

# Body size trends in fossil tortoises

```
## Warning in evalq(((as.numeric(as.character(MAmin)))) +
## (as.numeric(as.character(Mamax))))/2, : NAs durch Umwandlung erzeugt
```

**paleoTS Plot with the following bins (for fossil taxa):**

```
## Warning in bind_rows(x, .id): binding character and factor vector,
## coercing into character vector
```

```
## Warning in bind_rows(x, .id): binding character and factor vector,
## coercing into character vector
```

```
## Warning in bind_rows(x, .id): binding character and factor vector,
## coercing into character vector
```

```
## Warning in bind_rows(x, .id): binding character and factor vector,
## coercing into character vector
```

bin	n
(0,1e-06]	240
(1e-06,0.0117]	12
(0.0117,0.126]	46
(0.126,0.781]	46
(0.781,2.59]	68
(2.59,3.6]	19
(3.6,5.33]	22
(5.33,11.6]	41

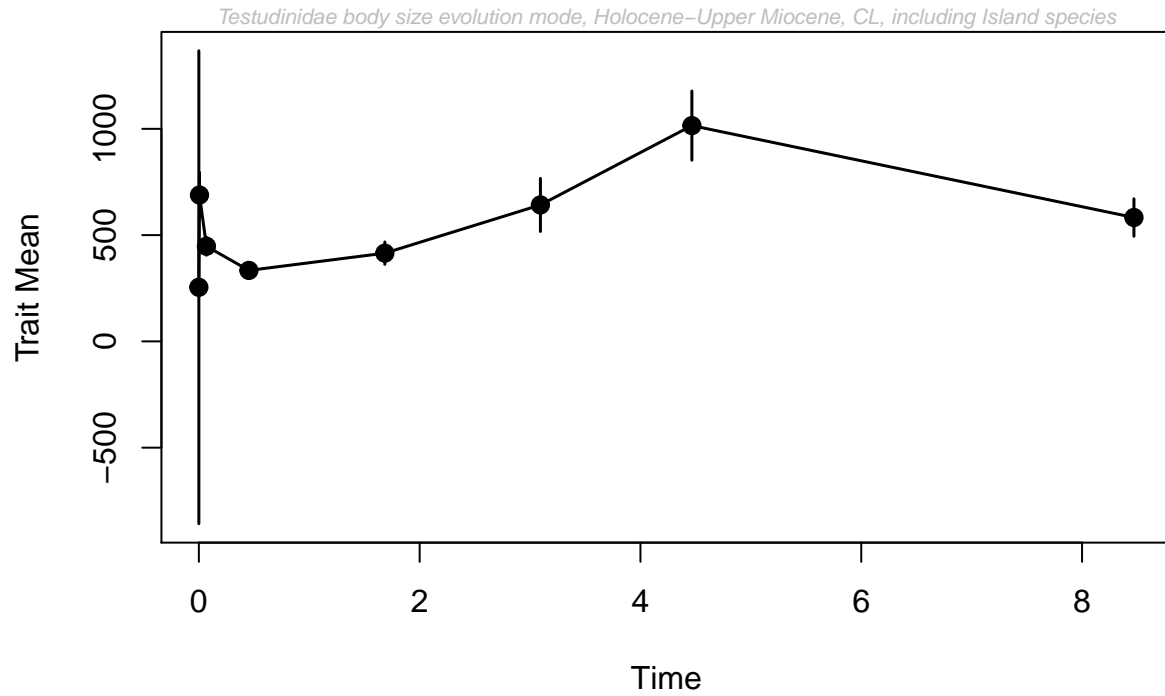
bin	EpochBins	MeanBins
(0,1e-06]	Modern	0.0000005
(1e-06,0.0117]	Holocene	0.0058500
(0.0117,0.126]	Upper Pleistocene	0.0688500
(0.126,0.781]	Middle Pleistocene	0.4535000
(0.781,2.59]	Lower Pleistocene	1.6845000
(2.59,3.6]	Upper Pliocene	3.0940000
(3.6,5.33]	Lower Pliocene	4.4660000
(5.33,11.6]	Upper Miocene	8.4700000

**including Island species (n=2214)**

paleoTS object (mm= mean CL, nn = sample size, vv = variance (CL), tt = Age):

mm	nn	vv	tt
254.6124	1968	2.435166e+09	0.0000005
688.5455	11	1.245041e+05	0.0058500
447.6480	45	8.098707e+04	0.0688500
333.8707	45	3.704545e+04	0.4535000

	mm	nn	vv	tt
	415.0939	66	1.833202e+05	1.6845000
	642.0167	18	2.812598e+05	3.0940000
	1015.2286	21	5.560846e+05	4.4660000
	582.7750	40	3.097159e+05	8.4700000



```
##
## Comparing 3 models [n = 7, method = AD]
##
##          logL K      AICc Akaike.wt
## GRW      -50.50691 2 108.0138    0.034
## URW      -51.20280 1 105.2056    0.137
## Stasis   -47.30219 2 101.6044    0.829
```

	logL	K	AICc	Akaike.wt
GRW	-50.50691	2	108.0138	0.034
URW	-51.20280	1	105.2056	0.137
Stasis	-47.30219	2	101.6044	0.829

including Island species, Species mean

```
SpeciesMean <- PleiPlioCL %>%
  filter(EpochBins != "Modern") %>%
  group_by(EpochBins, Taxon, Age) %>%
  summarise(meanCL = mean(CL), n=n()) %>%
  merge(BINS)

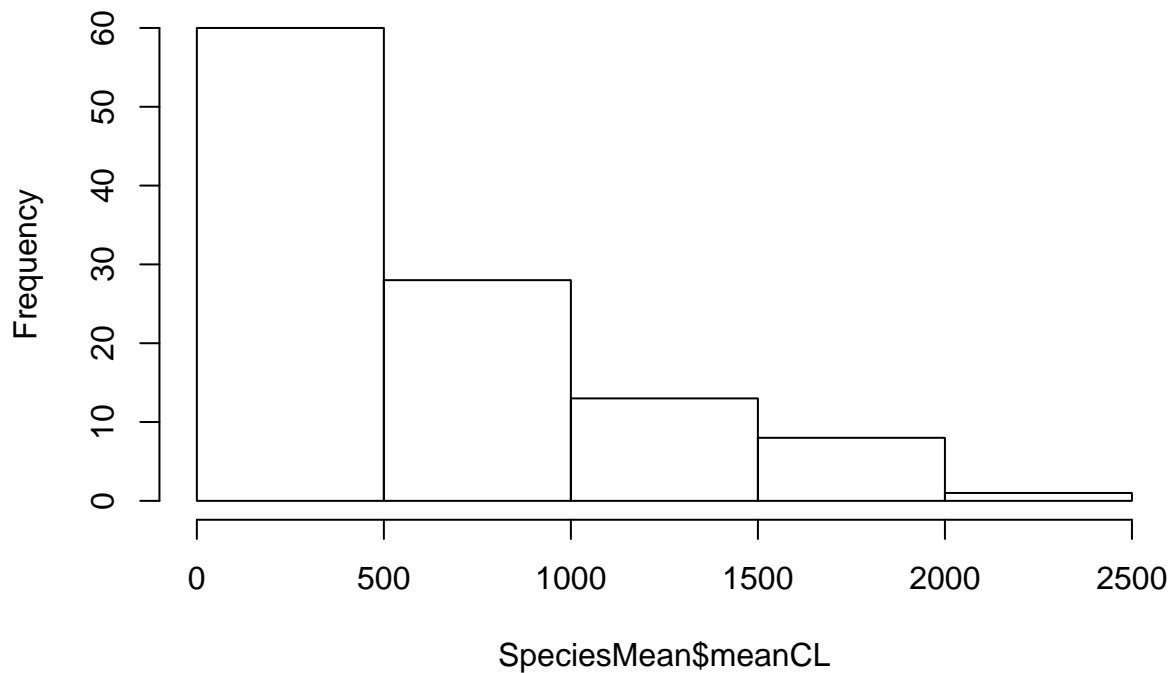
SpeciesModern <- PleiPlioCL %>%
  filter(EpochBins == "Modern") %>%
  group_by(Taxon) %>%
  summarise(meanCL=mean(CL), sdCL=sd(CL), n=n(), Age=mean(Age), EpochBins=unique(EpochBins), MeanBins=unique(MeanBins))

SpeciesModern[is.na(SpeciesModern)]<-0 #subset NAs with 0 for n=1

####

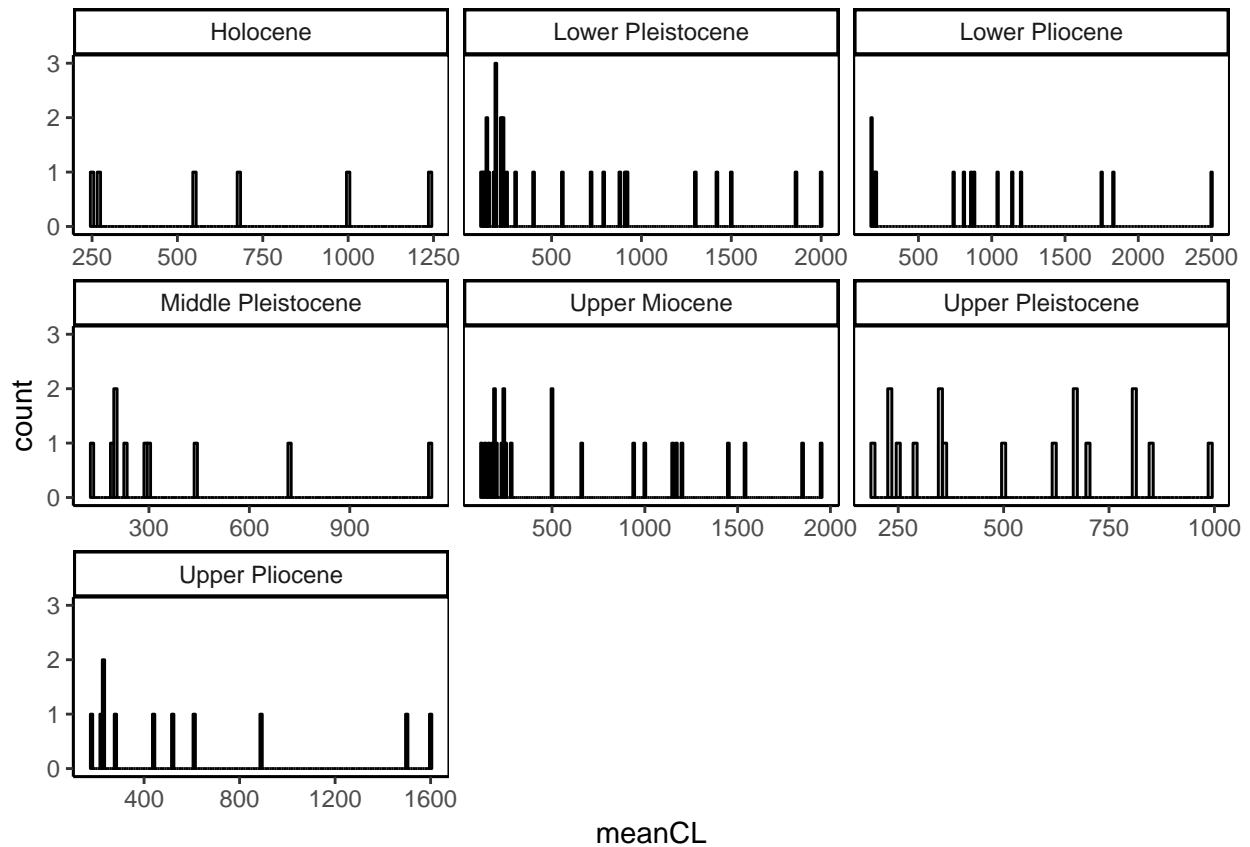
hist(SpeciesMean$meanCL)
```

