

# Body size trends in Neogene tortoises

30.05.2017

Test paleoTS with Fossil Checklist data (but is probably of no use, because they report average body sizes (means, median, something else? what are the respective sample size? maybe ask the authors!?), so this is just for playing around).

Raw data:

```
library(paleoTS)
#setwd("//naturkundemuseum-berlin.de/MuseumDFSRoot/Benutzer/Julia.Joos/Eigene Dateien/MA")
test<-read.csv("test26.5.csv", sep=";", header=TRUE)
test
```

| ##    |  | Taxon                            | Age_min | Age_max | Age_mean |
|-------|--|----------------------------------|---------|---------|----------|
| ## 1  |  | Gopherus pertenuis               | 0.7810  | 1.8060  | 1.29350  |
| ## 2  |  | Hesperotestudo johnstoni         | 0.7810  | 1.8060  | 1.29350  |
| ## 3  |  | Hesperotestudo oelrichi          | 0.7810  | 1.8060  | 1.29350  |
| ## 4  |  | Hesperotestudo turgida           | 0.7810  | 1.8060  | 1.29350  |
| ## 5  |  | Megalochelys margae              | 0.7810  | 1.8060  | 1.29350  |
| ## 6  |  | Megalochelys sondaari            | 0.7810  | 1.8060  | 1.29350  |
| ## 7  |  | Megalochelys sp. [Flores]        | 0.7810  | 1.8060  | 1.29350  |
| ## 8  |  | Megalochelys sp. [Java]          | 0.7810  | 1.8060  | 1.29350  |
| ## 9  |  | Psammobates antiquorum           | 0.7810  | 1.8060  | 1.29350  |
| ## 10 |  | Testudinidae sp. [China]         | 0.7810  | 1.8060  | 1.29350  |
| ## 11 |  | Testudo changshanesis            | 0.7810  | 1.8060  | 1.29350  |
| ## 12 |  | Hesperotestudo sp. [El Salvador] | 0.7810  | 1.8060  | 1.29350  |
| ## 13 |  | Aldabrachelys abrupta            | 0.0000  | 0.0117  | 0.00585  |
| ## 14 |  | Aldabrachelys grandidieri        | 0.0000  | 0.0117  | 0.00585  |
| ## 15 |  | Chelonoidis alburyorum           | 0.0000  | 0.0117  | 0.00585  |
| ## 16 |  | Chelonoidis sp. [Caicos]         | 0.0000  | 0.0117  | 0.00585  |
| ## 17 |  | Chelonoidis sp. [Turks]          | 0.0000  | 0.0117  | 0.00585  |
| ## 18 |  | Titanochelon schafferi           | 5.3320  | 7.2460  | 6.28900  |
| ## 19 |  | Chelonoidis elata                | 1.8060  | 7.2460  | 4.52600  |
| ## 20 |  | Homopus fenestratus              | 3.6000  | 1.8060  | 2.70300  |
| ## 21 |  | Chelonoidis lutzae               | 0.0117  | 0.1260  | 0.06885  |
| ## 22 |  | Chelonoidis sombreroensis        | 0.0117  | 0.1260  | 0.06885  |
| ## 23 |  | Chelonoidis sp. [Navassa]        | 0.0117  | 0.1260  | 0.06885  |
| ## 24 |  | Gopherus donlatoi                | 0.0117  | 0.1260  | 0.06885  |
| ## 25 |  | Hesperotestudo equicomes         | 0.0117  | 0.1260  | 0.06885  |
| ## 26 |  | Hesperotestudo incisa            | 0.0117  | 0.1260  | 0.06885  |
| ## 27 |  | Testudo suttoensis               | 0.0117  | 0.1260  | 0.06885  |
| ## 28 |  | Hesperotestudo wilsoni           | 0.0010  | 0.1260  | 0.06350  |
| ## 29 |  | Manouria oyamai                  | 0.0010  | 0.1260  | 0.06350  |
| ## 30 |  | Chelonoidis sp. [Hispaniola]     | 0.0010  | 0.1260  | 0.06350  |
| ## 31 |  | Chelonoidis monensis             | 0.0000  | 0.1260  | 0.06300  |
| ## 32 |  | Aldabrachelys laetoliensis       | 0.1260  | 3.6000  | 1.86300  |
| ## 33 |  | Centrochelys marocana            | 0.1260  | 3.6000  | 1.86300  |
| ## 34 |  | Gopherus sp. [Florida]           | 0.1260  | 3.6000  | 1.86300  |
| ## 35 |  | Hesperotestudo campester         | 0.1260  | 3.6000  | 1.86300  |
| ## 36 |  | Manouria punjabiensis            | 0.1260  | 3.6000  | 1.86300  |
| ## 37 |  | Megalochelys atlas               | 0.1260  | 3.6000  | 1.86300  |

