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 sombrerensis  0.0117  0.1260  0.06885
## 23        Chelonoidis sp. [Navassa]  0.0117  0.1260  0.06885
## 24                Gopherus donlaloi  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         Titatochelon 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             Chylindraspis indica  0.0000  0.0000  0.00000
## 66           Chylindraspis 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 Cl size for each taxon as a single data point, so each data point is one species (in

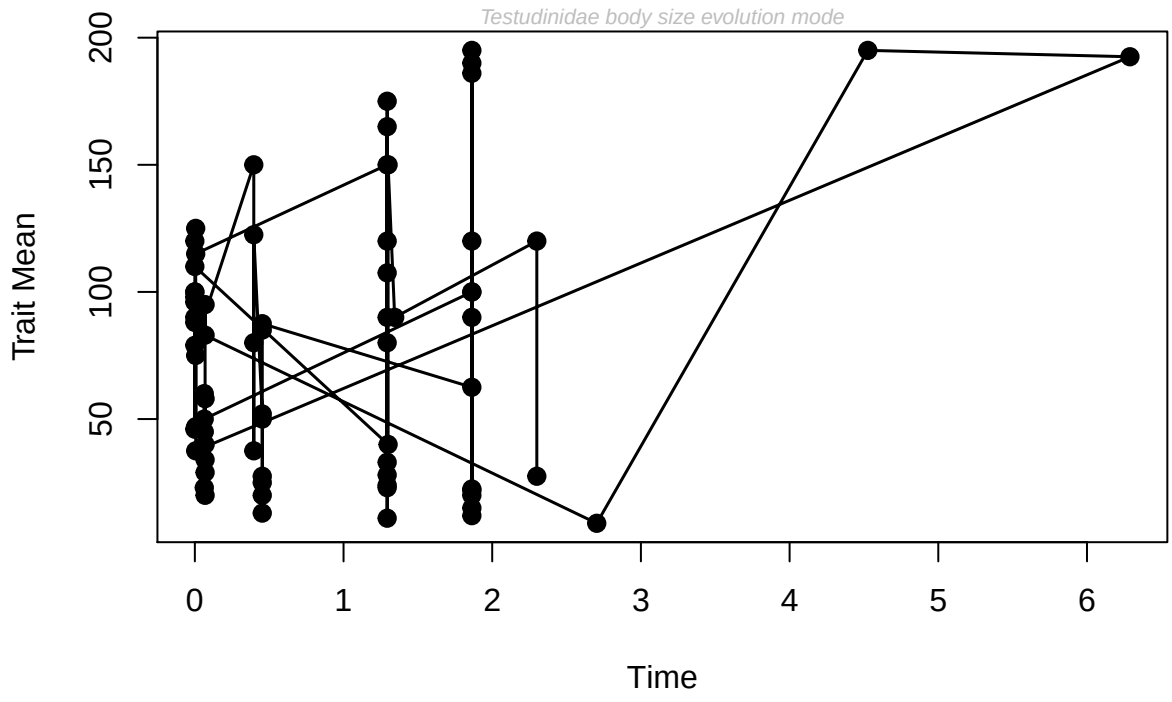
this case this equals one individual, since I don't have sample sizes), even within time bins.

```
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 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 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 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 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
```

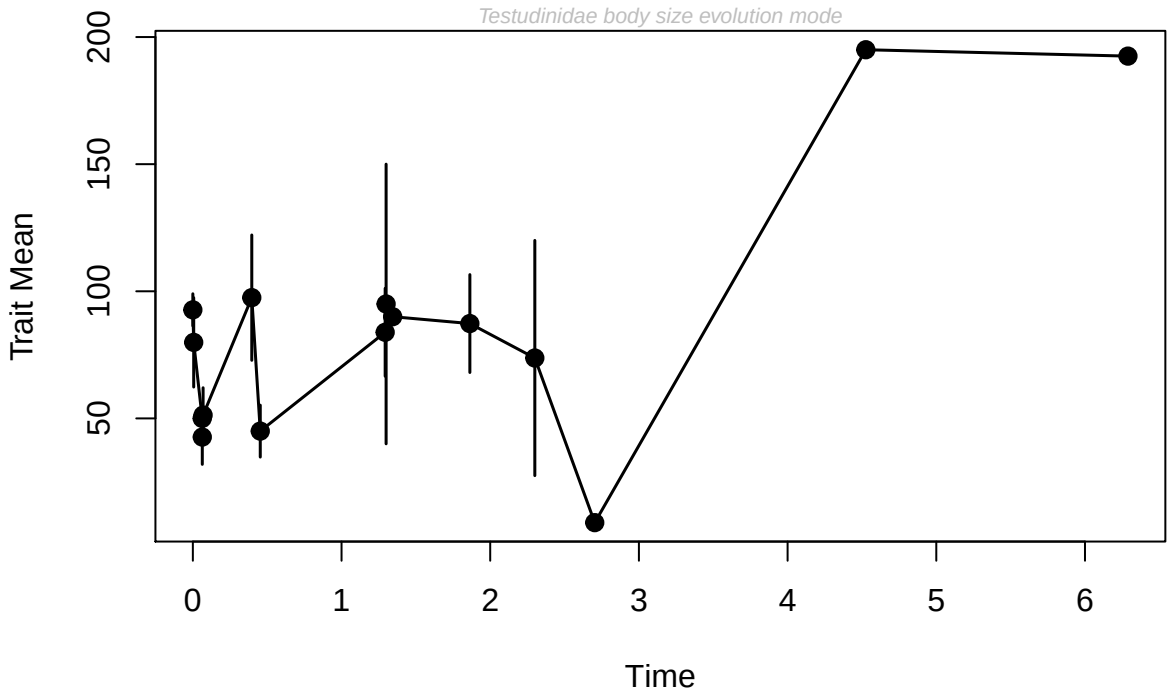
For the second plot, I averaged CL means across taxa for each time bin, which leaves one data point per time bin, comprising all taxa within the respective bin:

```
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)

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).