**Histogram of SpeciesMean\$meanCL**



```
HistCLSpcies <- SpeciesMean %>%
  filter(!is.na(meanCL)) %>%
  ggplot(aes(meanCL)) + geom_histogram(binwidth=10, col="black", fill="gray") + facet_wrap(~EpochBins, ncol=4) +
  theme_classic() +
  #theme_gray() +
  theme(panel.border = element_rect(colour = "black", fill=NA))

HistCLSpcies
```



```
HistEpoch <- SpeciesMean %>%
  filter( !is.na(meanCL)) %>%
  ggplot(aes(MeanBins)) + geom_histogram(bins=0.000001)
```

```
HistEpoch
```

```
## Warning: Computation failed in `stat_bin()`:
## Need at least one bin.
```

count

MeanBins

```
SpeciesOverview <- SpeciesMean %>%  
# filter(EpochBins != "Modern") %>%  
  filter( !is.na(meanCL)) %>%  
  group_by(EpochBins) %>%  
  summarise(meanSpeciesCL = mean(meanCL), nSpecies=n(), MeanBins = mean(MeanBins)) %>%  
  arrange(MeanBins)  
  
kable(SpeciesOverview)
```

EpochBins	meanSpeciesCL	nSpecies	MeanBins
Holocene	666.0000	6	0.00585
Upper Pleistocene	521.4533	17	0.06885
Middle Pleistocene	384.8626	10	0.45350
Lower Pleistocene	581.2039	28	1.68450
Upper Pliocene	610.4591	11	3.09400
Lower Pliocene	965.6167	14	4.46600
Upper Miocene	680.7708	24	8.47000

#####

```
SpeciesPaleo <- SpeciesMean %>%  
  dplyr::select(meanCL, MeanBins) %>%  
  dplyr::filter(meanCL != "NA") %>%  
  mutate(tt= MeanBins) %>% # create mean age
```

```

group_by(tt) %>% #create time bins
summarise(mm=mean(meanCL), vv=var(meanCL), nn=n()) #create means etc. for each time bin

#SpeciesPaleo[is.na(SpeciesPaleo)]<-0 #subset NAs with 0 for n=1

# ExTort <- extant %>%
#   mutate(CL = SCL * 10) %>%
#   dplyr::select(CL) %>%
#   summarise(mm=mean(CL), nn=n(), vv=var(CL), tt=0) %>%
#   dplyr::select(mm, nn, vv, tt)
#
# ExTort[is.na(ExTort)] <- 0 #subset NAs with 0 for n=1

sumTort <- read.csv("tortoises_summary.csv", sep=";", header=TRUE)
#colnames(sumTort)[1] <- "Taxon"
colnames(sumTort)[6] <- "meanCL"
colnames(sumTort)[7] <- "sdCL"
#sumTort$EpochBins <- "Modern"
#sumTort$MeanBins <- 0.0000005

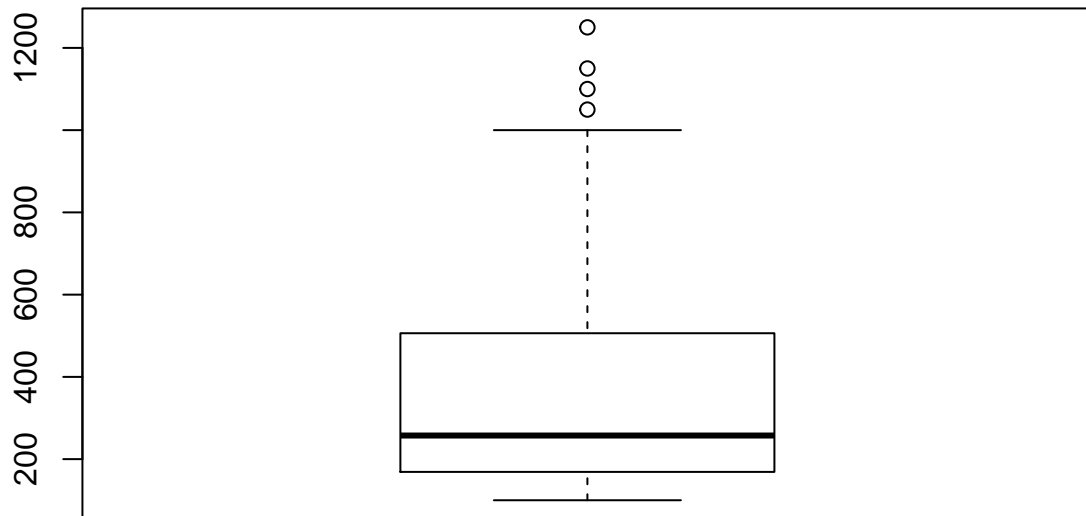
sumTortoises <- sumTort %>%
  mutate(Taxon= as.character(Species)) %>%
  mutate(MeanBins=(Mamin+Mamax)/2) %>%
  select(Taxon, MeanBins, n, meanCL, sdCL) %>%
  bind_rows(SpeciesModern)

SumTort <- sumTortoises %>%
  group_by(Taxon) %>%
  mutate(tt=MeanBins, vv=sdCL^2, nn=n, mm=meanCL) %>%
  dplyr::select(mm, nn, vv, tt, Taxon) %>%
  mutate(nx = nn*mm) %>%
  mutate(mmall=sum(nx)/sum(nn)) %>%
  mutate(SD=sqrt(nx), d=mm-mmall) %>%
  mutate(nsd=((nx^2+d^2)*nn)) %>%
  mutate(varall=sum(nsd)/sum(nn), n=sum(nn)) %>%
  dplyr::select(mm=mmall, vv=varall, nn=n, tt, Taxon) %>%
  unique() %>%
  dplyr::select(CL=mm, n=nn, var=vv, tt, Taxon)

# write.table(SumTort,file="SumTortModern.txt", sep="\t", row.names = FALSE)

boxplot(SumTort$CL)

```



```
modernMean <- SumTort %>%
  ungroup() %>%
  select(CL, n, tt) %>%
  filter(!is.na(CL)) %>%
  group_by(tt) %>%
  summarise(mm = mean(CL), vv=var(CL), nn=n())

#bis hier alle modernen taxa zusammengefasst (summarised and MFN_testudinidae)

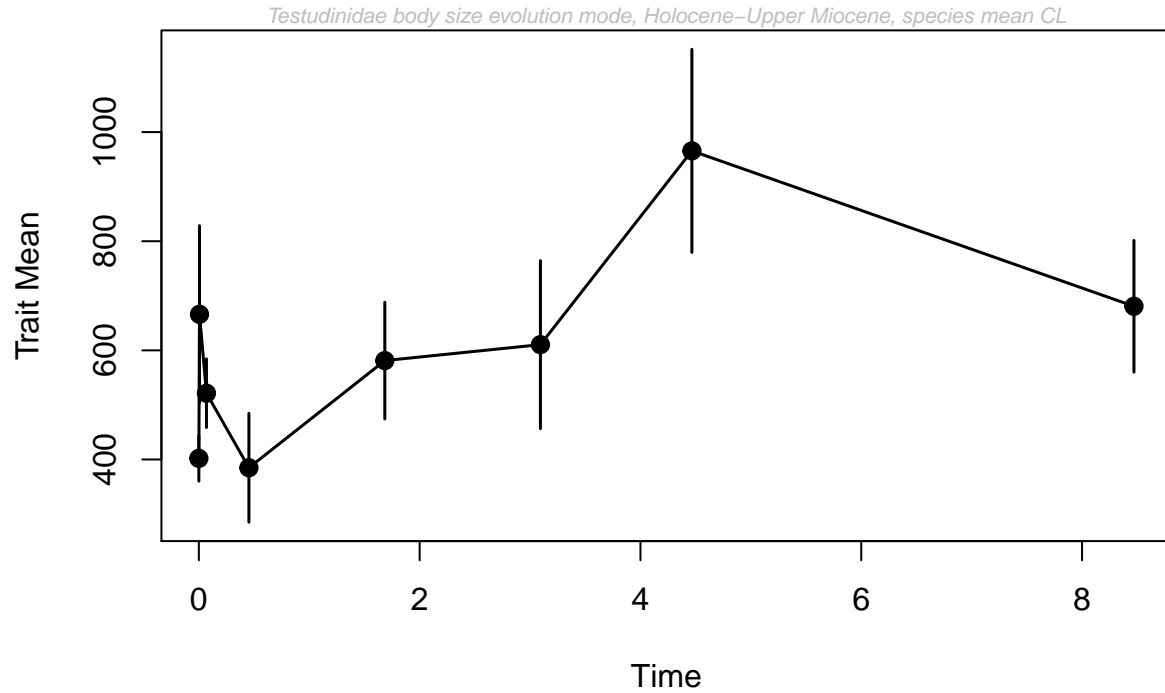
SpecPaleo <- bind_rows(modernMean,SpeciesPaleo) %>%
  arrange(tt)

kable(SpecPaleo)
```

tt	mm	vv	nn
0.0000005	402.0279	104275.52	60
0.0058500	666.0000	158400.40	6
0.0688500	521.4533	67149.55	17
0.4535000	384.8626	99603.12	10
1.6845000	581.2039	319998.46	28
3.0940000	610.4591	260640.34	11
4.4660000	965.6167	485060.72	14
8.4700000	680.7708	349806.99	24

tt	mm	vv	nn
----	----	----	----

```
paleoSpec <-as.paleoTS(SpecPaleo$mm, SpecPaleo$vv, SpecPaleo$nn, SpecPaleo$tt, MM = NULL, genpars = NULL)
plot(paleoSpec)
```



```
kable(fit3models(paleoSpec, silent=FALSE, method="AD", pool=FALSE))
```

