

# Species accumulation curves

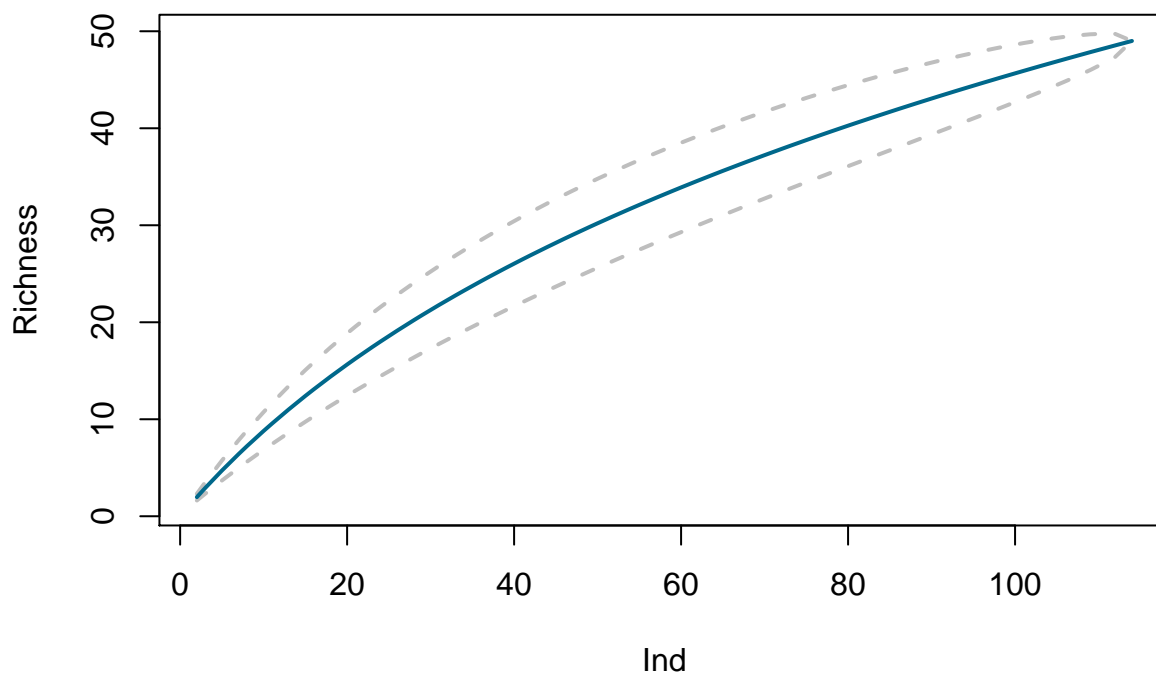
## Fossil species (n=50)

```
vegan <- tidyCL %>%
  dplyr::select(Locality, Taxon) %>%
  group_by(Locality, Taxon) %>%
  summarise(n=n()) %>%
  tidyr::spread(Taxon, n, fill=0)

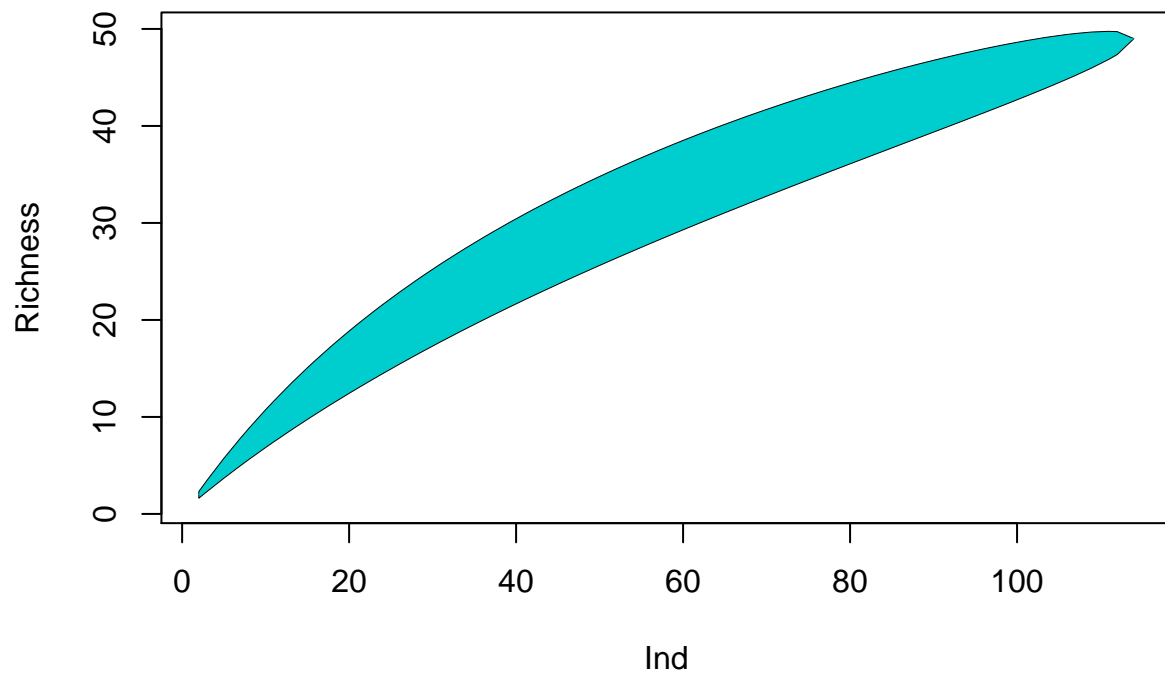
library(vegan)

## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.4-3

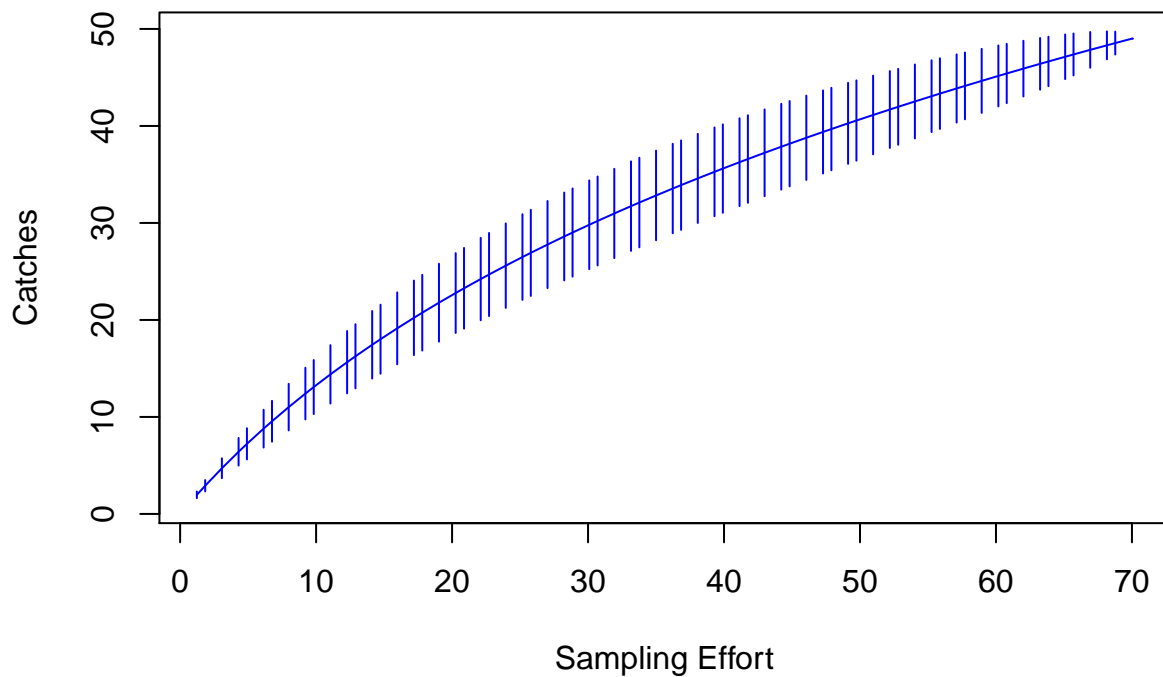
#head(vegan)
vegan=vegan[,-1]
vegansp=specaccum(vegan,method="rarefaction", permutations=1000)
plot(vegansp,xlab="Ind",ylab="Richness", xvar="individuals", ci.type="line", ci.lty=2, ci.col="grey", c
```



```
plot(vegansp,xlab="Ind",ylab="Richness", ci.type="polygon", xvar="individuals", col="cyan3", lwd=0.001)
```



```
veganc=specaccum(vegan,method="collector")  
plot(vegansp,xlab="Sampling Effort", ylab="Catches",col="blue")
```



