

Body size trends in fossil tortoises

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

- after including extant species, another bin is added: Modern, t=0

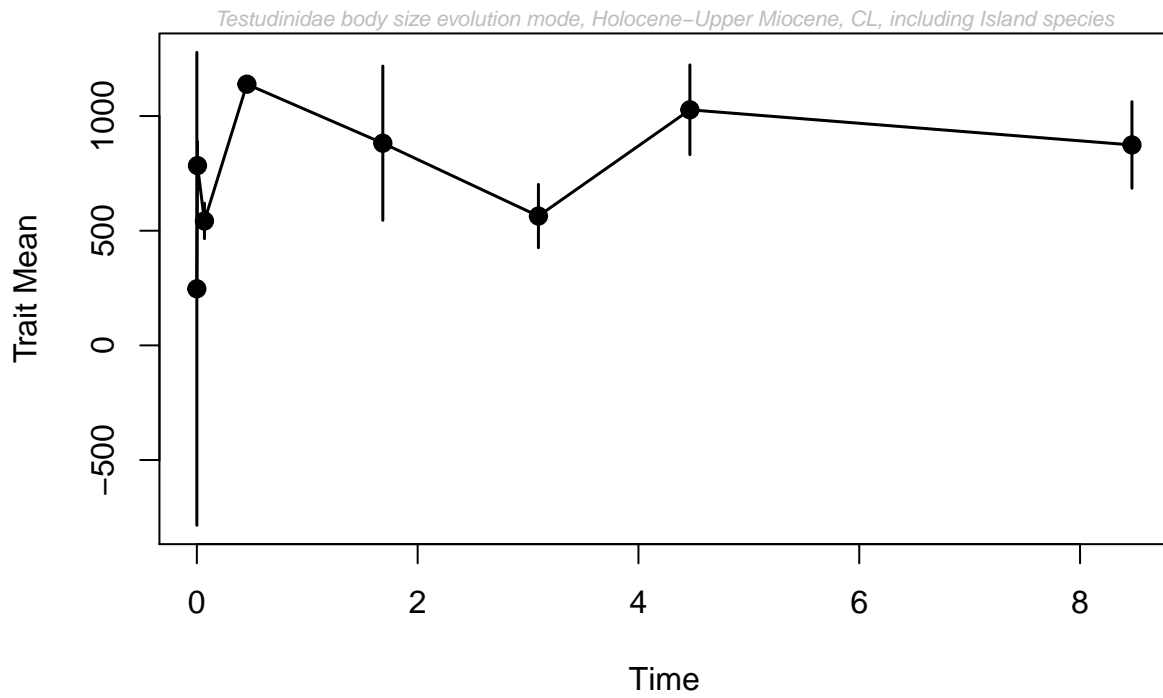
bin	n
(0,1e-06]	234
(1e-06,0.0117]	10
(0.0117,0.126]	12
(0.126,0.781]	2
(0.781,2.59]	24
(2.59,3.6]	13
(3.6,5.33]	15
(5.33,11.6]	16

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=2049)

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

mm	nn	vv	tt
246.7213	1962	2.085874e+09	0.0000005
784.0000	9	9.923200e+04	0.0058500
542.4800	12	7.186028e+04	0.0688500
1139.0000	1	0.000000e+00	0.4535000
881.6591	22	2.488497e+06	1.6845000
563.8583	12	2.288335e+05	3.0940000
1027.2667	15	5.753904e+05	4.4660000
873.9312	16	5.695508e+05	8.4700000

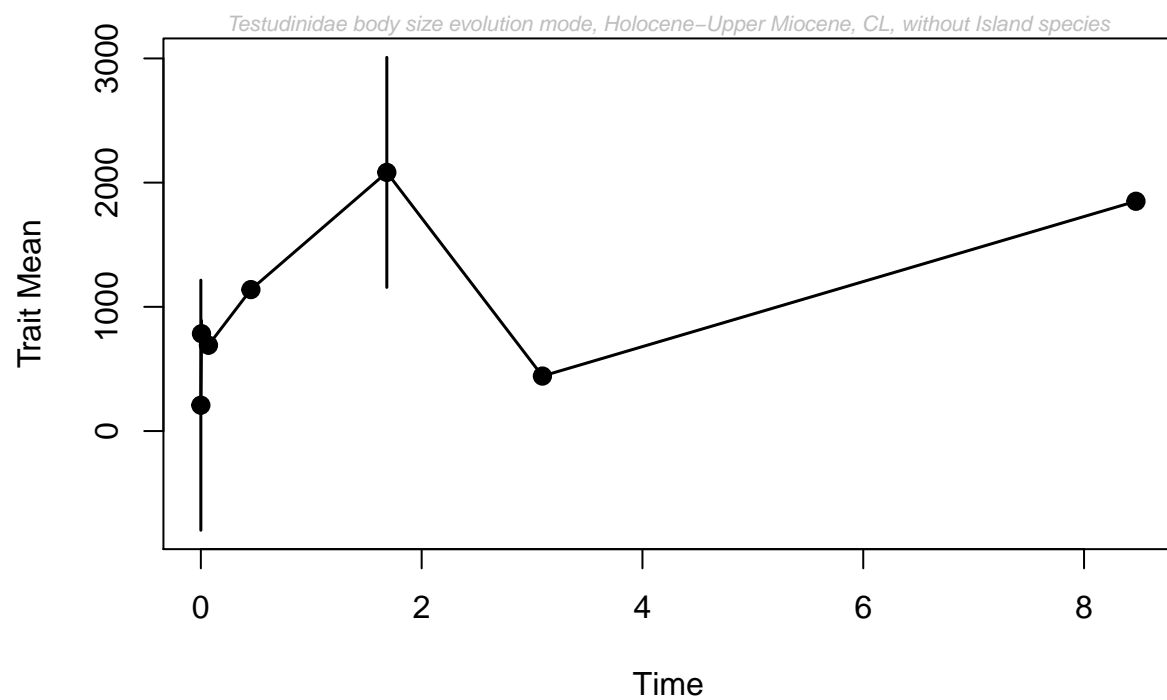


```
##
## Comparing 3 models [n = 7, method = AD]
##
##          logL K      AICc Akaike.wt
## GRW      -57.17115 2 121.3423    0.001
## URW      -57.87805 1 118.5561    0.002
## Stasis   -49.71594 2 106.4319    0.997
```

