

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	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	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

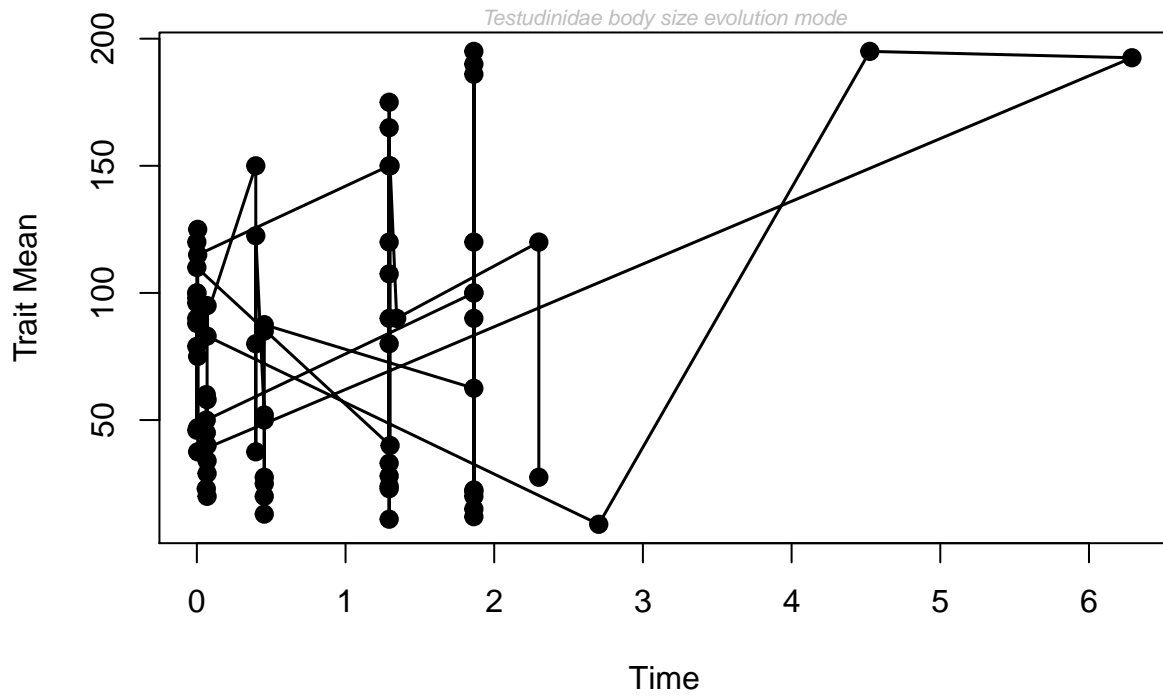
this case this equals one individual, since I don't have sample sizes), even within time bins.

```
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:

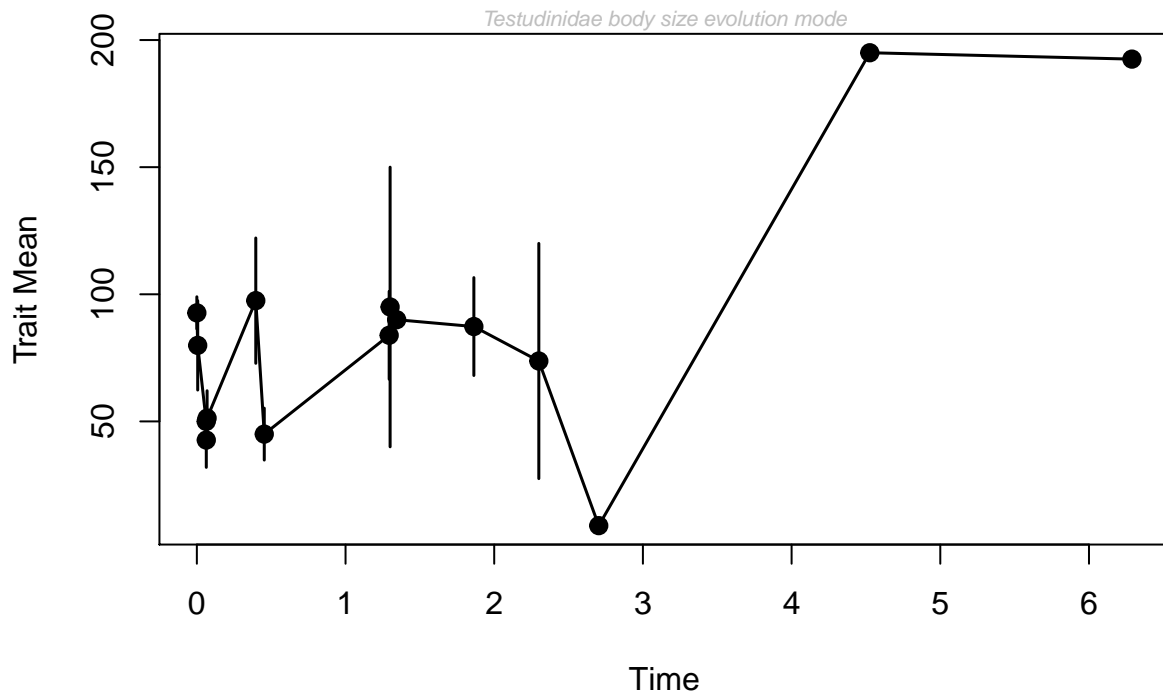
```
Test2 <- test %>%
  group_by(Age_mean) %>%
  summarise(mm = mean(CL_mean), nn=n(), vv=var(CL_mean)) %>%
  mutate(tt=Age_mean) %>%
  dplyr::select(mm, vv, nn, tt)

