

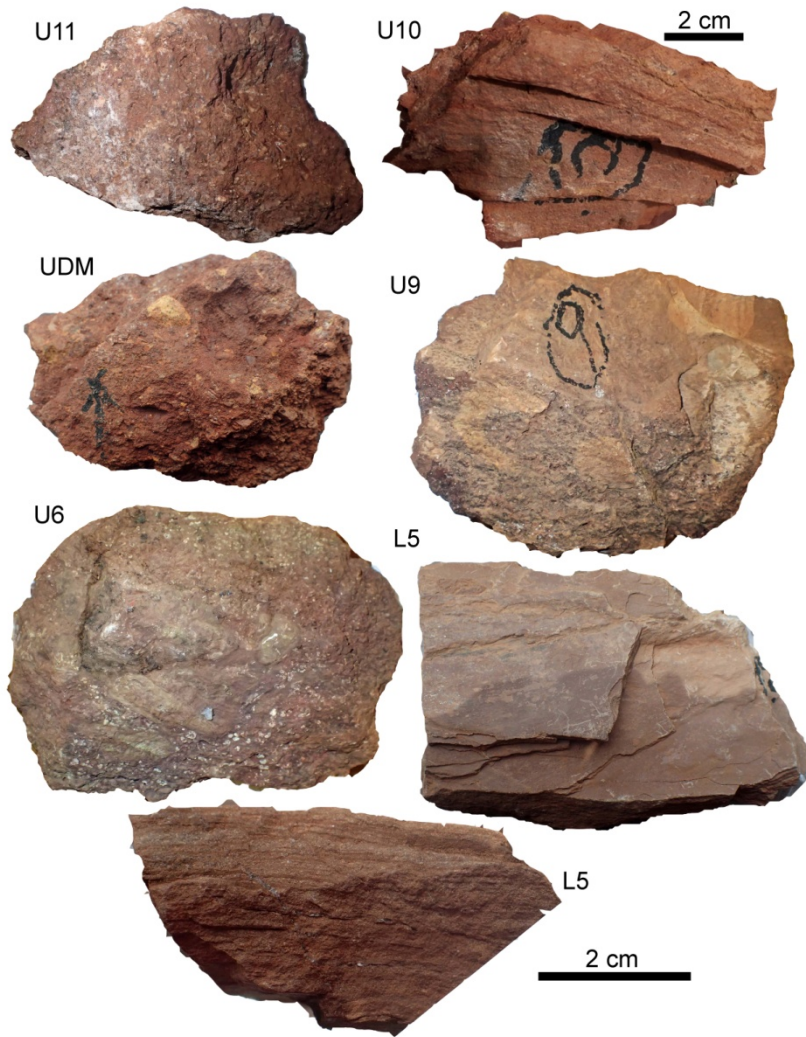
Anatomy of a Late Triassic Bristol fissure: Tytherington fissure 2

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Supplementary data

<i>Sample</i>	<i>Rock type</i>	<i>Original mass (g)</i>
Upper (U) 1	Quasi layered brown hard marl with small voids and some calcite.	283
U2	Conglomerate with brecciated clasts and some green clay film.	3409
U3	Reddish rock with some calcite veining and ooids.	308
U4	Reddish brown hard marl/conglomerate. Very few ooids.	168
U5	Conglomerate with yellow dolomitised Carboniferous limestone clasts, small voids and some authigenic clay pockets.	2062
U6	Conglomerate with ooids and travertine.	1240
U7	Brown rock with ooids and small voids-some calcite filled.	146
U9	Brecciated rock with variety of clasts, including layered clasts. Possible travertine clasts plus small dolomitised Carboniferous limestone clasts.	760
U10	Thick layered brown sandy limestone.	214
U11	Conglomerate-small clasts. Crystalline.	75
UDM	UDM Red detrital marl-conglomerate with yellow dolomitised Carboniferous limestone clasts.	229
Lower (L) 1	Brown hard marl with calcite-filled voids.	261
L2	Brown darker brown grey layered marl.	80
L3	Grey hard marl.	196
L4	Conglomerate with calcite-filled voids.	241
L5	Brown dark brown thinly layered marl. Bordered 'scallop'.	586
'Slump'	Small clast conglomerate. Top of lower section.	236

Appendix Table 1. Geological characteristics of the rock samples of the Ex17 of Fissure 2, based on Whiteside and Marshall (2008) and current study.



