

```
#Create marine taxa sub-tree
```

```
streeMarine <- subtreeBAMM(edata, tips = MarineTaxa)
```

```
#Create marine through-time matrix
```

```
rtt_M <- getRateThroughTimeMatrix(streeMarine)
```

```
#Plot marine speciation through time
```

```
plotRateThroughTime(streeMarine, ratetype='speciation', avgCol="blue", ylim=c(0,0.5),  
cex.axis=1, intervalCol='blue', intervals=c(0.05, 0.95), opacity=0.3)
```

```
#Plotting marine extinction through time
```

```
is.na(rtt_M$mu)
```

```
which(is.na(rtt_M$mu))
```

```
rtt_M$mu[is.na(rtt_M$mu)] <-0
```

```
plotRateThroughTime(rtt_M, ratetype = 'extinction', avgCol = "blue", cex.axis = 1, intervalCol  
= "blue", intervals = c(0.05, 0.95), opacity = 0.3, ylim = c(0,0.2))
```

```
#####
```

```
CCA <- function(x,y,s){
```

```
  xx<-cumsum(x)
```

```
  yy<-cumsum(y)
```

```
  t<-1:length(xx)
```

```
  F2sj_xy<-runif(floor(length(xx)/s))
```

```
  F2sj_xx<-F2sj_xy
```

```
  F2sj_yy<-F2sj_xy
```

```

for(ss in seq(1,(floor(length(xx)/s)*s),by=s)){
  F2sj_xy[(ss-1)/s+1]<-sum((summary(lm(xx[ss:(ss+s-1)]~t[ss:(ss+s-1)]))$residuals)*(summary(lm(yy[ss:(ss+s-1)]~t[ss:(ss+s-1)]))$residuals))/(s-1)
  F2sj_xx[(ss-1)/s+1]<-sum((summary(lm(xx[ss:(ss+s-1)]~t[ss:(ss+s-1)]))$residuals)*(summary(lm(xx[ss:(ss+s-1)]~t[ss:(ss+s-1)]))$residuals))/(s-1)
  F2sj_yy[(ss-1)/s+1]<-sum((summary(lm(yy[ss:(ss+s-1)]~t[ss:(ss+s-1)]))$residuals)*(summary(lm(yy[ss:(ss+s-1)]~t[ss:(ss+s-1)]))$residuals))/(s-1)
}
rho<-mean(F2sj_xy)/sqrt(mean(F2sj_xx)*mean(F2sj_yy))
return(c(rho,1/sqrt(length(xx)),1-pnorm(abs(rho),mean=0,sd=1/sqrt(length(xx))))))
}

```

#Generate data sets for terrestrial speciation-temperature analysis

```

Ttimes= abs(rtt_T$times-max(rtt_T$times))
TnumberOfSims = length(rtt_T$lambda)/length(rtt_T$times)
numberOfSamples = 2000
cors_temp_T <- rep(NA, numberOfSamples)
Tsamples = sample(1:TnumberOfSims, numberOfSamples, replace = F)
count = 1

```

#Generate correlation coefficients

This loops from 1 to the number of simulations, which is 9,001.

```

for (i in 1:TnumberOfSims ) {

```

Is it one of our samples?

```

if (i %in% Tsamples){

```

If yes, do the correlation.

Start by interpolating the data. We do this because the two time series are different lengths. We need them to start and end at the same times and we need the points in between to match up in order to carry out the correlation.

This line takes our speciation rates (lambda) and the corresponding times and interpolates the lambda onto the temperature times. We can only do a correlation for the temperature data that we have so if we have more lambda times than temperature we cannot use them

```

interpdiv = approx(Ttimes, rtt_T$lambda[i,], temperature$V1, method='linear', rule=1)

```

Here we check whether there is a lambda for every temperature time, if not it's left as NA

```
end = which(is.na(interpdiv$y))
```

If we have no NAs, ie. there is a time in the temperature time series for each lambda, we just use the interpolation as already calculated

```
if (length(end) == 0) {  
  div_rates = interpdiv$y  
  ft = finaltemp
```

Otherwise, we only grab and use the times that have both lambda and temperature data

```
} else {  
  div_rates = interpdiv$y[-end]  
  ft = finaltemp[-end]  
}
```

Now do the correlation using the interpolated data

```
c = DCCA(as.numeric(unlist(div_rates)),as.numeric(unlist(ft)),length(ft)/10)
```

Store the correlation co-efficient

```
cors_temp_T[count] = c[1]
```

Increase your count by 1 ready for the next correlation

```
count = count+1
```

```
}
```

```
}
```