# 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
## 36
## 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...from.verbal.description..ev..from.plastron..ep..or.measured..m..measured.from.figure
```

```
## #   tt <dbl>
```

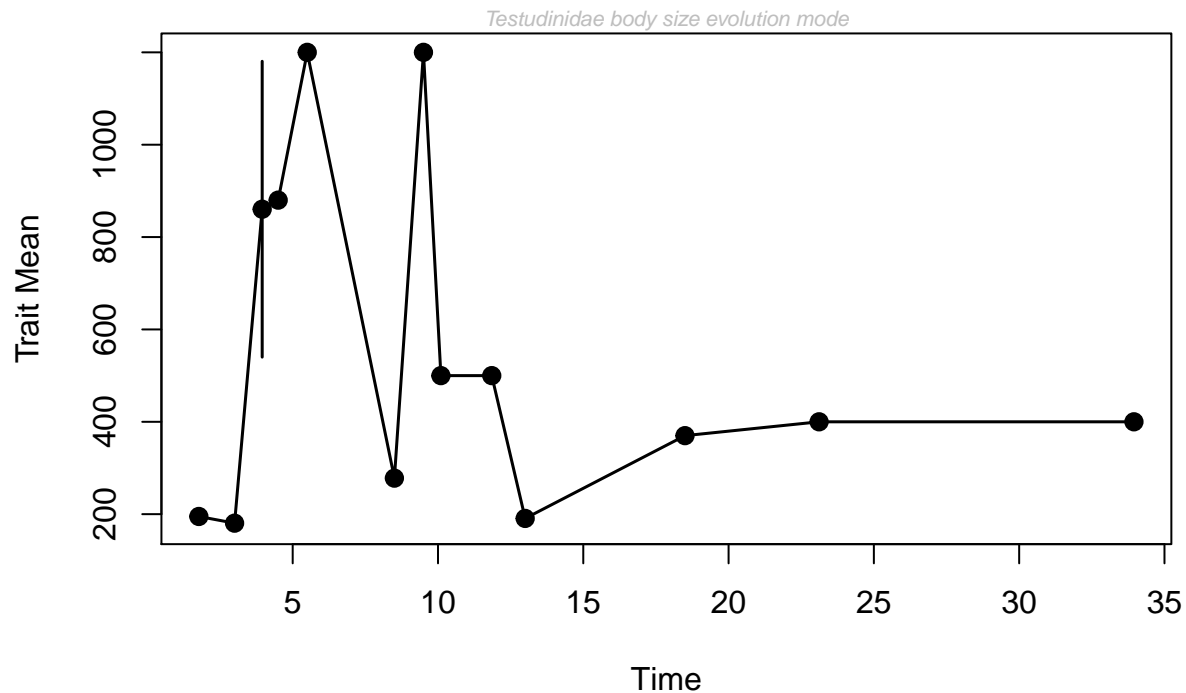
```
library(paleoTS)
```