	logL	K	AICc	Akaike.wt
GRW	-57.17115	2	121.3423	0.001
URW	-57.87805	1	118.5561	0.002
Stasis	-49.71594	2	106.4319	0.997

Excluding Island species (n= 1733)

mm	nn	vv	tt
208.0755	1703	1.725832e+09	0.0000005
784.0000	9	9.923200e+04	0.0058500
691.1250	8	3.611984e+04	0.0688500
1139.0000	1	0.000000e+00	0.4535000
2082.5714	7	6.003166e+06	1.6845000
442.7500	4	4.049167e+02	3.0940000
1850.0000	1	0.000000e+00	8.4700000



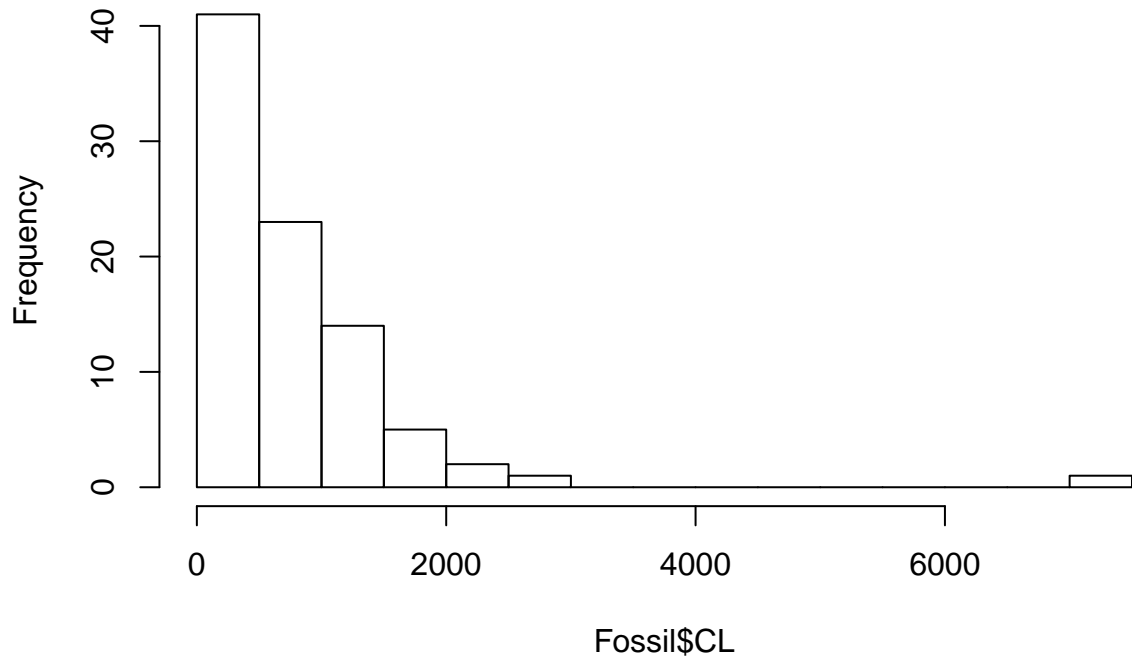
```
##
## Comparing 3 models [n = 6, method = AD]
##
##      logL K      AICc Akaike.wt
## GRW  -53.90808 2 115.8162    0.017
## URW  -52.71457 1 108.4291    0.692
## Stasis -51.08142 2 110.1628    0.291
```

	logL	K	AICc	Akaike.wt
GRW	-53.90808	2	115.8162	0.017
URW	-52.71457	1	108.4291	0.692
Stasis	-51.08142	2	110.1628	0.291