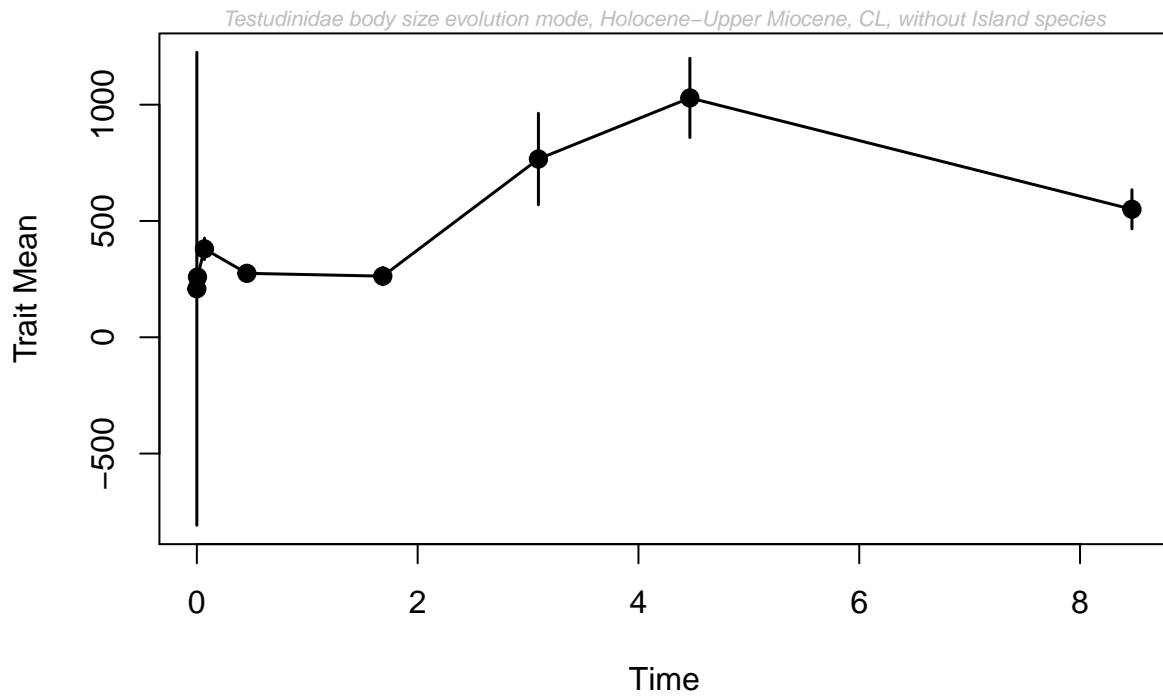
```
##
## Comparing 3 models [n = 7, method = AD]
##
##      logL K      AICc Akaike.wt
## GRW  -47.52095 2 102.04189    0.045
## URW  -47.65920 1  98.11839    0.320
## Stasis -44.87577 2  96.75155    0.635
```

	logL	K	AICc	Akaike.wt
GRW	-47.52095	2	102.04189	0.045
URW	-47.65920	1	98.11839	0.320
Stasis	-44.87577	2	96.75155	0.635

Excluding Island species (n= 1966)



	mm	nn	vv	tt
208.4249	1771	1.830244e+09	0.0000005	
259.0000	2	1.620000e+02	0.0058500	
380.0617	35	7.471306e+04	0.0688500	
274.8795	40	3.342617e+03	0.4535000	
262.7958	48	6.826984e+04	1.6845000	
766.3909	11	4.261398e+05	3.0940000	
1029.0400	20	5.811355e+05	4.4660000	
550.2821	39	2.745233e+05	8.4700000	



```
##
## Comparing 3 models [n = 7, method = AD]
##
##          logL K      AICc Akaike.wt
## GRW      -52.57801 2 112.1560    0.072
## URW      -53.51970 1 109.8394    0.231
## Stasis   -50.31407 2 107.6281    0.697
```

	logL	K	AICc	Akaike.wt
GRW	-52.57801	2	112.1560	0.072
URW	-53.51970	1	109.8394	0.231
Stasis	-50.31407	2	107.6281	0.697

excluding Island species, Species mean

```
SpeciesMean <- PleiPlioCL %>%
  filter(EpochBins != "Modern" & Island != "y") %>%
  group_by(EpochBins, Taxon, Age) %>%
  summarise(meanCL = mean(CL), n=n()) %>%
  merge(BINS)

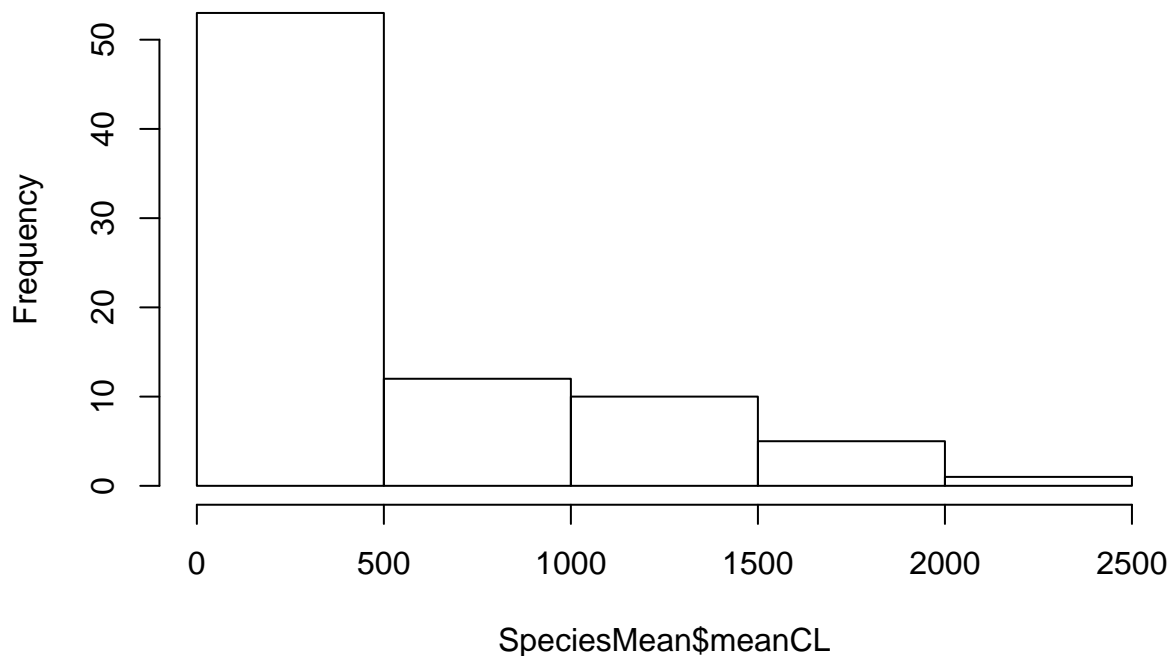
SpeciesModern <- PleiPlioCL %>%
  filter(EpochBins == "Modern" & Island != "y") %>%
  group_by(Taxon) %>%
  summarise(meanCL=mean(CL), sdCL=sd(CL), n=n(), Age=mean(Age), EpochBins=unique(EpochBins), MeanBins=u

SpeciesModern[is.na(SpeciesModern)]<-0 #subset NAs with 0 for n=1

####

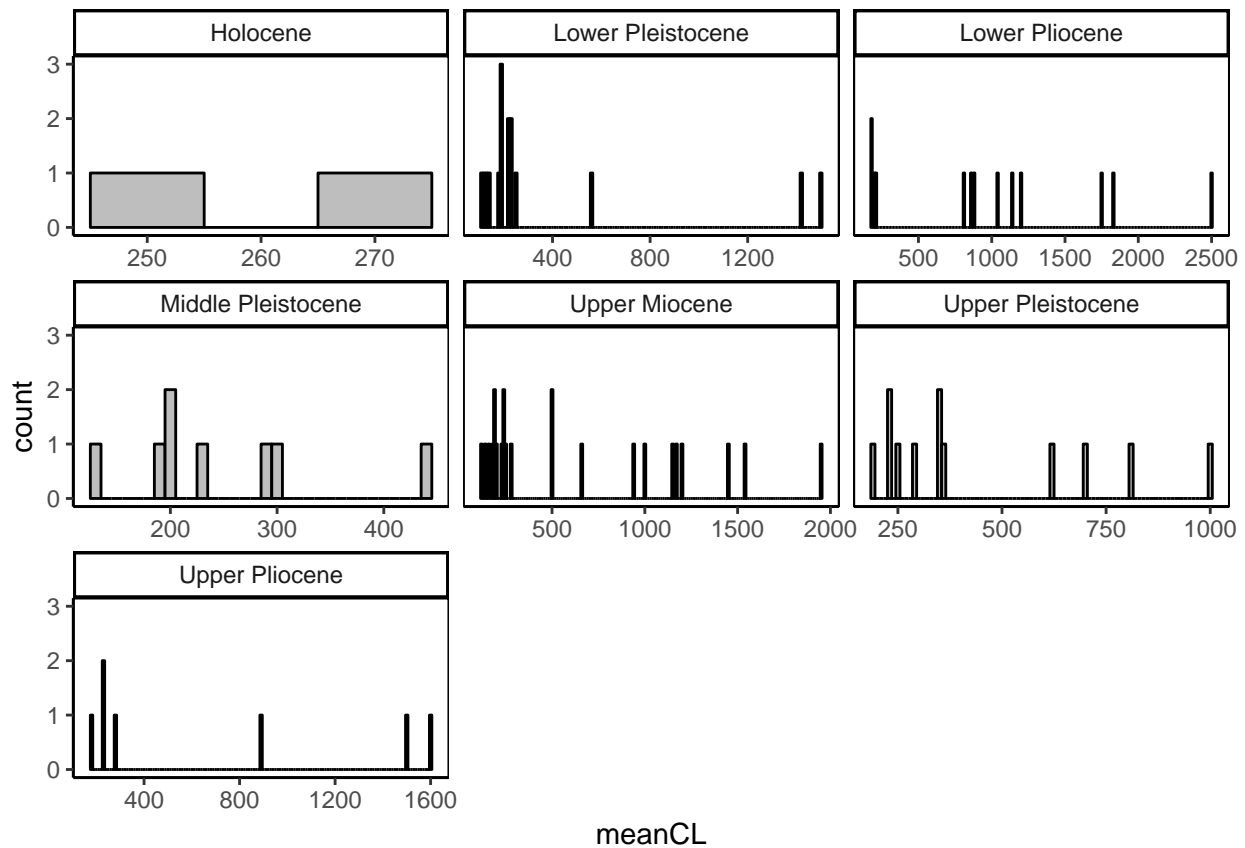
hist(SpeciesMean$meanCL)
```