```
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
```

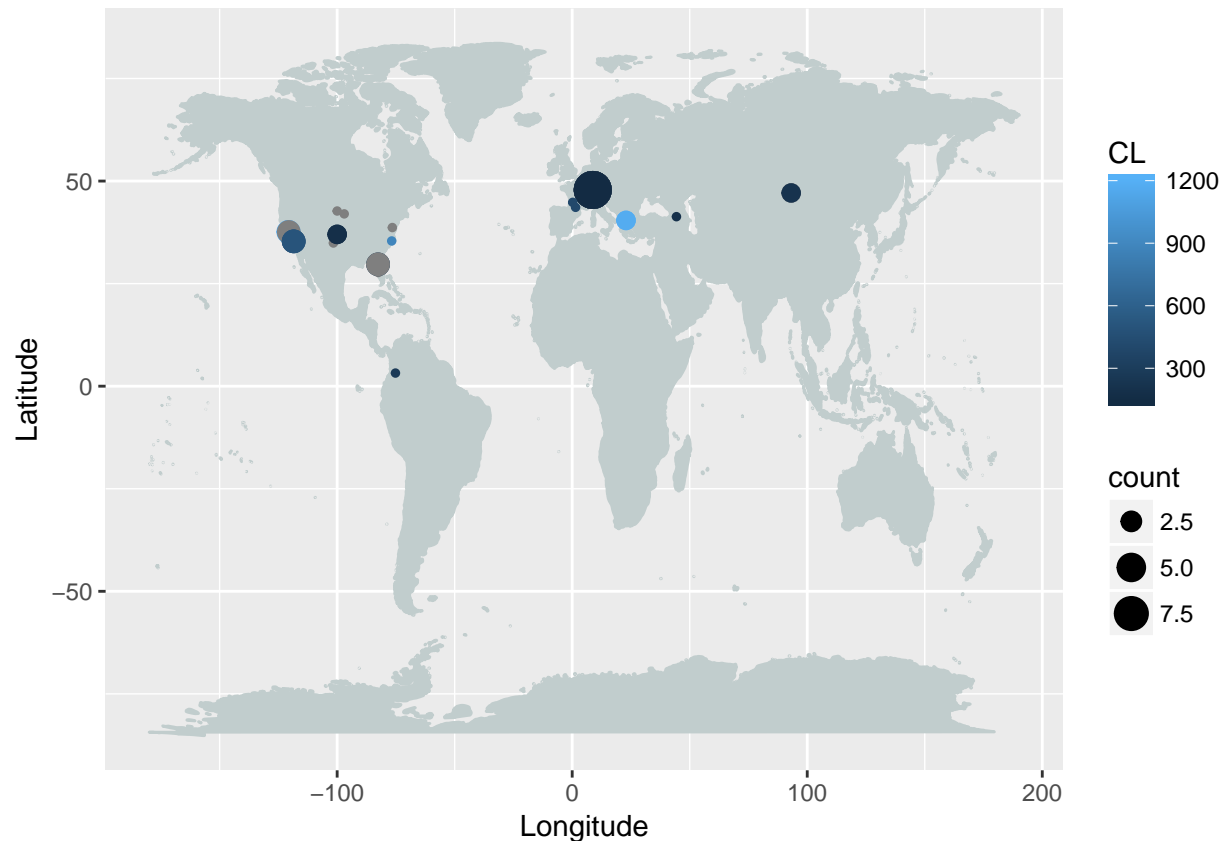
```
##
## Comparing 3 models [n = 12, method = AD]
##
##           logL K      AICc Akaike.wt
## GRW      -94.17833 2 193.6900    0.001
## URW     -104.38851 1 211.1770    0.000
## Stasis   -87.43929 2 180.2119    0.999
```

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

```
mapWorld <- borders("world", colour="azure3", fill="azure3") # create a layer of borders
```

```
mp <- Map %>%
  ggplot(aes(Longitude, Latitude)) + mapWorld +
  # geom_point(fill="red", colour="red", size=0.5) +
  geom_point(aes(Longitude, Latitude, colour=CL, size=count))
```

```
mp
```

```
library(plotly)
```

```
##
## Attaching package: 'plotly'
##
## The following object is masked from 'package:ggplot2':
##
##   last_plot
##
## The following object is masked from 'package:stats':
##
##   filter
##
## The following object is masked from 'package:graphics':
##
##   layout
```

