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

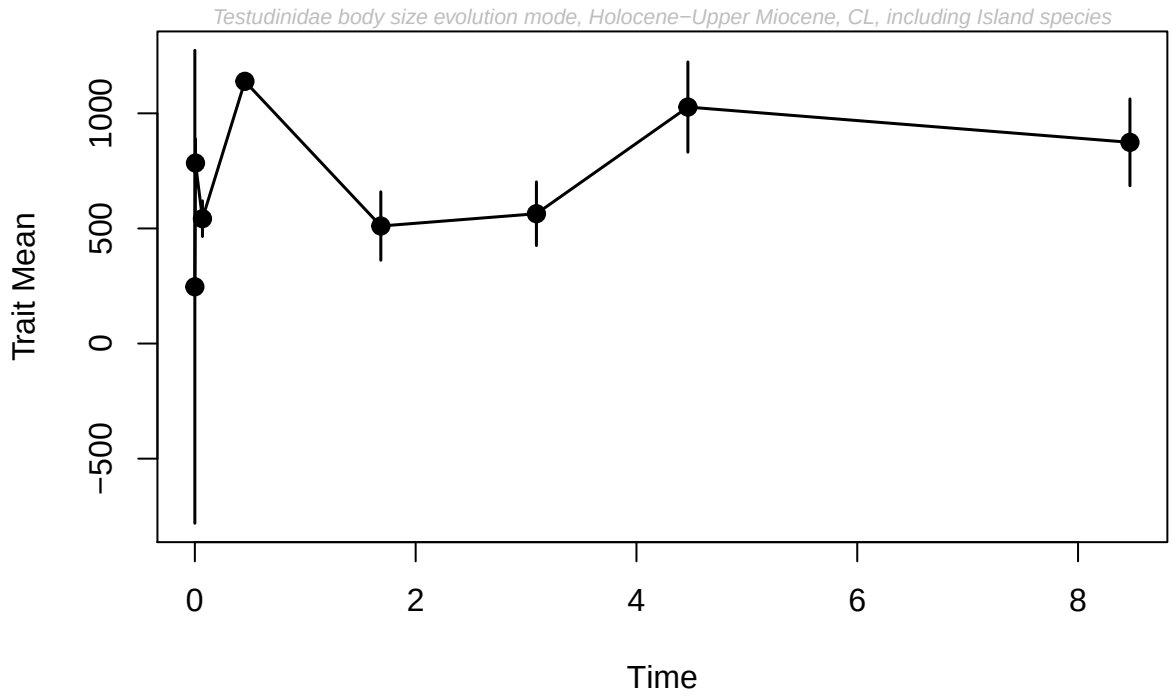
bin	n
(0,1e-06]	232
(1e-06,0.0117]	10
(0.0117,0.126]	12
(0.126,0.781]	2
(0.781,2.59]	19
(2.59,3.6]	13
(3.6,5.33]	15
(5.33,11.6]	16

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=2042)

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

mm	nn	vv	tt
246.5267	1960	2.067437e+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
510.5000	17	3.756274e+05	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