Appendix Fig. 1. A selection of labelled rock samples used in the analysis. Rock mass is given in Appendix table 1. Note the ooids in U6, the breccia (possibly travertine) of U9 and the well layered L5. UDM is a conglomerate with yellow (limonite) soft dolomitised clasts in a red matrix.

Appendix 3: complete R scripts and outputs of statistical analyses

Citation: R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria.

1) Analysis of differences in specimens percentages between upper, lower, and glauconitic clay sections of the 17 m exposure

```

>
> ## Diphydontosaurus
>
> diphy<-kwtable$Diphy
> group<-kwtable$group
>
> shapiro.test(kwtable$Diphy) #distribution not normal
> kruskal.test(diphy~ group, data = kwtable) #p=0.05069
>
> ## Clevosaurus
>
> clevo<-kwtable$Clevo
> group<-kwtable$group
>
> shapiro.test(clevo) #distribution not normal
>
> ktclevo<-kruskal.test(kwtable$Clevo~ kwtable$group, data = kwtable) >
require(PMCMR)
> posthoc.kruskal.dunn.test(clevo~ group, p.adjust.method="none")
> ##### p=0.006715, differences between u-1 and l-g >
>
> ##Planocephalosaurus
>
> plano<-kwtable$Plano
> group<-kwtable$group
>
> shapiro.test(kwtable$Plano) #distribution not normal
> kruskal.test(plano~ group, data = kwtable) #p=0.054
>
> ## Gyrolepis
> gyro<-kwtable$Gyrolepis
> group<-kwtable$group
>
> shapiro.test(kwtable$Gyrolepis) #distribution not normal
> kruskal.test(gyro~ group, data = kwtable) #####p=0.02822, diff.
between u- 1
> require(PMCMR)
> posthoc.kruskal.dunn.test(gyro~ group, p.adjust.method="none") >
>
>
> ## 'Euestheria'
> euestheria<-kwtable$Euestheria
> group<-kwtable$group
>
> shapiro.test(kwtable$Euestheria) #distribution not normal
> kruskal.test(euestheria~ group, data = kwtable) #p=0.1799
> ## Crossostoma
> cro<-kwtable$Crossostoma
> group<-kwtable$group
>
> shapiro.test(kwtable$Crossostoma) #distribution not normal
> kruskal.test(cro~ group, data = kwtable) #####p-value=0.01078, diff.
u-1
> require(PMCMR)
> posthoc.kruskal.dunn.test(cro~ group, p.adjust.method="none")
>
>
> ## Chemnitzia
> chem<-kwtable$Chemnitzia

```

```

> group<-kwttable$group
>
> shapiro.test(kwttable$Chemnitzia) #distribution not normal
> kruskal.test(chem~ group, data = kwttable) #p=0.2317
>
> ##Archosaurs (excluding Thecodontosaurus and Terrestrisuchus) >
> archos<-kwttable$Archos
> group<-kwttable$group
>
> shapiro.test(kwttable$Archos) #distribution not normal
> kruskal.test(archos~ group, data = kwttable) #p-value=0.4465
>
> ##Crinoids
> crinoids<-kwttable$Crinoids
> group<-kwttable$group
>
> shapiro.test(kwttable$Crinoids) #distribution not normal
> kruskal.test(crinoids~ group, data = kwttable) #####p-value =
0.001397, diff. u-l.
> require(PMCMR)
> posthoc.kruskal.dunn.test(crinoids~ group, p.adjust.method="none")
>
>
> ##Chimaeroids
>
> chimaeroids<-kwttable$Carbofish
> group<-kwttable$group
>
> shapiro.test(kwttable$Carbofish) #distribution not normal
> kruskal.test(chimaeroids~ group, data = kwttable) #p-value = 0.2387
>
> ##Fragments
>
> fragments<-kwttable$Fragments
> group<-kwttable$group
>
> shapiro.test(kwttable$Fragments) #distribution not normal
> kruskal.test(fragments~ group, data = kwttable) #p-value = 0.2098
>
> ##Sharks
> sharks<-kwttable$Sharks
> group<-kwttable$group
>
> shapiro.test(kwttable$Sharks) #distribution not normal
> kruskal.test(sharks~ group, data = kwttable) #p-value=0.1034