|       |                                 |                                    |        |                    |
|-------|---------------------------------|------------------------------------|--------|--------------------|
| ## 38 | Megalochelys cautleyi           | 0.1260                             | 3.6000 | 1.86300            |
| ## 39 | Testudo or Agrionemys ranovi    | 0.1260                             | 3.6000 | 1.86300            |
| ## 40 | Testudo oughlamensis            | 0.1260                             | 3.6000 | 1.86300            |
| ## 41 | Testudo pecorinii               | 0.1260                             | 3.6000 | 1.86300            |
| ## 42 | Testudo transcaucasia           | 0.1260                             | 3.6000 | 1.86300            |
| ## 43 | Titanochelon sp. [Lesvos]       | 0.1260                             | 3.6000 | 1.86300            |
| ## 44 | Centrochelys vulcanica          | 0.1260                             | 3.6000 | 1.86300            |
| ## 45 | Centrochelys burchardi          | 0.1260                             | 0.7810 | 0.45350            |
| ## 46 | Centrochelys robusta            | 0.1260                             | 0.7810 | 0.45350            |
| ## 47 | Hesperotestudo bermudae         | 0.1260                             | 0.7810 | 0.45350            |
| ## 48 | Hesperotestudo mlynarskii       | 0.1260                             | 0.7810 | 0.45350            |
| ## 49 | Hesperotestudo percrassa        | 0.1260                             | 0.7810 | 0.45350            |
| ## 50 | Testudo kenitrensis             | 0.1260                             | 0.7810 | 0.45350            |
| ## 51 | Testudo lunellensis             | 0.1260                             | 0.7810 | 0.45350            |
| ## 52 | Titanochelon sp. [Ibiza]        | 0.1260                             | 0.7810 | 0.45350            |
| ## 53 | Hesperotestudo crassicutata     | 0.7810                             | 0.0117 | 0.39635            |
| ## 54 | Chelonoidis sp. [Curaçao]       | 0.0117                             | 0.7810 | 0.39635            |
| ## 55 | Gopherus laticaudatus           | 0.0117                             | 0.7810 | 0.39635            |
| ## 56 | Megalochelys sp. [Timor]        | 0.0117                             | 0.7810 | 0.39635            |
| ## 57 | Aldabrachelys gigantea daudinii | 0.0000                             | 0.0000 | 0.00000            |
| ## 58 | Chelonoidis abingdonii          | 0.0000                             | 0.0000 | 0.00000            |
| ## 59 | Chelonoidis nigra               | 0.0000                             | 0.0000 | 0.00000            |
| ## 60 | Chelonoidis phantastica         | 0.0000                             | 0.0000 | 0.00000            |
| ## 61 | Chelonoidis sp. [Santa Fé]      | 0.0000                             | 0.0000 | 0.00000            |
| ## 62 | Chylindrapsis inepta            | 0.0000                             | 0.0000 | 0.00000            |
| ## 63 | Chylindrapsis peltastes         | 0.0000                             | 0.0000 | 0.00000            |
| ## 64 | Chylindrapsis triserrata        | 0.0000                             | 0.0000 | 0.00000            |
| ## 65 | Chylindrapsis indica            | 0.0000                             | 0.0000 | 0.00000            |
| ## 66 | Chylindrapsis vosmaeri          | 0.0000                             | 0.0000 | 0.00000            |
| ## 67 | Centrochelys atlantica          | 0.0117                             | 2.5880 | 1.29985            |
| ## 68 | Testudo sellovii                | 0.0117                             | 2.5880 | 1.29985            |
| ## 69 | Chelonoidis cubensis            | 0.1000                             | 2.5880 | 1.34400            |
| ## 70 | Titanochelon gymnesica          | 1.0000                             | 3.6000 | 2.30000            |
| ## 71 | Testudo kalganensis             | 1.0000                             | 3.6000 | 2.30000            |
| ##    |                                 |                                    | Age    | CL_mean CL_range n |
| ## 1  |                                 | Early Pleistocene                  | 107.5  | 1                  |
| ## 2  |                                 | Early Pleistocene                  | 24.0   | 1                  |
| ## 3  |                                 | Early Pleistocene                  | 28.0   | 1                  |
| ## 4  |                                 | Early Pleistocene                  | 23.0   | 1                  |
| ## 5  |                                 | Early Pleistocene                  | 165.0  | 1                  |
| ## 6  |                                 | Early Pleistocene                  | 80.0   | 80-95 1            |
| ## 7  |                                 | Early Pleistocene                  | 120.0  | 180-200 1          |
| ## 8  |                                 | Early Pleistocene                  | 175.0  | 1                  |
| ## 9  |                                 | Early Pleistocene                  | 11.0   | 60-65 1            |
| ## 10 |                                 | Early Pleistocene                  | 90.0   | 1                  |
| ## 11 |                                 | Early Pleistocene                  | 33.0   | 1                  |
| ## 12 |                                 | Early to Late Pleistocene          | 150.0  | 1                  |
| ## 13 |                                 | Late Holocene                      | 115.0  | 180-210 1          |
| ## 14 |                                 | Late Holocene                      | 125.0  | 1                  |
| ## 15 |                                 | Late Holocene                      | 47.0   | 1                  |
| ## 16 |                                 | Late Holocene                      | 75.0   | 1                  |
| ## 17 |                                 | Late Holocene                      | 37.5   | 1                  |
| ## 18 |                                 | Late Miocene                       | 192.5  | 90-100 1           |
| ## 19 |                                 | Late Miocene to Early Pleistocene? | 195.0  | 60-90 1            |

|       |  |       |         |   |
|-------|--|-------|---------|---|
| ## 20 | Late Neogene; possibly Pliocene to Early Pleistocene | 9.0   |         | 1 |
| ## 21 | Late Pleistocene                                     | 83.0  |         | 1 |
| ## 22 | Late Pleistocene                                     | 95.0  |         | 1 |
| ## 23 | Late Pleistocene                                     | 40.0  |         | 1 |
| ## 24 | Late Pleistocene                                     | 58.0  | 35-40   | 1 |
| ## 25 | Late Pleistocene                                     | 34.0  |         | 1 |
| ## 26 | Late Pleistocene                                     | 29.0  |         | 1 |
| ## 27 | Late Pleistocene                                     | 20.0  |         | 1 |
| ## 28 | Late Pleistocene to Early Holocene                   | 23.0  |         | 1 |
| ## 29 | Late Pleistocene to Early Holocene                   | 45.0  |         | 1 |
| ## 30 | Late Pleistocene to Early Holocene?                  | 60.0  |         | 1 |
| ## 31 | Late Pleistocene to Late Holocene                    | 50.0  | 35-40   | 1 |
| ## 32 | Late Pliocene to Early Pleistocene                   | 100.0 | 105-110 | 1 |
| ## 33 | Late Pliocene to Early Pleistocene                   | 190.0 | 18-26   | 1 |
| ## 34 | Late Pliocene to Early Pleistocene                   | 22.0  |         | 1 |
| ## 35 | Late Pliocene to Early Pleistocene                   | 100.0 |         | 1 |
| ## 36 | Late Pliocene to Early Pleistocene                   | 90.0  | 120-125 | 1 |
| ## 37 | Late Pliocene to Early Pleistocene                   | 195.0 |         | 1 |
| ## 38 | Late Pliocene to Early Pleistocene                   | 120.0 |         | 1 |
| ## 39 | Late Pliocene to Early Pleistocene                   | 20.0  |         | 1 |
| ## 40 | Late Pliocene to Early Pleistocene                   | 12.0  |         | 1 |
| ## 41 | Late Pliocene to Early Pleistocene                   | 22.5  |         | 1 |
| ## 42 | Late Pliocene to Early Pleistocene                   | 15.0  |         | 1 |
| ## 43 | Late Pliocene to Early Pleistocene                   | 186.0 |         | 1 |
| ## 44 | Late Pliocene to EarlyPleistocene?                   | 62.5  |         | 1 |
| ## 45 | Middle Pleistocene                                   | 87.5  |         | 1 |
| ## 46 | Middle Pleistocene                                   | 85.0  |         | 1 |
| ## 47 | Middle Pleistocene                                   | 50.0  |         | 1 |
| ## 48 | Middle Pleistocene                                   | 20.0  |         | 1 |
| ## 49 | Middle Pleistocene                                   | 25.0  | 180-210 | 1 |
| ## 50 | Middle Pleistocene                                   | 13.0  |         | 1 |
| ## 51 | Middle Pleistocene                                   | 27.5  | 140-190 | 1 |
| ## 52 | Middle Pleistocene                                   | 52.0  | 70-90   | 1 |
| ## 53 | Middle Pleistocene to Early Holocene                 | 122.5 | 100-140 | 1 |
| ## 54 | Middle to Late Pleistocene                           | 80.0  |         | 1 |
| ## 55 | Middle to Late Pleistocene                           | 37.5  |         | 1 |
| ## 56 | Middle to Late Pleistocene                           | 150.0 |         | 1 |
| ## 57 | Modern   | 79.0  |         | 1 |
| ## 58 | Modern   | 98.0  |         | 1 |
| ## 59 | Modern   | 96.0  | 27-28   | 1 |
| ## 60 | Modern   | 88.0  |         | 1 |
| ## 61 | Modern   | 90.0  | 25-30   | 1 |
| ## 62 | Modern   | 100.0 |         | 1 |
| ## 63 | Modern   | 46.0  |         | 1 |
| ## 64 | Modern   | 100.0 | 22-23   | 1 |
| ## 65 | Modern   | 120.0 |         | 1 |
| ## 66 | Modern   | 110.0 |         | 1 |
| ## 67 | Pleistocene  | 40.0  |         | 1 |
| ## 68 | Pleistocene  | 150.0 | 110-130 | 1 |
| ## 69 | Pleistocene to Early Holocene                        | 90.0  | 185-200 | 1 |
| ## 70 | Pliocene to Early Pleistocene?                       | 120.0 |         | 1 |
| ## 71 | Tertiary; Pliocene to Early Pleistocene?             | 27.5  | 48-56   | 1 |