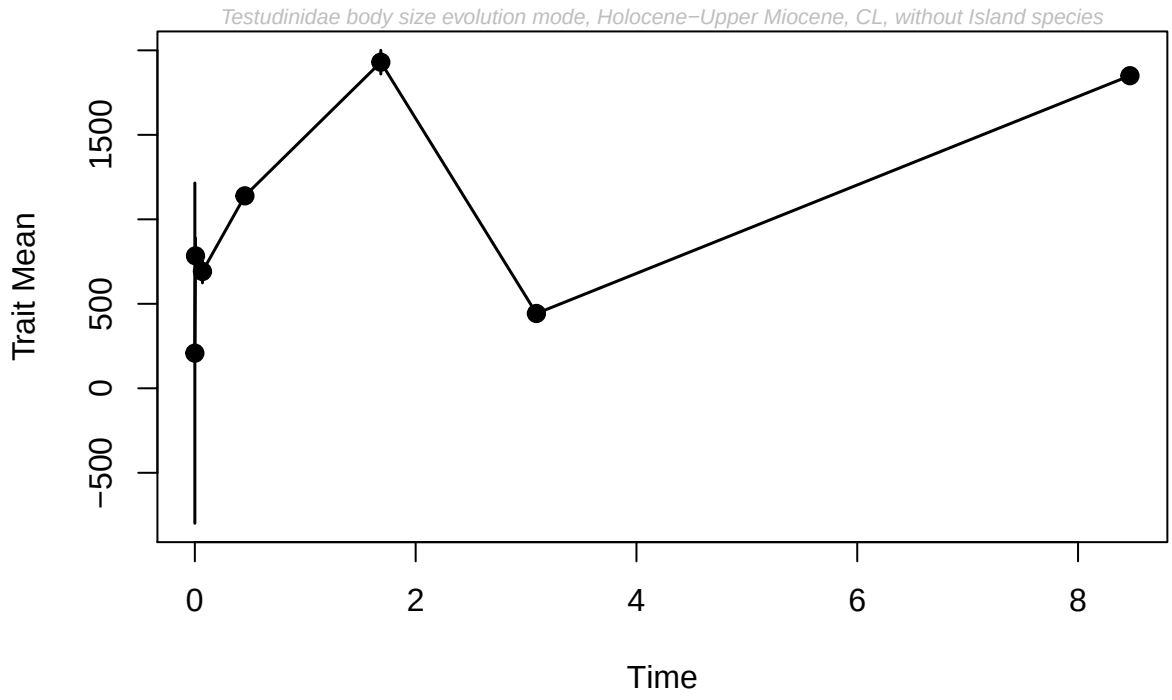



```
##
## Comparing 3 models [n = 7, method = AD]
##
##             logL K     AICc Akaike.wt
## GRW    -64.21910 2 135.4382     0.000
## URW    -60.07702 1 122.9540     0.001
## Stasis -50.50463 2 108.0093     0.999
```

	logL	K	AICc	Akaike.wt
GRW	-64.21910	2	135.4382	0.000
URW	-60.07702	1	122.9540	0.001
Stasis	-50.50463	2	108.0093	0.999

Excluding Island species (n= 1728)

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
1930.0000	2	9.800000e+03	1.6845000
442.7500	4	4.049167e+02	3.0940000
1850.0000	1	0.000000e+00	8.4700000