```

2) Fisher's exact test for interspecific associations across samples

```

> ## van den Berg's significant or quasi-significant associations: >
> #Diphydontosaurus-Clevosaurus
> #####- p-value = 0.01729 #####
> diphyclevo <- matrix( c(12, 1, 2, 4), nrow=2, ncol=2)
> fisher.test(diphyclevo, alternative="two.sided")
>
> #Diphydontosaurus-Thecodontosaurus
> diphytheco <- matrix( c(2,0 ,12 ,5 ), nrow=2, ncol=2)
> fisher.test(diphytheco, alternative="two.sided")
>
> #Diphydontosaurus-Planocephalosaurus p-value = 0.04455 #####
> diphyplano<- matrix( c(8, 0,6 ,5 ), nrow=2, ncol=2)
> fisher.test(diphyplano, alternative="two.sided")
>
> #Thecodontosaurus-Planocephalosaurus
> thecoplano<- matrix( c(2,6 ,0 ,11 ), nrow=2, ncol=2)
> fisher.test(thecoplano, alternative="two.sided")
>
> #Thecodontosaurus-Clevosaurus
>

```

```

> thecoclevo<- matrix( c(2,11 ,0 ,6 ), nrow=2, ncol=2)
> fisher.test(thecoclevo, alternative="two.sided")
>
> #Archosaurs-ClevoSaurus, p=0.0436 #####
>
> archoclevo<- matrix( c(7, 6,0 ,6 ), nrow=2, ncol=2)
> fisher.test(archoclevo, alternative="two.sided")
>
> #Archosaurs-Diphydontosaurus,
>
> archodiphy<- matrix( c(7, 0, 7,5 ), nrow=2, ncol=2)
> fisher.test(archodiphy, alternative="two.sided")
>
> #Planocephalosaurus-ClevoSaurus
>
> planoclevo<- matrix( c(7,6,1 ,5), nrow=2, ncol=2)
> fisher.test(planoclevo, alternative="two.sided")
>
> #Gyrolepis-Archosaurs
> gyroarcho <- matrix( c(4,3 ,3 ,9 ), nrow=2, ncol=2)
> fisher.test(gyroarcho, alternative="two.sided")
>
> #Diphydontosaurus-Chimaeroids
>
> diphychim<-matrix( c(11,1 ,4 ,3), nrow=2, ncol=2)
> fisher.test(diphychim, alternative="two.sided")
>
> ##Do sphenodontians associate with reworked taxa?
>
> #ClevoSaurus-Chimaeroids ##### p-value = 0.002912
> clevochim<-matrix( c(12, 1, 1, 5), nrow=2, ncol=2)
> fisher.test(clevochim, alternative="two.sided")
>
> #Planocephalosaurus-Chimaeroids
> planochim<-matrix( c(7,6 ,1 ,5), nrow=2, ncol=2)
> fisher.test(planochim, alternative="two.sided")
> #Diphydontosaurus-Crinoids ##### p-value = 0.006106 > diphycrino<-
matrix( c(13,1 ,1 ,4 ), nrow=2, ncol=2)
> fisher.test(diphycrino, alternative="two.sided")
> #ClevoSaurus-Crinoids p=0.000516 #####
> clevocrino<-matrix( c(13,1 ,0 ,5 ), nrow=2, ncol=2)
> fisher.test(clevocrino, alternative="two.sided")
>
> #Planocephalosaurus-Crinoids
> planocrino<-matrix( c(7,6 ,1 ,5), nrow=2, ncol=2)
> fisher.test(planocrino, alternative="two.sided")
>
> -----
> #Archosaurs-Planocephalosaurus p-value = 0.06233 ## >
> archoplano<-matrix( c(5, 2, 3,9), nrow=2, ncol=2)
> fisher.test(archoplano, alternative="two.sided")
>
> #Crossostoma-Archosaurs
>
> crossostomarcho<-matrix( c(6,1 ,5,7), nrow=2, ncol=2) >
fisher.test(crossostomarcho, alternative="two.sided")
>
> #Crossostoma-Planocephalosaurus, p-value = 0.05866 ##
> crossostomaplano<-matrix( c(7,4 ,1 ,7), nrow=2, ncol=2)
> fisher.test(crossostomaplano, alternative="two.sided")
>
> #Crossostoma-Chemnitzia p-value = 0.04455 #####
> crossostomachemnitzia<-matrix( c(5, 6, 0,8), nrow=2, ncol=2)
> fisher.test(crossostomachemnitzia, alternative="two.sided")
>
> #Crossostoma-Euestheria
> crossostomaeuestheria<-matrix( c(4,7 ,0 ,8), nrow=2, ncol=2)
> fisher.test(crossostomaeuestheria, alternative="two.sided")

