

```
setwd( "~/Documents/Christian Foth middle ear analyses/MIDDLE_EAR" )
```

```
require( sp )
require(rgl)
```

```
files.all <- list.files()
files.all <- files.all[ grepl( "Ascii" , files.all ) ]
```

```
files.FO <- files.all[ grepl( "fenestra-ovalis" , files.all ) | grepl( "fenestra_ovalis" , files.all ) | grepl( "fenestra-ovale" , files.all ) | grepl( "fenestra_ovale" , files.all ) | grepl( "fenstra_ovalis" , files.all ) ]
files.CA <- files.all[ grepl( "columella-auris" , files.all ) | grepl( "columella_auris" , files.all ) | grepl( "columella-auris" , files.all ) | grepl( "columnella-auris" , files.all ) | grepl( "culumella_auris" , files.all ) ]
files.CT <- files.all[ grepl( "cavum-tympanum" , files.all ) | grepl( "cavum_tympanum" , files.all ) | grepl( "cacum-tympanum" , files.all ) | grepl( "cavum_tympaani" , files.all ) | grepl( "cavum-typanum" , files.all ) ]
```

```
landmarks <- list()
```

```
for( i in 1:length( files.all ) ) {
  read.temp <- readLines( files.all[[ i ]], skip = 1 )
  from <- 2 + which( grepl( "# Data section follows" , read.temp ) )
  read.temp <- read.temp[ from:length(read.temp) ]
  read.temp <- matrix( unlist( lapply( read.temp , strsplit , split = " " ) ) , ncol = 3 , byrow = T )
  landmarks[[ i ]] <- matrix( as.numeric( read.temp ) , ncol = 3 , byrow = F )
}; names( landmarks ) <- files.all
```

```
fix.landmarks <- which( !( grepl( "Aldabrachelys" , files.all ) | grepl( "Batagur" , files.all ) | grepl( "Chelonia" , files.all ) | grepl( "Chelus" , files.all ) | grepl( "Chelodina" , files.all ) | grepl( "Cuora_BONE" , files.all ) | grepl( "Eretmochelys" , files.all ) | grepl( "Mauremys" , files.all ) | grepl( "Staurotypus" , files.all ) ) )
```

```
for( i in 1:length( fix.landmarks ) ) {
  landmarks[[ fix.landmarks[i] ]] <- landmarks[[ fix.landmarks[i] ]]/1000 }
```

```
landmarks.FO <- list()
landmarks.CA <- list()
landmarks.CT <- list()
```

```
for( i in 1:length(files.FO) ) { landmarks.FO[[ i ]] <- matrix( as.numeric( landmarks[[ which( files.all == files.FO[i] ) ]]) , ncol = 3 ) }
for( i in 1:length(files.CA) ) { landmarks.CA[[ i ]] <- matrix( as.numeric( landmarks[[ which( files.all == files.CA[i] ) ]]) , ncol = 3 ) }
for( i in 1:length(files.CT) ) { landmarks.CT[[ i ]] <- matrix( as.numeric( landmarks[[ which( files.all == files.CT[i] ) ]]) , ncol = 3 ) }
```

```
i = 1
plot3d( rbind( landmarks.FO[[ i ]], landmarks.CA[[ i ]], landmarks.CT[[ i ]]) )
i = i + 1
```

```
plane.calc <- function( input ) {
  PCresults.temp <- precomp( input )
  #dev.new() ; plot( PCresults.temp$x[, c(1,2) ] ); polygon( PCresults.temp$x[, c(1,2) ] )
  polygon.temp <- Polygon( PCresults.temp$x[, c(1,2) ] )
}
```

```

        output.temp <- c( polygon.temp@area , apply( input , 2 , mean ) , summary( PCresults.temp ) $
importance[ 2 , ] )
        names( output.temp ) <- c( "Area" , "CentroidX" , "CentroidY" , "CentroidZ" , "PC1var" , "PC2var"
, "PC3var" )
        output.temp }

```

```

params.FO <- matrix( ncol = 7 , nrow = length( landmarks.FO ) )
for( i in 1:length( landmarks.FO ) ) {
    params.FO[ i , ] <- plane.calc( landmarks.FO[[ i ]] ) }
colnames( params.FO ) <- c( "Area" , "CentroidX" , "CentroidY" , "CentroidZ" , "PC1var" , "PC2var" , "PC3var" )
rownames( params.FO ) <- files.FO

```

```

params.CT <- matrix( ncol = 7 , nrow = length( landmarks.CT ) )
for( i in 1:length( landmarks.CT ) ) {
    params.CT[ i , ] <- plane.calc( landmarks.CT[[ i ]] ) }
colnames( params.CT ) <- c( "Area" , "CentroidX" , "CentroidY" , "CentroidZ" , "PC1var" , "PC2var" , "PC3var" )
rownames( params.CT ) <- files.CT

```

```

params.CA <- matrix( ncol = 7 , nrow = length( landmarks.CT ) )
for( i in 1:length( landmarks.CA ) ) {
    params.CA[ i , ] <- plane.calc( landmarks.CA[[ i ]] ) }
colnames( params.CA ) <- c( "Area" , "CentroidX" , "CentroidY" , "CentroidZ" , "PC1var" , "PC2var" , "PC3var" )
rownames( params.CA ) <- files.CA

```

```

write.table( params.FO , "Fenestra ovalis measurements" )
write.table( params.CT , "Cavum tympanum measurements" )
write.table( params.CA , "Columella auris measurements" )

```

```

Edist <- function( A ) { sum( ( A[ c(1:3) ] - A[ c(4:6) ] ) ^ 2 ) ^ 0.5 }

```

```

straight.dist <- apply( cbind( params.FO[ , c( "CentroidX" , "CentroidY" , "CentroidZ" ) ] , params.CT[ , c(
"CentroidX" , "CentroidY" , "CentroidZ" ) ] ) , 1 , Edist )

```

```

bent.dist1 <- apply( cbind( params.FO[ , c( "CentroidX" , "CentroidY" , "CentroidZ" ) ] , params.CA[ , c(
"CentroidX" , "CentroidY" , "CentroidZ" ) ] ) , 1 , Edist )

```

```

bent.dist2 <- apply( cbind( params.CA[ , c( "CentroidX" , "CentroidY" , "CentroidZ" ) ] , params.CT[ , c(
"CentroidX" , "CentroidY" , "CentroidZ" ) ] ) , 1 , Edist )

```

```

bent.dist <- bent.dist1 + bent.dist2

```

BEGIN TREES;

LINK Taxa = Taxa;

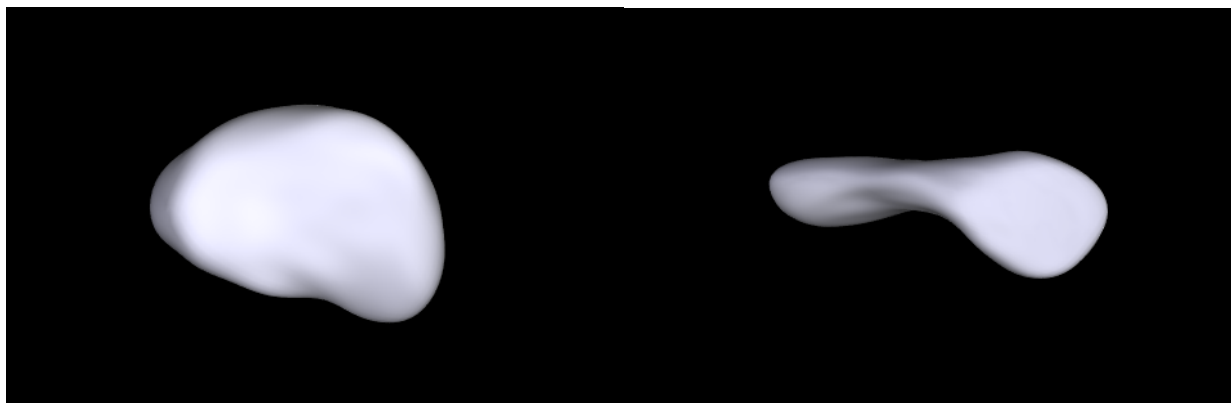
[! Trees from source: 'Current Tree (Tree(s) used from Trees from "tree2_equal_pruned.nex". Last tree used:
UNTITLED+ [tree: (((((1:94.6,2:94.6):21.4,(3:94,(4:72,5:72):22):22):48.1,(6:125,
(7:91.75,8:91.75):33.250000009):39.1):48.2,((9:162.8,(10:105,(11:101.26,
((12:46,13:46):51.52,14:97.52):3.74):3.74):57.8):27.6,(((15:91.1,(16:55.7,(17:21.700000003,(18:17.1,
(19:5.7,20:5.7):11.4):4.6):34):35.4):22,(21:78.02499999999999,(22:23.25,23:23.25):54.775000000000006):35.075):5.5,
((24:82.4,((25:28.8,((28:20.9,(26:16.4,27:16.4):4.5):4.5,(29:14.3,30:14.3):11.1):3.4):15.4,(31:31.8,
((32:6.966666667,33:6.966666667):13.933333334,34:20.9):10.9):12.4):38.2):3.4,(((35:38.325,(36:25.55,
(37:12.775,38:12.775):12.775):12.775):16.975,(((39:25.55,(40:12.775,41:12.775):12.775):12.775,42:38.325):12.775,
((43:21.29166667,44:21.29166666):21.29166666,
(45:34.06666666,46:34.066666668):8.516666667):8.516666667):4.2):17.35,((47:24.6,48:24.6):34.9,
((49:35.31428571,50:35.314285716):18.08571429,((51:20.6,52:20.6):20.6,((53:24.72,
(54:16.48,55:16.48):8.24):8.24,56:32.96):8.24):12.2):6.1):13.15):13.15):32.8):71.8):21.9):3.2000000010000003;)]]'