**Histogram of SpeciesMean\$meanCL**



```
HistCLSpcies <- SpeciesMean %>%
  filter(!is.na(meanCL)) %>%
  ggplot(aes(meanCL)) + geom_histogram(binwidth=10, col="black", fill="gray") + facet_wrap(~EpochBins, s
  theme_classic()+
  #theme_gray() +
  theme(panel.border = element_rect(colour = "black", fill=NA))
```

HistCLSpecies



```
HistEpoch <- SpeciesMean %>%
  filter( !is.na(meanCL)) %>%
  ggplot(aes(MeanBins)) + geom_histogram(bins=0.000001)
```

HistEpoch

```
## Warning: Computation failed in `stat_bin()`:
## Need at least one bin.
```

count

MeanBins

```
SpeciesOverview <- SpeciesMean %>%  
# filter(EpochBins != "Modern") %>%  
  filter( !is.na(meanCL)) %>%  
  group_by(EpochBins) %>%  
  summarise(meanSpeciesCL = mean(meanCL), nSpecies=n(), MeanBins = mean(MeanBins)) %>%  
  arrange(MeanBins)  
  
kable(SpeciesOverview)
```

EpochBins	meanSpeciesCL	nSpecies	MeanBins
Holocene	259.0000	2	0.00585
Upper Pleistocene	447.7325	12	0.06885
Middle Pleistocene	248.3908	8	0.45350
Lower Pleistocene	368.7943	16	1.68450
Upper Pliocene	702.4714	7	3.09400
Lower Pliocene	983.0487	13	4.46600
Upper Miocene	629.9348	23	8.47000

#####

```
SpeciesPaleo <- SpeciesMean %>%  
  dplyr::select(meanCL, MeanBins) %>%  
  dplyr::filter(meanCL != "NA") %>%  
  mutate(tt= MeanBins) %>% # create mean age
```

```

group_by(tt) %>% #create time bins
summarise(mm=mean(meanCL), vv=var(meanCL), nn=n()) #create means etc. for each time bin

#SpeciesPaleo[is.na(SpeciesPaleo)]<-0 #subset NAs with 0 for n=1

# ExTort <- extant %>%
#   mutate(CL = SCL * 10) %>%
#   dplyr::select(CL) %>%
#   summarise(mm=mean(CL), nn=n(), vv=var(CL), tt=0) %>%
#   dplyr::select(mm, nn, vv, tt)
#
# ExTort[is.na(ExTort)] <- 0 #subset NAs with 0 for n=1

sumTort <- read.csv("tortoises_summary.csv", sep=";", header=TRUE)
#colnames(sumTort)[1] <- "Taxon"
colnames(sumTort)[6] <- "meanCL"
colnames(sumTort)[7] <- "sdCL"
#sumTort$EpochBins <- "Modern"
#sumTort$MeanBins <- 0.0000005

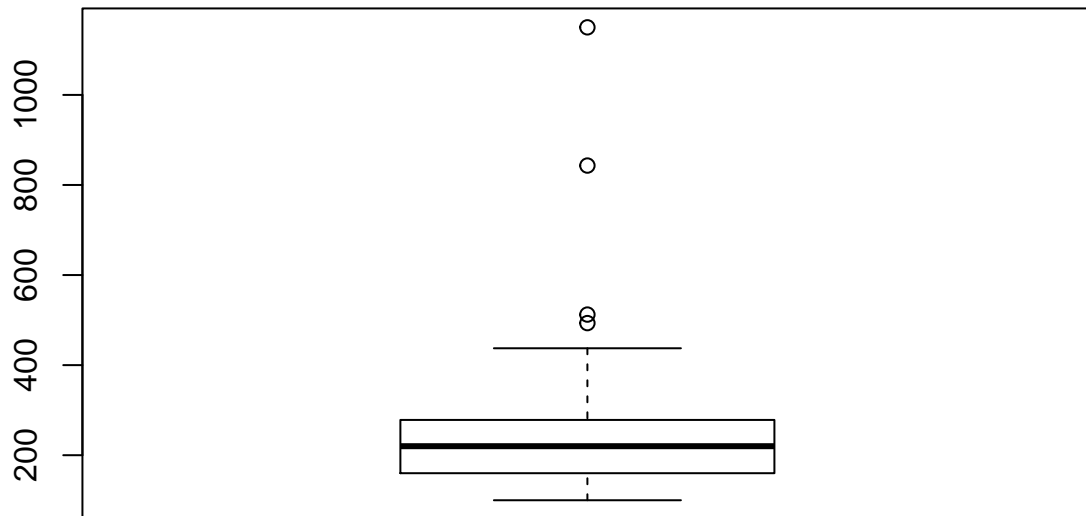
sumTortoises <- sumTort %>%
  mutate(Taxon= as.character(Species)) %>%
  mutate(MeanBins=(Mamin+Mamax)/2) %>%
  select(Taxon, MeanBins, n, meanCL, sdCL) %>%
  bind_rows(SpeciesModern)

SumTort <- sumTortoises %>%
  group_by(Taxon) %>%
  mutate(tt=MeanBins, vv=sdCL^2, nn=n, mm=meanCL) %>%
  dplyr::select(mm, nn, vv, tt, Taxon) %>%
  mutate(nx = nn*mm) %>%
  mutate(mmall=sum(nx)/sum(nn)) %>%
  mutate(SD=sqrt(nx), d=mm-mmall) %>%
  mutate(nsd=((nx^2+d^2)*nn)) %>%
  mutate(varall=sum(nsd)/sum(nn), n=sum(nn)) %>%
  dplyr::select(mm=mmall, vv=varall, nn=n, tt, Taxon) %>%
  unique() %>%
  dplyr::select(CL=mm, n=nn, var=vv, tt, Taxon)

# write.table(SumTort,file="SumTortModern.txt", sep="\t", row.names = FALSE)

boxplot(SumTort$CL)

```



```
modernMean <- SumTort %>%
  ungroup() %>%
  select(CL, n, tt) %>%
  filter( !is.na(CL)) %>%
  group_by(tt) %>%
  summarise(mm = mean(CL), vv=var(CL), nn=n())

#bis hier alle modernen taxa zusammengefasst (summarised and MFN_testudinidae)

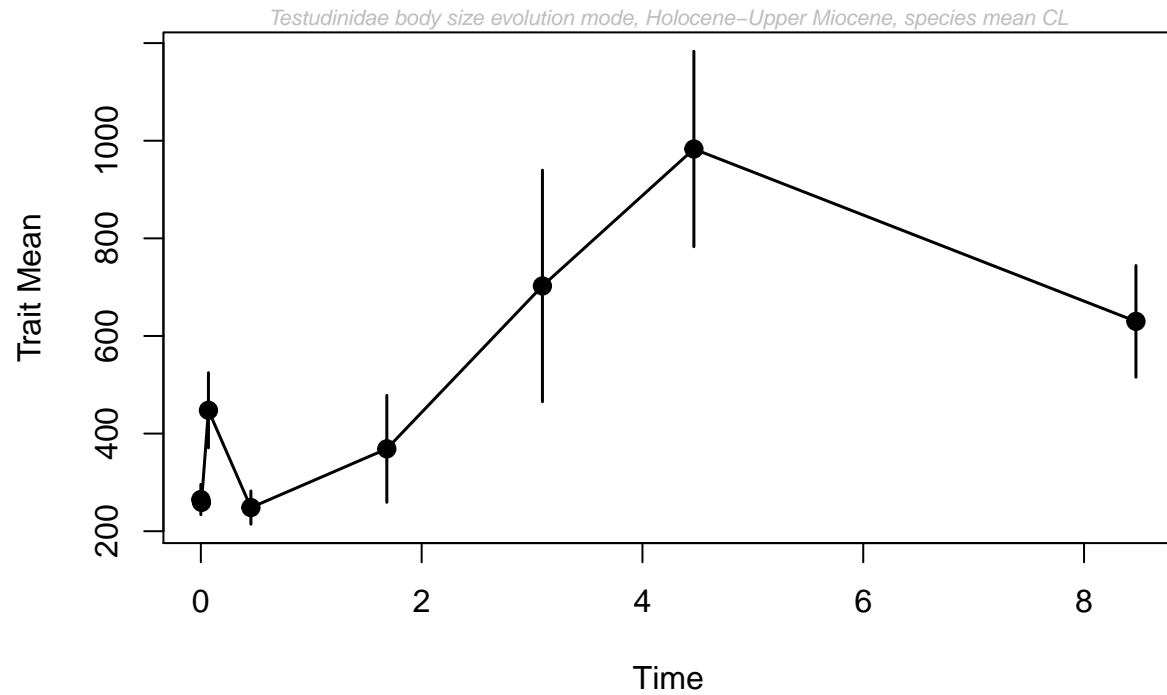
SpecPaleo <- bind_rows(modernMean,SpeciesPaleo) %>%
  arrange(tt)

kable(SpecPaleo)
```

tt	mm	vv	nn
0.0000005	264.9006	39605.260	41
0.0058500	259.0000	162.000	2
0.0688500	447.7325	71037.951	12
0.4535000	248.3908	9244.191	8
1.6845000	368.7943	192142.503	16
3.0940000	702.4714	393708.572	7
4.4660000	983.0487	520873.653	13
8.4700000	629.9348	300864.767	23

tt	mm	vv	nn
----	----	----	----

```
paleoSpec <-as.paleoTS(SpecPaleo$mm, SpecPaleo$vv, SpecPaleo$nn, SpecPaleo$tt, MM = NULL, genpars = NULL)
plot(paleoSpec)
```



