Paleobiology lab 12 answers

Problem set 1:

1)

TriassicSynapsids<-downloadPBDB("Synapsida","Triassic","Triassic")

TriassicDiapsids<-downloadPBDB("Diapsida","Triassic","Triassic")

JurassicDiapsids<-downloadPBDB("Diapsida","Jurassic","Neogene")

JurassicSynapsids<-downloadPBDB("Synapsida","Jurassic","Neogene")

2)

TriassicSynapsids<-cleanRank(TriassicSynapsids,"genus")

TriassicDiapsids<-cleanRank(TriassicDiapsids,"genus")

JurassicDiapsids<-cleanRank(JurassicDiapsids,"genus")

JurassicSynapsids<-cleanRank(JurassicSynapsids,"genus")

TriDiGenera<-subset(TriassicDiapsids[,28])

length(unique(TriDiGenera[,"genus"]))

[1] 430

TriSynGenera<-subset(TriassicSynapsids["genus"])

> length(unique(TriSynGenera[,"genus"]))

[1] 135

3)

JurSynGenera<-subset(JurassicSynapsids["genus"])

JurDiGenera<-subset(JurassicDiapsids["genus"])

length(unique(JurSynGenera[,"genus"]))

[1] 146

length(unique(JurDiGenera[,"genus"]))

[1] 517

##(this is kinda pointless)

TriSynSurvivors<-intersect(TriassicSynapsids[,"genus"],JurassicSynapsids[,"genus"])

[1] "Kuehneotherium" "Thomasia" "Morganucodon" "Pentasauropus"

[5] "Ameghinichnus" "Dicynodontipus" "Sinoconodon" "Oligokyphus"

[9] "Tritylodon"

TriSynVictims<-setdiff(TriassicSynapsids[,"genus"],JurassicSynapsids[,"genus"])

[1] "Therioherpeton" "Adelobasileus"

[3] "Massetognathus" "Ischigualastia"

[5] "Exaeretodon" "Dinodontosaurus"

[7] "Jachaleria" "Chiniquodon"

[9] "Probainognathus" "Brachyzostrodon"

[11] "Lystrosaurus" "Rhadiodromus"

## 126 genera of synapsids did not cross the Triassic/Jurassic boundary

TriDiSurvivors<-intersect(TriassicDiapsids[,"genus"],JurassicDiapsids[,"genus"])

intersect(TriassicDiapsids[,"genus"],JurassicDiapsids[,"genus"])

[1] "Clevosaurus" "Grallator" "Rhynchosauroides"

[4] "Rotodactylus" "Brachychirotherium" "Coelurosaurichnus"

[7] "Synaptichnium" "Chirotherium" "Coelophysis"

[10] "Euskelosaurus" "Melanorosaurus" "Kayentapus"

[13] "Dilophosauripus" "Anomoepus" "Thecodontosaurus"

[16] "Syntarsus" "Gruipeda" "Batrachopus"

[19] "Otozoum" "Tetrasauropus" "Walteria"

[22] "Platypterna" "Massospondylus" "Mystriosuchus"

[25] "Mafatrisauropus" "Megalosaurus" "Steropoides"

[28] "Sauropus" "Argoides" "Thalassiodracon"

[31] "Rhomaleosaurus" "Plesiosaurus" "Shenmuichnus"

[34] "Heterodontosaurus" "Plesiornis" "Moyenisauropus"

[37] "Nihilichnus"

TriDiVictims<-setdiff(TriassicDiapsids[,"genus"],JurassicDiapsids[,"genus"])

[1] "Icarosaurus" "Rutiodon" "Kuehneosuchus"

[4] "Kuehneosaurus" "Trilophosaurus" "Diphydontosaurus"

[7] "Terrestrisuchus" "Planocephalosaurus" "Sigmala"

[10] "Pelecymala" "Hyperodapedon" "Lewisuchus"

[13] "Lagerpeton" "Postosuchus" "Desmatosuchus"

[16] "Malerisaurus" "Efraasia" "Neusticosaurus"

[19] "Plateosaurus" "Aetosaurus" "Saltoposuchus"

[22] "Liliensternus" "Gresslyosaurus" "Doswellia"

393 genera of diapsids did not cross the Triassic/Jurassic boundary.