TRANSLATE

- 1 Chelodina_oblonga,
- 2 Emydura_subglobosa,
- 3 Hydromedusa_tectifera,
- 4 Chelus_fimbriata,
- 5 Phrynops_geoffroanus,
- 6 Pelomedusa_subrufa,
- 7 Podocnemis_unifilis,
- 8 Peltoccephalus_dumeriliana,
- 9 Carettochelys_insculpta,
- 10 Lissemys_punctata,
- 11 Chitra_indica,
- 12 Amyda_cartilaginea,
- 13 Pelodiscus_sinensis,
- 14 Apalone_spinifera,
- 15 Dermatemys_mawii,
- 16 Staurotypus_sp,
- 17 Sternotherus_minor,
- 18 Kinosternon_scorpioides,
- 19 Kinosternon_baurii,
- 20 Kinosternon_subrubrum,
- 21 Dermochelys_coriacea,
- 22 Chelonia_mydas,
- 23 Eretmochelys_imbricata,
- 24 Platysternon_megacephalum,
- 25 Glyptemys_insculpta,
- 26 Emydoidea_blandingii,
- 27 Emys_orbicularis,
- 28 Clemmys_guttata,
- 29 Terrapene_ornata,
- 30 Terrapene_coahuila,
- 31 Deirochelys_reticularia,
- 32 Pseudemys_concinna,
- 33 Pseudemys_floridana,
- 34 Malaclemys_terrapi,
- 35 Manouria_impressa,
- 36 Gopherus_agassizi,

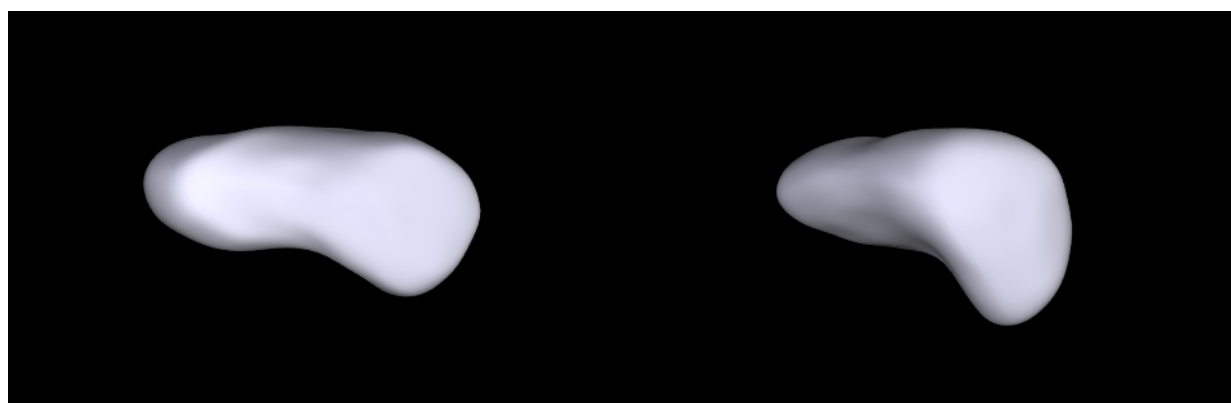
37 Gopherus_flavomarginatus,
38 Gopherus_polyphemus,
39 Malacochersus_tornieri,
40 Indotestudo_elongata,
41 Indotestudo_forstenii,
42 Testudo_marginata,
43 Chelonoidis_sp,
44 Kinixys_erosa,
45 Aldabrachelys_gigantea,
46 Psammobates_tentorius,
47 Rhinoclemmys_melanosterna,
48 Rhinoclemmys_pulcherrima,
49 Geoemyda_spengleri,
50 Batagur_baska,
51 Heosemys_annandalii,
52 Notochelys_platynota,
53 Cuora_amboinensis,
54 Cuora_flavomarginata,
55 Cuora_mouhotii,
56 Mauremys_leprosa;

TREE 'UNTITLED+' = (((((1:94.6,2:94.6):21.4,(3:94,(4:72,5:72):22):22):48.1,(6:125,
(7:91.75,8:91.75):33.250000009):39.1):48.2,((9:162.8,(10:105,(11:101.26,
((12:46,13:46):51.52,14:97.52):3.74):3.74):57.8):27.6,(((15:91.1,(16:55.7,(17:21.700000003,(18:17.1,
(19:5.7,20:5.7):11.4):4.6):34):35.4):22,(21:78.02499999999999,(22:23.25,23:23.25):54.775000000000006):35.075):5.5,
((24:82.4,((25:28.8,((28:20.9,(26:16.4,27:16.4):4.5):4.5,(29:14.3,30:14.3):11.1):3.4):15.4,(31:31.8,
((32:6.966666667,33:6.966666667):13.933333334,34:20.9):10.9):12.4):38.2):3.4,(((35:38.325,(36:25.55,
(37:12.775,38:12.775):12.775):12.775):16.975,(((39:25.55,(40:12.775,41:12.775):12.775):12.775,42:38.325):12.775,
((43:21.29166667,44:21.29166666):21.29166666,
(45:34.06666666,46:34.066666668):8.516666667):8.516666667):4.2):17.35,((47:24.6,48:24.6):34.9,
((49:35.31428571,50:35.314285716):18.08571429,((51:20.6,52:20.6):20.6,((53:24.72,
(54:16.48,55:16.48):8.24):8.24,56:32.96):8.24):12.2):6.1):13.15):13.15):32.8):71.8):21.9):3.2000000010000003;
END;



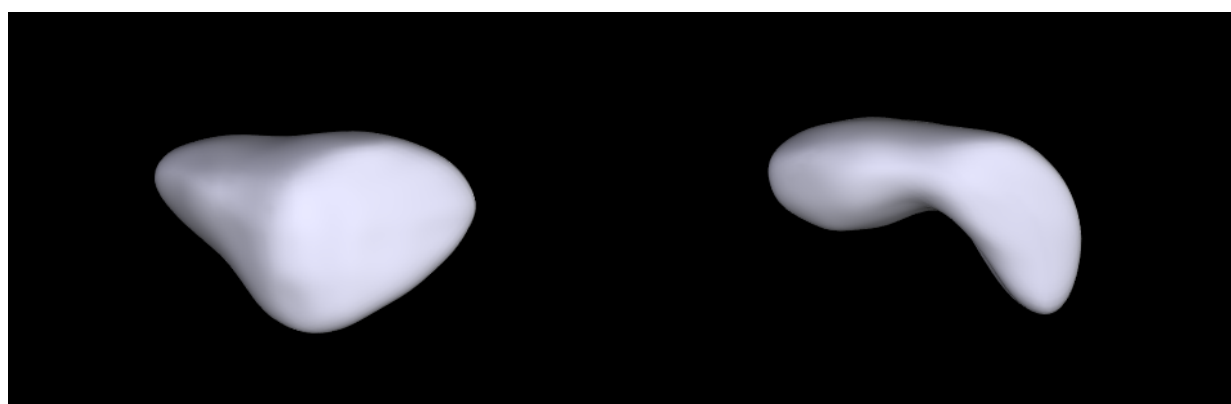
PC1 (+)