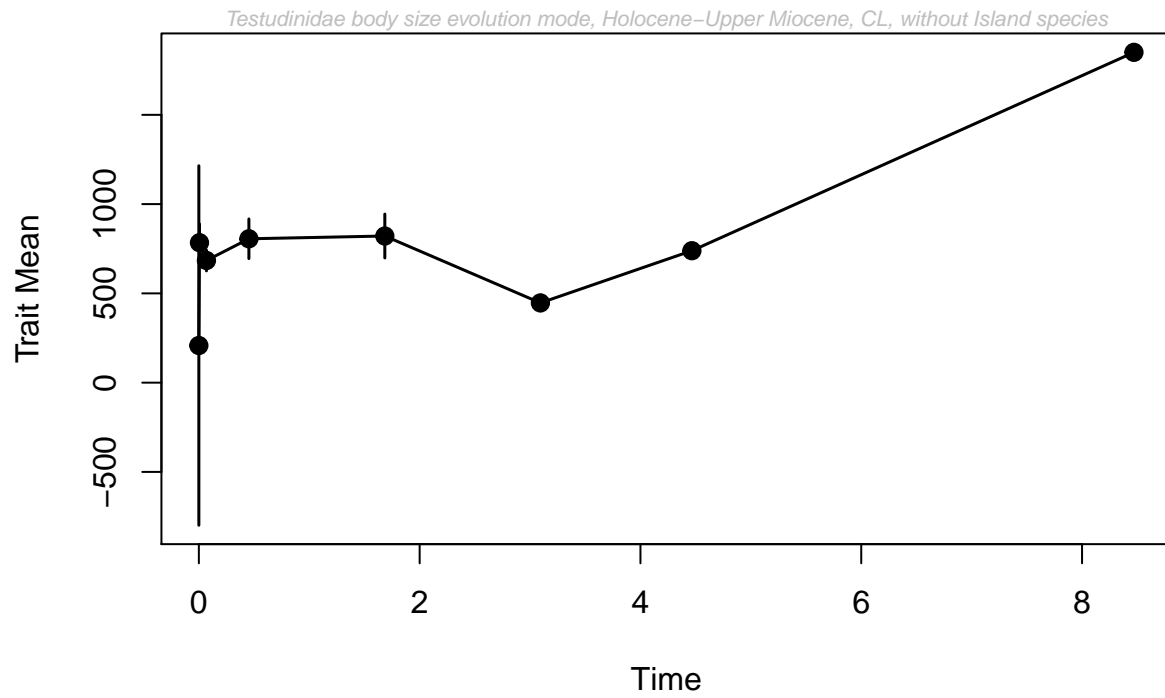
```
kable(fit3models(paleoSpec, silent=FALSE, method="AD", pool=FALSE))
```

```
##
## Comparing 3 models [n = 7, method = AD]
##
##          logL K      AICc Akaike.wt
## GRW      -47.13089 2 101.26178    0.119
## URW      -47.28326 1  97.36652    0.833
## Stasis   -48.03479 2 103.06957    0.048
```

	logL	K	AICc	Akaike.wt
GRW	-47.13089	2	101.26178	0.119
URW	-47.28326	1	97.36652	0.833
Stasis	-48.03479	2	103.06957	0.048

Only Island species

mm	nn	vv	tt
208.0755	1703	1.725832e+09	0.0000005
784.0000	9	9.923200e+04	0.0058500
684.2000	10	3.374907e+04	0.0688500
805.8000	5	6.171320e+04	0.4535000
821.2222	18	2.720508e+05	1.6845000
446.5714	7	1.374462e+04	3.0940000
739.0000	1	0.000000e+00	4.4660000
1850.0000	1	0.000000e+00	8.4700000

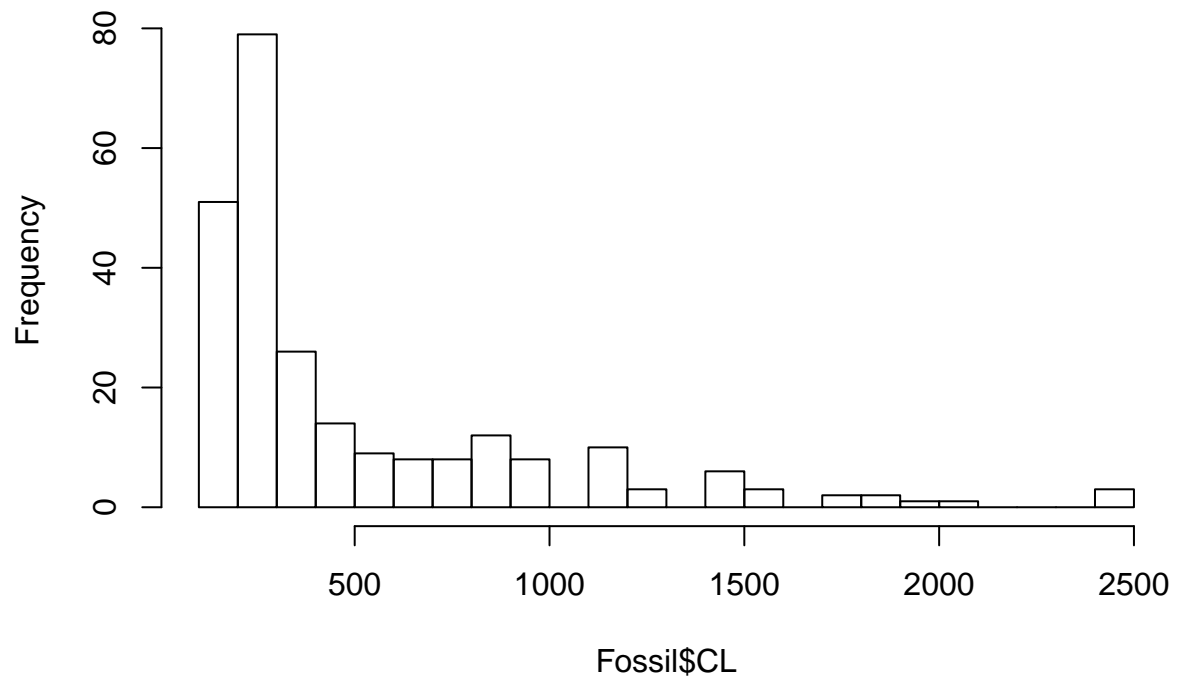


## Histograms

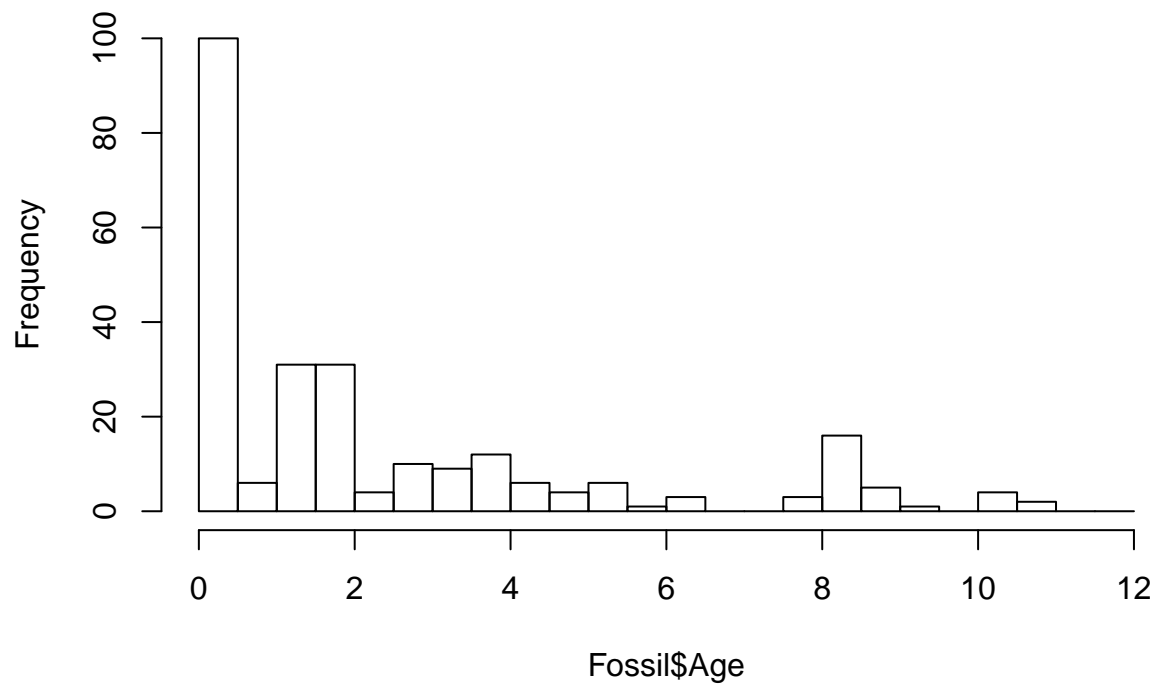
Frequency of body size data and distribution over time