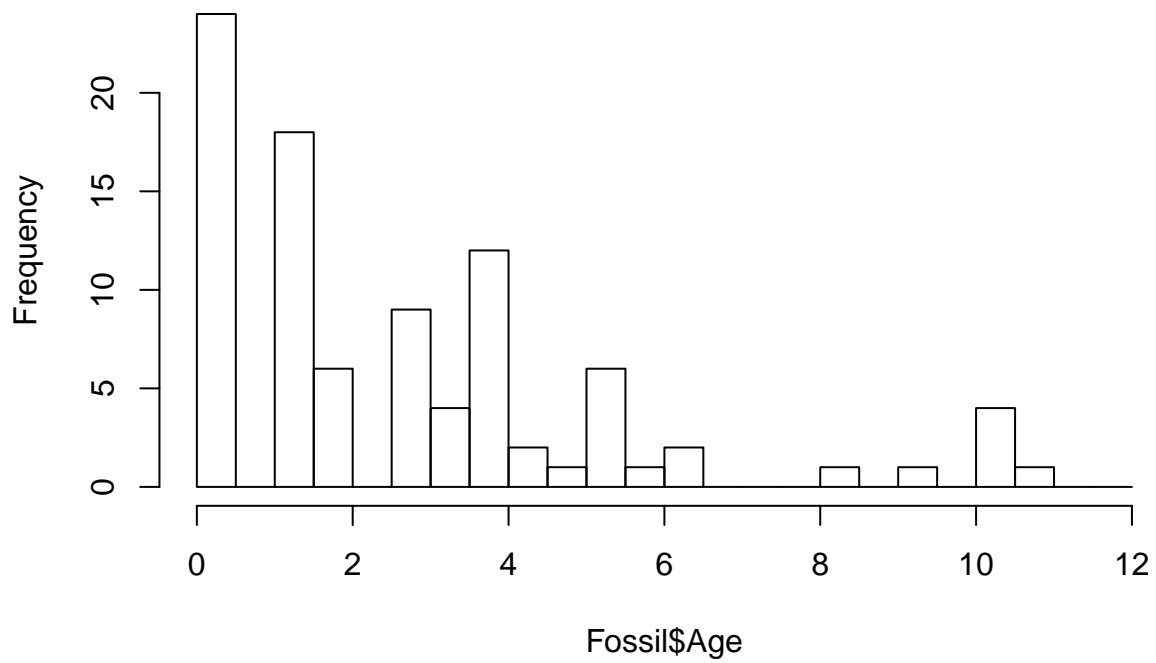
Histograms

Frequency of body size data and distribution over time

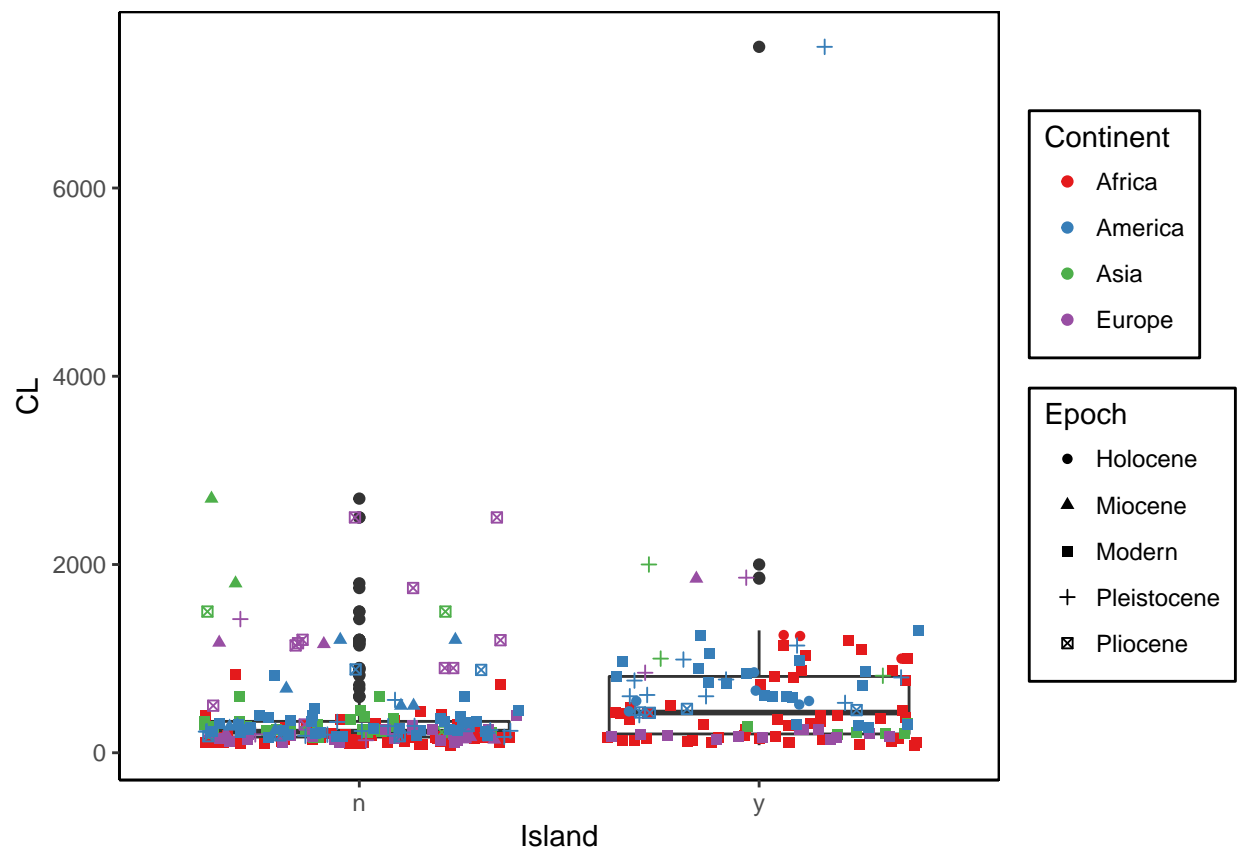
Histogram of Fossil\$CL