The first plot shows mean CI size for each taxon as a single data point, so each data point is one species (in

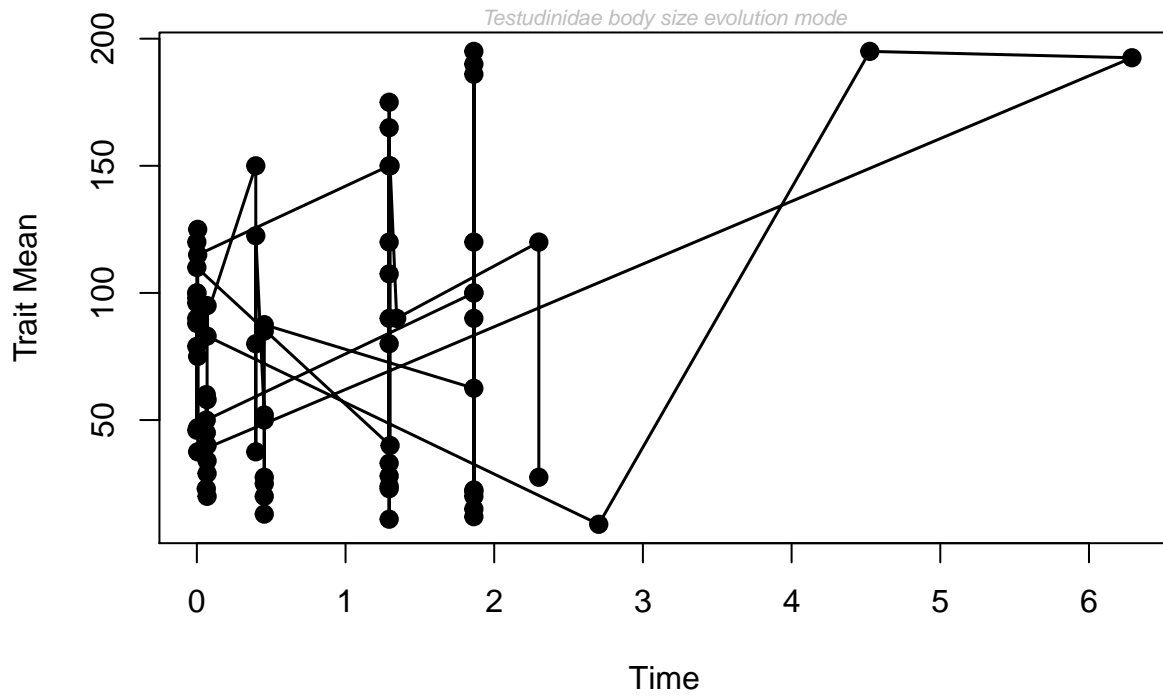
this case this equals one individual, since I don't have sample sizes), even within time bins.

```
Test1 <- test %>%
  mutate(mm = CL_mean, vv=0, nn= n, tt=Age_mean) %>%
  dplyr::select(mm, vv, nn, tt)

paleoTest1 <-as.paleoTS(Test1$mm, Test1$vv, Test1$nn, Test1$tt, MM = NULL,
  genpars = NULL, label = "Testudinidae body size evolution mode")
paleoTest1

## $mm
## [1] 107.5 24.0 28.0 23.0 165.0 80.0 120.0 175.0 11.0 90.0 33.0
## [12] 150.0 115.0 125.0 47.0 75.0 37.5 192.5 195.0 9.0 83.0 95.0
## [23] 40.0 58.0 34.0 29.0 20.0 23.0 45.0 60.0 50.0 100.0 190.0
## [34] 22.0 100.0 90.0 195.0 120.0 20.0 12.0 22.5 15.0 186.0 62.5
## [45] 87.5 85.0 50.0 20.0 25.0 13.0 27.5 52.0 122.5 80.0 37.5
## [56] 150.0 79.0 98.0 96.0 88.0 90.0 100.0 46.0 100.0 120.0 110.0
## [67] 40.0 150.0 90.0 120.0 27.5
##
## $vv
## [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [36] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
## [71] 0
##
## $nn
## [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [36] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [71] 1
##
## $tt
## [1] 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000 0.00000
## [8] 0.00000 0.00000 0.00000 0.00000 0.00000 -1.28765 -1.28765
## [15] -1.28765 -1.28765 -1.28765 4.99550 3.23250 1.40950 -1.22465
## [22] -1.22465 -1.22465 -1.22465 -1.22465 -1.22465 -1.22465 -1.23000
## [29] -1.23000 -1.23000 -1.23050 0.56950 0.56950 0.56950 0.56950
## [36] 0.56950 0.56950 0.56950 0.56950 0.56950 0.56950 0.56950
## [43] 0.56950 0.56950 -0.84000 -0.84000 -0.84000 -0.84000 -0.84000
## [50] -0.84000 -0.84000 -0.84000 -0.89715 -0.89715 -0.89715 -0.89715
## [57] -1.29350 -1.29350 -1.29350 -1.29350 -1.29350 -1.29350 -1.29350
## [64] -1.29350 -1.29350 -1.29350 0.00635 0.00635 0.05050 1.00650
## [71] 1.00650
##
## $MM
## NULL
##
## $genpars
## NULL
##
## $label
## [1] "Testudinidae body size evolution mode"
##
## $start.age
## [1] 1.2935
##
## $timeDir
```

```
## [1] "increasing"
##
## attr(,"class")
## [1] "paleoTS"
plot(paleoTest1)
```