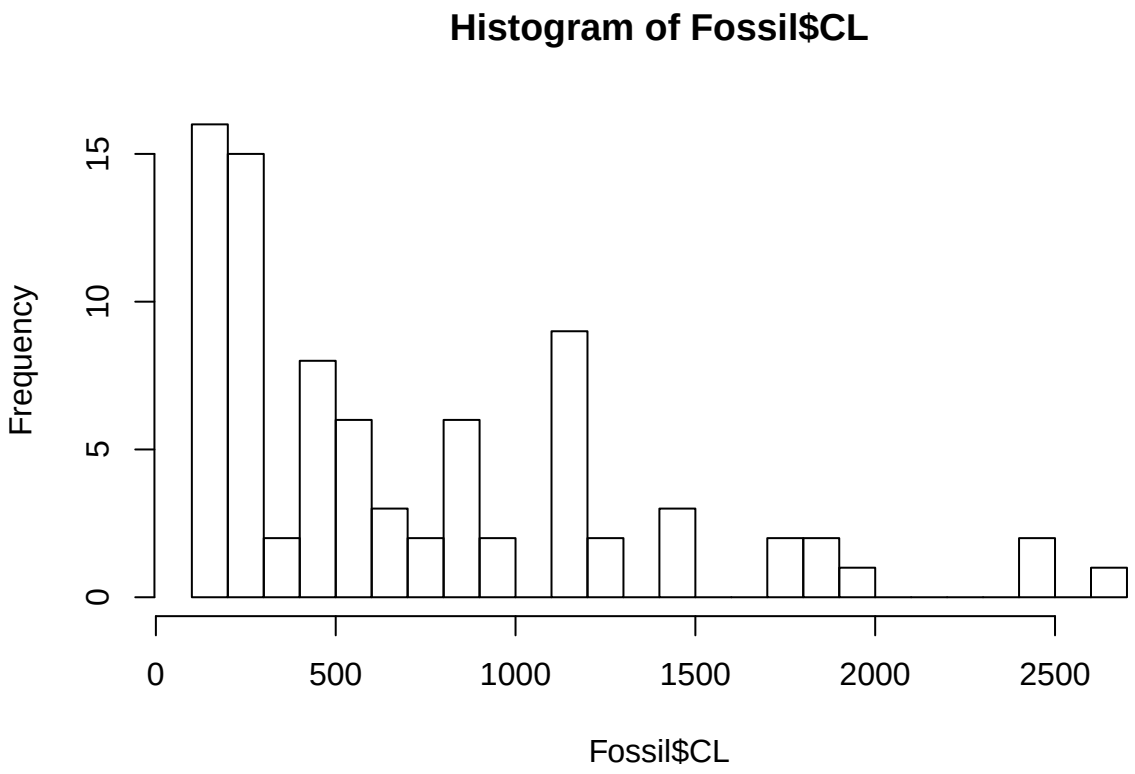


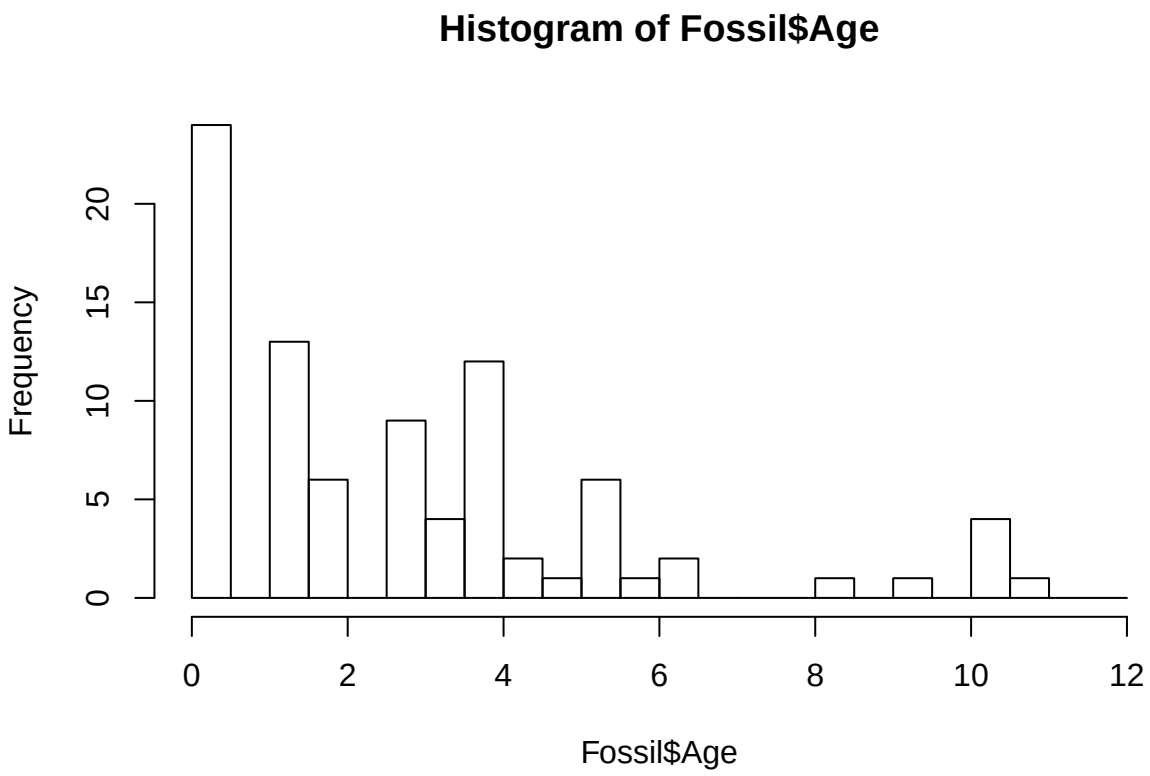

```
##
## Comparing 3 models [n = 6, method = AD]
##
##             logL K     AICc Akaike.wt
## GRW    -53.20994 2 114.4199     0.027
## URW    -57.87959 1 118.7592     0.003
## Stasis -49.61560 2 107.2312     0.970
```

	logL	K	AICc	Akaike.wt
GRW	-53.20994	2	114.4199	0.027
URW	-57.87959	1	118.7592	0.003
Stasis	-49.61560	2	107.2312	0.970