```

```

>
> ##Are sharks associated with marine (Trias) or reworked taxa? >
#Gyrolepis-Sharks
> gyroshark<-matrix( c(3,2 ,4 ,10), nrow=2, ncol=2)
> fisher.test(gyroshark, alternative="two.sided")
>
> #Crossostoma-Sharks
  • > crossostomashark<-matrix( c(4,1 ,7 ,7), nrow=2, ncol=2)
  • > fisher.test(crossostomashark, alternative="two.sided")
>
> #Crinoids-Sharks
> crinoshark<-matrix( c(5,0 ,9 ,5), nrow=2, ncol=2)
> fisher.test(crinoshark, alternative="two.sided")
>
> #Chimaeroids-Sharks
>
> chimaeroidshark<-matrix( c(5, 0, 8,6), nrow=2, ncol=2) >
fisher.test(chimaeroidshark, alternative="two.sided")
>
> #Thecodontosaurus and Terrestrisuchus occur always together
>
> # Terrestrisuchus-Thecodontosaurus p-value = 0.005848 ##### >
terrestritheco<-matrix( c(2,0 ,0 ,17), nrow=2, ncol=2)
> fisher.test(terrestritheco, alternative="two.sided")
>
> ##Marine taxa associations?
>
> #Crossostoma-Gyrolepis p-value = 0.01282 ##### crossostoma-
chemnitzia p-value = 0.04455
>
> crossostomagyro<-matrix( c(7,0 ,4 ,8), nrow=2, ncol=2)
> fisher.test(crossostomagyro, alternative="two.sided")
>
> #Gyrolepis-Chemnitzia
>
> chemgyro<-matrix( c(3, 4, 2,10), nrow=2, ncol=2) > fisher.test(chemgyro,
alternative="two.sided")
> #Associations between Clevosaurus and marine taxa
>
> clevogyro<-matrix( c(7, 6, 0,6), nrow=2, ncol=2) #####
> fisher.test(clevogyro, alternative="two.sided")
>
> clevocrossostoma<-matrix( c(11,2 ,0 ,6), nrow=2, ncol=2) #####
> fisher.test(clevocrossostoma, alternative="two.sided")
>
> clevosharks<-matrix( c(5,8 ,0 ,6), nrow=2, ncol=2)
> fisher.test(clevosharks, alternative="two.sided")
> clevochemnitzia<-matrix( c(5,8 ,0 ,6), nrow=2, ncol=2)
> fisher.test(clevochemnitzia, alternative="two.sided")
#Diphydontosaurus and marine taxa
>
>
> diphygyro<-matrix( c(7, 7, 0,5), nrow=2, ncol=2)
fisher.test(diphygyro, alternative="two.sided")
>
> diphycrossostoma<-matrix( c(10,1 ,4 ,4), nrow=2, ncol=2)
> fisher.test(diphycrossostoma, alternative="two.sided")
>
> diphysharks<-matrix( c(5,9 ,0 ,5), nrow=2, ncol=2)
> fisher.test(diphysharks, alternative="two.sided")
>
> diphychemnitzia<-matrix( c(5, 9,0 ,5), nrow=2, ncol=2) >
fisher.test(diphychemnitzia, alternative="two.sided")
>
> #Planocephalosaurus and marine taxa
>
>
> planogyro<-matrix( c(4,4 ,3 ,8), nrow=2, ncol=2)

```

```

> fisher.test(planogyro, alternative="two.sided")
>
> planocrossostoma<-matrix( c(7,1 ,4 ,7), nrow=2, ncol=2)
> fisher.test(planocrossostoma, alternative="two.sided")
>
> planosharks<-matrix( c(4,1 ,5 ,9), nrow=2, ncol=2)
> fisher.test(planosharks, alternative="two.sided")
> planochemnitzia<-matrix( c(3,2 ,5 ,9), nrow=2, ncol=2)
> fisher.test(planochemnitzia, alternative="two.sided")