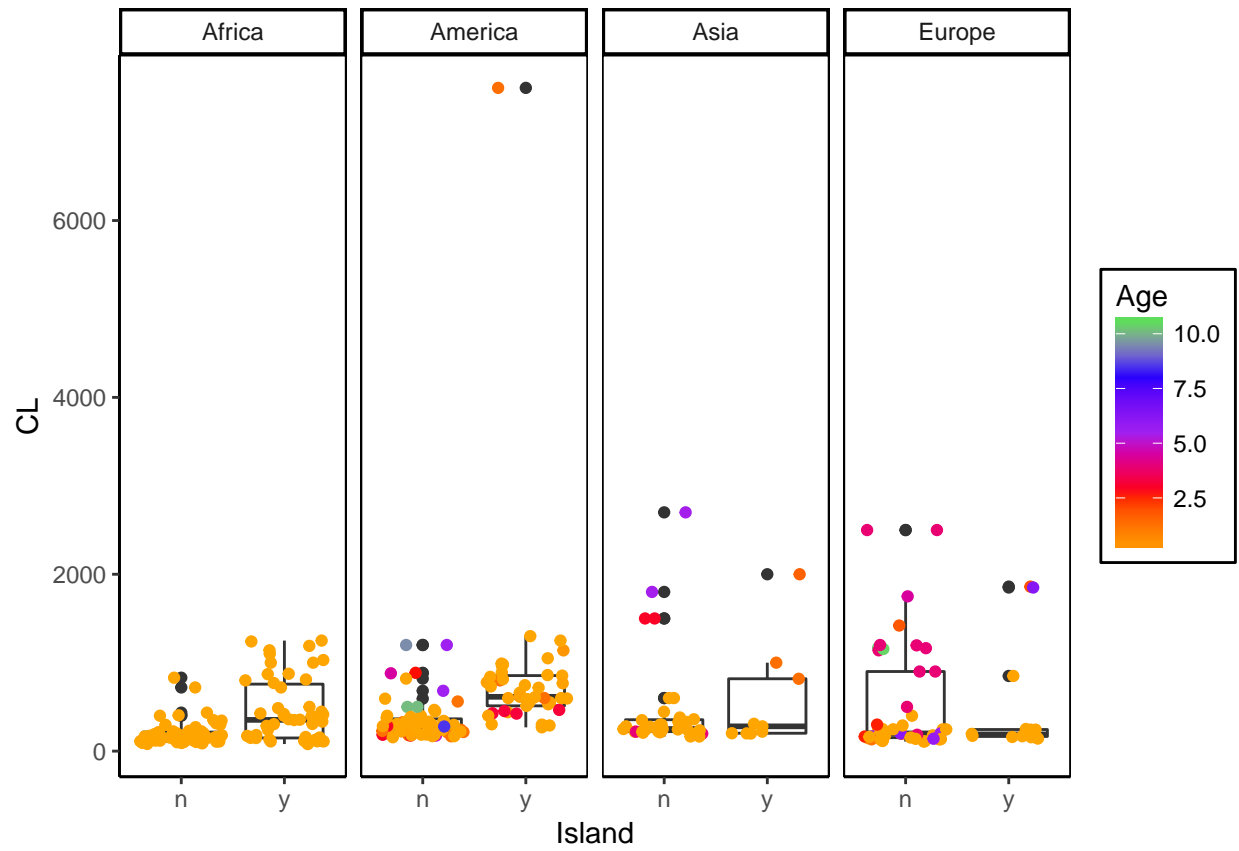


Histogram of Fossil\$Age

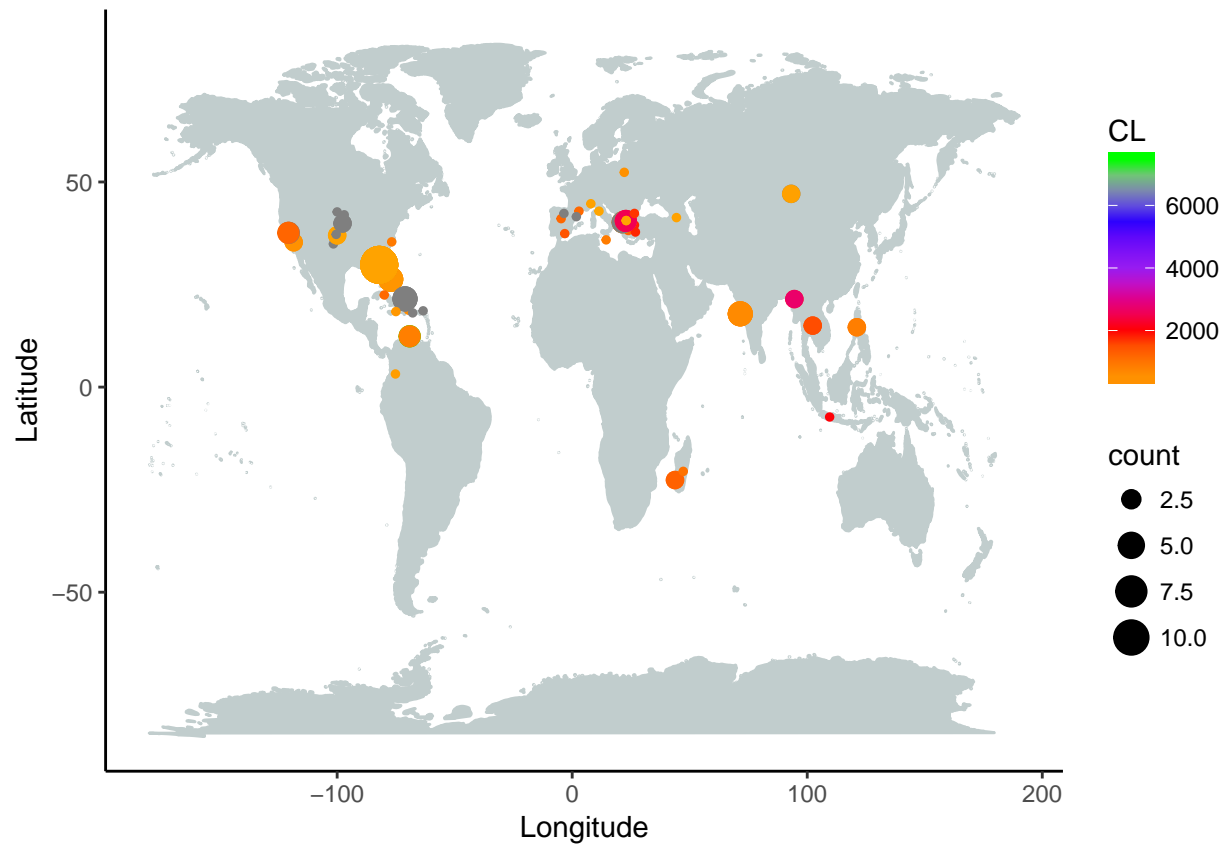


Boxplots (continental (n) vs. Island (y) species)