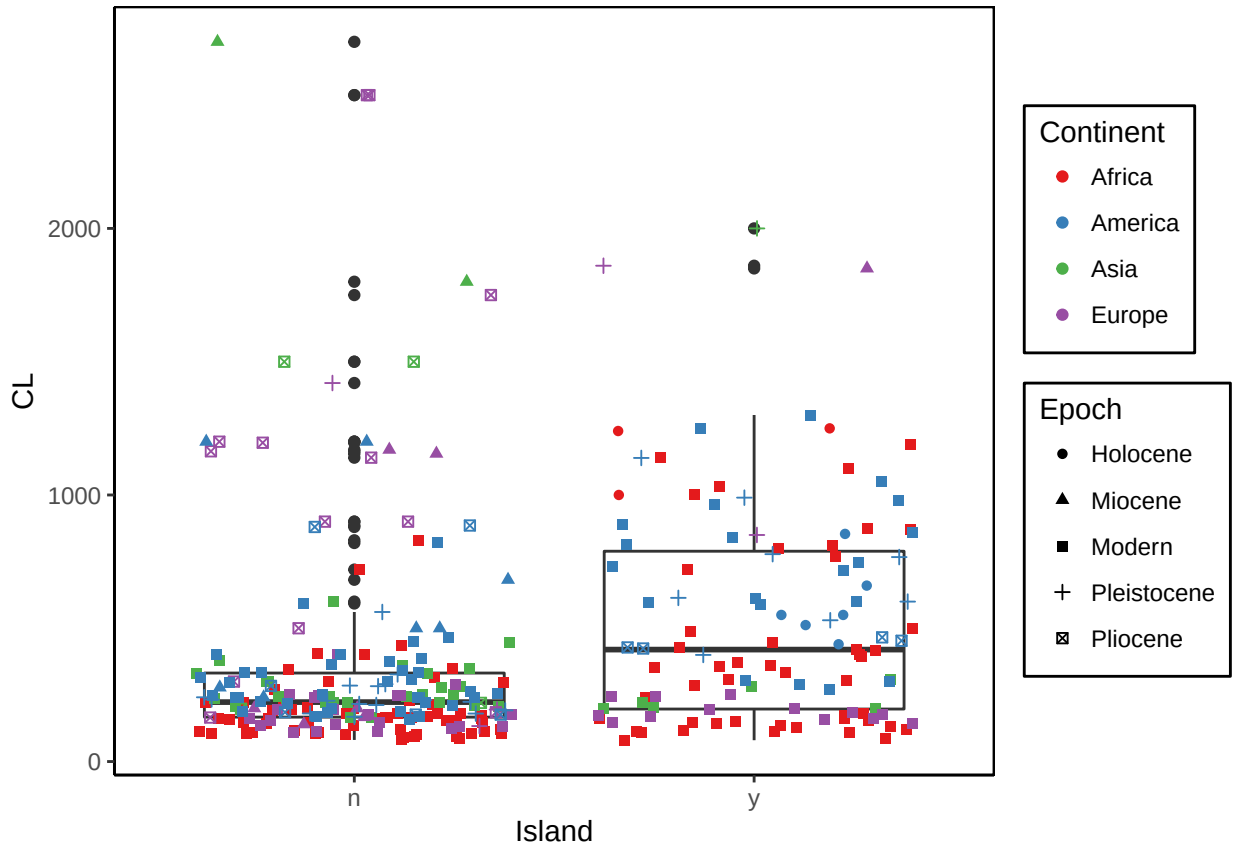
Histograms

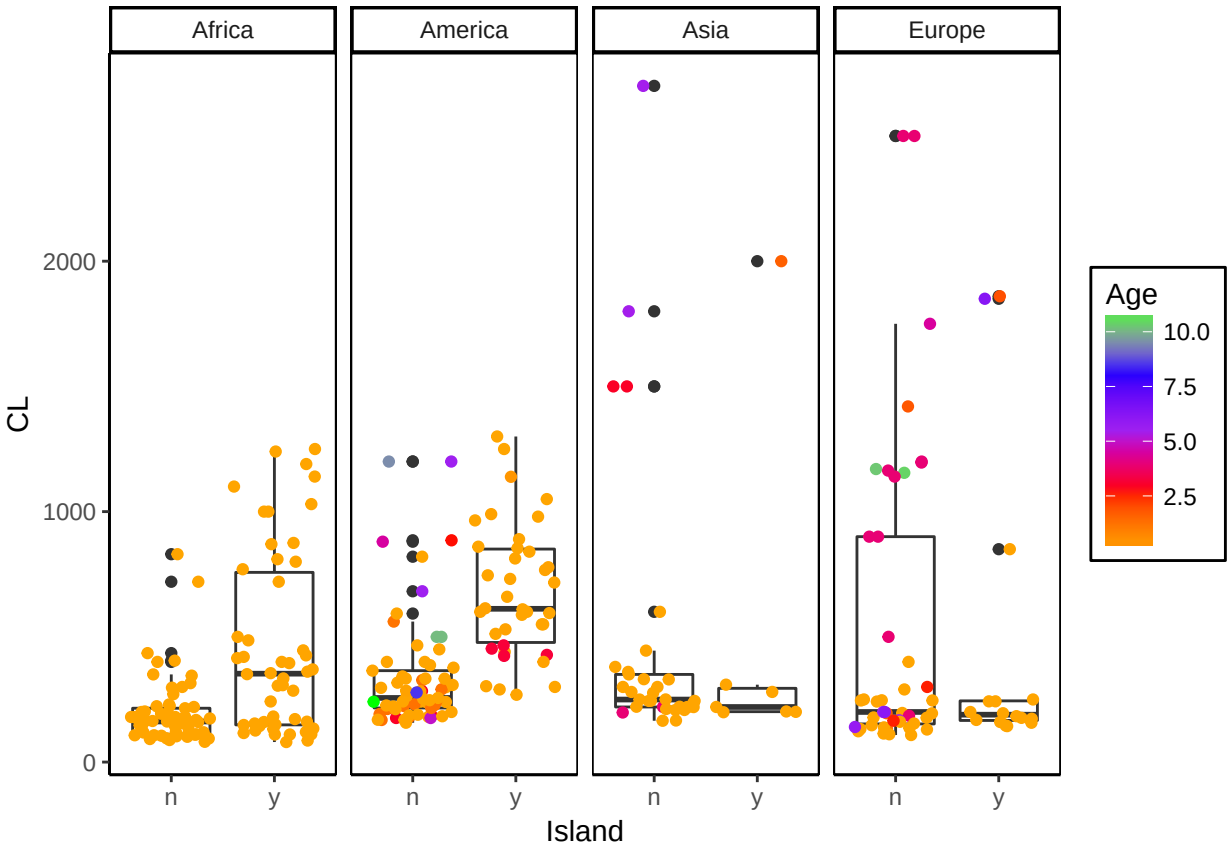
Frequency of body size data and distribution over time