```

3) Linear models for testing interspecific correlations

```

>
> #check correlation between reworked and Triassic fossil density: >
> Triasdens<-my_data$`Trias. Density`
> Rewdens<-my_data$`Rew. Density`
> taphomodel<-lm(Rewdens ~Triasdens, data = my_data)
> summary(taphomodel) #significant
> qqplot(x=Rewdens, y=Triasdens, data=my_data, xlab= "Rewdens",
ylab="Triasdens" ) + theme_bw()
> #Clevosaurus/Diphydontosaurus
>
> clevo<-my_data$Clevo
> diphy<-my_data$Diphy
>
> library(ggplot2)
> qqplot(x=diphy, y=clevo, data=my_data, xlab= "Diphydontosaurus",
ylab="Clevosaurus") + theme_bw()
>
>
> model<-lm(clevo ~ diphy, data = my_data)
> summary(model)
> #Planocephalosaurus/Chimaeroids
> plano<-my_data$Plano
> carbofish<-my_data$CarboFish
>
> library(ggplot2)
> qqplot(x=carbofish, y=plano, data=my_data, xlab= "CarboFish",
ylab="Planocephalosaurus") + theme_bw()
>
>
> model0<-lm(plano ~ carbofish, data = my_data)
> summary(model0)
>
> #Planocephalosaurus/Crinoids
> plano<-my_data$Plano
> crinoids<-my_data$Crinoids
>
> library(ggplot2)
> qqplot(x=crinoids, y=plano, data=my_data, xlab= "Crinoids",
ylab="Planocephalosaurus") + theme_bw()
>
>
> model.<-lm(plano ~ crinoids, data = my_data)
> summary(model.)
>
> #Clevosaurus/Chimaeroids
>
> clevo<-my_data$Clevo
> carbofish<-my_data$CarboFish
>
> library(ggplot2)
> qqplot(x=carbofish, y=clevo, data=my_data, xlab= "CarboFish",
ylab="Clevosaurus") + theme_bw()
>
>
> model1<-lm(clevo ~ carbofish, data = my_data)
> summary(model1)

```

```

# Clevosaurus/Crinoids: p-value: 0.03473
> #####
>
> clevo<-my_data$Clevo
> crinoids<-my_data$Crinoids
>
> library(ggplot2)
> qplot(x=crinoids, y=clevo, data=my_data, xlab= "Crinoids",
ylab="Clevosaurus" ) + theme_bw()
>
>
> model1<-lm(clevo ~ crinoids, data = my_data)
> summary(model1)
>
> #Thecodontosaurus/Diphydontosaurus
>
> theco<-my_data$Theco
> diphy<-my_data$Diphy
>
> library(ggplot2)
> qplot(x=diphy, y=theco, data=my_data, xlab= "Diphydontosaurus",
ylab="Thecodontosaurus") + theme_bw()
>
>
> model2<-lm(theco ~ diphy, data = my_data)
> summary(model2)
>
> #Diphydontosaurus/Planocephalosaurus
>
> plano<-my_data$Plano
> diphy<-my_data$Diphy
>
> library(ggplot2)
> qplot(x=diphy, y=plano, data=my_data, xlab= "Diphydontosaurus",
ylab="Planocephalosaurus") + theme_bw()
>
>
> model3<-lm(plano ~ diphy, data = my_data)
> summary(model3)
>
> #Clevosaurus/Planocephalosaurus
>
> plano<-my_data$Plano
> clevo<-my_data$Clevo
>
> library(ggplot2)
> qplot(x=clevo, y=plano, data=my_data, xlab= "Clevosaurus",
ylab="Planocephalosaurus") + theme_bw()
>
>
> model13<-lm(plano ~ clevo, data = my_data)
> summary(model13)
>
> #Thecodontosaurus/Planocephalosaurus
>
> plano<-my_data$Plano
> theco<-my_data$Theco
>
> library(ggplot2)
> qplot(x=theco, y=plano, data=my_data, xlab= "Thecodontosaurus",
ylab="Planocephalosaurus") + theme_bw()
>
>
> model4<-lm(plano ~ theco, data = my_data)
> summary(model4)
>
> #Thecodontosaurus/Clevosaurus