## Fossil genera (n=16)

```
vegan <- tidyCL %>%
  dplyr::select(Locality, Genus) %>%
  group_by(Locality, Genus) %>%
  summarise(n=n()) %>%
  tidyr::spread(Genus, n, fill=0)
```

```
library(vegan)
```

```
head(vegan)
```

```
## Source: local data frame [6 x 16]
```

```
## Groups: Locality [6]
```

```
##
```

```
##                                     Locality
##                                     <fctr>
```

```
## 1 Alcalá de Henares, Cerro del Viso (Barranco de los Mártires y Santos de la
```

```
## 2      Allatini, eastern part of Thessaloniki, western Chalkidiki peninsula
```

```
## 3                                     Altan-Teli main fossiliferous bed (Dzereg valley)
```

```
## 4                                     Altenstadt, 7 km S Illertissen
```

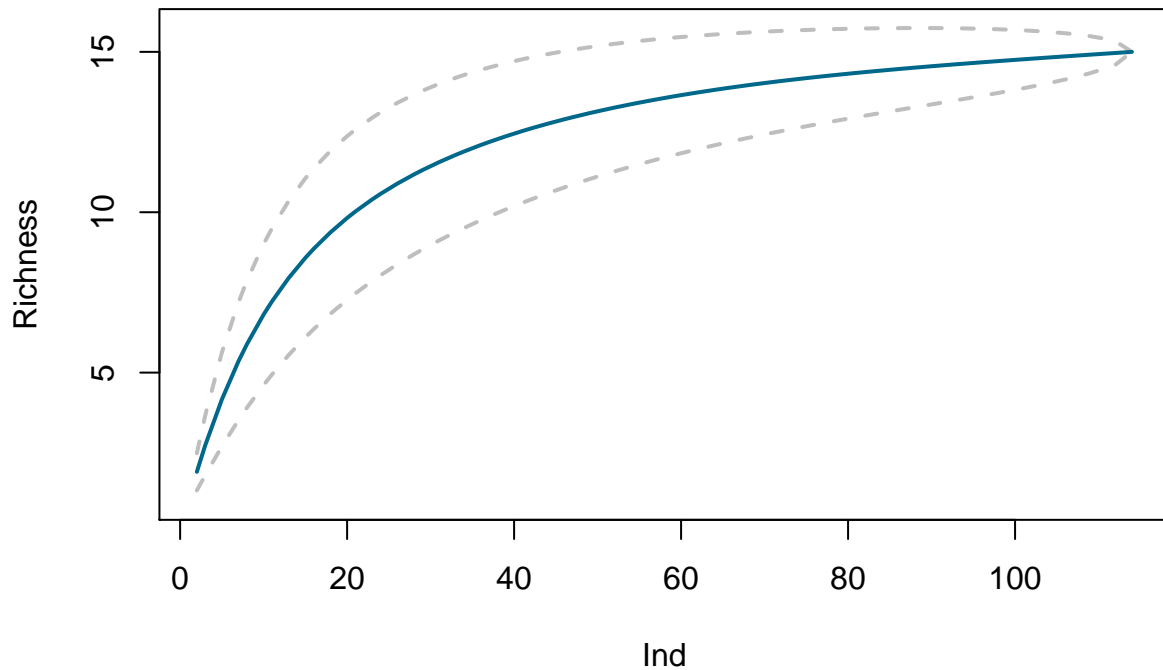
```
## 5                                     Ambositra
```

```
## 6                                     Arredondo IIA, Alachua County, Florida
```

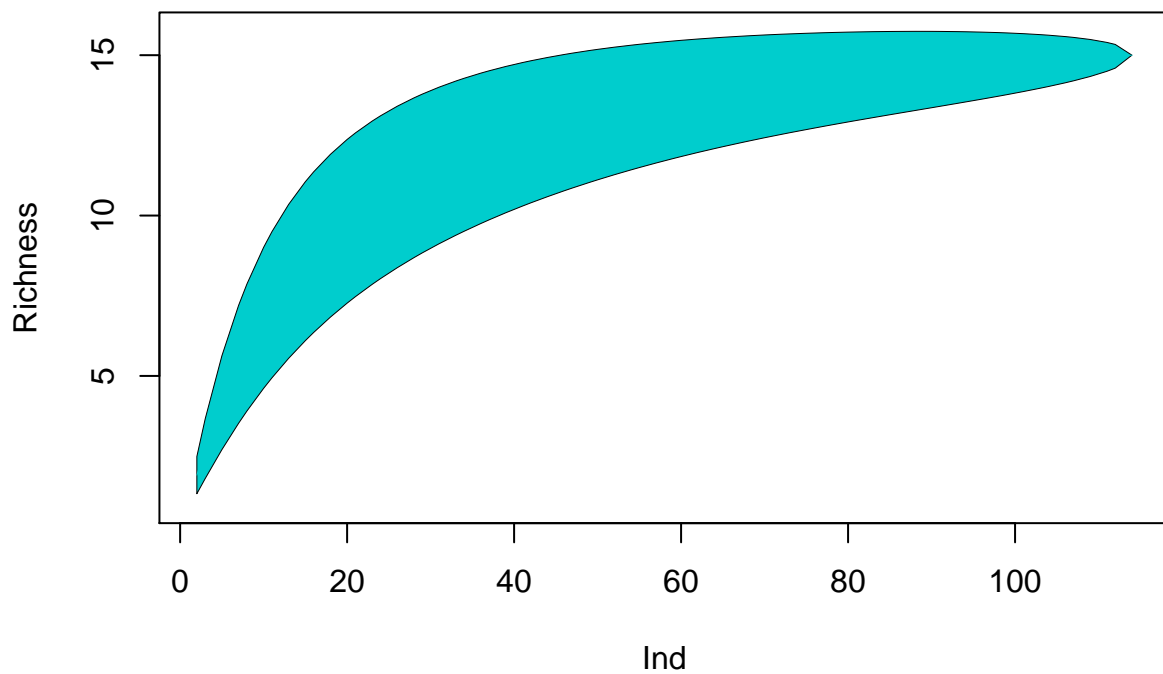
```
## # ... with 15 more variables: Aldabrachelys <dbl>, Cheirogaster <dbl>,
```

```
## # Chelonoidis <dbl>, Ergilemys <dbl>, Eurotestudo <dbl>,
## # Floridemys <dbl>, Geochelone <dbl>, Gopherus <dbl>,
## # Hesperotestudo <dbl>, Megalochelys <dbl>, Mesocherus <dbl>,
## # Namibchersus <dbl>, Paleotestudo <dbl>, Testudo <dbl>,
## # Titanochelon <dbl>
```