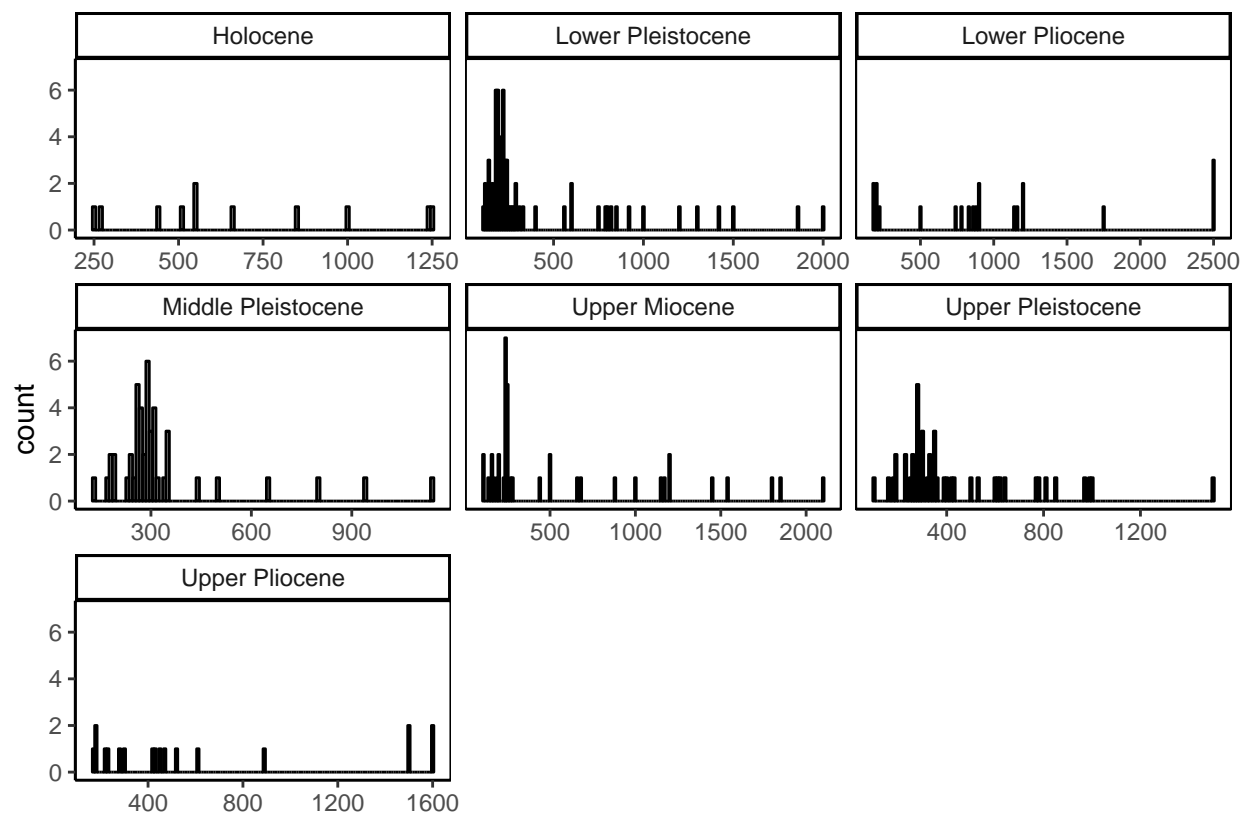
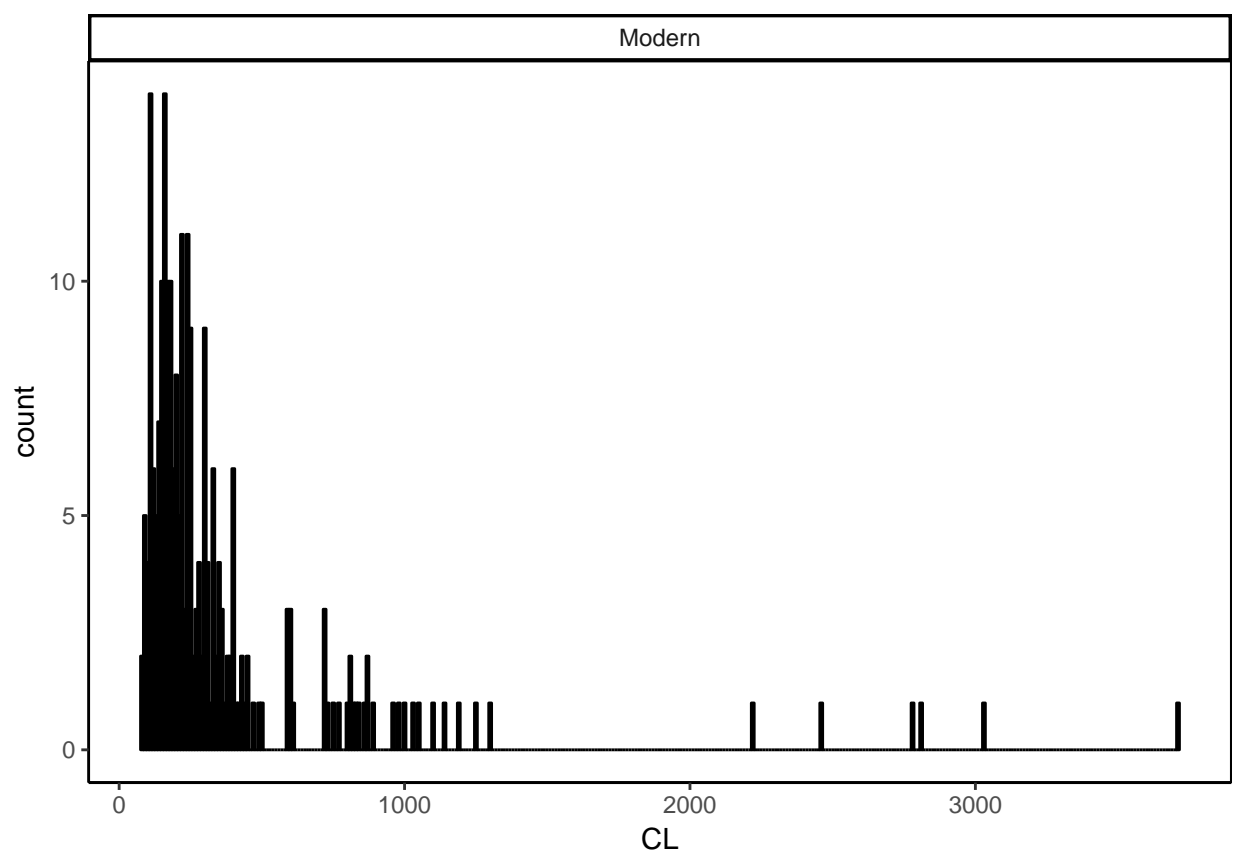
**Histogram of Fossil\$CL**