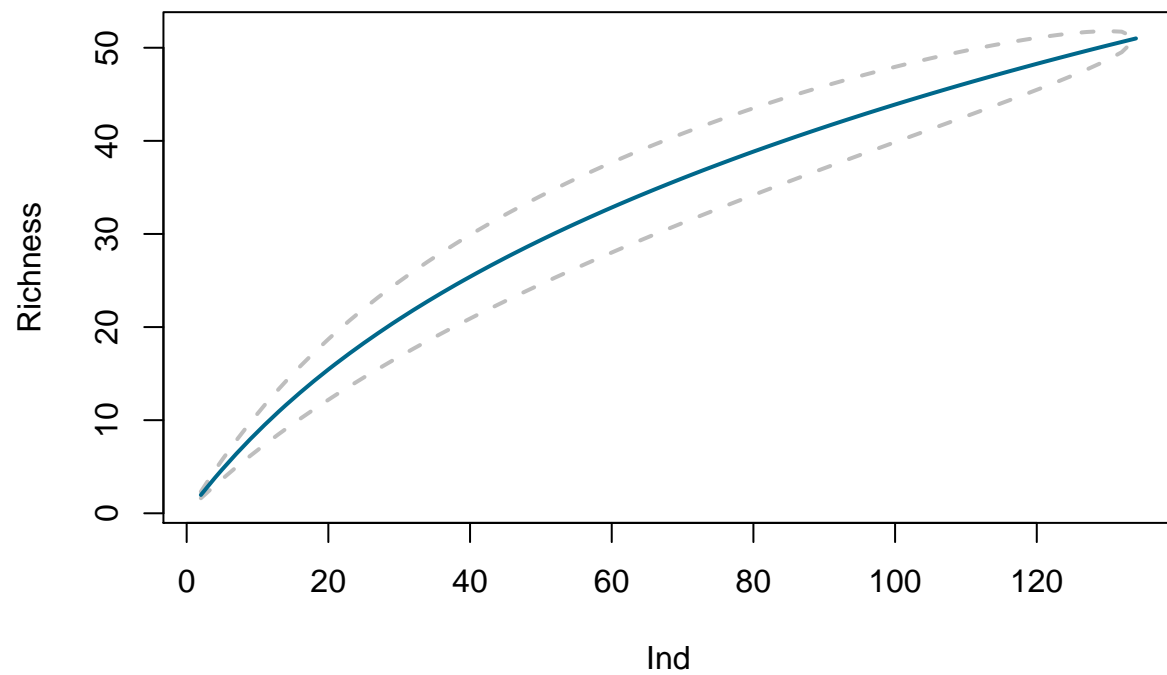


Map



Species Accumulation Curve

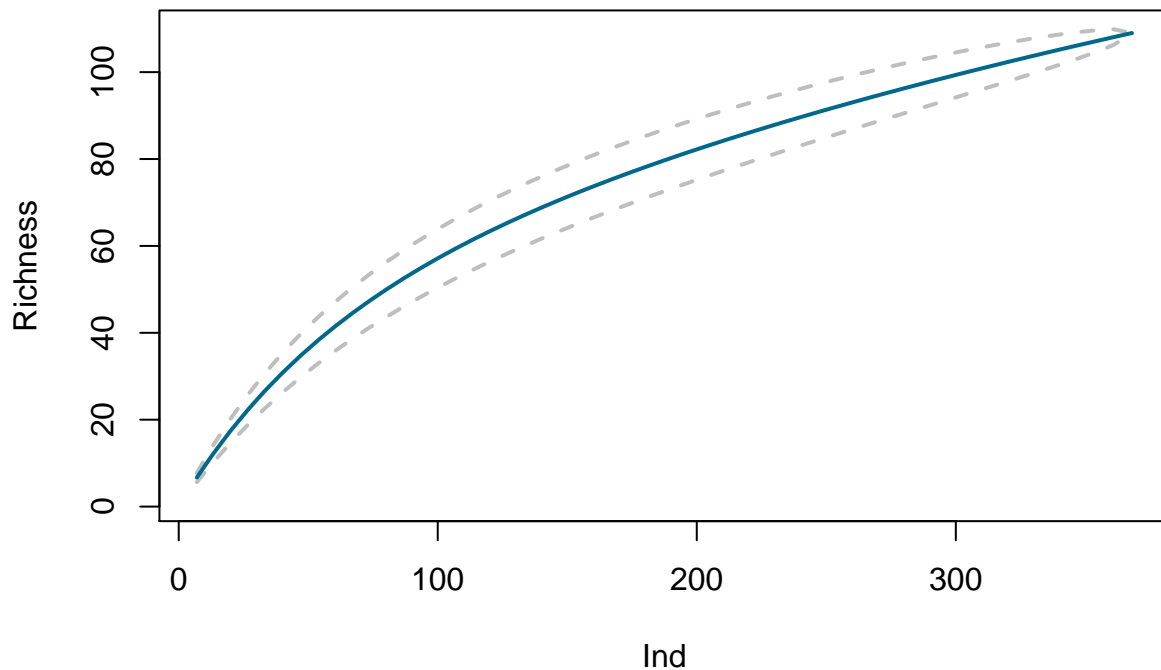
Only for fossils (per Locality)



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 factor and character vector,  
## coercing into character vector
```

```
All<-read.csv("tortoises13-04.csv", sep=";", header=TRUE)
```

```
allSp <- All %>%
  dplyr::select(Reference, Taxon) %>%
  rename(Species=Taxon)
```

```
extantSp <- extant %>%
  dplyr::select(Reference, Species)
```

```
veganAll <- allSp %>%