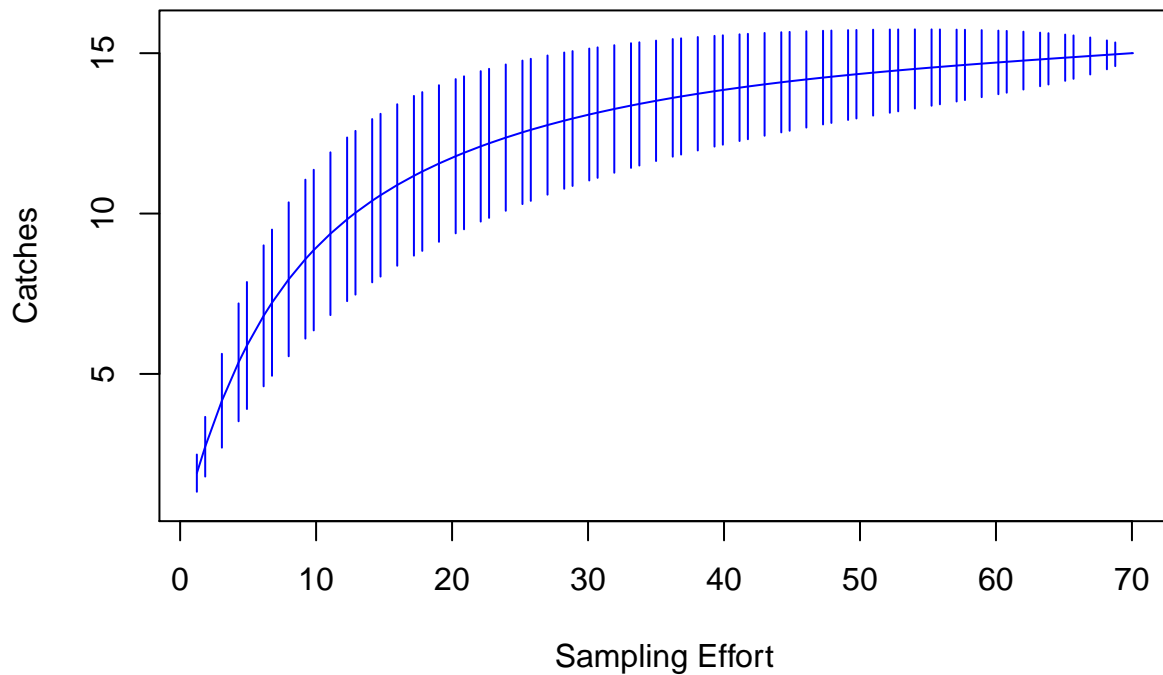
```
vegan=vegan[,-1]
vegansp=specaccum(vegan,method="rarefaction", permutations=1000)
plot(vegansp,xlab="Ind",ylab="Richness", xvar="individuals", ci.type="line", ci.lty=2, ci.col="grey", c
```



```
plot(vegansp,xlab="Ind",ylab="Richness", ci.type="polygon", xvar="individuals", col="cyan3", lwd=0.001)
```



```
veganc=specaccum(vegan,method="collector")  
plot(vegansp,xlab="Sampling Effort", ylab="Catches",col="blue")
```



## Extant species (n=62)

```
vegan <- Extant %>%
  dplyr::select(Continent, Species) %>%
  group_by(Continent, Species) %>%
  summarise(n=n()) %>%
  tidyr::spread(Species, n, fill=0)
```

```
library(vegan)
```

```
head(vegan)
```

```
## Source: local data frame [6 x 61]
## Groups: Continent [6]
##
##   Continent `Aldabrachelys gigantea` `Astrochelys radiata`
##   <chr>          <dbl>          <dbl>
## 1 Africa         9              7
## 2 Asia           0              0
## 3 C-America      0              0
## 4 Europe         0              0
## 5 N-America      0              0
## 6 S-America      0              0
## # ... with 58 more variables: `Astrochelys yniphora` <dbl>, `Centrochelys`
```

```

## #   sulcata` <dbl>, `Chelonoidis abingdonii` <dbl>, `Chelonoidis
## #   becki` <dbl>, `Chelonoidis carbonaria` <dbl>, `Chelonoidis
## #   chathamensis` <dbl>, `Chelonoidis chilensis` <dbl>, `Chelonoidis
## #   darwini` <dbl>, `Chelonoidis denticulata` <dbl>, `Chelonoidis
## #   duncanensis` <dbl>, `Chelonoidis hoodensis` <dbl>, `Chelonoidis
## #   nigra` <dbl>, `Chelonoidis phantastica` <dbl>, `Chelonoidis
## #   vicina` <dbl>, `Chersina angulata` <dbl>, `Cylindraspis indica` <dbl>,
## #   `Cylindraspis inepta` <dbl>, `Cylindraspis peltastes` <dbl>,
## #   `Cylindraspis triserrata` <dbl>, `Cylindraspis vosmaeri` <dbl>,
## #   `Geochelone elegans` <dbl>, `Geochelone platynota` <dbl>, `Gopherus
## #   sp.` <dbl>, `Gopherus agassizii` <dbl>, `Gopherus berlandieri` <dbl>,
## #   `Gopherus flavomarginatus` <dbl>, `Gopherus morafkai` <dbl>, `Gopherus
## #   polyphemus` <dbl>, `Homopus aerolatus` <dbl>, `Homopus
## #   boulengeri` <dbl>, `Homopus femoralis` <dbl>, `Homopus
## #   signatus` <dbl>, `Homopus solus` <dbl>, `Indotestudo elongata` <dbl>,
## #   `Indotestudo forstenii` <dbl>, `Indotestudo travancorica` <dbl>,
## #   `Kinixys belliana` <dbl>, `Kinixys erosa` <dbl>, `Kinixys
## #   homeana` <dbl>, `Kinixys lobatsiana` <dbl>, `Kinixys
## #   natalensis` <dbl>, `Kinixys spekii` <dbl>, `Malacochersus
## #   tornieri` <dbl>, `Manouria emys` <dbl>, `Manouria impressa` <dbl>,
## #   `Pixys arachnoides` <dbl>, `Psammobates geometricus` <dbl>,
## #   `Psammobates oculifer` <dbl>, `Psammobates tentorius` <dbl>,
## #   `Psammobates tentorius trimeni` <dbl>, `Pyxis arachnoides` <dbl>,
## #   `Pyxis planicauda` <dbl>, `Stigmochelys pardalis` <dbl>, `Testudo
## #   graeca` <dbl>, `Testudo hermanni` <dbl>, `Testudo horsfieldii` <dbl>,
## #   `Testudo kleinmanni` <dbl>, `Testudo marginata` <dbl>