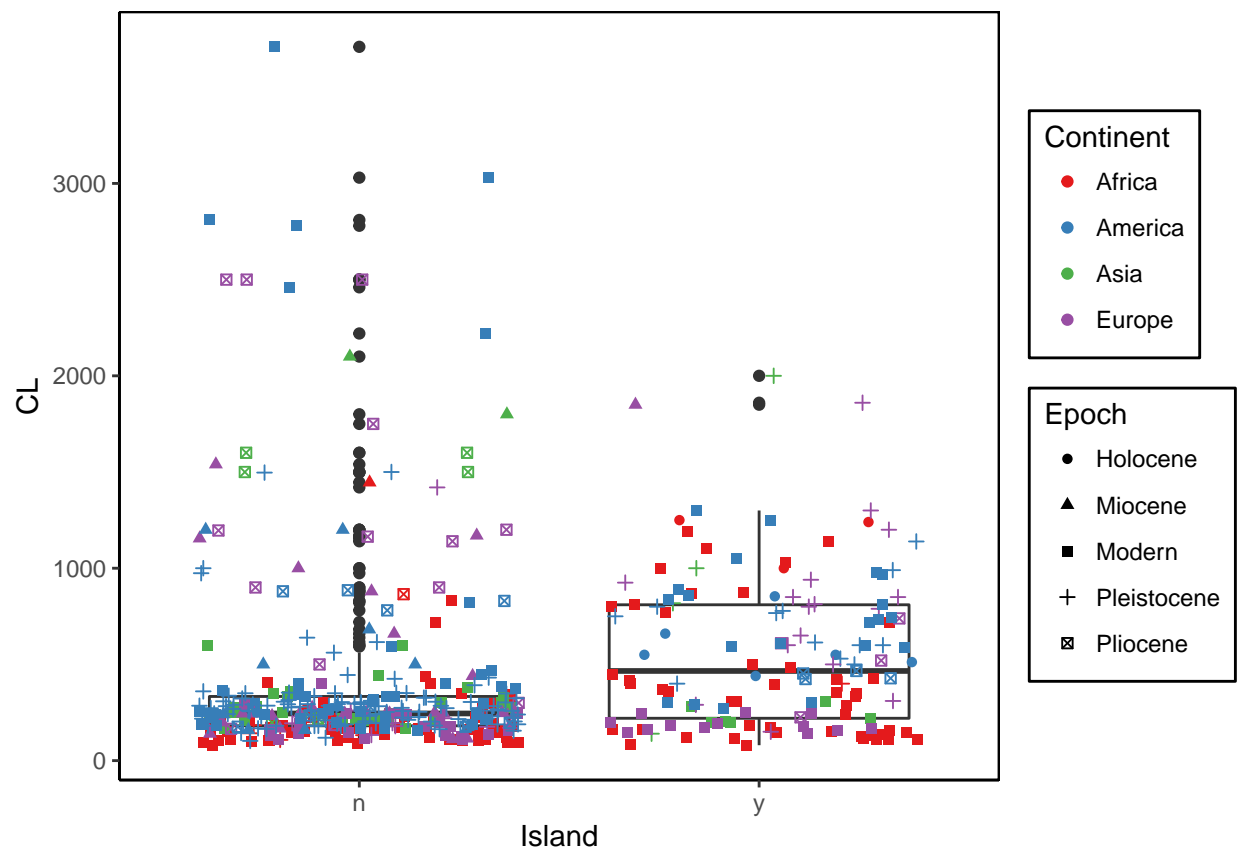
**Histogram of Fossil\$Age**

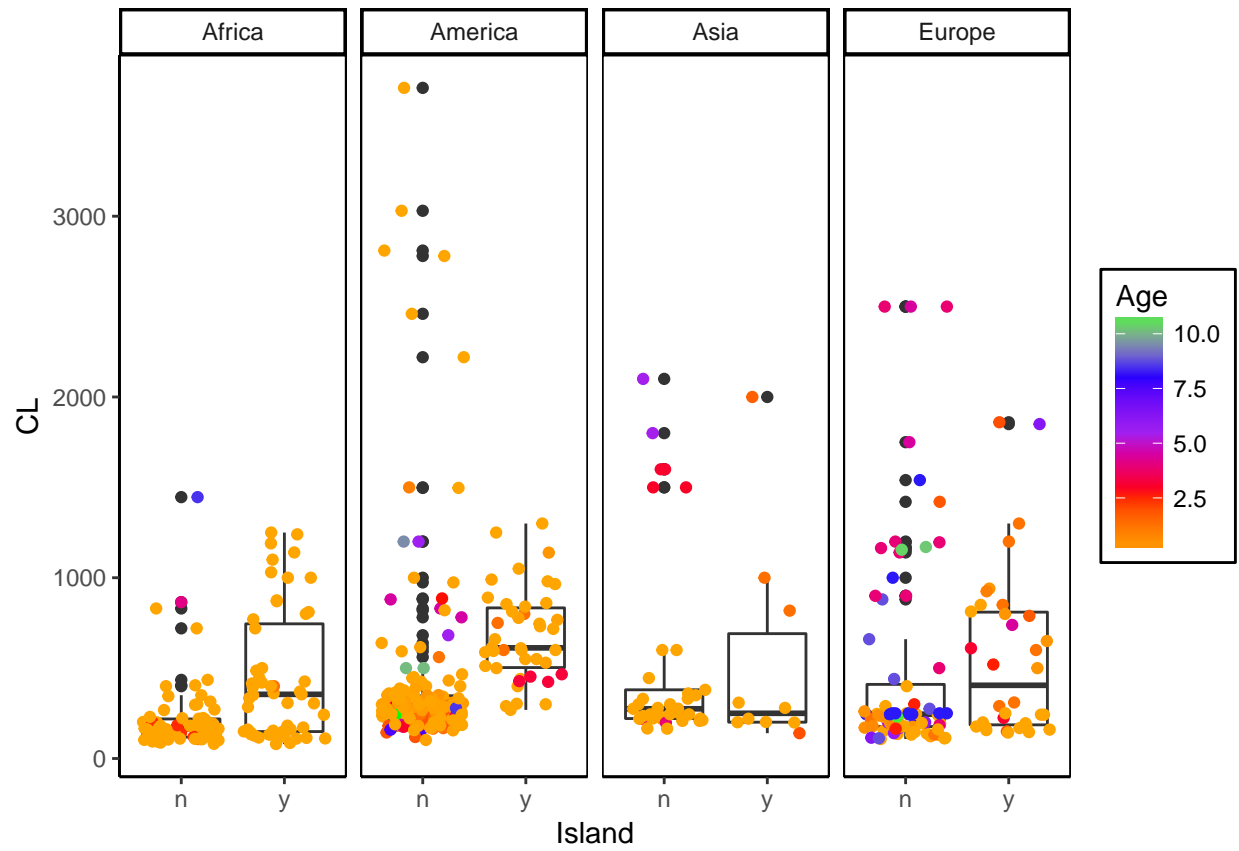


# CL histogram per bin



# Boxplots (continental (n) vs. Island (y) species)

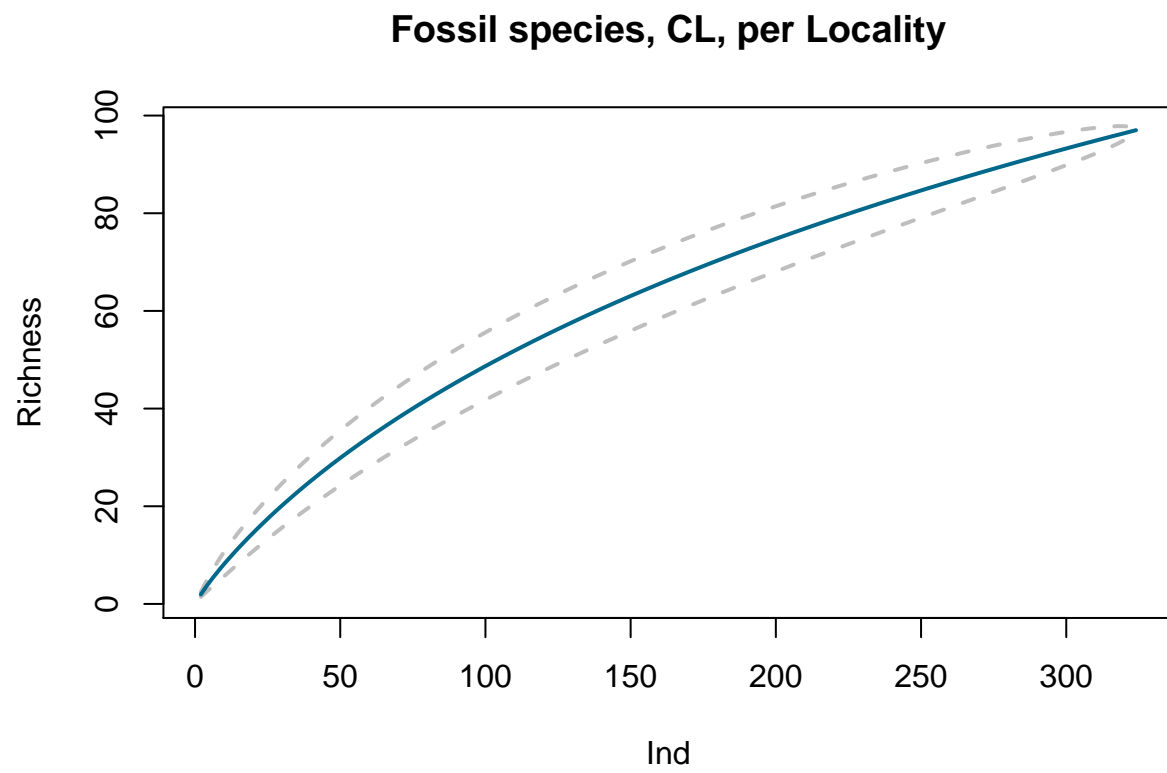




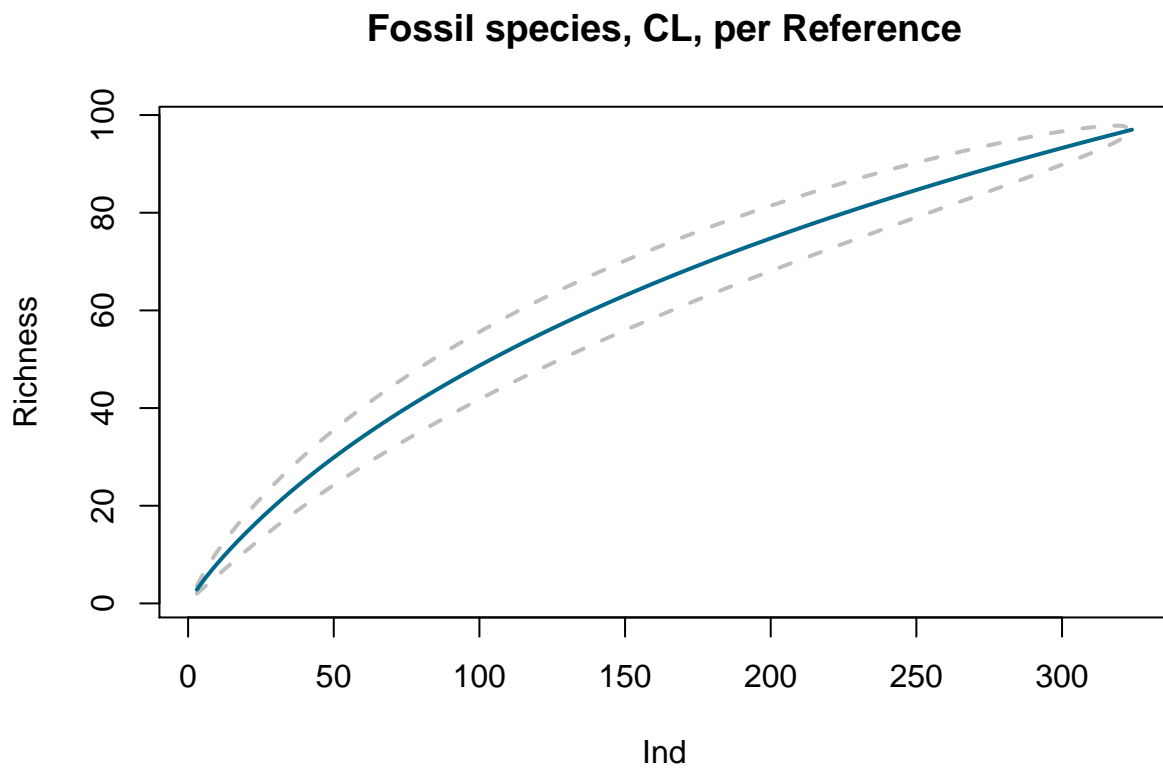
Map

Species Accumulation Curve

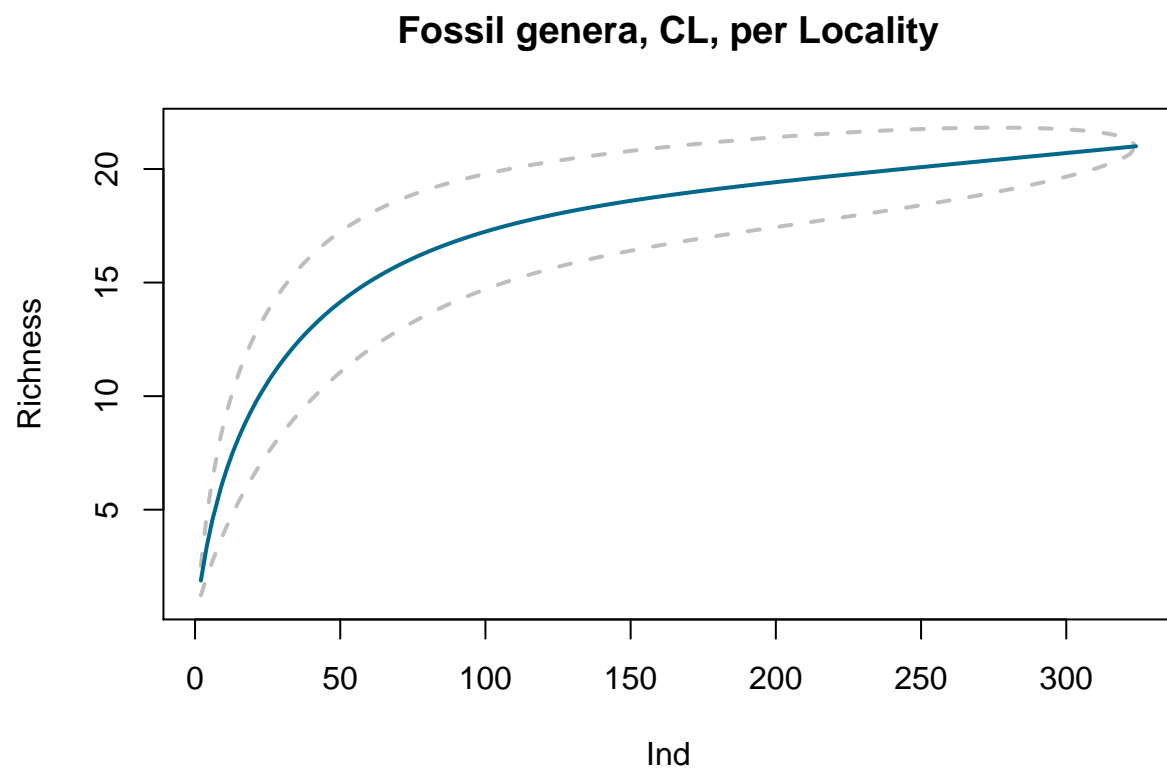
Fossil species (per Locality)