This is the underlying data for Test1:

```
Test1
```

```
##      mm vv nn      tt
## 1  107.5 0  1 1.29350
## 2   24.0 0  1 1.29350
## 3   28.0 0  1 1.29350
## 4   23.0 0  1 1.29350
## 5  165.0 0  1 1.29350
## 6   80.0 0  1 1.29350
## 7  120.0 0  1 1.29350
## 8  175.0 0  1 1.29350
## 9   11.0 0  1 1.29350
## 10  90.0 0  1 1.29350
## 11  33.0 0  1 1.29350
## 12 150.0 0  1 1.29350
## 13 115.0 0  1 0.00585
## 14 125.0 0  1 0.00585
## 15  47.0 0  1 0.00585
## 16  75.0 0  1 0.00585
```

```

## 17 37.5 0 1 0.00585
## 18 192.5 0 1 6.28900
## 19 195.0 0 1 4.52600
## 20 9.0 0 1 2.70300
## 21 83.0 0 1 0.06885
## 22 95.0 0 1 0.06885
## 23 40.0 0 1 0.06885
## 24 58.0 0 1 0.06885
## 25 34.0 0 1 0.06885
## 26 29.0 0 1 0.06885
## 27 20.0 0 1 0.06885
## 28 23.0 0 1 0.06350
## 29 45.0 0 1 0.06350
## 30 60.0 0 1 0.06350
## 31 50.0 0 1 0.06300
## 32 100.0 0 1 1.86300
## 33 190.0 0 1 1.86300
## 34 22.0 0 1 1.86300
## 35 100.0 0 1 1.86300
## 36 90.0 0 1 1.86300
## 37 195.0 0 1 1.86300
## 38 120.0 0 1 1.86300
## 39 20.0 0 1 1.86300
## 40 12.0 0 1 1.86300
## 41 22.5 0 1 1.86300
## 42 15.0 0 1 1.86300
## 43 186.0 0 1 1.86300
## 44 62.5 0 1 1.86300
## 45 87.5 0 1 0.45350
## 46 85.0 0 1 0.45350
## 47 50.0 0 1 0.45350
## 48 20.0 0 1 0.45350
## 49 25.0 0 1 0.45350
## 50 13.0 0 1 0.45350
## 51 27.5 0 1 0.45350
## 52 52.0 0 1 0.45350
## 53 122.5 0 1 0.39635
## 54 80.0 0 1 0.39635
## 55 37.5 0 1 0.39635
## 56 150.0 0 1 0.39635
## 57 79.0 0 1 0.00000
## 58 98.0 0 1 0.00000
## 59 96.0 0 1 0.00000
## 60 88.0 0 1 0.00000
## 61 90.0 0 1 0.00000
## 62 100.0 0 1 0.00000
## 63 46.0 0 1 0.00000
## 64 100.0 0 1 0.00000
## 65 120.0 0 1 0.00000
## 66 110.0 0 1 0.00000
## 67 40.0 0 1 1.29985
## 68 150.0 0 1 1.29985
## 69 90.0 0 1 1.34400
## 70 120.0 0 1 2.30000

```

```
## 71 27.5 0 1 2.30000
```

For the second plot, I averaged CL means across taxa for each time bin, which leaves one data point per time bin, comprising all taxa within the respective bin:

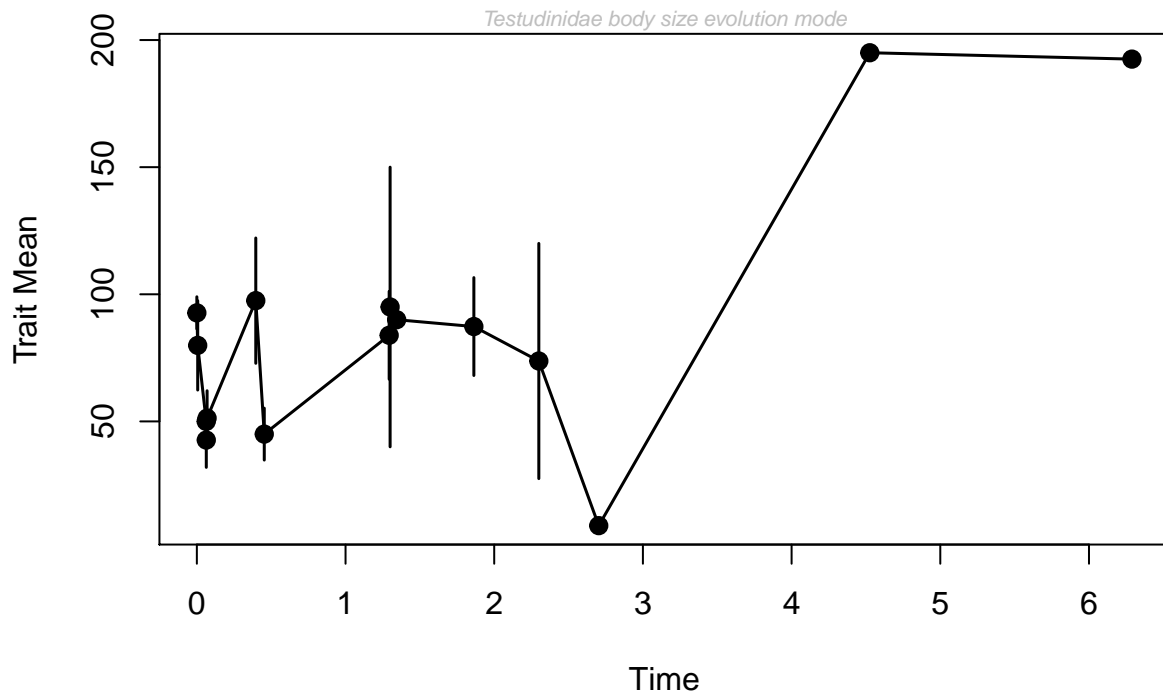
```
Test2 <- test %>%
  group_by(Age_mean) %>%
  summarise(mm = mean(CL_mean), nn=n(), vv=var(CL_mean)) %>%
  mutate(tt=Age_mean) %>%
  dplyr::select(mm, vv, nn, tt)

# NA: column 2, rows 3, 10, 13, 14, 15
Test2[3,2] <- 0
Test2[10,2] <- 0
Test2[13,2] <- 0
Test2[14,2] <- 0
Test2[15,2] <- 0

paleoTest2 <-as.paleoTS(Test2$mm, Test2$vv, Test2$nn, Test2$tt, MM = NULL,
  genpars = NULL, label = "Testudinidae body size evolution mode")
paleoTest2
```

```
## $mm
## [1] 92.70000 79.90000 50.00000 42.66667 51.28571 97.50000 45.00000
## [8] 83.87500 95.00000 90.00000 87.30769 73.75000 9.00000 195.00000
## [15] 192.50000
##
## $vv
## [1] 398.6778 1542.5500 0.0000 346.3333 810.5714 2429.1667 833.6429
## [8] 3589.5511 6050.0000 0.0000 4816.0224 4278.1250 0.0000 0.0000
## [15] 0.0000
##
## $nn
## [1] 10 5 1 3 7 4 8 12 2 1 13 2 1 1 1
##
## $tt
## [1] 0.00000 0.00585 0.06300 0.06350 0.06885 0.39635 0.45350 1.29350
## [9] 1.29985 1.34400 1.86300 2.30000 2.70300 4.52600 6.28900
##
## $MM
## NULL
##
## $genpars
## NULL
##
## $label
## [1] "Testudinidae body size evolution mode"
##
## $start.age
## NULL
##
## $timeDir
## [1] "increasing"
##
## attr(,"class")
```

```
## [1] "paleoTS"
plot(paleoTest2)
```



Since “real” variances and sample sizes are available when pooling all taxa, you can even fit models (as you should be able to in the end). (when I remember correctly, the model with the highest Akaike.wt is the best supported one, in this case this would be URW = random walk)

```
a=fit3models(paleoTest2, silent=FALSE, method="AD", pool=FALSE) #not working with Test1, because no v
```

```
##
## Comparing 3 models [n = 14, method = AD]
##
##          logL K      AICc Akaike.wt
## GRW      -70.40398 2 145.8989    0.373
## URW      -71.26818 1 144.8697    0.625
## Stasis   -75.70460 2 156.5001    0.002
```

```
str(a)
```

```
## 'data.frame':   3 obs. of  4 variables:
## $ logL      : num  -70.4 -71.3 -75.7
## $ K         : num   2  1  2
## $ AICc       : num   146 145 157
## $ Akaike.wt : num   0.373 0.625 0.002
```

```
a$AICc[1] # not sure what this tells me...
```

```
## [1] 145.8989
```



This is the underlying data for Test2:

Test2

```
## # A tibble: 15 × 4
##       mm      vv    nn     tt
##   <dbl>  <dbl> <int>  <dbl>
## 1  92.70000 398.6778   10 0.00000
## 2  79.90000 1542.5500    5 0.00585
## 3  50.00000   0.0000    1 0.06300
## 4  42.66667 346.3333    3 0.06350
## 5  51.28571 810.5714    7 0.06885
## 6  97.50000 2429.1667    4 0.39635
## 7  45.00000 833.6429    8 0.45350
## 8  83.87500 3589.5511   12 1.29350
## 9  95.00000 6050.0000    2 1.29985
## 10 90.00000   0.0000    1 1.34400
## 11 87.30769 4816.0224   13 1.86300
## 12 73.75000 4278.1250    2 2.30000
## 13  9.00000   0.0000    1 2.70300
## 14 195.00000 0.0000    1 4.52600
## 15 192.50000 0.0000    1 6.28900
```

## TO DO:

- figure out if Checklist data is of any use (means? medians? sample size?) or see if authors can provide necessary data
- do paleoTS analyses with FFB data set
- read Hunt papers (see citations in Catalina's paper 2006, 2008, 2008, 2010; also 2015)
- figure out how to implement phylogeny... well, figure out how to do paleoTS analyses with more than one taxon without pooling everything together (as in Test2)

06.06.2017

Try paleoTS with some first real data. Here is the underlying data:

```
tidyCL<-read.csv("tortoises_tidy.csv", sep=";", header=TRUE)
tidyCL
```

```
##      Country Latitude Longitude
## 1      USA  37.6000 -120.6000
## 2      USA  37.6000 -120.8000
## 3      USA  37.6000 -120.6000
## 4      USA  38.6665  -76.5298
## 5      USA  37.2242 -100.4176
## 6      USA  42.0000  -97.0000
## 7      USA  34.9000 -101.6000
## 8      USA  27.7000  -82.5000
## 9      USA  42.7000 -100.0000
## 10     USA  29.7000  -82.6000
## 11     USA  29.6000  -82.4000
## 12  Greece  40.4046   22.8980
```