#Create a sink for wilcox test of terrestrial temperature-speciation coefficients

```
sink(file='SpeciationTerrestrialTemperature.txt')
```

```
print(summary(cors_temp_T))
```

```
print(quantile(cors_temp_T, c(0.025, 0.975)))
```

```
Tstats <- (wilcox.test(cors_temp_T, mu=0.0, paired = F))
```

```
Tstats$p.value
```

```
sink()
```

#Generate data sets for marine speciation-temperature analysis

```

Mtimes= abs(rtt_M$times-max(rtt_M$times))
MnumberOfSims = length(rtt_M$lambda)/length(rtt_M$times)
numberOfSamples = 2000
cors_temp_M <- rep(NA, numberOfSamples)
Msamples = sample(1:MnumberOfSims, numberOfSamples, replace = F)
count = 1
#Generate correlation coefficients
for (i in 1:MnumberOfSims ) {

  # Is it one of our samples?
  if (i %in% Msamples){

    # If yes, do the correlation.

    # Start by interpolating the data. We do this because the two time series are
different lengths. We need them to start and end at the same times and we need the
points in between to match up in order to carry out the correlation.

    # This line takes our speciation rates (lambda) and the corresponding times and
interpolates the lambda onto the temperature times. We can only do a correlation for
the temperature data that we have so if we have more lambda times than temperature
we cannot use them

    interpdiv = approx(Mtimes, rtt_M$lambda[i,], temperature$V1, method='linear', rule=1)

    # Here we check whether there is a lambda for every temperature time, if not it's left
as NA

    end = which(is.na(interpdiv$y))

    # If we have no NAs, ie. there is a time in the temperature time series for each
lambda, we just use the interpolation as already calculated

    if (length(end) == 0) {
      div_rates = interpdiv$y
      ft = finaltemp

    # Otherwise, we only grab and use the times that have both lambda and
temperature data

    } else {
      div_rates = interpdiv$y[-end]
    }
  }
}

```

```

    ft = finaltemp[-end]
  }

# Now do the correlation using the interpolated data
c = DCCA(as.numeric(unlist(div_rates)),as.numeric(unlist(ft)),length(ft)/10)

# Store the correlation co-efficient
cors_temp_M[count] = c[1]

# Increase your count by 1 ready for the next correlation
count = count+1
}
}

#Create a sink for wilcox test of marine temperature-speciation coefficients
sink(file='SpeciationMarineTemperature.txt')
print(summary(cors_temp_M))
print(quantile(cors_temp_M, c(0.025, 0.975)))
Mstats <- (wilcox.test(cors_temp_M, mu=0.0, paired = F))
Mstats$p.value
sink()

#Generate data sets for terrestrial speciation-sea level analysis
Ttimes= abs(rtt_T$times-max(rtt_T$times))
TnumberOfSims = length(rtt_T$lambda)/length(rtt_T$times)
numberOfSamples = 2000
cors_seaLevel_T <- rep(NA, numberOfSamples)
Tsamples = sample(1:TnumberOfSims, numberOfSamples, replace = F)
count = 1

#Generate correlation coefficients
# This loops from 1 to the number of simulations, which is 9,001.
for (i in 1:TnumberOfSims ) {

# Is it one of our samples?

```

```

if (i %in% Tsamples){

# If yes, do the correlation.
# Again, we have to start by interpolating the data.
interpdiv = approx(Ttimes, rtt_T$lambda[i,], seaLevel$Age, method='linear', rule=1)
end = which(is.na(interpdiv$y))
if (length(end) == 0) {
  div_rates = interpdiv$y
  ft = seaLevel$SL
} else {
  div_rates = interpdiv$y[-end]
  ft = seaLevel$SL[-end]
}

# Now do the correlation
c = DCCA(as.numeric(unlist(div_rates)),as.numeric(unlist(ft)),length(ft)/10)

## Store the correlation co-efficient
cors_seaLevel_T[count] = c[1]

# Increase your count by 1 ready to do the next.
count = count+1
}
}

#Create a sink for wilcox test of terrestrial speciation-sea level coefficients
sink(file='SpeciationTerrestrialSealevel.txt')
print(summary(cors_seaLevel_T))
print(quantile(cors_seaLevel_T, c(0.025, 0.975)))
Tstats2 <- (wilcox.test(cors_seaLevel_T, mu=0.0, paired = F))
Tstats2$p.value
sink()

#Generate data sets for marine speciation-sea level analysis
Mtimes= abs(rtt_M$times-max(rtt_M$times))