PC1 (-)



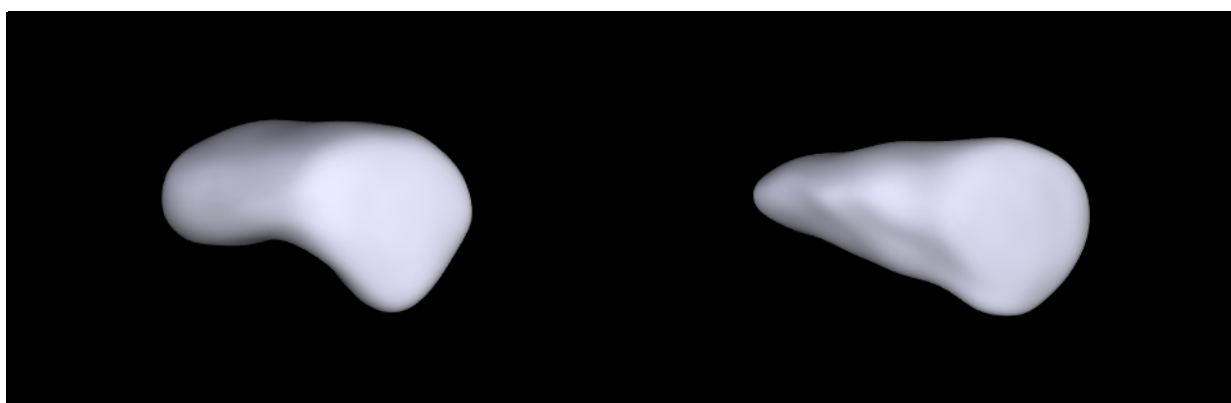
PC2 (+)

PC2 (-)



PC3 (+)

PC3 (-)



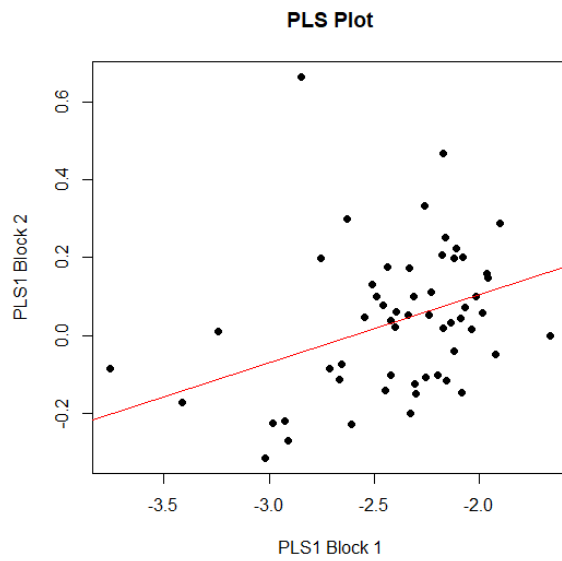
PC4 (+)

PC4 (-)

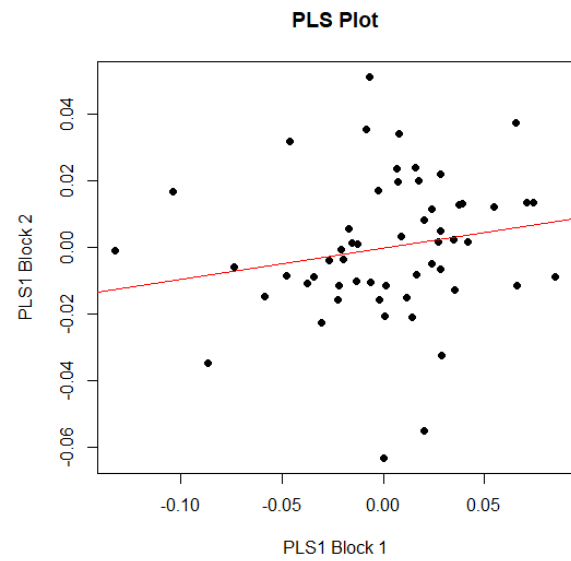
Two-block partial least squares analysis

Phylogenetic Two-Block Partial Least Squares Analyses

Morphometric measurements

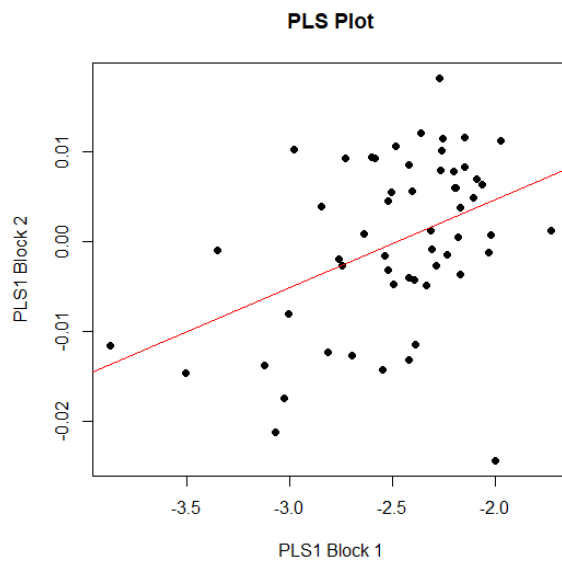


$r\text{-PLS: } 0.298$; P-value: 0.12

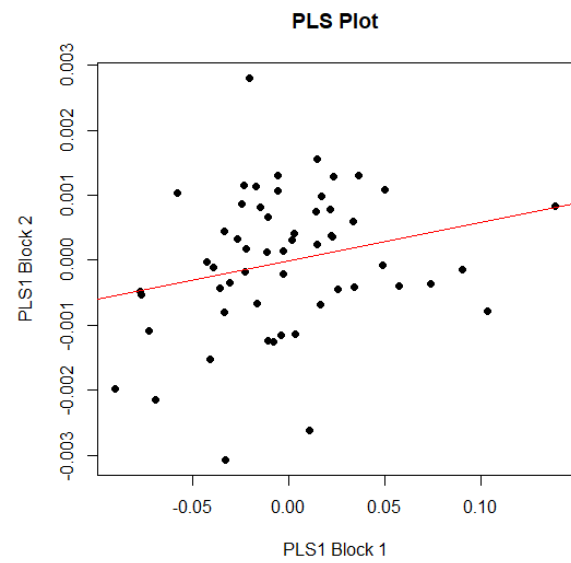


$r\text{-PLS: } 0.144$; P-value: 0.802

PC1-PC4

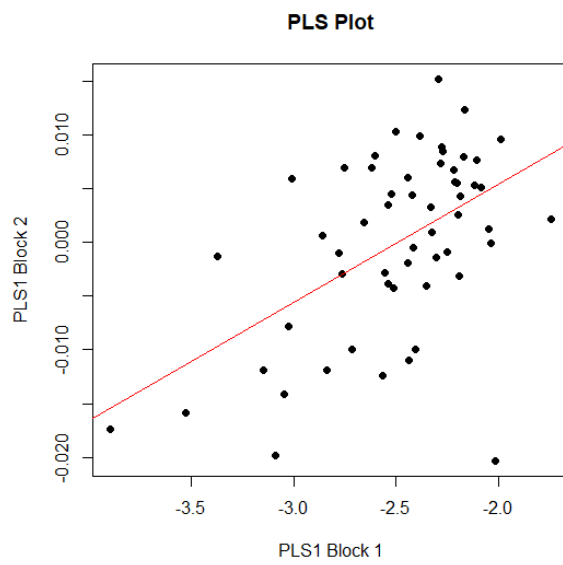


$r\text{-PLS: } 0.419$; P-value: 0.02

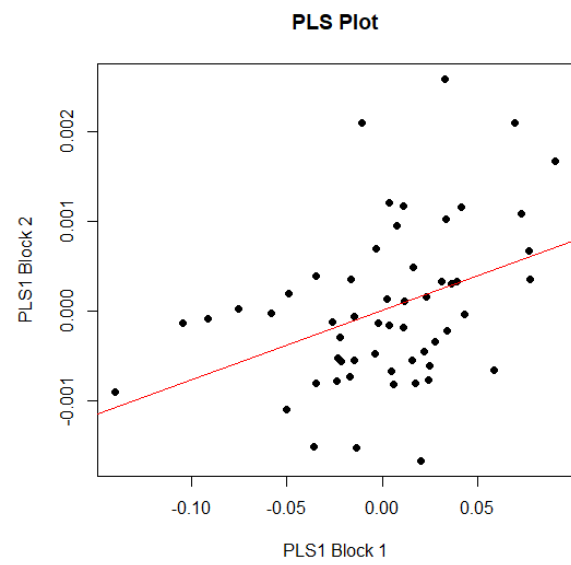


$r\text{-PLS: } 0.242$; P-value: 0.391

All PCs



r-PLS: 0.527; P-value: 0.008



r-PLS: 0.388; P-value: 0.246

Table S1. Specimens used in this study and CT data repository information.