4)

TriDiOdds<-(length(TriDiSurvivors)/length(TriDiGenera))/(length(TriDiVictims)/(length(TriDiGenera)))

> TriDiOdds

[1] 0.09414758

TriSynOdds<-(length(TriSynSurvivors)/length(TriSynGenera))/(length(TriSynVictims)/(length(TriSynGenera)))

> TriSynOdds

[1] 0.07142857

FlippedOddsRatio<-TriDiOdds/TriSynOdds

> FlippedOddsRatio

[1] 1.318066

> log(FlippedOddsRatio)

[1] 0.2761656

>

5)

StandardError<-sqrt(1/length(TriDiSurvivors) + 1/length(TriDiVictims) + 1/length(TriSynSurvivors) + 1/length(TriSynVictims))

> StandardError

[1] 0.3855116

UpperLimit<-log(FlippedOddsRatio)+StandardError\*1.96

> LowerLimit<-log(FlippedOddsRatio)-StandardError\*1.96

> UpperLimit

[1] 1.031768

> LowerLimit

[1] -0.4794371

So, the 95% confidence interval is -0.479 to 1.0317. So, while Triassic diapsids were more likely than synapsids to cross the Triassic/Jurassic, this likelihood is not unusual enough to count as statistically significant. The lower limit intersects 0, indication that the confidence interval overlaps the perfect 1:1 odds.

(???????????)

Problem set 2

1)

MidLateTri<-downloadPBDB(Taxa=c("Synapsida","Diapsida"),"Anisian","Rhaetian")

MidLateTri<-cleanRank(MidLateTri,"genus")

PostTri<-downloadPBDB(Taxa=c("Synapsida","Diapsida"),"Jurassic","Neogene")

PostTri<-cleanRank(PostTri,"genus")

2)

MeanTriLat<- tapply(MidLateTri[,"paleolat"],MidLateTri[,"genus"],mean)

head(MeanTriLat)

Acaenasuchus Acallosuchus Acompsosaurus

10.116 10.430 10.740

Actiosaurus Adamanasuchus Adelobasileus

32.120 10.145 10.170

3)

TriSurvivors<-intersect(MidLateTri[,"genus"],PostTri[,"genus"])

TriVictims<-setdiff(MidLateTri[,"genus"],PostTri[,"genus"])

4)

TriSynapsids<-subset(MidLateTri,MidLateTri[,"genus"]%in%TriassicSynapsids[,"genus"]==TRUE)

TriDiapsids<-subset(MidLateTri,MidLateTri[,"genus"]%in%TriassicDiapsids[,"genus"]==TRUE)

5)

TriVictims<-array(0,dim=length(TriVictims),dimnames=list(TriVictims))

> head(TriVictims)

Icarosaurus Rutiodon Kuehneosuchus

0 0 0

Kuehneosaurus Trilophosaurus Diphydontosaurus

0 0 0

TriMatrix<-merge(TriVictims,MeanTriLat,all=TRUE,by="row.names")

> head(TriMatrix)

Row.names x y

1 Acaenasuchus 0 10.116

2 Acallosuchus 0 10.430

3 Acompsosaurus 0 10.740

4 Actiosaurus 0 32.120

5 Adamanasuchus 0 10.145

6 Adelobasileus 0 10.170

colnames(TriMatrix)<-c("genus name"," Survivor/Victim"," Mean Latitude")

> head(TriMatrix)

genus name Survivor/Victim Mean Latitude

1 Acaenasuchus 0 10.116

2 Acallosuchus 0 10.430

3 Acompsosaurus 0 10.740

4 Actiosaurus 0 32.120

5 Adamanasuchus 0 10.145

6 Adelobasileus 0 10.170

> Regression<-glm(TriMatrix[,"Survivor/Victim"]~TriMatrix[,"Mean Latitude"],family="binomial")

summary(Regression)

Call:

glm(formula = TriMatrix[, "Survivor/Victim"] ~ TriMatrix[, "Mean Latitude"],

family = "binomial")

Deviance Residuals:

Min 1Q Median 3Q Max

-0.4474 -0.4411 -0.4385 -0.4308 2.1889

Coefficients:

Estimate Std. Error

(Intercept) -2.3009122 0.1547326

TriMatrix[, "Mean Latitude"] 0.0007725 0.0051555

z value Pr(>|z|)

(Intercept) -14.87 <2e-16 \*\*\*

TriMatrix[, "Mean Latitude"] 0.15 0.881

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Signif. codes:

0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 308.10 on 504 degrees of freedom

Residual deviance: 308.08 on 503 degrees of freedom

AIC: 312.08

Number of Fisher Scoring iterations: 5

Was the mean latitude of a Triassic genus a good predictor of its survival across the T/J extinction?