Histogram of Fossil$CL
Frequency
0
5
10
15
0
500
1000
1500
2000
2500
Fossil$CL

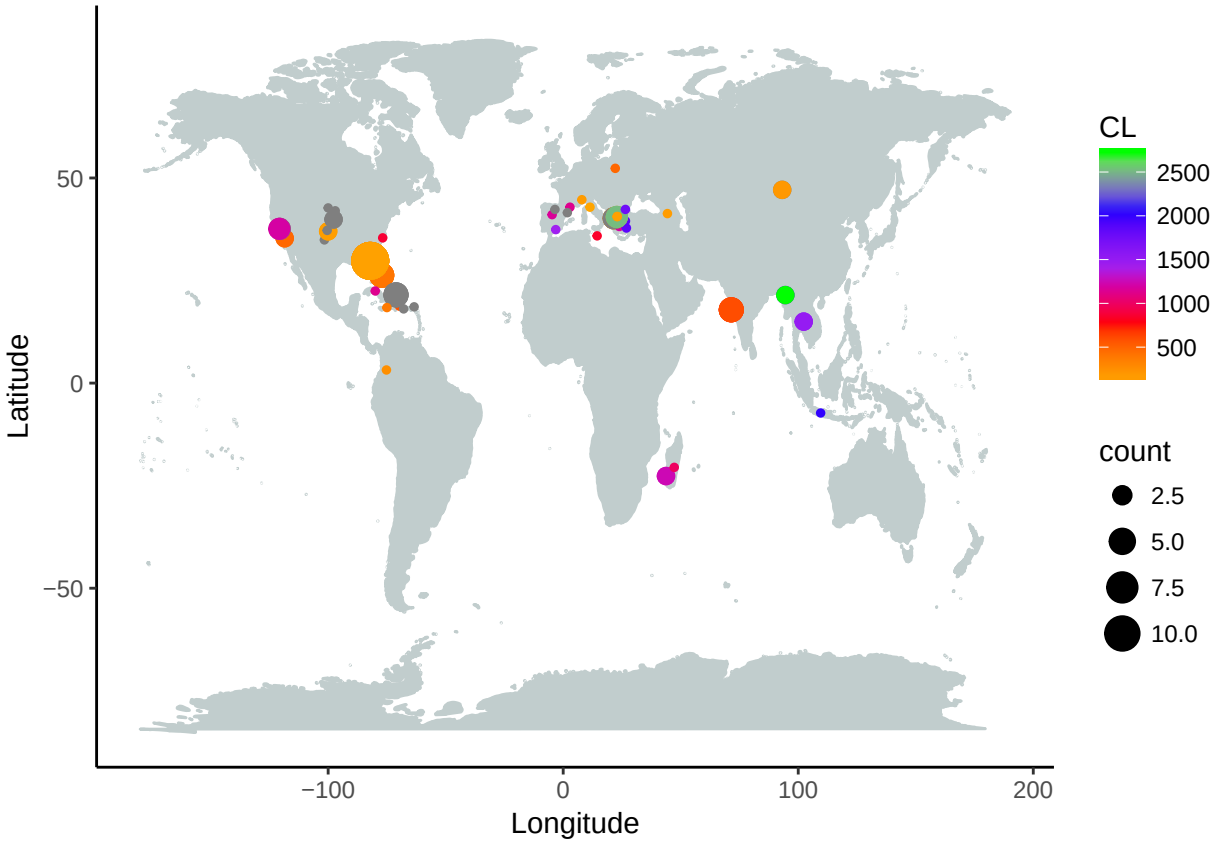

Histogram of Fossil$Age
Frequency
0
5
10
15
20
0
2
4
6
8
10
12
Fossil$Age

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



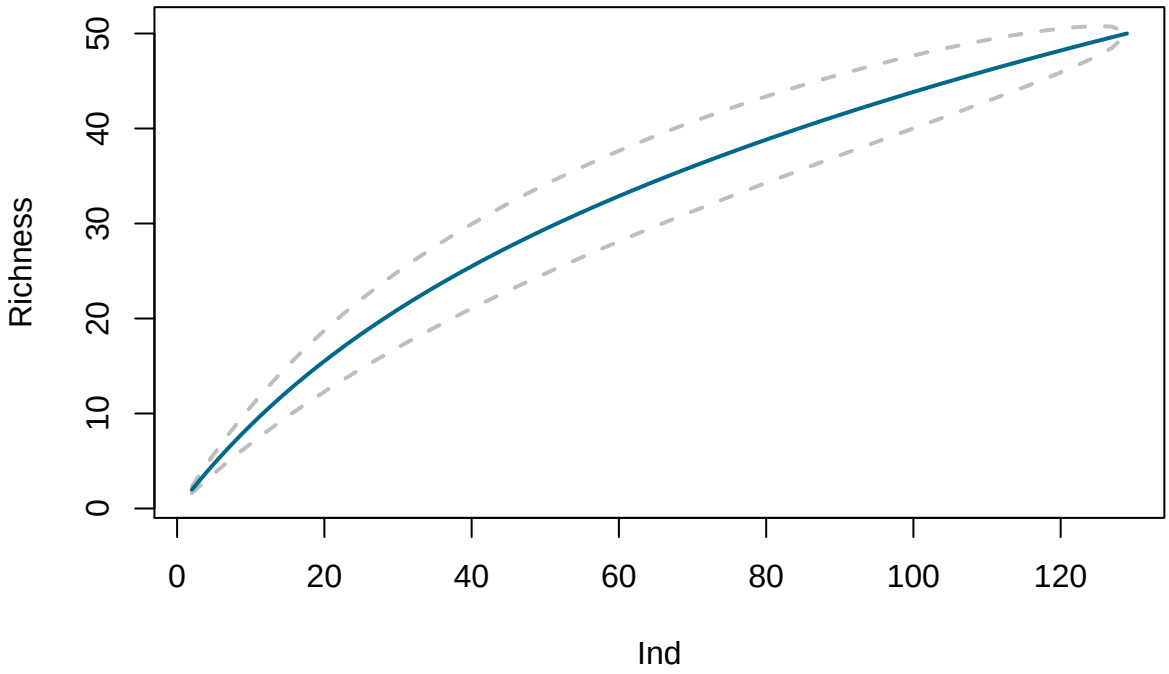

Africa
America
Asia
Europe
CL
2000
1000
0
n
y
Island
Age
10.0
7.5
5.0
2.5

Map


Latitude
50
0
−50
−100
0
100
200
Longitude
CL
2500
2000
1500
1000
500
count
2.5
5.0
7.5
10.0