Note that all CT scans for which we had explicit copyright holder permission have been made available.

"For scans for which we have no copyright or no permission, individuals that shared the scans with us are indicated, and, if applicable, the first literature mentioning of those data are indicated with an asterisk (*). "

Citations without asterisks refer to the MorphoSource projects.

Taxon	SpecimenRepository	Project	Media accession number	Data Source	Citation
<i>Aldabrachelys gigantea</i>	NHMUK 77.11.12.2	MorphoSourceP769	M42855	own scan	Evers (2019)
<i>Amyda cartilaginea</i>	FMNH 244117	MorphoSourceP769	M42876	own scan	Evers (2019)
<i>Apalone spinifera</i>	FMNH 22178	MorphoSourceP462	M22038	own scan	Evers & Benson (2018)
<i>Batagur baska</i>	NHMUK 67.9.28.7	MorphoSourceP769	M42851	own scan	Evers (2019)
<i>Carettochelys insculpta</i>	SMF 56626	noneNA	NA	shared by I. Werneburg	none
<i>Chelodina oblonga</i>	NHMUK 64.12.22	MorphoSourceP769	M42849	own scan	Evers (2019)
<i>Chelonia mydas</i>	NHMUK 1969.776	MorphoSourceP769	M42846	own scan	Evers (2019)
<i>Chelonoidis</i> sp.	SMF 67582	noneNA	NA	shared by I. Werneburg	none
<i>Chelus fimbriatus</i>	NHMUK 81.9.27.4	MorphoSourceP769	M42856	own scan	Evers (2019)
<i>Chitra chitra</i>	NHMUK 1936.12.16.1	MorphoSourceP769	M42842	own scan	Evers (2019)
<i>Clemmys guttata</i>	FMNH 22114	MorphoSourceP769	M42870	own scan	Evers (2019)
<i>Cuora amboinensis</i>	NHMUK 69.42.145	MorphoSourceP769	M42852	own scan	Evers (2019)
<i>Cuora flavomarginata</i>	FMNH 21515	MorphoSourceP769	M42867	own scan	Evers (2019)
<i>Cuora mouhotii</i>	SMF 71599	noneNA	NA	shared by I. Werneburg	none
<i>Deirochelys reticularia</i>	FMNH 98754	MorphoSourceP769	M42883	own scan	Evers (2019)
<i>Dermatemys mawii</i>	SMF 59463	noneNA	NA	shared by I. Werneburg	none
<i>Dermochelys coriacea</i>	FMNH 171756	MorphoSourceP769	M42864	own scan	Evers (2019)
<i>Emydoidea blandingii</i>	FMNH 22144	MorphoSourceP769	M42871	own scan	Evers (2019)
<i>Emydura subglobosa</i>	PIMUZ lab# 2009.37	noneNA	NA	shared by I. Werneburg	Lautenschlager et al. (2018)*
<i>Emys orbicularis</i>	SMF 1987	noneNA	NA	shared by I. Werneburg	Lautenschlager et al. (2018)*
<i>Eretmochelys imbricata</i>	NMB C2417	noneNA	NA	shared by I. Raselli	Raselli 2018*
<i>Geoemyda spengleri</i>	FMNH 260381	MorphoSourceP769	M42877	own scan	Evers (2019)
<i>Glyptemys insculpta</i>	FMNH 22240	MorphoSourceP769	M42873	own scan	Evers (2019)
<i>Gopherus agassizi</i>	FMNH 216746	MorphoSourceP769	M42868	own scan	Evers (2019)
<i>Gopherus flavomarginatus</i>	FMNH 98916	MorphoSourceP769	M42884	own scan	Evers (2019)
<i>Gopherus polyphemus</i>	FMNH 211815	MorphoSourceP462	M22041	own scan	Evers & Benson (2018)
<i>Heosemys annandalei</i>	FMNH 260389	MorphoSourceP769	M42878	own scan	Evers (2019)
<i>Hydromedusa tectifera</i>	SMF 70500	noneNA	NA	shared by I. Werneburg	none
<i>Indotestudo forstenii</i>	SMF 73257	noneNA	NA	shared by I. Werneburg	none
<i>Intestudo elongata</i>	SMF 71585	noneNA	NA	shared by I. Werneburg	none
<i>Kinosternon baurii</i>	FMNH 211705	MorphoSourceP769	M42865	own scan	Evers (2019)
<i>Kinosternon scorpioides</i>	SMF 71893	noneNA	NA	shared by I. Werneburg	none
<i>Kinosternon suburum</i>	FMNH 211711	MorphoSourceP769	M42866	own scan	Evers (2019)
<i>Kinyxis erosa</i>	SMF 40166	noneNA	NA	shared by I. Werneburg	none
<i>Lissemys punctata</i>	SMF 74141	noneNA	NA	shared by I. Werneburg	none
<i>Malaclemys terrapin</i>	SMF 36419	noneNA	NA	shared by I. Werneburg	none
<i>Malacochersus tornieri</i>	SMF 58702	noneNA	NA	shared by I. Werneburg	Lautenschlager et al. (2018)*
<i>Manouria impressa</i>	SMF 69777	noneNA	NA	shared by I. Werneburg	none
<i>Mauremys leprosa</i>	NHMUK unnumbered	MorphoSourceP769	M42862	own scan	Evers (2019)
<i>Notochelys platynota</i>	FMNH 224048	MorphoSourceP769	M42874	own scan	Evers (2019)
<i>Pelodiscus sinensis</i>	IW576-2b	noneNA	NA	shared by I. Werneburg	Lautenschlager et al. (2018)*
<i>Peltocephalus dumerilianus</i>	SMF 55470	noneNA	NA	shared by I. Werneburg	Lautenschlager et al. (2018)*
<i>Pelomedusa subrufa</i>	SMF 70504	noneNA	NA	shared by I. Werneburg	none
<i>Phrynops geoffroanus</i>	SMF 45470	MorphoSourceP462	M22118	own scan	Evers & Benson (2018)
<i>Platysternon megacephalum</i>	SMF 69684	noneNA	NA	shared by I. Werneburg	none
<i>Podocnemis unifilis</i>	FMNH 45657	MorphoSourceP769	M42880	own scan	Evers (2019)
<i>Psammobates tentorius</i>	SMF 57142	noneNA	NA	shared by I. Werneburg	none
<i>Pseudemys concinna</i>	FMNH 22146	MorphoSourceP769	M42872	own scan	Evers (2019)
<i>Pseudemys floridana</i>	FMNH 8222	MorphoSourceP769	M42882	own scan	Evers (2019)
<i>Rhinoclemmys melanosterna</i>	FMNH 44446	MorphoSourceP769	M42879	own scan	Evers (2019)

Rhinoclemmys pulcherrima	Digimorph unnumbered	Digimorph	NA	NA	downloaded	none
Staurotypus salvinii	NHMUK 1879.1.7.5	MorphoSourceP769	M42838	own scan	Evers (2019)	
Sternotherus minor	FMNH 211696	MorphoSourceP462	M22123	own scan	Evers & Benson (2018)	
Terrapene coahuila	FMNH 47372	MorphoSourceP769	M42881	own scan	Evers (2019)	
Terrapene ornata	FMNH 23014	MorphoSourceP769	M42875	own scan	Evers (2019)	
Testudo marginata	FMNH 51672	MorphoSourceP769	M42885	own scan	Evers (2019)	

References

"Evers SW, Benson RBJ (2018) Project: Evers & Benson 2018, Turtle CT data and 3D models. MorphoSource. Available at http://www.morphosource.org/Detail/ProjectDetail/Show/project_id/462. "

"Evers SW (2019) Project: Evers 2019, CT scans of extant turtle skulls. MorphoSource. Available at https://www.morphosource.org/Detail/ProjectDetail/Show/project_id/769."

"Lautenschlager S, Ferreira GS, Werneburg I (2018) Sensory evolution and ecology of early turtles revealed by digital endocranial reconstructions. Front Ecol Evol 6, 7:1-16."