```

```

MnumberOfSims = length(rtt_M$lambda)/length(rtt_M$times)
numberOfSamples = 2000
cors_sealevel_M <- rep(NA, numberOfSamples)
Msamples = sample(1:MnumberOfSims, numberOfSamples, replace = F)
count = 1
#Generate correlation coefficients
# This loops from 1 to the number of simulations, which is 9,001.
for (i in 1:MnumberOfSims ) {

# Is it one of our samples?
if (i %in% Msamples){

# If yes, do the correlation.
# Again, we have to start by interpolating the data.
interpdiv = approx(Mtimes, rtt_M$lambda[i,], seaLevel$Age, method='linear', rule=1)
end = which(is.na(interpdiv$y))
if (length(end) == 0) {
  div_rates = interpdiv$y
  ft = seaLevel$SL
} else {
  div_rates = interpdiv$y[-end]
  ft = seaLevel$SL[-end]
}

# Now do the correlation
c = DCCA(as.numeric(unlist(div_rates)),as.numeric(unlist(ft)),length(ft)/10)

## Store the correlation co-efficient
cors_seaLevel_M[count] = c[1]

# Increase your count by 1 ready to do the next.
count = count+1
}
}

```


#Create a sink for wilcox test of marine speciation-sea level coefficients

```
sink(file='SpeciationMarineSealevel.txt')
print(summary(cors_seaLevel_M))
print(quantile(cors_seaLevel_M, c(0.025, 0.975)))
Mstats2 <- (wilcox.test(cors_seaLevel_M, mu=0.0, paired = F))
Mstats2$p.value
sink()
```

#Generate data sets for terrestrial extinction-temperature analysis

```
Ttimes= abs(rtt_T$times-max(rtt_T$times))
TnumberOfSims2 = length(rtt_T$mu)/length(rtt_T$times)
numberOfSamples = 2000
cors_temp_T_E <- rep(NA, numberOfSamples)
Tsamples2 = sample(1:TnumberOfSims2, numberOfSamples, replace = F)
count = 1
```

#Generate correlation coefficients

This loops from 1 to the number of simulations, which is 9,001.

```
for (i in 1:TnumberOfSims2 ) {
```

Is it one of our samples?

```
if (i %in% Tsamples2){
```

If yes, do the correlation.

Start by interpolating the data. We do this because the two time series are different lengths. We need them to start and end at the same times and we need the points in between to match up in order to carry out the correlation.

This line takes our extinction rates (mu) and the corresponding times and interpolates the mu onto the temperature times. We can only do a correlation for the temperature data that we have so if we have more mu times than temperature we cannot use them

```
interpdiv = approx(Ttimes, rtt_T$mu[i,], temperature$V1, method='linear', rule=1)
```

Here we check whether there is a mu for every temperature time, if not it's left as NA

```
end = which(is.na(interpdiv$y))
```

If we have no NAs, ie. there is a time in the temperature time series for each mu, we just use the interpolation as already calculated

```
if (length(end) == 0) {  
  div_rates = interpdiv$y  
  ft = finaltemp
```

Otherwise, we only grab and use the times that have both mu and temperature data

```
} else {  
  div_rates = interpdiv$y[-end]  
  ft = finaltemp[-end]  
}
```

Now do the correlation using the interpolated data

```
c = DCCA(as.numeric(unlist(div_rates)),as.numeric(unlist(ft)),length(ft)/10)
```

Store the correlation co-efficient

```
cors_temp_T_E[count] = c[1]
```

Increase your count by 1 ready for the next correlation

```
count = count+1
```

```
}
```

```
}
```

#Create a sink for wilcox test of terrestrial extinction-temperature coefficients

```
sink(file='ExtinctionTerrestrialTemperature.txt')
```

```
print(summary(cors_temp_T_E))
```

```
print(quantile(cors_temp_T_E, c(0.025, 0.975)))
```

```
Tstats3 <- (wilcox.test(cors_temp_T_E, mu=0.0, paired = F))
```

```
Tstats3$p.value
```

```
sink()
```