```

```

vegan=vegan[,-1]

```

```

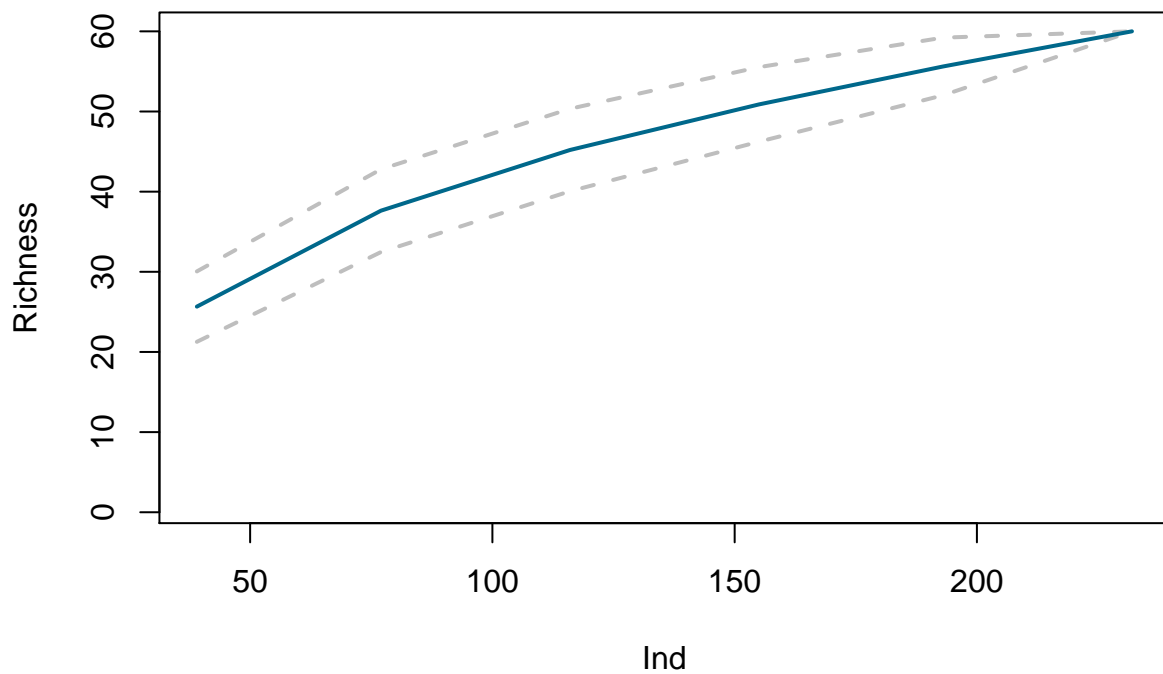
vegansp=specaccum(vegan,method="rarefaction", permutations=1000)

```

```

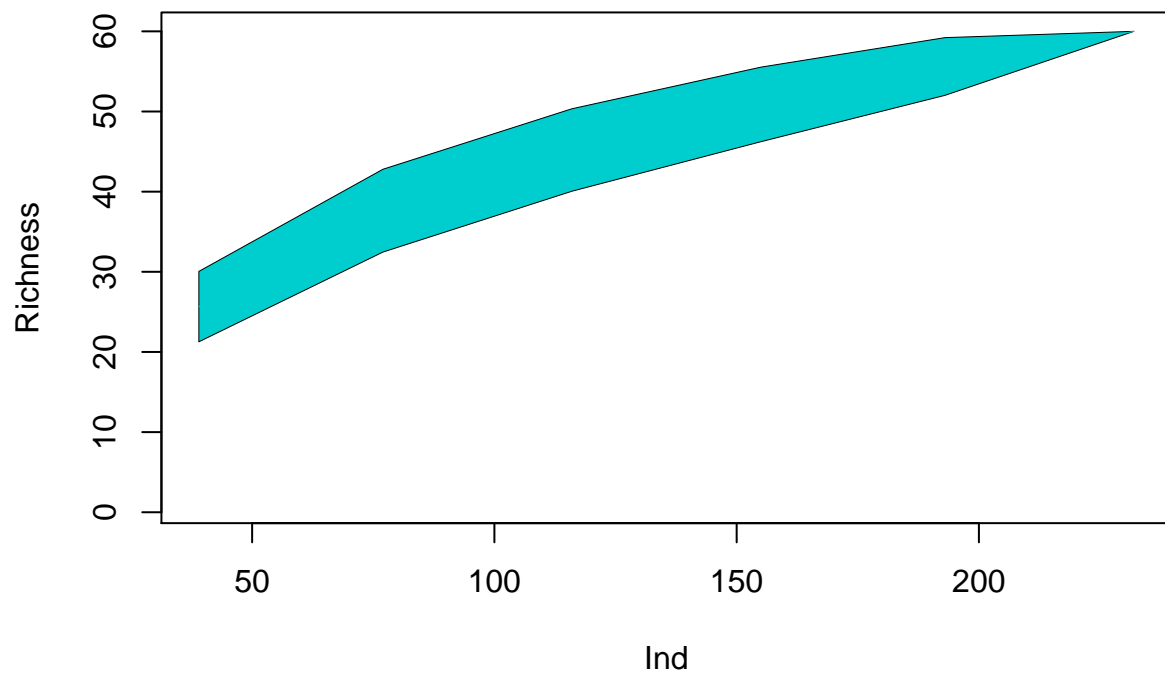
plot(vegansp,xlab="Ind",ylab="Richness", xvar="individuals", ci.type="line", ci.lty=2, ci.col="grey", c