```



```

>
> theco<-my_data$Theco
> clevo<-my_data$Clevo
>
> library(ggplot2)
> qplot(x=theco, y=clevo, data=my_data, xlab= "Thecodontosaurus",
ylab="Clevosa urus") + theme_bw()
>
>
> model6<-lm(clevo ~ theco, data = my_data)
> summary(model6)
>
> #Clevosaurus/Archosaus
>
> clevo<-my_data$Clevo
> archo<-my_data$Archos
>
> library(ggplot2)
> qplot(x=clevo, y=archo, data=my_data, xlab= "Clevosaurus",
ylab="Archosaurs") + theme_bw()
>
>
> model7<-lm(archo ~ clevo, data = my_data)
> summary(model7)
>
> #Planocephalosaurus/Archosaurs
>
> plano<-my_data$Plano
> archo<-my_data$Archos
>
> library(ggplot2)
> qplot(x=plano, y=archo, data=my_data, xlab= "Planocephalosaurus",
ylab="Archo saurs") + theme_bw()
>
>
> model12<-lm(archo ~ plano, data = my_data)
> summary(model12)
>
> # Diphydontosaurus/Archosaurs
>
> diphy<-my_data$Diphy
> archo<-my_data$Archos
>
> library(ggplot2)
> qplot(x=diphy, y=archo, data=my_data, xlab= "Diphydontosaurus",
ylab="Archosa urs") + theme_bw()
>
>
> model11<-lm(archo ~ diphy, data = my_data)
> summary(model11)
>
> #Planocephalosaurus/Clevosaurus
>
> clevo<-my_data$Clevo
> plano<-my_data$Plano
>
> library(ggplot2)
> qplot(x=plano, y=clevo, data=my_data, xlab= "Planocephalosaurus",
ylab="Clevo saurus") + theme_bw()
>
>
> model8<-lm(clevo ~ plano, data = my_data)
> summary(model8)
#Archosaurs/Gyrolepis
>
> gyrolepis<-my_data$Gyrolepis
> archo<-my_data$Archos
>
> library(ggplot2)

```

```

> qplot(x=archo, y=gyrolepis, data=my_data, xlab= "Archosaurs",
ylab="Gyrolepis ") + theme_bw()
>
>
> model9<-lm(gyrolepis ~ archo, data = my_data)
> summary(model9)
>
> #Diphydontosaurus/Chimaeroids
>
> carbofish<-my_data$CarboFish
> diphy<-my_data$Diphy
>
> library(ggplot2)
> qplot(x=diphy, y=carbofish, data=my_data, xlab= "Diphydontosaurus",
ylab="Car boniferous fishes") + theme_bw()
>
>
> model10<-lm(carbofish ~ diphy, data = my_data)
> summary(model10)
>
> #Diphydontosaurus/Crinoids
> crinoids<-my_data$Crinoids
> diphy<-my_data$Diphy
>
> library(ggplot2)
> qplot(x=diphy, y=crinoids, data=my_data, xlab= "Diphydontosaurus",
ylab="Crin oids") + theme_bw()
>
>
> model10a<-lm(crinoids ~ diphy, data = my_data)
> summary(model10a)
>
> # Diphydontosaurus/Crossostoma
>
> cro<-my_data$Crossostoma
> diphy<-my_data$Diphy
>
> library(ggplot2)
> qplot(x=diphy, y=cro, data=my_data, xlab= "Diphydontosaurus",
ylab="Crossosto ma") + theme_bw()
>
>
> model14<-lm(cro ~ diphy, data = my_data)
> summary(model14)
> # Clevosaurus/Crossostoma
> ##### p-value: 0.008005
>
>
> cro<-my_data$Crossostoma
> clevo<-my_data$Clevo
>
> library(ggplot2)
> qplot(x=clevo, y=cro, data=my_data, xlab= "Clevosaurus",
ylab="Crossostoma") + theme_bw()
>
>
> model15<-lm(cro ~ clevo, data = my_data)
> summary(model15)
>
> # Planocephalosaurus/Crossostoma
>
>
> cro<-my_data$Crossostoma
> plano<-my_data$Plano
>
> library(ggplot2)
> qplot(x=plano, y=cro, data=my_data, xlab= "Planocephalosaurus",
ylab="Crossos toma") + theme_bw()
>