#Generate data sets for marine extinction-temperature analysis

```
Mtimes= abs(rtt_M$times-max(rtt_M$times))
```

```
MnumberOfSims2 = length(rtt_M$mu)/length(rtt_M$times)
```

```

numberOfSamples = 2000
cors_temp_M_E <- rep(NA, numberOfSamples)
Msamples2 = sample(1:MnumberOfSims2, numberOfSamples, replace = F)
count = 1
#Generate correlation coefficients
for (i in 1:MnumberOfSims2 ) {

  # Is it one of our samples?
  if (i %in% Msamples2){

    # If yes, do the correlation.

    # Start by interpolating the data. We do this because the two time series are different lengths. We need them to start and end at the same times and we need the points in between to match up in order to carry out the correlation.

    # This line takes our extinction rates (mu) and the corresponding times and interpolates the mu onto the temperature times. We can only do a correlation for the temperature data that we have so if we have more mu times than temperature we cannot use them
    interpdiv = approx(Mtimes, rtt_M$mu[i,], temperature$V1, method='linear', rule=1)

    # Here we check whether there is a mu for every temperature time, if not it's left as NA
    end = which(is.na(interpdiv$y))

    # If we have no NAs, ie. there is a time in the temperature time series for each mu, we just use the interpolation as already calculated
    if (length(end) == 0) {
      div_rates = interpdiv$y
      ft = finaltemp
    }

    # Otherwise, we only grab and use the times that have both mu and temperature data
    } else {
      div_rates = interpdiv$y[-end]
      ft = finaltemp[-end]
    }
  }
}

```

Now do the correlation using the interpolated data

```
c = DCCA(as.numeric(unlist(div_rates)),as.numeric(unlist(ft)),length(ft)/10)
```

Store the correlation co-efficient

```
cors_temp_M_E[count] = c[1]
```

Increase your count by 1 ready for the next correlation

```
count = count+1
```

```
}
```

```
}
```

#Create a sink for wilcox test of marine extinction-temperature coefficients

```
sink(file='ExtinctionMarineTemperature.txt')
```

```
print(summary(cors_temp_M_E))
```

```
print(quantile(cors_temp_M_E, c(0.025, 0.975)))
```

```
Mstats3 <- (wilcox.test(cors_temp_M_E, mu=0.0, paired = F))
```

```
Mstats3$p.value
```

```
sink()
```

#Generate data sets for terrestrial extinction-sea level analysis

```
Ttimes= abs(rtt_T$times-max(rtt_T$times))
```

```
TnumberOfSims2 = length(rtt_T$m)/length(rtt_T$times)
```

```
numberOfSamples = 2000
```

```
cors_seaLevel_T_E <- rep(NA, numberOfSamples)
```

```
Tsamples2 = sample(1:TnumberOfSims2, numberOfSamples, replace = F)
```

```
count = 1
```

#Generate correlation coefficients

This loops from 1 to the number of simulations, which is 9,001.

```
for (i in 1:TnumberOfSims2 ) {
```

Is it one of our samples?

```
if (i %in% Tsamples2){
```

If yes, do the correlation.

Again, we have to start by interpolating the data.

```
interpdiv = approx(Ttimes, rtt_T$mu[i,], seaLevel$Age, method='linear', rule=1)
end = which(is.na(interpdiv$y))
if (length(end) == 0) {
  div_rates = interpdiv$y
  ft = seaLevel$SL
} else {
  div_rates = interpdiv$y[-end]
  ft = seaLevel$SL[-end]
}
```

Now do the correlation

```
c = DCCA(as.numeric(unlist(div_rates)),as.numeric(unlist(ft)),length(ft)/10)
```

Store the correlation co-efficient

```
cors_seaLevel_T_E[count] = c[1]
```

Increase your count by 1 ready to do the next.

```
count = count+1
```

```
}
```

```
}
```

#Create a sink for wilcox test of terrestrial extinction-sea level coefficients

```
sink(file='ExtinctionTerrestrialSealevel.txt')
```

```
print(summary(cors_seaLevel_T_E))
```

```
print(quantile(cors_seaLevel_T_E, c(0.025, 0.975)))
```

```
Tstats4 <- (wilcox.test(cors_seaLevel_T_E, mu=0.0, paired = F))
```

```
Tstats4$p.value
```

```
sink()
```