```

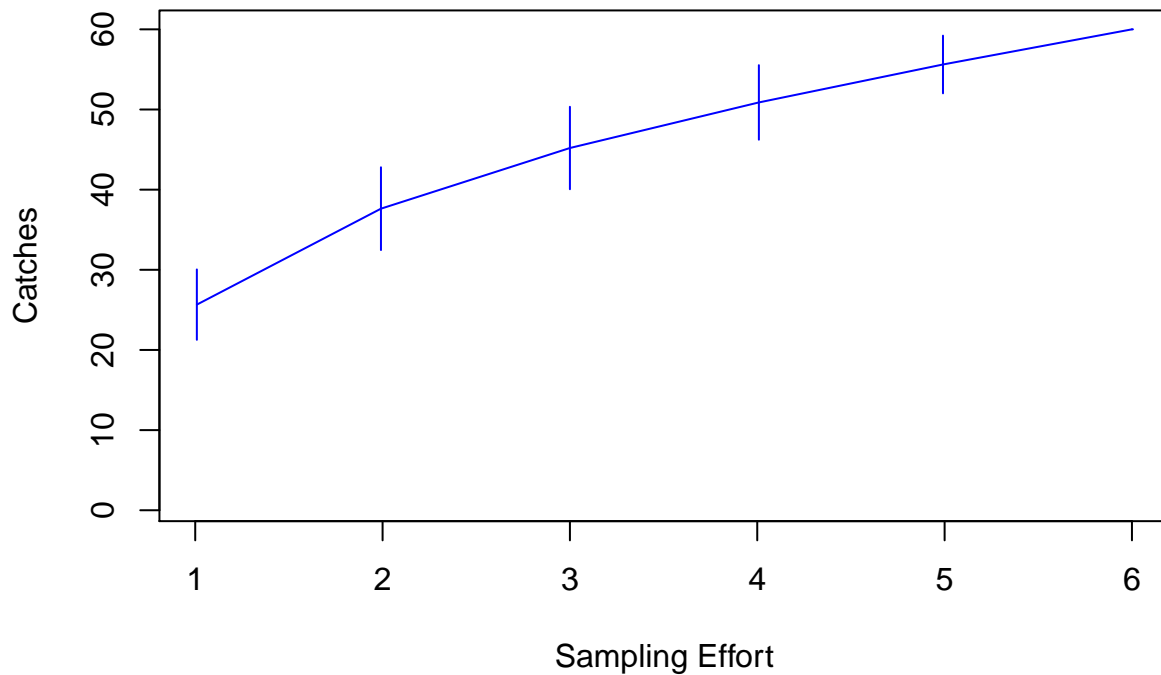


```
plot(vegansp,xlab="Ind",ylab="Richness", ci.type="polygon", xvar="individuals", col="cyan3", lwd=0.001)
```





```
veganc=specaccum(vegan,method="collector")  
plot(vegansp,xlab="Sampling Effort", ylab="Catches",col="blue")
```