|       |          |         |           |
|-------|----------|---------|-----------|
| ## 13 | Greece   | 40.4046 | 22.8980   |
| ## 14 | Germany  | 47.8356 | 8.7490    |
| ## 15 | Germany  | 47.8356 | 8.7490    |
| ## 16 | Germany  | 47.8356 | 8.7490    |
| ## 17 | Germany  | 47.8356 | 8.7490    |
| ## 18 | Germany  | 47.8356 | 8.7490    |
| ## 19 | Germany  | 47.8356 | 8.7490    |
| ## 20 | Germany  | 47.8356 | 8.7490    |
| ## 21 | Germany  | 47.8356 | 8.7490    |
| ## 22 | Germany  | 47.8356 | 8.7490    |
| ## 23 | Mongolia | 47.1000 | 93.1667   |
| ## 24 | Mongolia | 47.1000 | 93.1667   |
| ## 25 | USA      | 37.0000 | -100.0000 |
| ## 26 | USA      | 37.0000 | -100.0000 |
| ## 27 | France   | 44.8120 | 0.2133    |
| ## 28 | France   | 43.6000 | 1.4333    |
| ## 29 | Georgia  | 41.3200 | 44.3500   |
| ## 30 | USA      | 35.4000 | -76.8000  |
| ## 31 | USA      | 35.3000 | -118.5000 |
| ## 32 | USA      | 35.3000 | -118.5000 |
| ## 33 | USA      | 35.3000 | -118.5000 |
| ## 34 | USA      | 29.7000 | -82.6000  |
| ## 35 | USA      | 29.7000 | -82.6000  |
| ## 36 | Colombia | 3.2000  | -75.2000  |
| ##    |          |         |           |
| ## 1  |          |         |           |
| ## 2  |          |         |           |
| ## 3  |          |         |           |
| ## 4  |          |         |           |
| ## 5  |          |         |           |
| ## 6  |          |         |           |
| ## 7  |          |         |           |
| ## 8  |          |         |           |
| ## 9  |          |         |           |
| ## 10 |          |         |           |
| ## 11 |          |         |           |
| ## 12 |          |         |           |
| ## 13 |          |         |           |
| ## 14 |          |         |           |
| ## 15 |          |         |           |
| ## 16 |          |         |           |
| ## 17 |          |         |           |
| ## 18 |          |         |           |
| ## 19 |          |         |           |
| ## 20 |          |         |           |
| ## 21 |          |         |           |
| ## 22 |          |         |           |
| ## 23 |          |         |           |
| ## 24 |          |         |           |
| ## 25 |          |         |           |
| ## 26 |          |         |           |
| ## 27 |          |         |           |
| ## 28 |          |         |           |
| ## 29 |          |         |           |

```

## 30
## 31
## 32
## 33
## 34 a sinkhole lake that then collapsed into a larger underground chamber earliest Hemmingfordian Nor
## 35 a sinkhole lake that then collapsed into a larger underground chamber earliest Hemmingfordian Nor
## 36
##      MAmin  Mamax      Genus      Species      Taxon
## 1    5.000  6.000 Hesperotestudo orthopygia Hesperotestudo orthopygia
## 2    9.000 10.000 Hesperotestudo      sp.      Hesperotestudo sp.
## 3    5.000  6.000 Hesperotestudo orthopygia Hesperotestudo orthopygia
## 4   15.000 15.800      Floridemys      hurdi      Floridemys hurdi
## 5    0.300  0.300 Hesperotestudo equicomes Hesperotestudo equicomes
## 6    4.800  5.200      Geochelone      sp.      Geochelone sp.
## 7    1.800  3.600      Gopherus canyonensis Gopherus canyonensis
## 8    1.000  1.500 Hesperotestudo crassiscutata Hesperotestudo crassiscutata
## 9    3.000  3.000 Hesperotestudo oelrichi Hesperotestudo oelrichi
## 10   10.900 11.000 Hesperotestudo alleni Hesperotestudo alleni
## 11    0.012  0.126 Hesperotestudo incisa Hesperotestudo incisa
## 12    2.600  5.300 Titanochelon bacharidisi Titanochelon bacharidisi
## 13    2.600  5.300 Titanochelon bacharidisi Titanochelon bacharidisi
## 14   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 15   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 16   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 17   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 18   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 19   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 20   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 21   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 22   13.000 13.000 Paleotestudo antiqua Paleotestudo antiqua
## 23    2.600  5.300 Ergilemys oskarkuhni Ergilemys oskarkuhni
## 24    2.600  5.300 Ergilemys oskarkuhni Ergilemys oskarkuhni
## 25    3.000  3.000 Hesperotestudo riggsi Hesperotestudo riggsi
## 26    3.000  3.000 Hesperotestudo riggsi Hesperotestudo riggsi
## 27   33.900 34.000 Cheirogaster maurini Cheirogaster maurini
## 28   23.030 23.200 Ergilemys bruneti Ergilemys bruneti
## 29    1.770  1.770 Testudo graeca Testudo graeca
## 30    4.000  5.000 Geochelone sp. Geochelone sp.
## 31   11.200 12.500 Gopherus ? sp. Gopherus ? sp.
## 32    9.000 11.200 Geochelone sp. Geochelone sp.
## 33    9.000 11.200 Gopherus ? sp. Gopherus ? sp.
## 34   18.000 19.000 Geochelone tedwhitei Geochelone tedwhitei
## 35   18.000 19.000 Geochelone tedwhitei Geochelone tedwhitei
## 36    6.000 11.000 Geochelone hesterna Geochelone hesterna
##      CL      PL
## 1    1200      NA
## 2    1200      NA
## 3      NA    620.0
## 4      NA      NA
## 5      NA      NA
## 6      NA    160.0
## 7      NA    805.0
## 8      NA    510.0
## 9      NA    258.0

```

|    |    |      |        |
|----|----|------|--------|
| ## | 10 | NA   | 219.0  |
| ## | 11 | NA   | 211.6  |
| ## | 12 | 1196 | 1150.0 |
| ## | 13 | 1165 | 1120.0 |
| ## | 14 | 185  | NA     |
| ## | 15 | 229  | NA     |
| ## | 16 | 220  | NA     |
| ## | 17 | 195  | NA     |
| ## | 18 | 206  | NA     |
| ## | 19 | 196  | NA     |
| ## | 20 | NA   | 102.0  |
| ## | 21 | 150  | NA     |
| ## | 22 | 145  | NA     |
| ## | 23 | NA   | 180.0  |
| ## | 24 | 220  | NA     |
| ## | 25 | 176  | 189.0  |
| ## | 26 | 185  | NA     |
| ## | 27 | 400  | NA     |
| ## | 28 | 400  | NA     |
| ## | 29 | 195  | NA     |
| ## | 30 | 880  | 700.0  |
| ## | 31 | 500  | NA     |
| ## | 32 | 500  | NA     |
| ## | 33 | 500  | NA     |
| ## | 34 | 370  | NA     |
| ## | 35 | NA   | 400.0  |
| ## | 36 | 278  | NA     |