"Raselli I (2018) Comparative cranial morphology of the Late Cretaceous protostegid sea turtle Desmatochelys lowii. PeerJ 6, e5964."

"Table S2. Morphometric measurements of turtle skulls and middle ears, habitat preferences, and values for the first four PCs."

Skull paramters parameters (against logCS)				Habitat grouping PCA Results [SPHARM]				Middle ear parameters						Ratio:		Residuals of Middle					
Species	Specimen	Skull length [mm]	Skull width [mm]	Skull height [mm]	logV [mm3]	Forelimb	Forelimb1	Forelimb2	Forelimb3	Forelimb4	Forelimb5	Forelimb6	CS								
logCS	V [mm3]	logV	AreaCT [mm2]	logCT	AreaFO [mm2]	logFO	LengthD	logD	AreaCT/AreaFO	RESlogV	RESlogCT	RESlogFO	RESlogD	Axis 1	Axis 2						
Axis 3	Axis 4																				
Aldabrachelys gigantea	NHMUK77.11.12.2	147.7800	108.4300	51.7900	5.9190	not webbed	-00	0	0	0	0	0	800.4643	2.9033	11887.3330	4.0751	510.8319	2.7083			
34.6161	1.5393	38.2408	1.5825	14.7571	0.208760	-0.135713	0.079780	-0.034821	0.002615	-0.003391	-0.002486	0.000440									
Amyda cartilaginea	FMNH 244117	97.7600	70.2300	32.8800	5.3536	extensive	-3	3	2	2	1	1	497.9813	2.6972	2674.1254	3.4272	364.1208	2.5612	17.7427		
1.2490	20.3903	1.3094	20.5223	0.147856	0.171765	0.114323	-0.053519	0.010312	0.002873	0.016150	-0.001394										
Apalone spinifera	FMNH 22178	65.9500	41.9300	22.0200	4.7846	extensive	-3	3	2	2	1	1	297.6649	2.4737	530.1349	2.7244	117.7513	2.0710	9.7697	0.9899	
11.6729	1.0672	12.0527	0.081483	0.174268	0.207337	-0.019937	0.005710	0.001272	0.013473	-0.004849											
Batagur baska	NHMUK 67.9.28.791.2100	67.6500	33.5100	5.3155	extensive	-3	3	2	2	1	1	1	492.8359	2.6927	2103.3687	3.3229	391.1809	2.5924	26.7536	1.4274	
20.9059	1.3203	14.6216	0.056435	0.212845	0.299795	-0.037107	0.008017	-0.000593	0.003055	-0.009007											
Carettochelys insculpta	SMF 56626	101.0000	86.6700	38.2500	5.5248	flipper	-44	3	3	2	1	1	549.6876	2.7401	3222.2785	3.5082	600.0117	2.7782	21.4677	1.3318	
24.3648	1.3868	27.9495	0.106661	0.294080	0.129487	-0.029131	0.010663	0.009607	0.012304	0.002946											
Chelodina oblonga	NHMUK 64.12.22	51.7000	30.8200	10.6000	4.2276	extensive	-3	3	3	2	2	1	1	301.2057	2.4789	361.0728	2.5576	46.6082	1.6685	3.3186	0.5210
10.6051	1.0255	14.0444	-0.099931	-0.239559	-0.269678	-0.067937	-0.012088	-0.001772	-0.005612	-0.002780											
Chelonia mydas	NHMUK 1969.776	159.5100	113.4300	80.8300	6.1651	flipper	-44	3	3	2	1	1	710.8949	2.8518	6805.1353	3.8328	666.3803	2.8237	31.2758	1.4952	
40.8983	1.6117	21.3066	0.113276	0.093369	0.116919	0.057964	0.016877	-0.003885	0.002300	-0.006360											
Chelonoidis sp.	SMF 67582	43.5500	31.6500	14.6100	4.3040	not webbed	0	0	0	0	0	0	230.2957	2.3623	300.6277	2.4780	35.4527	1.5496	3.7989	0.5797	
7.2153	0.8583	9.3324	0.152482	-0.101321	-0.027289	-0.091320	0.010757	-0.000013	-0.005850	0.007481											
Chelus fimbriata	NHMUK 81.9.27.4	98.4700	104.1000	20.5600	5.3238	extensive	-2	2	2	1	1	1	0	771.3347	2.8872	2488.1763	3.3959	220.1778	2.3428	12.1015	
1.0828	38.0000	1.5798	18.1943	-0.424598	-0.465719	-0.351291	-0.017695	-0.027440	-0.031787	0.005464	0.012390										
Chitra chitra	NHMUK 1926.12.16.1	89.1400	53.7600	21.3400	5.0097	extensive	-3	3	3	2	2	1	1	325.5846	2.5127	697.2859	2.8434	106.3584	2.0268	7.2314	0.8592
14.3712	1.1575	14.7079	0.089629	0.044220	0.015323	0.022322	0.013404	-0.002627	0.002950	-0.007651											
Clemmys guttata	FMNH 22114	24.2600	15.6900	8.5300	3.5115	small	-1	1	0	0	0	0	158.3839	2.1997	55.9437	1.7478	10.7499	1.0314	1.9921	0.2993	5.0588
0.7040	5.3963	-0.114827	-0.261092	-0.051467	-0.044876	-0.012227	0.006213	-0.001618	-0.003141												
Cuora amboinensis	NHMUK 69.42.145	34.7700	22.0800	10.8000	3.9186	extensive	-2	2	2	1	1	1	0	231.8457	2.3652	190.5400	2.2800	31.1311	1.4932	3.5744	
0.5532	7.3278	0.8650	8.7096	-0.053856	-0.164198	-0.058337	-0.088192	-0.004795	0.003149	-0.005656	-0.003591										
Cuora flavomarginata	FMNH 21515	33.2600	21.7400	10.1800	3.8669	small	-1	1	0	0	0	0	206.5600	2.3150	176.4465	2.2466	29.8874	1.4755	3.5914	0.5553	
6.8146	0.8334	8.3218	0.055593	-0.071318	0.022762	-0.057829	-0.002444	0.006158	-0.001117	-0.002172											
Cuora mouhotii	SMF 71599	36.5800	25.7100	13.2800	4.0965	not webbed	-00	0	0	0	0	0	239.3363	2.3790	332.7875	2.5222	29.4373	1.4689	4.9952	0.6986	
8.3941	0.9240	5.8931	0.148998	-0.218946	0.065258	-0.046237	0.003027	0.001824	-0.001448	0.003708											
Deirochelys reticularia	FMNH 98754	41.0800	24.3300	10.8000	4.0332	extensive	-2	2	2	1	1	1	0	221.2665	2.3449	169.1333	2.2282	42.7948	1.6314	3.8368	0.5840
7.4058	0.8696	11.1539	-0.047853	0.018721	0.004390	-0.058560	-0.011358	0.003035	-0.001913	-0.001722											
Dermatemys mawii	SMF 59463	66.9700	49.6200	23.3900	4.8906	extensive	-2	2	2	1	1	1	0	412.4972	2.6154	1270.0393	3.1038	192.0737	2.2835	15.2399	1.1830
15.3454	1.1860	12.6034	0.057412	0.074339	0.177166	-0.076015	-0.001257	0.006571	0.006581	0.001454											
Dermochelys coriacea	FMNH 171756	219.0000	250.3800	117.3700	6.8086	flipper	-44	3	3	2	1	1	1318.8044	3.1202	45042.5803	4.6536	2323.2833	3.3661			
43.5020	1.6385	93.3719	1.9702	53.4063	0.169805	0.043986	-0.162665	0.085245	0.012734	0.008770	0.006427	0.009015									
Emydoidea blandingii	FMNH 22144	40.2500	26.2500	10.1500	4.0304	small	-1	1	0	0	0	0	267.4280	2.4272	246.1861	2.3913	44.8232	1.6515	3.0437	0.4834	
9.0167	0.9550	14.7265	-0.119160	-0.142618	-0.225838	-0.074650	-0.013760	0.005339	-0.000509	-0.003836											
Emydura subglobosa	PIMUZ lab# 2009.37	15.9300	12.3300	6.1900	3.0849	extensive	-2	2	2	1	1	1	0	97.0596	1.9870	19.2604	1.2847	6.4547	0.8099	1.0173	
0.0075	3.1567	0.4992	6.3449	0.027718	-0.013680	-0.008206	0.012794	0.001796	-0.002519	-0.004728	-0.000190										
Emys orbicularis	SMF 1987	28.4500	19.9400	8.6200	3.6893	small	-1	1	0	0	0	0	197.7575	2.2961	134.0057	2.1271	28.2260	1.4506	3.2980	0.5182	6.5520
0.8164	8.5586	-0.010038	-0.054454	0.015539	-0.051551	-0.005070	0.001872	-0.003589	-0.005118												
Eretmochelys imbricata	NMB C2417	96.6000	67.2800	40.3000	5.4182	flipper	-44	3	3	2	1	1	437.2608	2.6407	1777.8015	3.2499	250.3808	2.3986	16.0126	1.2045	
22.4357	1.3509	15.6365	0.131377	0.133644	0.158753	0.057696	0.022410	-0.007111	0.005228	-0.002990											
Geoemyda spengleri	FMNH 260381	23.9200	15.5300	10.3200	3.5836	not webbed	-00	0	0	0	0	0	156.8814	2.1956	84.0010	1.9243	12.2612	1.0885	2.3448		
0.3701	4.4084	0.6443	5.2292	0.073492	-0.194834	0.025848	-0.099529	0.002852	0.009633	-0.001228	0.002977										
Glyptemys insculpta	FMNH 22240	41.0000	33.9600	14.4800	4.3045	small	-1	1	0	0	0	0	276.2149	2.4412	345.7768	2.5388	40.8428	1.6111	5.6691	0.7535	
11.2005	1.0492	7.2045	-0.011610	-0.213962	0.022147	0.002211	-0.005259	0.004442	-0.005932	-0.001423											
Gopherus agassizi	FMNH 216746	44.9600	37.4800	18.3300	4.4898	not webbed	-00	0	0	0	0	0	270.5898	2.4323	442.0455	2.6455	71.6636	1.8553	7.6102	0.8814	
11.3547	1.0552	9.4167	0.120508	0.049924	0.164113	0.019179	0.006237	0.008279	-0.001873	0.008154											
Gopherus flavomarginatus	FMNH 98916	50.1900	39.5500	16.9000	4.5257	not webbed	-00	0	0	0	0	0	325.1360	2.5121	831.4995	2.9199	64.4825	1.8094	7.4230		
0.8706	12.0649	1.0815	8.6869	0.167786	-0.171789	0.027624	-0.052907	0.023812	-0.014335	-0.009296	0.000520										
Gopherus polyphemus	FMNH 211815	43.0600	41.3200	15.2200	4.4326	not webbed	-00	0	0	0	0	0	274.7341	2.4389	447.9904	2.6513	43.1594	1.6351	14.6989		
1.1673	8.1512	0.9112	2.9362	0.107510	-0.184856	0.439598	-0.132927	0.011976	-0.004312	-0.007317	0.005767										
Heosemys annandalii	FMNH 260389	54.5700	41.2900	17.4000	4.5933	extensive	-2	2	2	1	1	1	0	356.2682	2.5518	685.2824	2.8359	87.3079	1.9411	10.4951	
1.0210	13.5513	1.1320	8.3189	-0.029295	-0.127741	0.115457	-0.051465	-0.008993	0.002546	-0.003385	-0.001139										
Hydromedusa tectifera	SMF 70500	46.1200	28.0000	9.2000	4.0748	extensive	-3	3	3	2	2	1	1	267.1395	2.4267	170.7259	2.2323	25.6322	1.4088	4.4273	0.6461
9.0976	0.9589	5.7896	-0.276789	-0.384300	-0.062363	-0.070191	-0.024566	-0.000812	-0.000588	-0.005792											
Indotestudo elongata	SMF 71585	51.4900	39.2200	15.1200	4.4848	not webbed	-00	0	0	0	0	0	268.4538	2.4289	401.0904	2.6032	63.7809	1.8047	7.8476	0.8947	
11.4678	1.0595	8.1274	0.088082	0.060904	0.182877	0.027727	0.001811	0.005179	-0.007539	-0.006524											
Indotestudo forstenii	SMF 73257	33.8500	28.0900	12.1800	4.0638	not webbed	-00	0	0	0	0	0	213.3865	2.3292	258.9144	2.4132	38.8185	1.5890	4.2096	0.6242	
7.9402	0.8998	9.2214	0.181923	0.011096	0.069484	-0.008868	0.007410	0.003748	-0.002857	0.008591											
Kinixys erosa	SMF 40166	46.0800	30.0800	13.3400	4.2669	not webbed	-00	0	0	0	0	0	273.5445	2.4370	542.5592	2.7344	68.9256	1.8384	7.9823	0.9021	8.9343
0.9511	8.6348	0.196056	0.022606	0.177413	-0.090762	0.004956	0.003543	0.002282	0.006139												
Kinosternon baurii	FMNH 211705	24.2800	17.2400	9.7900	3.6126	extensive	-2	2	2	1	1										