  # bind_rows(extantSp) %>%
  group_by(Reference, Species) %>%
  summarise(n=n()) %>%
  tidyr::spread(Species, n, fill=0)
```

```
veganAllEx <- allSp %>%
  bind_rows(extantSp) %>%
  group_by(Reference, Species) %>%
  summarise(n=n()) %>%
  tidyr::spread(Species, n, fill=0)
```

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

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

```
library(vegan)
```

```
#head(vegan)
```

```
veganAll=veganAll[,-1]
```

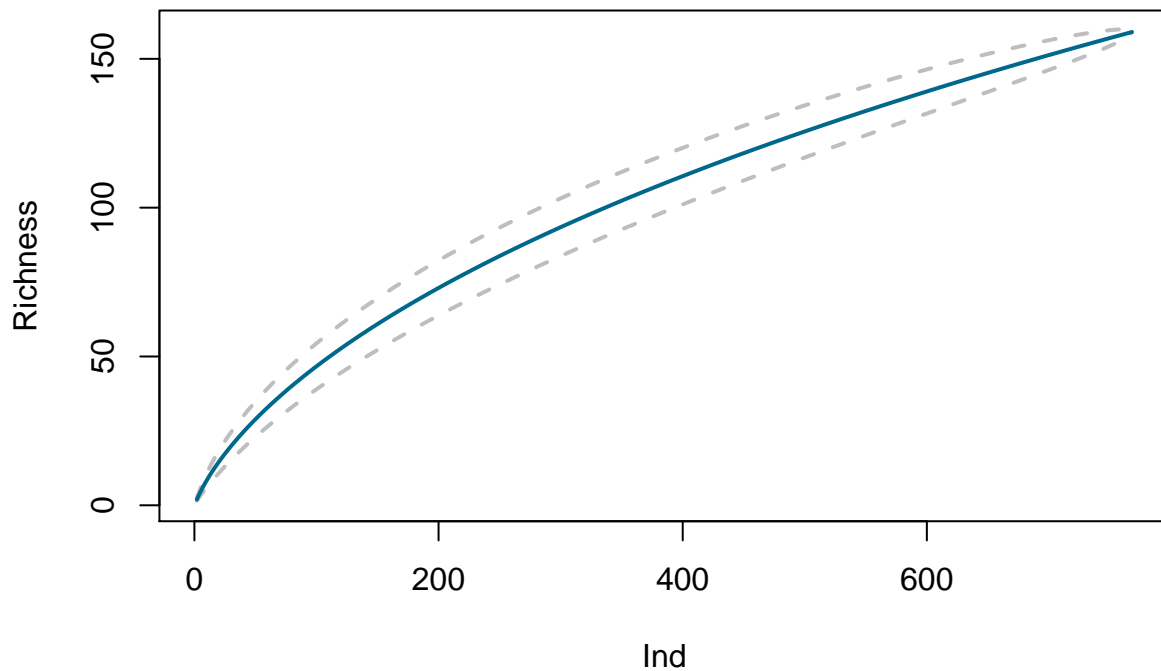
```
vegansp=specaccum(veganAll,method="rarefaction", permutations=1000)
```