## Extant and fossil combined, Continents as sites (n=109)

(because I do not have localities for extant data)

```
fossil <- tidyCL %>%
  dplyr::select(Continent, Taxon) %>%
  group_by(Continent, Taxon) %>%
  rename(Species=Taxon)

ExtantSpecies <- Extant %>%
  dplyr::select(Continent, Species) %>%
  group_by(Continent, Species)

vegan <- fossil %>%
  bind_rows(ExtantSpecies) %>%
  group_by(Continent, 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)
```

```
## Source: local data frame [6 x 108]
```

```
## Groups: Continent [6]
```

```
##
```

```
##   Continent `Aldabrachelys ? sp.` `Aldabrachelys abrupta`
```

```
##           <chr>                <dbl>                <dbl>
```

```
## 1   Africa                0                1
```

```
## 2   Asia                  2                0
```

```
## 3 C-America              0                0
```

```
## 4   Eurasia              0                0
```

```
## 5   Europe               0                0
```

```
## 6 N-America             0                0
```

```
## # ... with 105 more variables: `Aldabrachelys gigantea` <dbl>,
```

```
## # `Aldabrachelys grandidieri` <dbl>, `Astrochelys radiata` <dbl>,
```

```
## # `Astrochelys yniphora` <dbl>, `Centrochelys sulcata` <dbl>,
```

```
## # `Cheirogaster maurini` <dbl>, `Cheirogaster richardi` <dbl>,
```

```
## # `Cheirogaster sp.` <dbl>, `Chelonoidis abingdonii` <dbl>, `Chelonoidis
```

```
## # alburyorum` <dbl>, `Chelonoidis becki` <dbl>, `Chelonoidis
```

```
## # carbonaria` <dbl>, `Chelonoidis chathamensis` <dbl>, `Chelonoidis
```

```
## # chilensis` <dbl>, `Chelonoidis cubensis` <dbl>, `Chelonoidis
```

```
## # darwini` <dbl>, `Chelonoidis denticulata` <dbl>, `Chelonoidis
```

```
## # duncanensis` <dbl>, `Chelonoidis hoodensis` <dbl>, `Chelonoidis
```

```
## # marcanoi` <dbl>, `Chelonoidis monensis` <dbl>, `Chelonoidis
```

```
## # nigra` <dbl>, `Chelonoidis phantastica` <dbl>, `Chelonoidis
```

```
## # sombreroensis` <dbl>, `Chelonoidis sp.` <dbl>, `Chelonoidis
```

```
## # vicina` <dbl>, `Chersina angulata` <dbl>, `Cylindraspis indica` <dbl>,
```

```
## # `Cylindraspis inepta` <dbl>, `Cylindraspis peltastes` <dbl>,
```

```
## # `Cylindraspis triserrata` <dbl>, `Cylindraspis vosmaeri` <dbl>,
```

```
## # `Ergilemys bruneti` <dbl>, `Ergilemys oskarkuhni` <dbl>, `Ergilemys
```

```
## # sp.` <dbl>, `Floridemys hurdi` <dbl>, `Geochelone elegans` <dbl>,
```

```
## # `Geochelone hesternae` <dbl>, `Geochelone platynota` <dbl>, `Geochelone
```

```
## # sp.` <dbl>, `Geochelone tedwhitei` <dbl>, `Gopherus sp.` <dbl>,
```

```
## # `Gopherus ? sp.` <dbl>, `Gopherus agassizii` <dbl>, `Gopherus
```

```
## # berlandieri` <dbl>, `Gopherus canyonensis` <dbl>, `Gopherus
```

```
## # flavomarginatus` <dbl>, `Gopherus morafkai` <dbl>, `Gopherus
```

```
## # polyphemus` <dbl>, `Hesperotestudo alleni` <dbl>, `Hesperotestudo
```

```
## # crassiscutata` <dbl>, `Hesperotestudo equicomes` <dbl>,
```

```
## # `Hesperotestudo incisa` <dbl>, `Hesperotestudo oelrichi` <dbl>,
```

```
## # `Hesperotestudo orthopygia` <dbl>, `Hesperotestudo riggsi` <dbl>,
```

```
## # `Hesperotestudo sp.` <dbl>, `Homopus aerolatus` <dbl>, `Homopus
```

```
## # boulengeri` <dbl>, `Homopus femoralis` <dbl>, `Homopus
```

```
## # signatus` <dbl>, `Homopus solus` <dbl>, `Indotestudo elongata` <dbl>,
```

```
## # `Indotestudo forstenii` <dbl>, `Indotestudo travancorica` <dbl>,
```

```
## # `Kinixys belliana` <dbl>, `Kinixys erosa` <dbl>, `Kinixys
```

```
## # homeana` <dbl>, `Kinixys lobatsiana` <dbl>, `Kinixys
```

```
## # natalensis` <dbl>, `Kinixys spekii` <dbl>, `Malacochersus
```

```
## # tornieri` <dbl>, `Manouria emys` <dbl>, `Manouria impressa` <dbl>,
```

```
## # `Megalochelys atlas` <dbl>, `Mesochersus orangeus` <dbl>, `Namibchersus
```

```
## # aff. namaquensis` <dbl>, `Namibchersus namaquensis` <dbl>,
```

```
## # `Paleotestudo antiqua` <dbl>, `Pixys arachnoides` <dbl>, `Psammobates
```