Fossil species (per Reference)

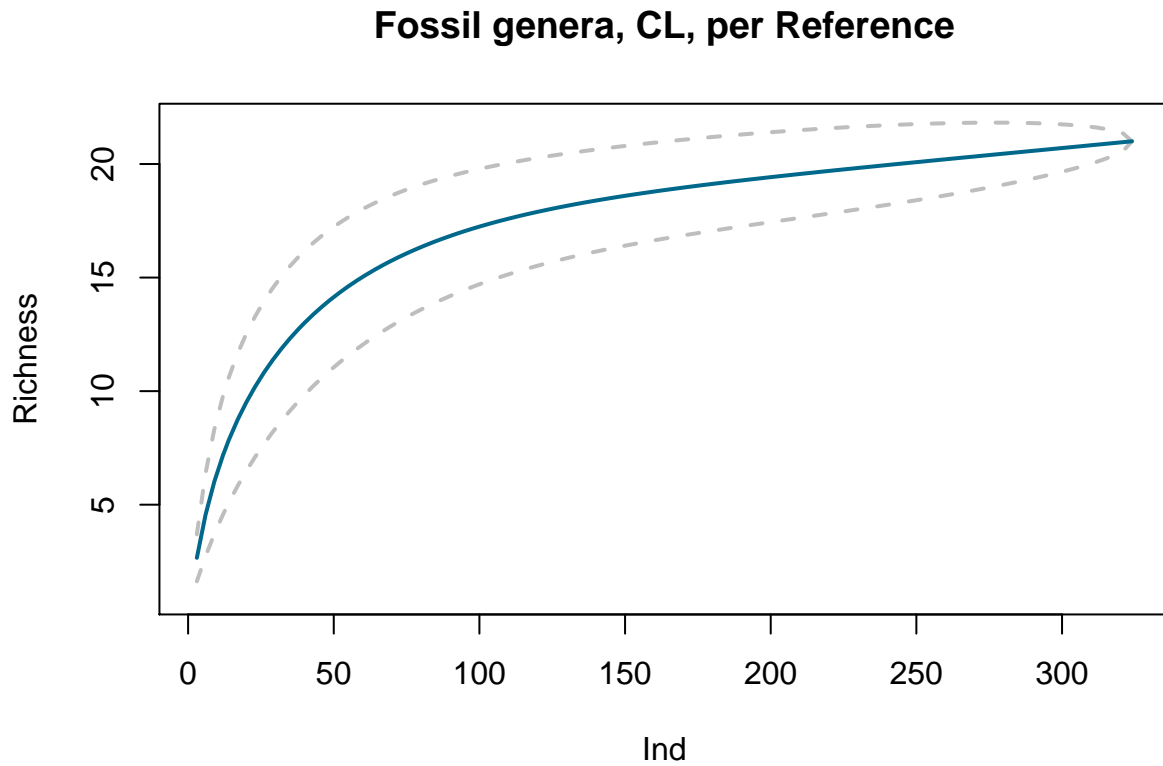


Fossil genera (per Locality)





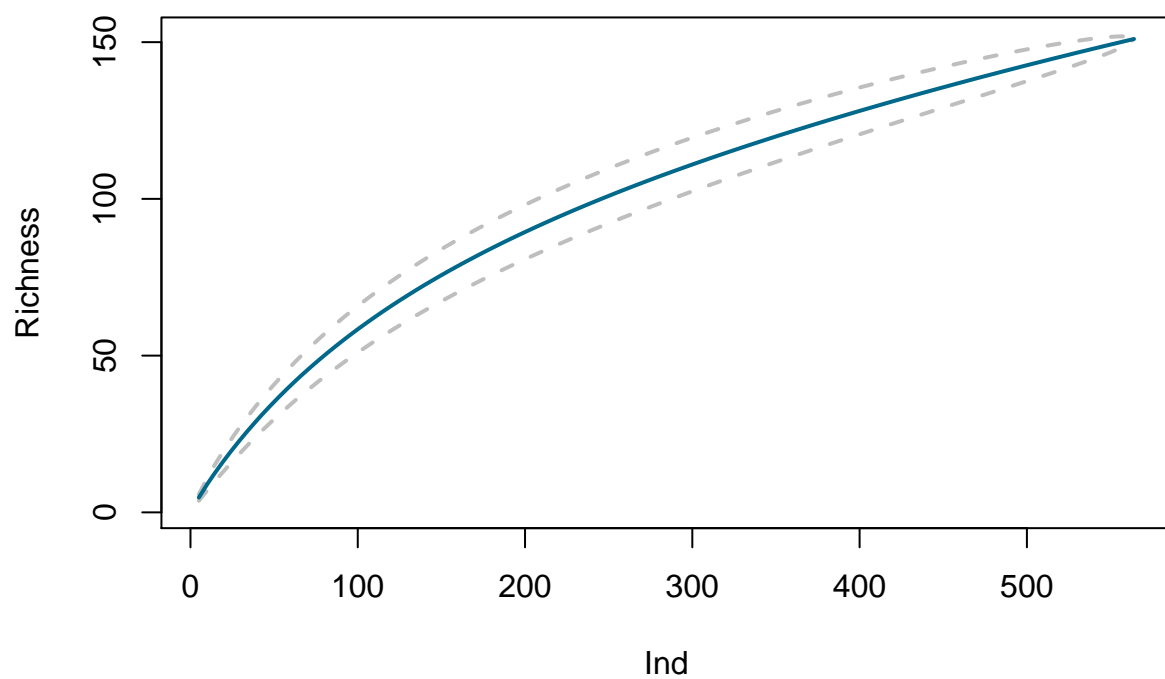
Fossil genera (per Reference)



Fossil and extant species (per Reference)

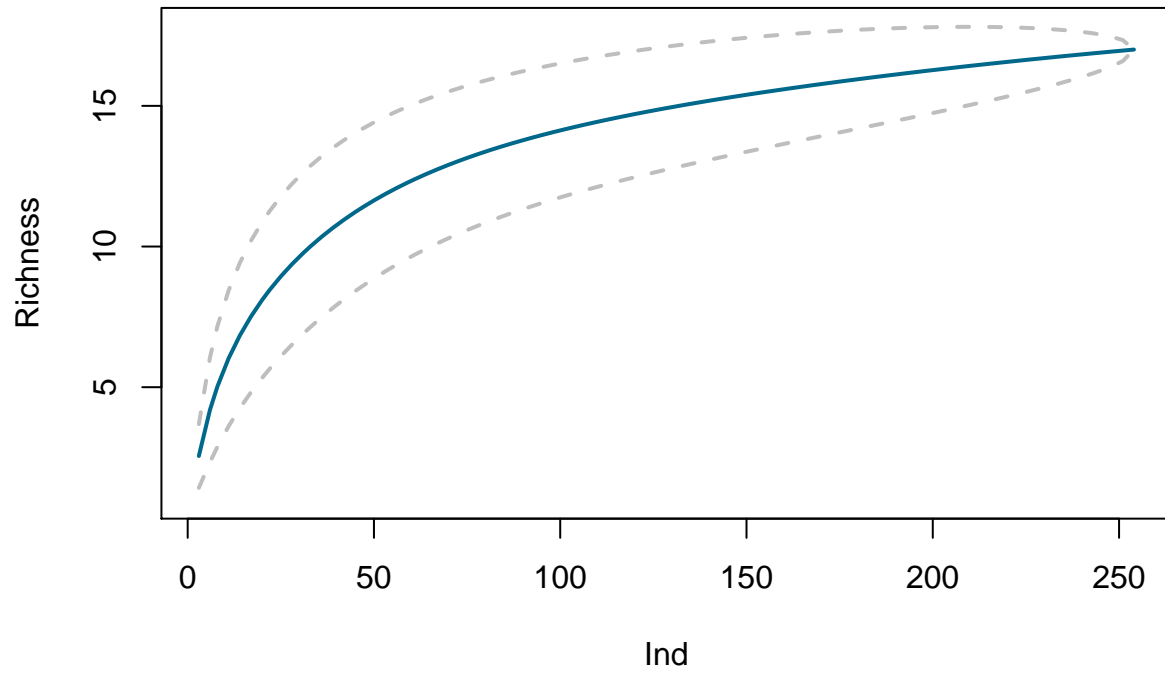
```
## Warning in bind_rows(x, .id): binding factor and character vector,  
## coercing into character vector  
  
## Warning in bind_rows(x, .id): binding character and factor vector,  
## coercing into character vector  
  
## Warning in bind_rows(x, .id): binding factor and character vector,  
## coercing into character vector  
  
## Warning in bind_rows(x, .id): binding character and factor vector,  
## coercing into character vector
```

### Fossil and extant species, CL, per Reference



Occurrences from FosFarBase per Reference (all known occurrences, disregarding availability of CL-data)

### All fossil genera, per Reference



Occurrences from FosFarBase per Locality (all known occurrences, disregarding availability of CL-data)

### All fossil genera, per Locality