Table S3. All results of the phylogenetic generalized least square (pGLS) regression analyses

Model formula	R ²	AICc weight	AICc	Lambda	Variable	Slope	p value	Model formula	R ²	AICc weight	AICc	Lambda	Variable	Slope	p value	Model formula	R ²	AICc weight	AICc	Lambda	Variable	Slope	p value	Model formula	R ²	AICc weight	AICc	Lambda	Variable	Slope	p value				
CT_area ~ log10(head_size)	0.85	0.54**	-34.21	0.6	intercept	-1.157	<0.001	FO_area ~ log10(head_size)	0.83	0.823**	-54.51	0.23	intercept	-1.337	<0.001	chamber_size ~ log10(head_size)	0.91	0.931**	-155.65	0.85	intercept	1.134	<0.001	chamber_volume ~ log10(head_size) + forelimb 1	0.93	0.57**	-52.25	-0.1	intercept	-1.205	<0.001				
0.855** -138.04	0.7	intercept	-0.626	<0.001	CT_area/FO_area ~ log10(head_size)	0.3	0.458**	-31.25	0.44	intercept	0.21	0.195	chamber_width ~ log10(head_size)	0.9	0.969**	-120.49	0.26	intercept	-0.846	<0.001	chamber_crosssection ~ log10(head_size)	0.85	0.83**	-64.78	0.77	intercept	-0.344	0.012	log10(head_size)	0.194	<0.001				
log10(head_size)	0.669	<0.001			log10(head_size)	0.469	<0.001			log10(head_size)	0.867	<0.001			log10(head_size)	0.867	<0.001			log10(head_size)	0.376	<0.001													
log10(head_size)	0.353	<0.001			log10(head_size)	0.489	<0.001			log10(head_size)	0.82	0.036			chamber_size ~ log10(head_size) + forelimb 5	0.9	0.016	-147.51	0.85	intercept	1.131	<0.001	forelimb 1	-0.044	0.001	distCT_FO ~ log10(head_size) + forelimb 6	0.92								
CT_area ~ log10(head_size) + forelimb 4	0.85	0.116*	-31.13	0.69	intercept	-1.146	<0.001	FO_area ~ log10(head_size) + forelimb 3	0.3	0.17*	-29.27	0.33	intercept	0.278	0.075	chamber_size ~ log10(head_size) + forelimb 6	0.89	0.026	-113.38	0.32	intercept	-0.874	<0.001	chamber_crosssection ~ log10(head_size) + forelimb 5	0.84	0.041	-58.75	0.77	intercept	-0.332	0.016				
0.078 -133.26	0.61	intercept	-0.649	<0.001	CT_area/FO_area ~ log10(head_size) + forelimb 3	0.487	<0.001			chamber_width ~ log10(head_size)	0.294	<0.001			chamber_volume ~ log10(head_size)	0.93	0.262*	-50.69	0.34	intercept	-1.154	<0.001	log10(head_size)	0.387	<0.001	log10(head_size)	0.154	<0.001							
log10(head_size)	0.363	<0.001			log10(head_size)	0.493	<0.001			log10(head_size)	0.298	<0.001			log10(head_size)	0.837	<0.001			forelimb 6	-0.031	0.039				forelimb 3	0.079	0.021	forelimb 6	-0.02					
0.206					forelimb 3	-0.037	0.141			forelimb 5	0.007	0.705			log10(head_size)	0.837	<0.001			forelimb 6	-0.031	0.039				forelimb 3	0.079	0.021	forelimb 6	-0.02					
CT_area ~ log10(head_size) + forelimb 3	0.85	0.102*	-30.87	0.69	intercept	-1.11	<0.001	FO_area ~ log10(head_size) + forelimb 1	0.82	0.032	-48.02	0.08	intercept	-1.33	<0.001	chamber_size ~ log10(head_size) + forelimb 6	0.9	0.014	-147.32	0.84	intercept	1.127	<0.001	chamber_volume ~ log10(head_size) + forelimb 2	0.93	0.097*	-48.71	-0.07	intercept	-1.104	<0.001				
distCT_FO ~ log10(head_size) + forelimb 4	0.92	0.023	-130.82	0.69	intercept	-0.632	<0.001	CT_area/FO_area ~ log10(head_size) + forelimb 4	0.29	0.1*	-28.21	0.33	intercept	0.217	0.156	chamber_width ~ log10(head_size) + forelimb 5	0.89	0.019	-112.79	0.22	intercept	-0.847	<0.001	chamber_crosssection ~ log10(head_size) + forelimb 2	0.83	0.032	-58.27	0.75	intercept	-0.327	0.016				
log10(head_size)	0.351	<0.001			log10(head_size)	0.499	<0.001			log10(head_size)	0.298	<0.001			log10(head_size)	0.845	<0.001			log10(head_size)	0.374	<0.001				log10(head_size)	0.169	<0.001							
forelimb 2	-0.028	0.226			forelimb 3	0.073	0.057			forelimb 6	-0.011	0.439			forelimb 2	-0.038	0.021			forelimb 5	0.02	0.375				forelimb 4	0.079	0.046	forelimb 5	0.012	0.599				
CT_area ~ log10(head_size) + forelimb 5	0.84	0.09*	-30.62	0.65	intercept	-1.184	<0.001	FO_area ~ log10(head_size) + forelimb 5	0.82	0.031	-47.99	0.19	intercept	-1.325	<0.001	chamber_size ~ log10(head_size) + forelimb 4	0.9	0.011	-146.83	0.85	intercept	1.134	<0.001	chamber_volume ~ log10(head_size) + forelimb 3	0.93	0.022	-45.7	0.01	intercept	-1.177	<0.001				
distCT_FO ~ log10(head_size) + forelimb 4	0.92	0.012	-129.58	0.7	intercept	-0.626	<0.001	CT_area/FO_area ~ log10(head_size) + forelimb 1	0.29	0.099*	-28.19	0.37	intercept	0.219	0.154	chamber_width ~ log10(head_size) + forelimb 3	0.89	0.014	-112.16	0.34	intercept	-0.861	<0.001	chamber_crosssection ~ log10(head_size) + forelimb 1	0.83	0.028	-57.99	0.75	intercept	-0.34					
log10(head_size)	0.36	<0.001			log10(head_size)	0.471	<0.001			log10(head_size)	0.295	<0.001			log10(head_size)	0.863	<0.001			log10(head_size)	0.378	<0.001				log10(head_size)	0.164	<0.001							
forelimb 1	-0.024	0.254			forelimb 5	0.091	0.112			forelimb 5	-0.022	0.602			log10(head_size)	0.863	<0.001			log10(head_size)	0.378	<0.001				log10(head_size)	0.164	<0.001							
CT_area ~ log10(head_size) + forelimb 1	0.84	0.057	-29.71	0.73	intercept	-1.156	<0.001	FO_area ~ log10(head_size) + forelimb 4	0.82	0.028	-47.76	0.13	intercept	-1.334	<0.001	chamber_size ~ log10(head_size) + forelimb 3	0.9	0.011	-146.78	0.84	intercept	1.132	<0.001	chamber_volume ~ log10(head_size) + forelimb 4	0.93	0.021	-45.63	-0.01	intercept	-1.124	<0.001				
distCT_FO ~ log10(head_size) + forelimb 3	0.92	0.012	-129.55	0.7	intercept	-0.631	<0.001	CT_area/FO_area ~ log10(head_size) + forelimb 5	0.28	0.063*	-27.28	0.42	intercept	0.182	0.253	chamber_width ~ log10(head_size) + forelimb 4	0.89	0.014	-112.12	0.33	intercept	-0.851	<0.001	chamber_crosssection ~ log10(head_size) + forelimb 4	0.83	0.025	-57.79	0.78	intercept	-0.345					