Species Accumulation Curve

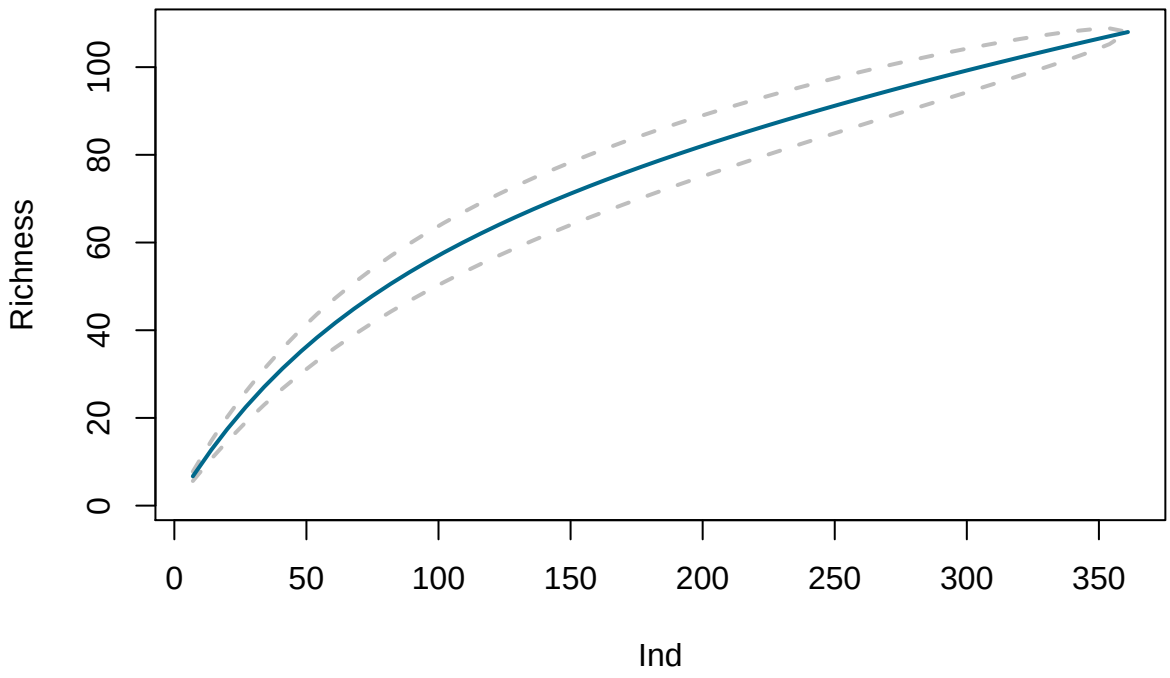
Only for fossils (per Locality)