#Generate data sets for marine extinction-sea level analysis

```
Mtimes= abs(rtt_M$times-max(rtt_M$times))
```

```
MnumberOfSims2 = length(rtt_M$mu)/length(rtt_M$times)
```

```

numberOfSamples = 2000
cors_sealevel_M_E <- rep(NA, numberOfSamples)
Msamples2 = sample(1:MnumberOfSims2, numberOfSamples, replace = F)
count = 1
#Generate correlation coefficients
# This loops from 1 to the number of simulations, which is 9,001.
for (i in 1:MnumberOfSims2 ) {

  # Is it one of our samples?
  if (i %in% Msamples2){

    # If yes, do the correlation.
    # Again, we have to start by interpolating the data.
    interpdiv = approx(Mtimes, rtt_M$mu[i,], seaLevel$Age, method='linear', rule=1)
    end = which(is.na(interpdiv$y))
    if (length(end) == 0) {
      div_rates = interpdiv$y
      ft = seaLevel$SL
    } else {
      div_rates = interpdiv$y[-end]
      ft = seaLevel$SL[-end]
    }

    # Now do the correlation
    c = DCCA(as.numeric(unlist(div_rates)),as.numeric(unlist(ft)),length(ft)/10)

    ## Store the correlation co-efficient
    cors_sealevel_M_E[count] = c[1]

    # Increase your count by 1 ready to do the next.
    count = count+1
  }
}
#Create a sink for wilcox test of marine extinction-sea level coefficients

```

```
sink(file='ExtinctionMarineSealevel.txt')
print(summary(cors_sealevel_M_E))
print(quantile(cors_sealevel_M_E, c(0.025, 0.975)))
Mstats4 <- (wilcox.test(cors_sealevel_M_E, mu=0.0, paired = F))
Mstats4$p.value
sink()
```

```
#####
```

#Plotting speciation-temperature for terrestrial

```
qplot(cors_temp_T, geom = 'histogram', bins=30) +
  theme_classic(base_size=17)+
  scale_y_continuous(expand = c(0,0)) +
  scale_x_continuous(expand = c(0,0)) +
  xlab("Correlation coefficient") +
  ylab("Count") +
  annotate('text', x=0, y=150, label="Mean: 0.2713")
```

#Plotting speciation-temperature for marine

```
qplot(cors_temp_M, geom = 'histogram', bins=30) +
  theme_classic(base_size=17)+
  scale_y_continuous(expand = c(0,0)) +
  scale_x_continuous(expand = c(0,0)) +
  xlab("Correlation coefficient") +
  ylab("Count") +
  annotate('text', x=0, y=150, label="Mean: 0.2388")
```

#Plotting speciation-sealevel for terrestrial

```
qplot(cors_seaLevel_T, geom = 'histogram', bins=30) +
  theme_classic(base_size=17)+
  scale_y_continuous(expand = c(0,0)) +
  scale_x_continuous(expand = c(0,0)) +
  xlab("Correlation coefficient") +
  ylab("Count") +
  annotate('text', x=-0.05, y=150, label="Mean: -0.4214")
```

#Plotting speciation-sealevel for marine

```
qplot(cors_seaLevel_M, geom = 'histogram', bins=30) +  
  theme_classic(base_size=17)+  
  scale_y_continuous(expand = c(0,0)) +  
  scale_x_continuous(expand = c(0,0)) +  
  xlab("Correlation coefficient") +  
  ylab("Count") +  
  annotate('text', x=0.1, y=100, label="Mean: -0.17586")
```

#Plotting extinction-temperature for terrestrial

```
qplot(cors_temp_T_E, geom = 'histogram', bins=30) +  
  theme_classic(base_size=17)+  
  scale_y_continuous(expand = c(0,0)) +  
  scale_x_continuous(expand = c(0,0)) +  
  xlab("Correlation coefficient") +  
  ylab("Count") +  
  annotate('text', x=-0.2, y=150, label="Mean: 0.035943")
```

#Plotting extinction-temperature for marine

```
qplot(cors_temp_M_E, geom = 'histogram', bins=30) +  
  theme_classic(base_size=17)+  
  scale_y_continuous(expand = c(0,0)) +  
  scale_x_continuous(expand = c(0,0)) +  
  xlab("Correlation coefficient") +  
  ylab("Count") +  
  annotate('text', x=-0.1, y=150, label="Mean: -0.33712")
```

#Plotting extinction-SeaLevel for terrestrial

```
qplot(cors_seaLevel_T_E, geom = 'histogram', bins=30) +  
  theme_classic(base_size=17)+  
  scale_y_continuous(expand = c(0,0)) +  
  scale_x_continuous(expand = c(0,0)) +  
  xlab("Correlation coefficient") +
```



```
ylab("Count") +  
annotate('text', x=0, y=150, label="Mean: 0.2937")
```

#Plotting extinction-sealevel for marine

```
qplot(cors_sealevel_M_E, geom = 'histogram', bins=30) +  
theme_classic(base_size=17)+  
scale_y_continuous(expand = c(0,0)) +  
scale_x_continuous(expand = c(0,0)) +  
xlab("Correlation coefficient") +  
ylab("Count") +  
annotate('text', x=0.1, y=150, label="Mean: 0.2983")
```