log10(head_size)	0.357	<0.001			log10(head_size)	0.477	<0.001			log10(head_size)	0.297	<0.001			log10(head_size)	0.852	<0.001			log10(head_size)	0.38	<0.001				log10(head_size)	0.184	<0.001							
forelimb 4	-0.015	0.662			forelimb 1	0.051	0.072			forelimb 4	-0.006	0.675			forelimb 4	-0.066	0.01			forelimb 3	-0.009	0.567				forelimb 5	0.083	0.139	forelimb 4	-0.008	0.655				
CT_area ~ log10(head_size) + forelimb 2	0.84	0.055	-29.65	0.73	intercept	-1.181	<0.001	FO_area ~ log10(head_size) + forelimb 2	0.82	0.025	-47.54	0.1	intercept	-1.307	<0.001	chamber_size ~ log10(head_size) + forelimb 2	0.9	0.009	-146.32	0.85	intercept	1.13	<0.001	chamber_volume ~ log10(head_size) + forelimb 5	0.92	0.019	-45.41	0.16	intercept	-1.107	<0.001				
distCT_FO ~ log10(head_size) + forelimb 2	0.92	0.011	-129.3	0.71	intercept	-0.631	<0.001	CT_area/FO_area ~ log10(head_size) + forelimb 2	0.28	0.062*	-27.25	0.37	intercept	0.18	0.245	chamber_width ~ log10(head_size) + forelimb 2	0.88	0.009	-111.35	0.25	intercept	-0.846	<0.001	chamber_crosssection ~ log10(head_size) + forelimb 6	0.83	0.022	-57.56	0.79	intercept	-0.339	0.016				
log10(head_size)	0.351	<0.001			log10(head_size)	0.476	<0.001			log10(head_size)	0.293	<0.001			log10(head_size)	0.839	<0.001			log10(head_size)	0.373	<0.001				log10(head_size)	0.175	<0.001							
forelimb 6	0.009	0.789			forelimb 2	0.052	0.08			forelimb 2	-0.027	0.15			forelimb 5	-0.06	0.161			forelimb 2	0.009	0.439				forelimb 2	0.052	0.056	forelimb 2	0.005	0.629				
CT_area ~ log10(head_size) + forelimb 6	0.84	0.04	-29.02	0.69	intercept	-1.108	<0.001	FO_area ~ log10(head_size) + forelimb 6	0.82	0.025	-47.52	0.18	intercept	-1.361	<0.001	chamber_size ~ log10(head_size) + forelimb 1	0.9	0.008	-146.01	0.85	intercept	1.133	<0.001	chamber_volume ~ log10(head_size) + forelimb 6	0.92	0.01	-44.08	0.26	intercept	-1.179	<0.001				
distCT_FO ~ log10(head_size) + forelimb 1	0.92	0.009	-128.86	0.71	intercept	-0.627	<0.001	CT_area/FO_area ~ log10(head_size) + forelimb 6	0.27	0.044	-26.58	0.33	intercept	0.261	0.107	chamber_width ~ log10(head_size) + forelimb 1	0.88	0.008	-111.04	0.28	intercept	-0.845	<0.001	chamber_crosssection ~ log10(head_size) + forelimb 3	0.83	0.022	-57.52	0.78	intercept	-0.35					
log10(head_size)	0.352	<0.001			log10(head_size)	0.479	<0.001			log10(head_size)	0.293	<0.001			log10(head_size)	0.848	<0.001			log10(head_size)	0.373	<0.001				log10(head_size)	0.171	<0.001							
forelimb 6	0.053	0.192			forelimb 6	-0.022	0.421			forelimb 1	0.003	0.785			forelimb 6	-0.028	0.341			forelimb 1	0.006	0.589				forelimb 6	0.058	0.112	forelimb 1	0.002					
CT_area ~ forelimb 6	0.140	0.63	-1.03	intercept	1.582	<0.001	FO_area ~ forelimb 3	0.11	0.39	0.05	0.63	intercept	0.482	0.006	chamber_size ~ forelimb 2	0.05	0	-21.86	0.96	intercept	2.303	<0.001	chamber_volume ~ forelimb 6	0.09	0	92.05	1.01	intercept	2.344	<0.001					
CT_area/FO_area ~ forelimb 3	0.15	0.002	-20.7	0.52	intercept	0.885	<0.001	chamber_width ~ forelimb 3	0.07	0	2.96	0.69	intercept	0.552	<0.001	chamber_crosssection ~ forelimb 6	0.08	0	35.34	1.01	intercept	1.691	<0.001	forelimb 6	0.09	0	92.05	1.01	intercept	2.344	<0.001				
forelimb 6	0.41	0.001			forelimb 3	0.222	0.001			forelimb 3	0.13	0.005			forelimb 6	0.413	0.008			forelimb 3	0.167	0.004				forelimb 3	0.152	<0.001	forelimb 3	0.159	0.002				
forelimb 6	0.252	0.006			forelimb 6	0.09	0	40.43	0.78	intercept	0.61	0.001			chamber_size ~ forelimb 6	0.05	0	-21.63	1.01	intercept	2.374	<0.001	chamber_volume ~ forelimb 3	0.08	0	92.79	0.87	intercept	2.149	<0.001					
CT_area ~ forelimb 3	0.12	0.64	-1.03	intercept	1.382	<0.001	chamber_width ~ forelimb 1	0.04	0	4.64	0.86	intercept	0.527	0.002	chamber_crosssection ~ forelimb 3	0.05	0	37.09	0.99	intercept	1.609	<0.001	forelimb 3	0.08	0	92.79	0.87	intercept	2.149	<0.001					
-forelimb 1	0.11	0.001			forelimb 6	0.229	0.004			forelimb 6	0.14	0.01			forelimb 3	0.372	0.003			forelimb 6	0.169	0.013				forelimb 1	0.106	0.001	forelimb 1	0.109	0.007				
forelimb 3	0.204	0.011			FO_area ~ forelimb 4	0.06	0	41.77	0.75	intercept	0.514	0.012			chamber_size ~ intercept	0	0	-20.98	1.01	intercept	2.507	<0.001	chamber_volume ~ forelimb 4	0.05	0	94.76	1	intercept	2.28	<0.001					
CT_area ~ forelimb 4	-16.4	0.68	intercept	0.912	<0.001	chamber_width ~ forelimb 6	0.04	0	4.83	0.94	intercept	0.658	<0.001	chamber_crosssection ~ intercept	0	0	37.81	1.01	intercept	1.93	<0.001	forelimb 4	0.328	0.033	forelimb 1	0.113	0.007	forelimb 4	0.152	0.002					
forelimb 4	0.08	0			forelimb 4	0.225	0.009			chamber_size ~ forelimb 1	0.03	0	-20.34	0.99	intercept	2.292	<0.001			forelimb 4	0.328	0.033				forelimb 1	0.113	0.007	forelimb 4	0.152	0.002				
forelimb 6	0.154	0.015			chamber_crosssection ~ forelimb 4	0.02	0	38.79	1.01	intercept	1.67	<0.001			FO_area ~ forelimb 1	0.04	0	43	0.74	intercept	0.476	0.024	chamber_volume ~ intercept	0	0	95.22	1.01	intercept	2.738	<0.001					
CT_area ~ forelimb 1	0.09	0.659	1.03	intercept	1.404	0.001	FO_area ~ forelimb 1	0.04	0	43	0.74	intercept	0.476	0.024	forelimb 1	0.085	0.01			chamber_volume ~ intercept	0	0	95.22	1.01	intercept	2.738	<0.001	distCT_FO ~ intercept	0	0	5.69	1	intercept	1.128	<0.001
0.62	intercept	0.997			chamber_width ~ intercept	0	0	5	0.97	intercept	0.805	<0.001			forelimb 4	0.186	0.043			chamber_volume ~ forelimb 1	0.03	0	95.51	0.99	intercept	2.199	<0.001	distCT_FO ~ forelimb 4	0.03	0	5.93	0.99	intercept	0.908	<0.001
chamber_width ~ forelimb 4	0.03	0	57	0.88	intercept	0.597	0.001	chamber_crosssection ~ forelimb 1	-0.01	0	40.54	1	intercept	1.661	<0.001	forelimb 4	0.124	0.02			chamber_volume ~ forelimb 1	0.03	0	95.51	0.99	intercept	2.199	<0.001	distCT_FO ~ forelimb 4	0.03	0	5.93	0.99		