```
veganAllEx=veganAllEx[,-1]
```

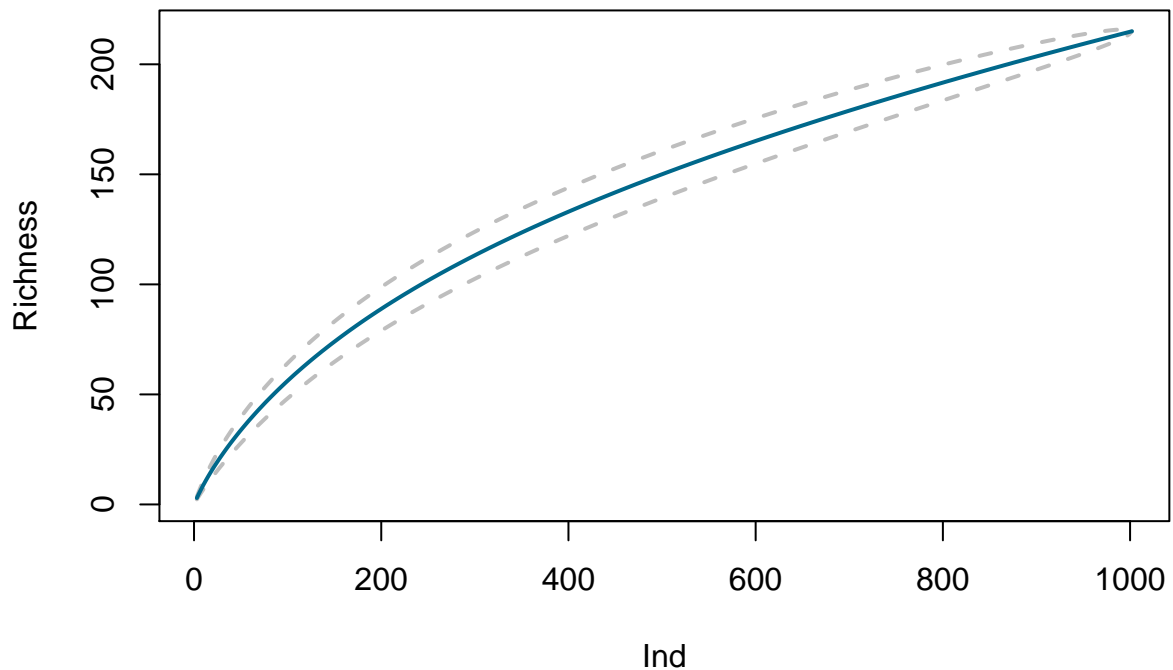
```
veganspAll=specaccum(veganAllEx,method="rarefaction", permutations=1000)
```

```
#par(mfcol=c(2, 1)) # mfrow: side by side
```

```
plot(vegansp,xlab="Ind",ylab="Richness", xvar="individuals", ci.type="line", ci.lty=2, ci.col="grey", c
```



```
plot(veganspAll,xlab="Ind",ylab="Richness", xvar="individuals", ci.type="line", ci.lty=2, ci.col="grey"
```



```
All<-read.csv("tortoises13-04.csv", sep=";", header=TRUE)
```

```
allGen <- tidyCL %>% #All or tidyCL
  filter(Age < 11.000) %>%
  dplyr::select(Reference, Genus) %>%
  # rename(Species=Taxon)
```

```
# extantSp <- extant %>%
# dplyr::select(Reference, Species)
```

```
veganGenera <- allGen %>%
  # bind_rows(extantSp) %>%
  group_by(Reference, Genus) %>%
  summarise(n=n()) %>%
  tidyr::spread(Genus, n, fill=0)