```

```

>
> model16<-lm(cro ~ plano, data = my_data)
> summary(model16)
> #Euestheria/Crossostoma,
>
> cro<-my_data$Crossostoma
> euestheria<-my_data$Euestheria
>
> library(ggplot2)
> qplot(x=euestheria, y=cro, data=my_data, xlab= "Euestheria",
ylab="Crossostoma") + theme_bw()
>
>
> model17<-lm(cro ~ euestheria, data = my_data)
> summary(model17)
>
> #Planocephalosaurus/Gyrolepis
>
> plano<-my_data$Plano
> gyrolepis<-my_data$Gyrolepis
>
> qplot(x=gyrolepis, y=plano, data=my_data,
xlab="Gyrolepis",ylab="Planocephalosaurus")
>
> model18<-lm(plano~gyrolepis, data=my_data)
> summary(model18)
>
> #Gyrolepis/Crossostoma
>
> cro<-my_data$Crossostoma
> gyrolepis<-my_data$Gyrolepis
>
> library(ggplot2)
> qplot(x=gyrolepis, y=cro, data=my_data, xlab= "Gyrolepis",
ylab="Crossostoma" ) + theme_bw()
>
>
> model19<-lm(cro ~ gyrolepis, data = my_data)
> summary(model19)
>
> #Gyrolepis/Euestheria
>
> gyrolepis<-my_data$Gyrolepis
> euestheria<-my_data$Euestheria
>
> library(ggplot2)
> qplot(x=euestheria, y=gyrolepis, data=my_data, xlab= "Euestheria",
ylab="Gyrolepis") + theme_bw()
>
>
> model20<-lm(gyrolepis ~ euestheria, data = my_data)
> summary(model20)
> #C.granum/Crossostoma p-value: 0.003407
> #####
> cro<-my_data$Crossostoma
> chemnitzia<-my_data$`Chemnitzia granum`
>
> library(ggplot2)
> qplot(x=chemnitzia, y=cro, data=my_data, xlab= "Chemnitzia granum",
ylab="Crossostoma") + theme_bw()
>
>
> model21<-lm(cro ~ chemnitzia, data = my_data)
> summary(model21)
>
> #Euestheria/C.granum
>
> euestheria<-my_data$Euestheria
> chemnitzia<-my_data$`Chemnitzia granum`

```

```

>
> library(ggplot2)
> qplot(x=chemnitzia, y=euestheria, data=my_data, xlab= "Chemnitzia
granum", ylab="Euestheria") + theme_bw()
>
>
> model22<-lm(euestheria ~ chemnitzia, data = my_data)
> summary(model22)
>
> #Chimaeroids/Sharks
>
> carbofish<-my_data$CarboFish
> sharks<-my_data$Sharks
>
> qplot(x=carbofish, y=sharks, data=my_data, xlab="Chimaeroids",
ylab="Shark denticles")
>
> model23<-lm(sharks~carbofish, data=my_data)
> summary(model23)
>
> #Crossostoma/Sharks
>
> cro<-my_data$Crossostoma
> sharks<-my_data$Sharks
>
> qplot(x=cro, y=sharks, data=my_data, xlab="Crossostoma", ylab="Shark
denticle s")
>
> model24<-lm(sharks~cro, data=my_data)
> summary(model24)
>
> #'Euestheria'/Sharks
>
> euestheria<-my_data$Euestheria
> sharks<-my_data$Sharks
>
> qplot(x=euestheria, y=sharks, data=my_data, xlab="Euestheria",
ylab="Shark denticles")
>
> model25<-lm(sharks~euestheria, data=my_data)
> summary(model25)
>
> #Sharks/Archosaurs
>
> archos<-my_data$Archos
> sharks<-my_data$Sharks
>
> qplot(x=archos, y=sharks, data=my_data, xlab="Archosaurs", ylab="Shark
dentic les")
>
> model26<-lm(sharks~archos, data=my_data)
> summary(model26)
>
> #Shark-sphenodonts regressions
> #Sharks/Clevo ##### p-value: 0.04586 > sharks<-my_data$Sharks
> clevo<-my_data$Clevo
>
> qplot(x=clevo, y=sharks, data=my_data, xlab="Clevosaurus", ylab="Shark
dentic les")
>
> model27<-lm(sharks~clevo, data=my_data)
> summary(model27)
>
> #Sharks/Plano
>
> sharks<-my_data$Sharks
> plano<-my_data$Plano
>
> qplot(x=plano, y=sharks, data=my_data, xlab="Planocephalosaurus",