##

## 1

## 2

very large (comparable to specimens from Mel

## 3

## 4

smaller than Hesperotes

## 5

medium to large-sized Hesperotestudo, smaller

## 6

## 7

## 8

small (subgenus Hesper

## 9

*G. oelrichi* is among the largest of the *Geochelone* (*Hesperotestudo*

## 10

## 11

## 12

## 13

## 14

## 15

## 16

## 17

## 18

## 19

## 20

## 21

## 22

## 23

## 24

## 25

Holotype KUMVP 6789: CL: 176 mm(, C width: 155 mm, C height: 85 mm), PL: 189 mm(, I

## 26

Paratype KUMVP 6790: CL: 185

```

## 27
## 28
## 29
## 30
## 31 Tortoises (Geochelone sp. and ?Gopherus sp. with carapaces up to 0.5 m in length are found through
## 32 Tortoises (Geochelone sp. and ?Gopherus sp. with carapaces up to 0.5 m in length are found through
## 33 Tortoises (Geochelone sp. and ?Gopherus sp. with carapaces up to 0.5 m in length are found through
## 34
## 35 CL: 370 mm, CW: 300 mm, CL
## 36 several specimens: not exceeded
## estimated..e..from.verbal.description..ev..from.plastron..ep..or.measured..m..measured.from.figure
## 1
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21
## 22
## 23
## 24
## 25
## 26
## 27
## 28
## 29
## 30
## 31
## 32
## 33
## 34
## 35
## 36

```

Prepare data for conversion to paleoTS-object:

```

TidyCL <- tidyCL %>%
  select(MAmin, Mamax, CL) %>%
  filter(CL != "NA") %>%
  mutate(tt= (MAmin+Mamax)/2) %>% # create mean age
  group_by(tt) %>% #create time bins

```

```

summarise(mm=mean(CL), vv=var(CL), nn=n()) #create means etc. for each time bin

TidyCL[is.na(TidyCL)]<-0 #subset NAs with 0 for

TidyCL

```

```

## # A tibble: 13 × 4
##       tt      mm      vv    nn
##   <dbl>   <dbl>   <dbl> <int>
## 1  1.770 195.0000   0.0000     1
## 2  3.000 180.5000  40.5000     2
## 3  3.950 860.3333 307760.3333     3
## 4  4.500 880.0000   0.0000     1
## 5  5.500 1200.0000   0.0000     1
## 6  8.500 278.0000   0.0000     1
## 7  9.500 1200.0000   0.0000     1
## 8 10.100 500.0000   0.0000     2
## 9 11.850 500.0000   0.0000     1
##10 13.000 190.7500  911.9286     8
##11 18.500 370.0000   0.0000     1
##12 23.115 400.0000   0.0000     1
##13 33.950 400.0000   0.0000     1

```

```

bins <- tidyCL %>%
# select(MAmin, Mamax, CL) %>%
  filter(CL != "NA") %>%
  mutate(tt= (MAmin+Mamax)/2) %>% # create mean age
  group_by(tt)

```

```
bins
```

```

## Source: local data frame [24 x 14]
## Groups: tt [13]
##
##   Country Latitude Longitude
##   <fctr>   <dbl>   <dbl>
## 1     USA  37.6000 -120.600
## 2     USA  37.6000 -120.800
## 3  Greece 40.4046   22.898
## 4  Greece 40.4046   22.898
## 5  Germany 47.8356    8.749
## 6  Germany 47.8356    8.749
## 7  Germany 47.8356    8.749
## 8  Germany 47.8356    8.749
## 9  Germany 47.8356    8.749
##10 Germany 47.8356    8.749
## # ... with 14 more rows, and 11 more variables:
## #   Formation.Location.comment <fctr>, MAmin <dbl>, Mamax <dbl>,
## #   Genus <fctr>, Species <fctr>, Taxon <fctr>, CL <int>, PL <dbl>,
## #   verbal <fctr>,
## #   estimated..e..from.verbal.description..ev..from.plastron..ep..or.measured..m..measured.from.figure
## #   tt <dbl>

```

```

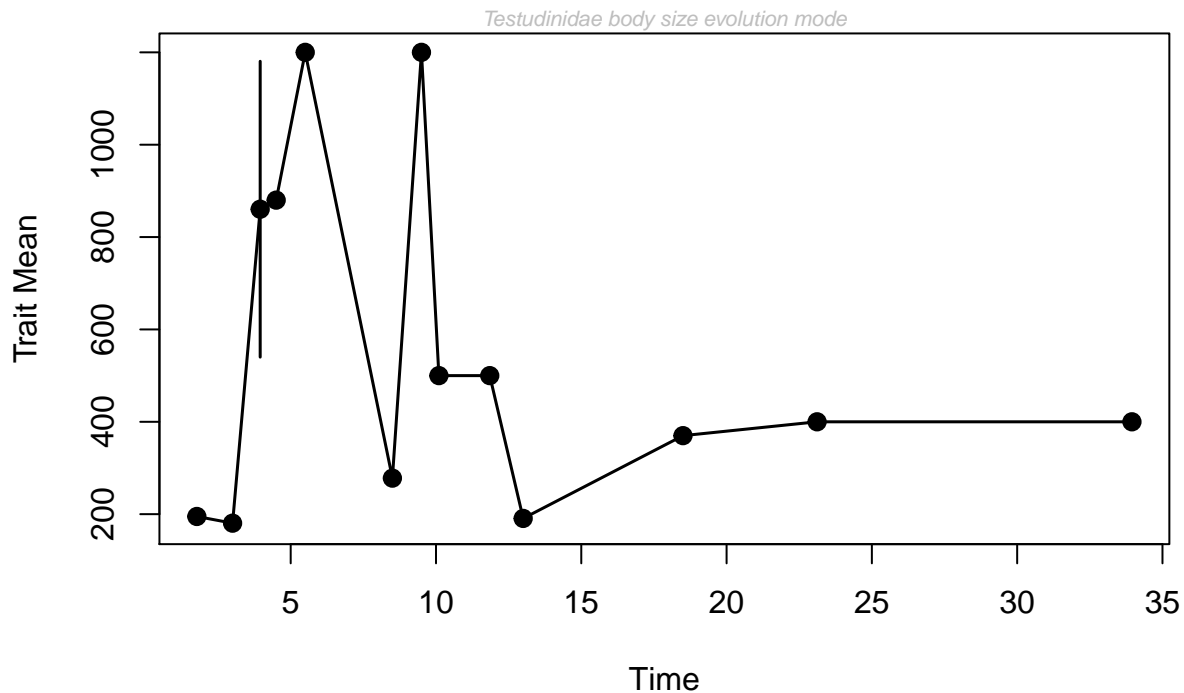
library(paleoTS)
paleoTidyCL <-as.paleoTS(TidyCL$mm, TidyCL$vv, TidyCL$nn, TidyCL$tt, MM = NULL, genpars = NULL, label =