# veganAllEx <- allSp %>%
# bind_rows(extantSp) %>%
# group_by(Reference, Species) %>%
# summarise(n=n()) %>%
# tidyr::spread(Species, n, fill=0)
```

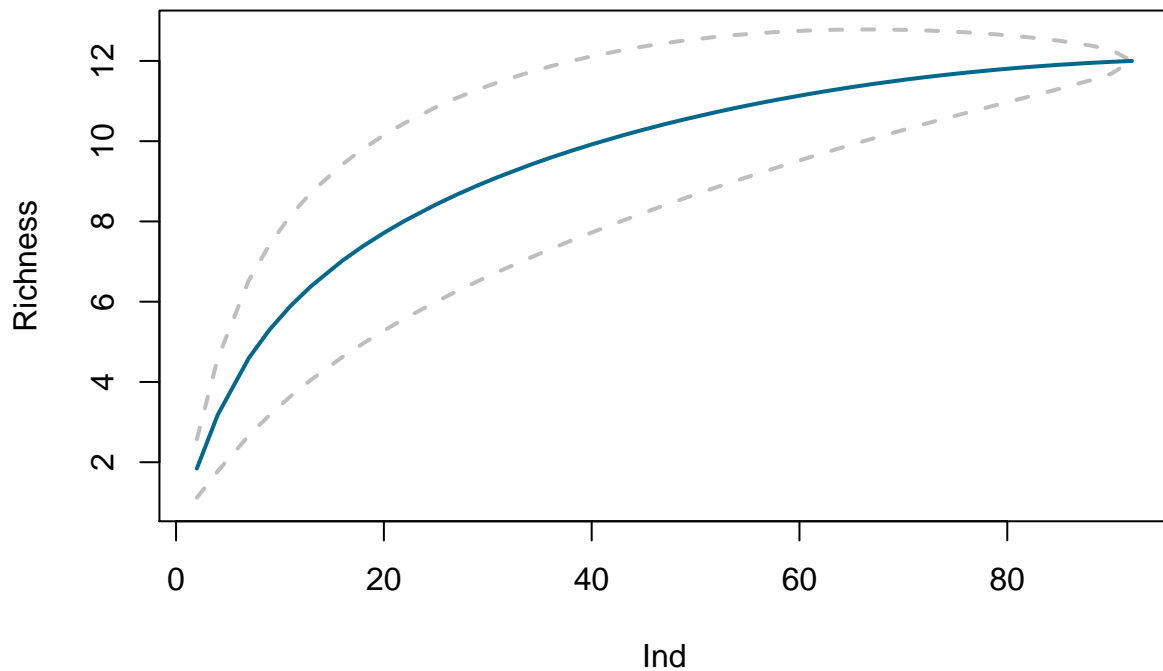
```
library(vegan)
```

```

#head(vegan)
veganGenera=veganGenera[,-1]
veganG=specaccum(veganGenera,method="rarefaction", permutations=1000)
# veganAllEx=veganAllEx[,-1]
# veganspAll=specaccum(veganAllEx,method="rarefaction", permutations=1000)

#par(mfcol=c(2, 1)) # mfrow: side by side
plot(veganG,xlab="Ind",ylab="Richness", xvar="individuals", ci.type="line", ci.lty=2, ci.col="grey", col="blue", lty=1)

```



```

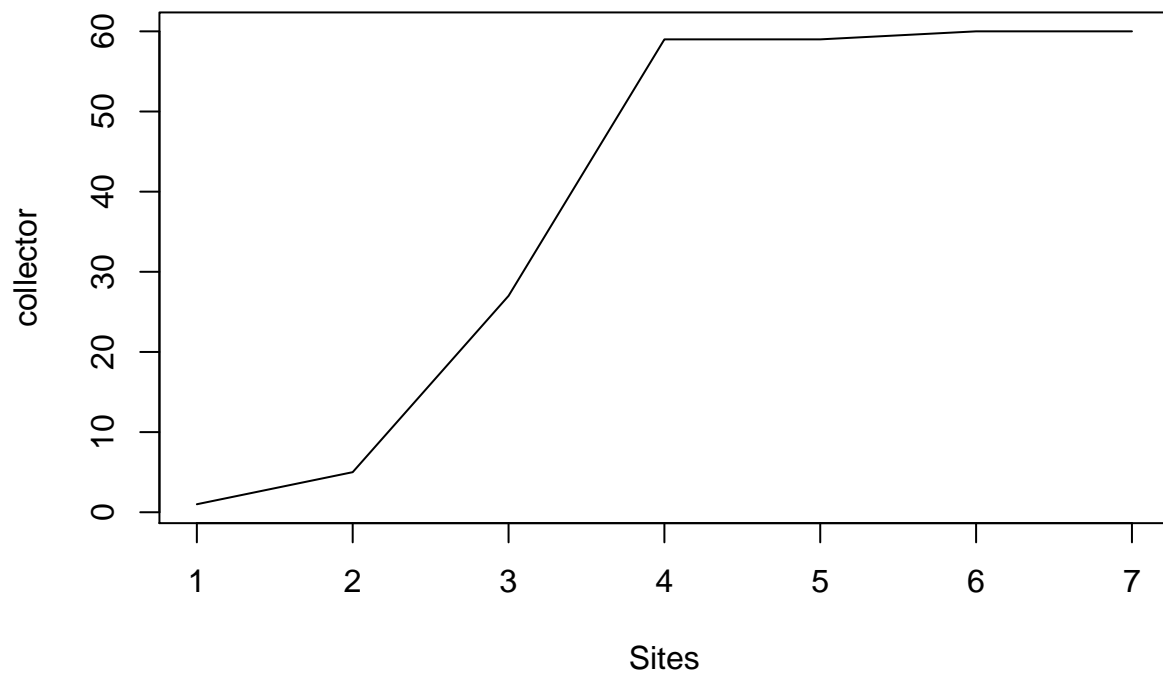
# plot(veganspAll,xlab="Ind",ylab="Richness", xvar="individuals", ci.type="line", ci.lty=2, ci.col="grey", col="blue", lty=1)

extantSp <- extant %>%
  dplyr::select(Reference, Species)

veganEx <- extantSp %>%
  group_by(Reference, Species) %>%
  summarise(n=n()) %>%
  tidyr::spread(Species, n, fill=0)

veganEx=veganEx[,-1]
veganE=specaccum(veganEx,method="collector" )#, permutations=1000)
plot(veganE)

```



```
# plot(veganE,xlab="Ind",ylab="Richness", xvar="individuals", ci.type="line", ci.lty=2, ci.col="grey",
```