```
ggplotly(mp)
```

```
## We recommend that you use the dev version of ggplot2 with `ggplotly()`
## Install it with: `devtools::install_github('hadley/ggplot2')`
```

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

08.06.17

Map all localities with sample size and age indicated (regardless of whether CL information is available):

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

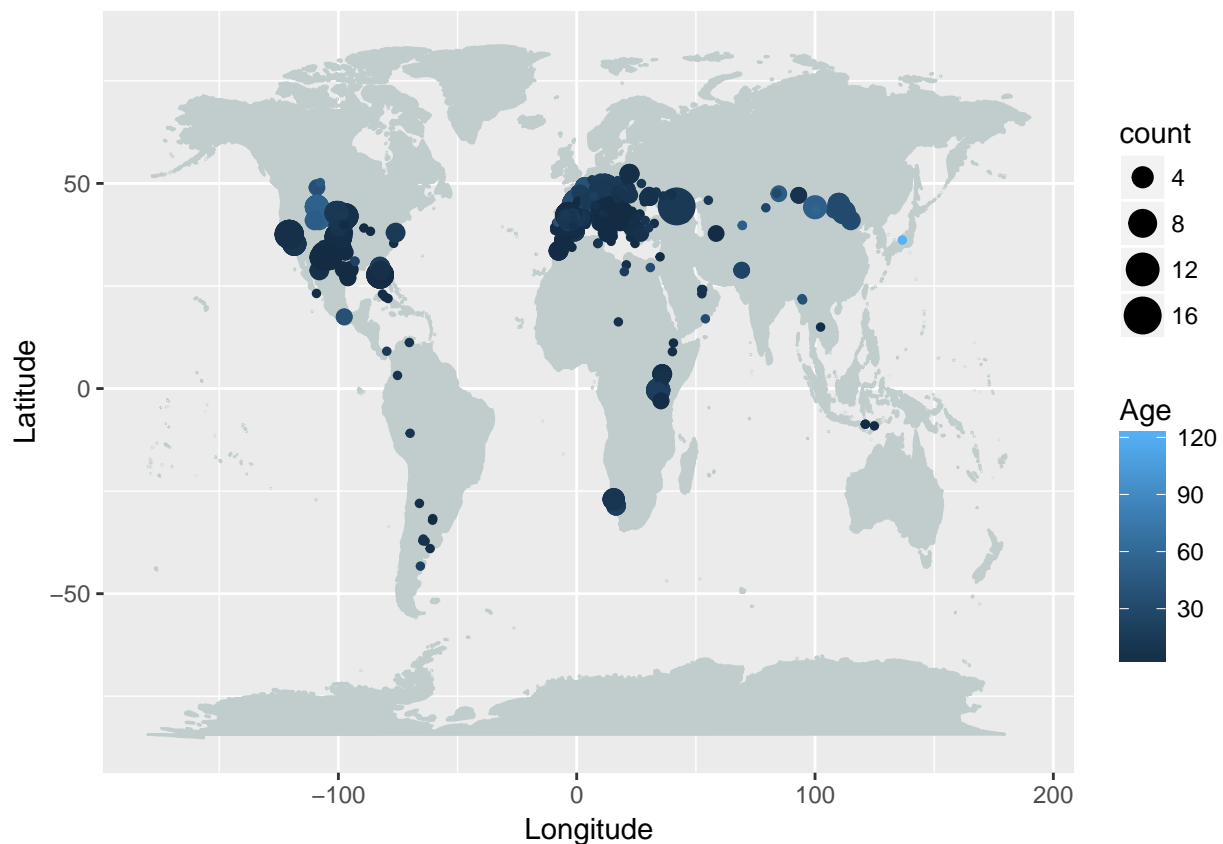
colnames(test)[6] <- "Mamin"
colnames(test)[7] <- "Mamax"

Test <- test %>%
  select(Locality, Country, Latitude, Longitude, Mamin, Mamax, Epoch, Genus, Species, Taxon, CL) %>%
  mutate(Age= (Mamin+Mamax)/2) %>% # create mean age
  group_by(Latitude) %>%
  mutate(count= n())

mapWorld <- borders("world", colour="azure3", fill="azure3") # create a layer of borders

map <- Test %>%
  ggplot(aes(Longitude, Latitude)) + mapWorld +
  #geom_point(fill="red", colour="red", size=0.5) +
  geom_point(aes(Longitude, Latitude, colour=Age, size=count))

map
```



```
ggplotly(map)
```

We recommend that you use the dev version of ggplot2 with `ggplotly()`

```
## Install it with: `devtools::install_github('hadley/ggplot2')`
```

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).