```

```

ylab="Shark denticles")
>
> model28<-lm(sharks~plano, data=my_data)
> summary(model28)
>
> # Sharks/Diphy
>
> sharks<-my_data$Sharks
> diphy<-my_data$Diphy
>
> qqplot(x=diphy, y=sharks, data=my_data, xlab="Diphydontosaurus",
ylab="Shark denticles")
>
> model29<-lm(sharks~diphy, data=my_data)
> summary(model29)
>
> #Sharks/Gyrolepis
>
> sharks<-my_data$Sharks
> gyrolepis<-my_data$Gyrolepis
>
> qqplot(x=gyrolepis, y=sharks, data=my_data, xlab="Gyrolepis", ylab="Shark
denticles")
>
> model30<-lm(sharks~gyrolepis, data=my_data)
> summary(model30)
> #Archosaurs/Crossostoma p-value: 0.02977
> #####
> archos<-my_data$Archos
> cro<-my_data$Crossostoma
>
> qqplot(x=archos, y=cro, data=my_data, xlab="Archosaurs",
ylab="Cylindrobullina ")
>
> model31<-lm(cro~archos, data=my_data)
> summary(model31)
>
> #Archosaurs/Euestheria
>
> archos<-my_data$Archos
> euestheria<-my_data$Euestheria
>
> qqplot(x=archos, y=euestheria, data=my_data, xlab="Archosaurs",
ylab="Euestheria")
>
> model32<-lm(euestheria~archos, data=my_data)
> summary(model32)
>
> #Archosaurs/Chemnitzia
> archos<-my_data$Archos
> chemnitzia<-my_data$`Chemnitzia granum`
>
> qqplot(x=archos, y=chemnitzia, data=my_data, xlab="Archosaurs",
ylab="Chemnitzia granum")
>
> model33<-lm(chemnitzia~archos, data=my_data)
> summary(model33)
> #Chimaeroid elements/Crinoids
>
> crinoids<-my_data$Crinoids
> carbofish<-my_data$CarboFish
>
> qqplot(x=crinoids, y=carbofish, data=my_data, xlab="Crinoids",
ylab="Chimaeroid elements")
>
> model34<-lm(carbofish~crinoids, data=my_data) > summary(model34)
>
> #Gyrolepis/Chimaeroid elements

```

```

>
> carbofish<-my_data$CarboFish
> gyrolepis<-my_data$Gyrolepis
>
> qqplot(x=gyrolepis, y=carbofish, data=my_data, xlab="Gyrolepis",
ylab="Chimaeroid elements")
>
> model35<-lm(carbofish~gyrolepis, data=my_data)
> summary(model35)
>
> #Gyrolepis/Crinoids
>
> crinoids<-my_data$Crinoids
> gyrolepis<-my_data$Gyrolepis
>
> qqplot(x=gyrolepis, y=crinoids, data=my_data, xlab="Gyrolepis",
ylab="Crinoids ")
>
> model35a<-lm(crinoids~gyrolepis, data=my_data) > summary(model35a)
>
> #Gyrolepis/Euestheria
> euestheria<-my_data$Euestheria
> gyrolepis<-my_data$Gyrolepis
>
> qqplot(x=gyrolepis, y=euestheria, data=my_data, xlab="Gyrolepis",
ylab="Euestheria")
>
> model37<-lm(euestheria~gyrolepis, data=my_data)
> summary(model37)
>
> #Gyrolepis/Chemnitzia p-value: 2.085e-05
> #####
> chemnitzia<-my_data$`Chemnitzia granum`
> gyrolepis<-my_data$Gyrolepis
>
> qqplot(x=gyrolepis, y=chemnitzia, data=my_data, xlab="Gyrolepis",
ylab="Chemnitzia")
>
> model38<-lm(chemnitzia~gyrolepis, data=my_data)
> summary(model38)
>
> #Archos/Chimaeroid elements
>
> carbofish<-my_data$CarboFish
> archos<-my_data$Archos
>
> qqplot(x=archos, y=carbofish, data=my_data, xlab="Archosaurs",
ylab="Chimaeroid elements")
>
> model39<-lm(carbofish~archos, data=my_data)
> summary(model39)
>
> #Archos/Chimaeroid elements
>
> carbofish<-my_data$Crinoids
> archos<-my_data$Archos
>
> qqplot(x=archos, y=crinoids, data=my_data, xlab="Archosaurs",
ylab="Crinoids") >
> model39a<-lm(crinoids~archos, data=my_data)
> summary(model39a)

```