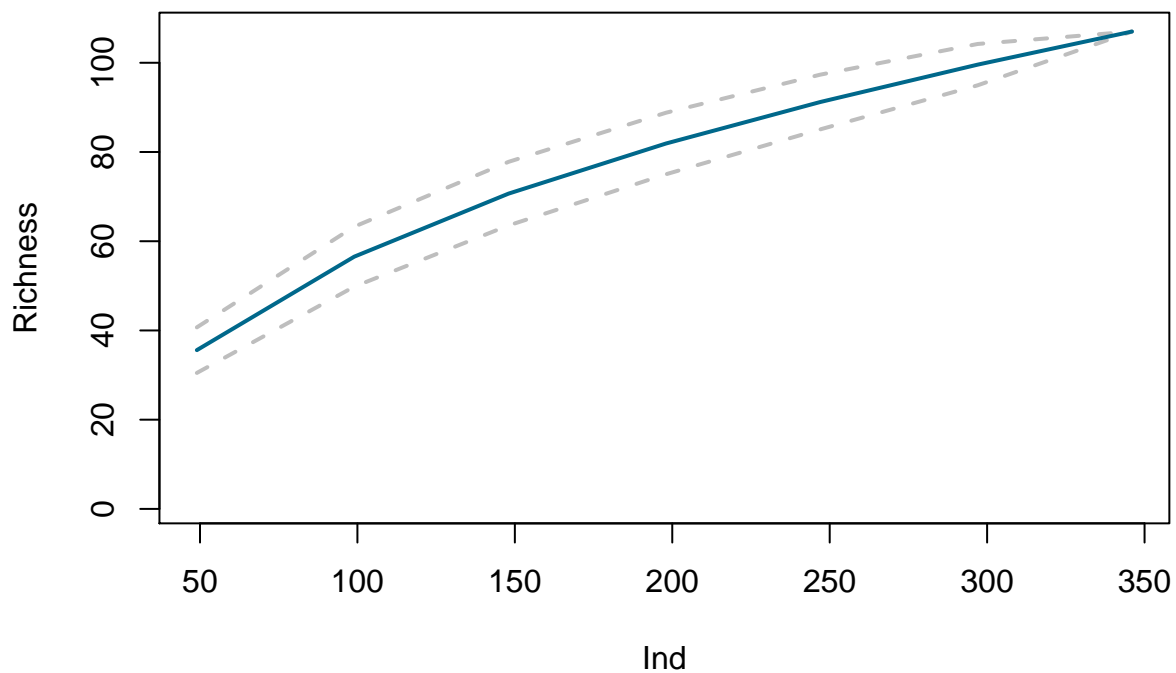
```
## # geometricus` <dbl>, `Psammobates oculifer` <dbl>, `Psammobates
```

```
## # tentorius` <dbl>, `Psammobates tentorius trimeni` <dbl>, `Pyxis
## # arachnoides` <dbl>, `Pyxis planicauda` <dbl>, `Stigmochelys
## # pardalis` <dbl>, `Testudo amiatae` <dbl>, `Testudo brevitesta` <dbl>,
## # `Testudo cf. graeca` <dbl>, `Testudo graeca` <dbl>, `Testudo
## # hermanni` <dbl>, `Testudo horsfieldii` <dbl>, `Testudo
## # kleinmanni` <dbl>, `Testudo marginata` <dbl>, `Testudo
## # rectogularis` <dbl>, `Testudo sp.` <dbl>, `Testudo
## # steinheimensis` <dbl>, `Titanochelon aff. schafferi` <dbl>,
## # `Titanochelon bacharidisi` <dbl>, ...
```

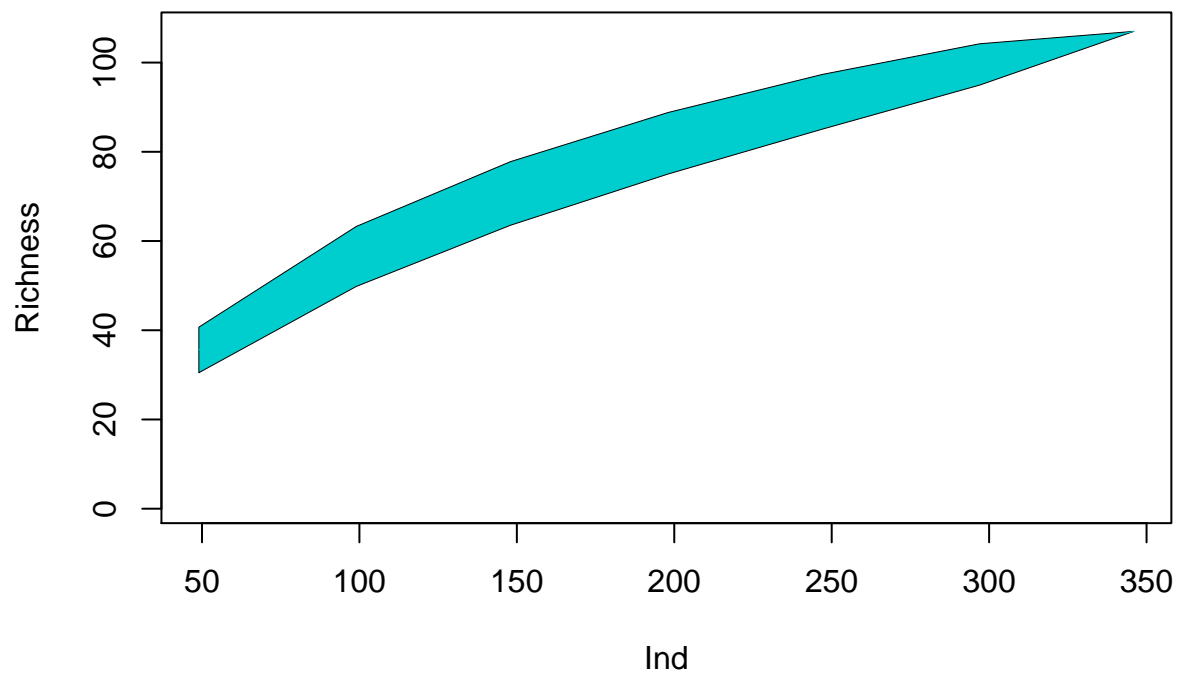
```
vegan=vegan[,-1]
```

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

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



```
plot(vegansp,xlab="Ind",ylab="Richness", ci.type="polygon", xvar="individuals", col="cyan3", lwd=0.001)
```



```
veganc=specaccum(vegan,method="collector")  
plot(vegansp,xlab="Sampling Effort", ylab="Catches",col="blue")
```