[illegible]

Variable	Mean	Std. Deviation	Minimum	Maximum	Skewness	Kurtosis	Skewness Z	Kurtosis Z	Shapiro-Wilk	Normality Test										
0.055274	0.052336	0.051878	0.046603	0.044154	0.043806	0.043364	0.039597	0.035291	0.031737	0.028252	0.026355	0.025770	0.019111	0.013836	0.012867	0.011293	0.008692	0.006441	0.004780	0.003826

Table S5. Results of phylogenetic flexible discriminant analyses (pFDA) exploring shape of the lateral middle ear cavity against habitat preferences for morphometric measurements and principal components.

	Forelimb1	Forelimb2	Forelimb3	Forelimb4	Forelimb5	Forelimb6
"Middle ear volume, length of columella, size of cavum tympani, size of fenestra ovale (all log-transformed)"						
Lambda	0.17	0.16	0.22	0.21	0.24	0.36
Error	0.43	0.41	0.46	0.43	0.29	0.14
"Lenght of columella, size of cavum tympani, size of fenestra ovale (all log-transformed)"						
Lambda	0.2	0.19	0.24	0.23	0.27	0.36
Error	0.61	0.54	0.55	0.5	0.39	0.14
"Size of cavum tympani, size of fenestra ovale (all log-transformed)"						
Lambda	0.22	0.21	0.27	0.26	0.3	0.36
Error	0.59	0.52	0.59	0.54	0.41	0.14
PC1 -PC4 (PCA from SPHARM analysis)						
Lambda	0.09	0.05	0.14	0.1	0.11	0.22
Error	0.3	0.3	0.34	0.3	0.27	0.09

Table S6. Results of the D.pGLS testing ecological constraints (Forelimb1 to Forelimb6) for middle ear measurements and shape.

PC 1-4	logCS	Forelimb01	Forelimb02	Forelimb03	Forelimb04	Forelimb05	Forelimb06
Sums of squares	0.00001	0.00001	0.00001	0.00000	0.00000	0.00000	0.00000
Mean square	0.00001	0.00001	0.00001	0.00000	0.00000	0.00000	0.00000
R ²	0.03005	0.03431	0.04373	0.01181	0.01287	0.01089	0.02730
F value	1.67290	1.91870	2.46950	0.64510	0.70390	0.59430	1.51530
Z score	0.91662	1.19550	1.35980	0.42370	0.34183	0.01547	1.54380
p value	0.16900	0.09900	0.06200	0.35900	0.38200	0.50800	0.04800

all PCs

Sums of squares	0.00001	0.00001	0.00001	0.00000	0.00000	0.00000	0.00001
Mean square	0.00001	0.00001	0.00001	0.00000	0.00000	0.00000	0.00001
R ²	0.02819	0.03243	0.03945	0.01314	0.01454	0.01225	0.02284
F value	1.56640	1.80970	2.21800	0.71890	0.79690	0.66980	1.26240
Z score	1.04210	1.46070	1.63620	0.53814	0.42817	-0.07725	1.74580
p value	0.14900	0.07600	0.05300	0.31000	0.34000	0.50800	0.05100

"logV,logD,logCT, logFO"

Sums of squares	0.00160	0.00159	0.00175	0.00166	0.00099	0.00201
Mean square	0.00160	0.00159	0.00175	0.00166	0.00099	0.00201
R ²	0.03323	0.03307	0.03626	0.03454	0.02049	0.04182
F value	1.85620	1.84710	2.03190	1.93200	1.12960	2.35700
Z score	1.16950	1.05610	1.65940	1.41260	0.70197	1.97770
p value	0.11300	0.13400	0.03300	0.06100	0.24500	0.02500

"logD,logCT, logFO"

Sums of squares	0.00115	0.00099	0.00171	0.00156	0.00066	0.00197
Mean square	0.00115	0.00099	0.00171	0.00156	0.00066	0.00197
R ²	0.02668	0.02290	0.03959	0.03614	0.00153	0.04560
F value	1.48010	1.26580	2.22620	2.02470	0.84040	2.58000
Z score	0.91184	0.68551	1.59060	1.35990	0.42168	1.82530
p value	0.18200	0.26100	0.03100	0.06300	0.36200	0.01400

"logCT, logFO"

Sums of squares	0.00115	0.00099	0.00170	0.00156	0.00065	0.00197
Mean square	0.00115	0.00099	0.00170	0.00156	0.00065	0.00197
R ²	0.02857	0.02457	0.04229	0.03870	0.01616	0.04892
F value	1.58820	1.36010	2.38430	2.17400	0.88690	2.77730
Z score	0.93546	0.73292	1.49420	1.28780	0.48412	1.66370
p value	0.17200	0.23500	0.02800	0.06100	0.34300	0.01400