```

```
paleoTidyCL
```

```
## $mm
## [1] 195.0000 180.5000 860.3333 880.0000 1200.0000 278.0000 1200.0000
## [8] 500.0000 500.0000 190.7500 370.0000 400.0000 400.0000
##
## $vv
## [1] 0.0000 40.5000 307760.3333 0.0000 0.0000
## [6] 0.0000 0.0000 0.0000 0.0000 911.9286
## [11] 0.0000 0.0000 0.0000
##
## $nn
## [1] 1 2 3 1 1 1 1 2 1 8 1 1 1
##
## $tt
## [1] 0.000 1.230 2.180 2.730 3.730 6.730 7.730 8.330 10.080 11.230
## [11] 16.730 21.345 32.180
##
## $MM
## NULL
##
## $genpars
## NULL
##
## $label
## [1] "Testudinidae body size evolution mode"
##
## $start.age
## [1] 1.77
##
## $timeDir
## [1] "increasing"
##
## attr(,"class")
## [1] "paleoTS"
```

```
plot(paleoTidyCL)
```



```
fit3models(paleoTidyCL, silent=FALSE, method="AD", pool=FALSE) #not working with Test1, because no va
```

```
##
## Comparing 3 models [n = 12, method = AD]
##
##           logL K      AICc Akaike.wt
## GRW      -94.17833 2 193.6900    0.001
## URW     -104.38851 1 211.1770    0.000
## Stasis   -87.43929 2 180.2119    0.999
```

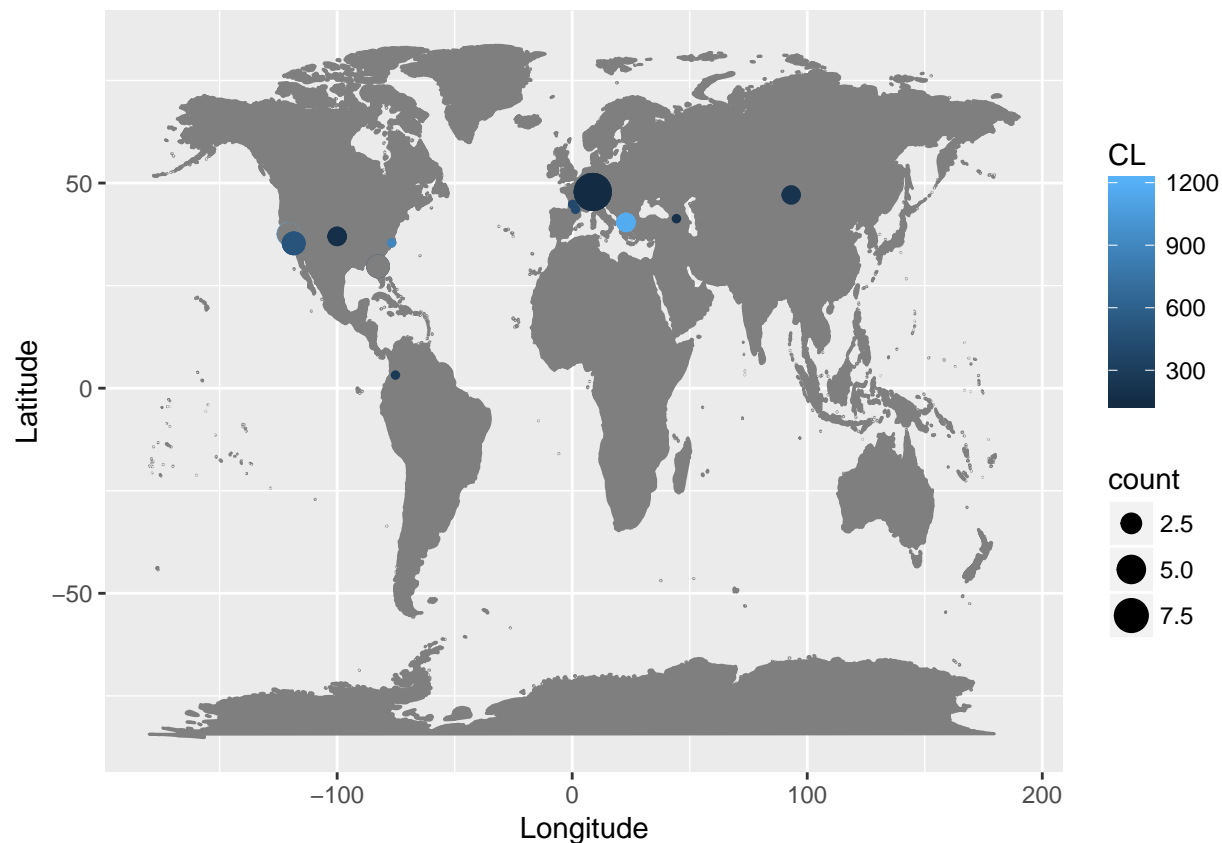
```
Map <- tidyCL %>%
  select(Genus, Taxon, Latitude, Longitude, Country, CL, PL) %>%
  group_by(Latitude) %>%
  mutate(count= n())
```

```
mapWorld <- borders("world", colour="gray50", fill="gray50") # create a layer of borders
```

```
mp <- Map %>%
  ggplot(aes( Longitude, Latitude, colour=CL)) + mapWorld +
  geom_point(aes(size=count))
```

```
mp
```





## TO DO:

- map localities with differing colors for: CL available, CL extrapolated (from PL or figures), CL missing
- complete data set!
- get missing references/make list of missing references

This is an R Markdown Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).