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)
```

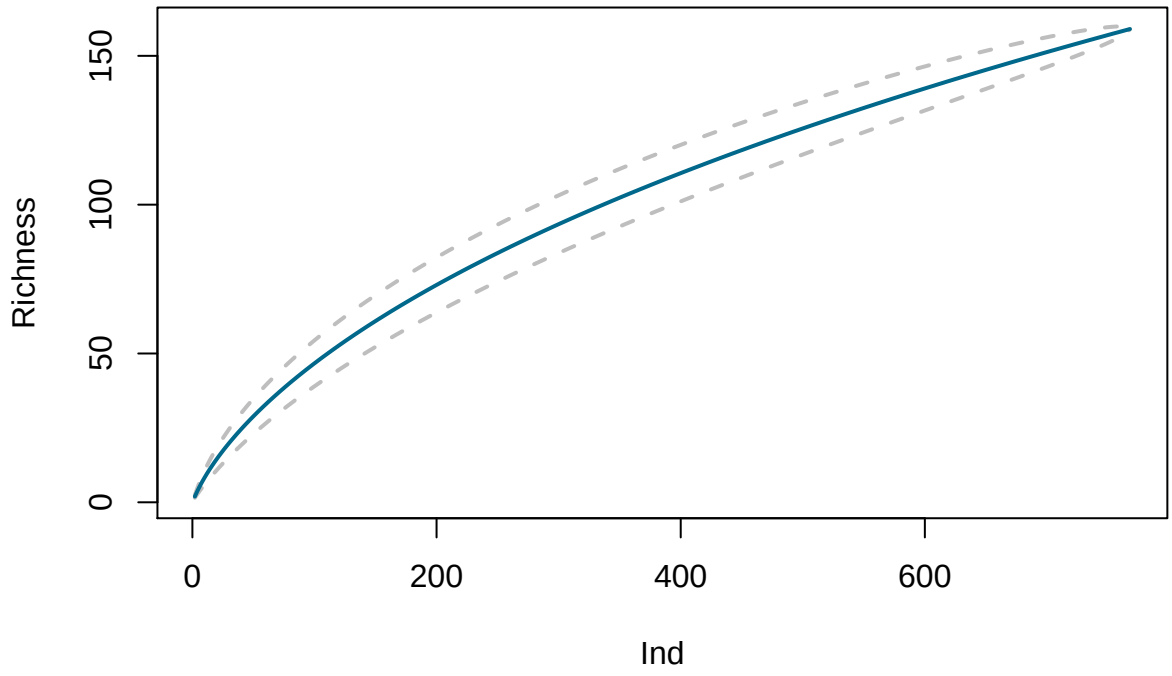
```
## Warning in bind_rows_(x, .id): binding factor and character vector,
## coercing into character vector
```

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

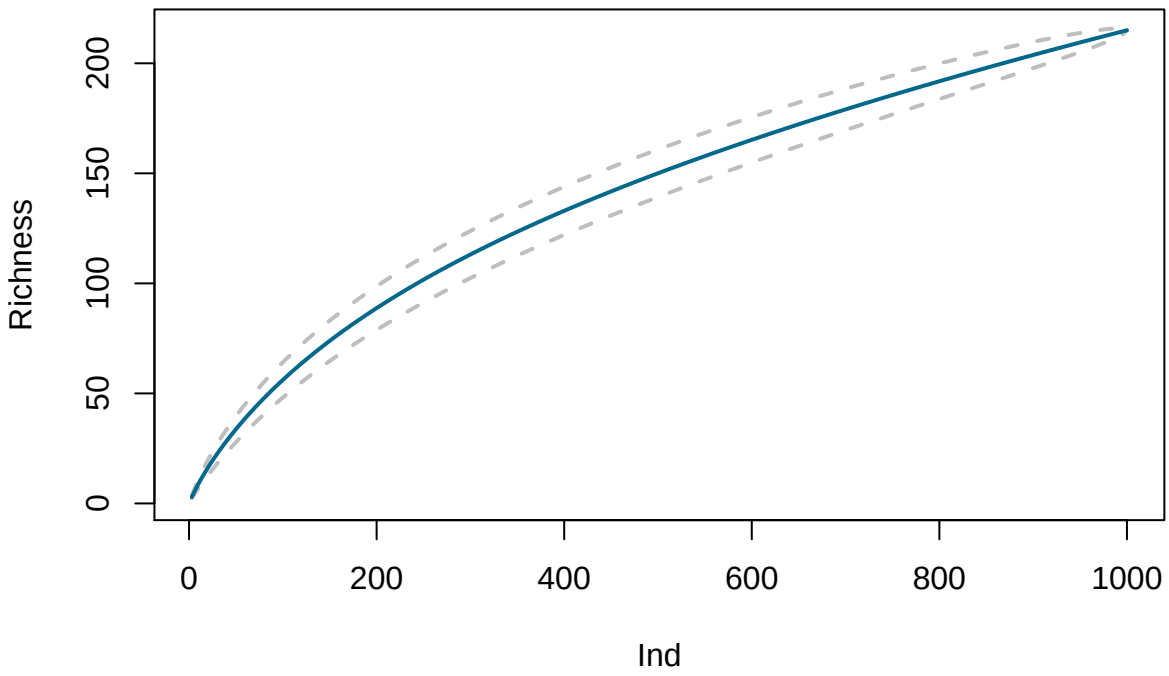
```r
library(vegan)

#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
```




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


Richness
0
50
100
150
200
0
200
400
600
800
1000
Ind