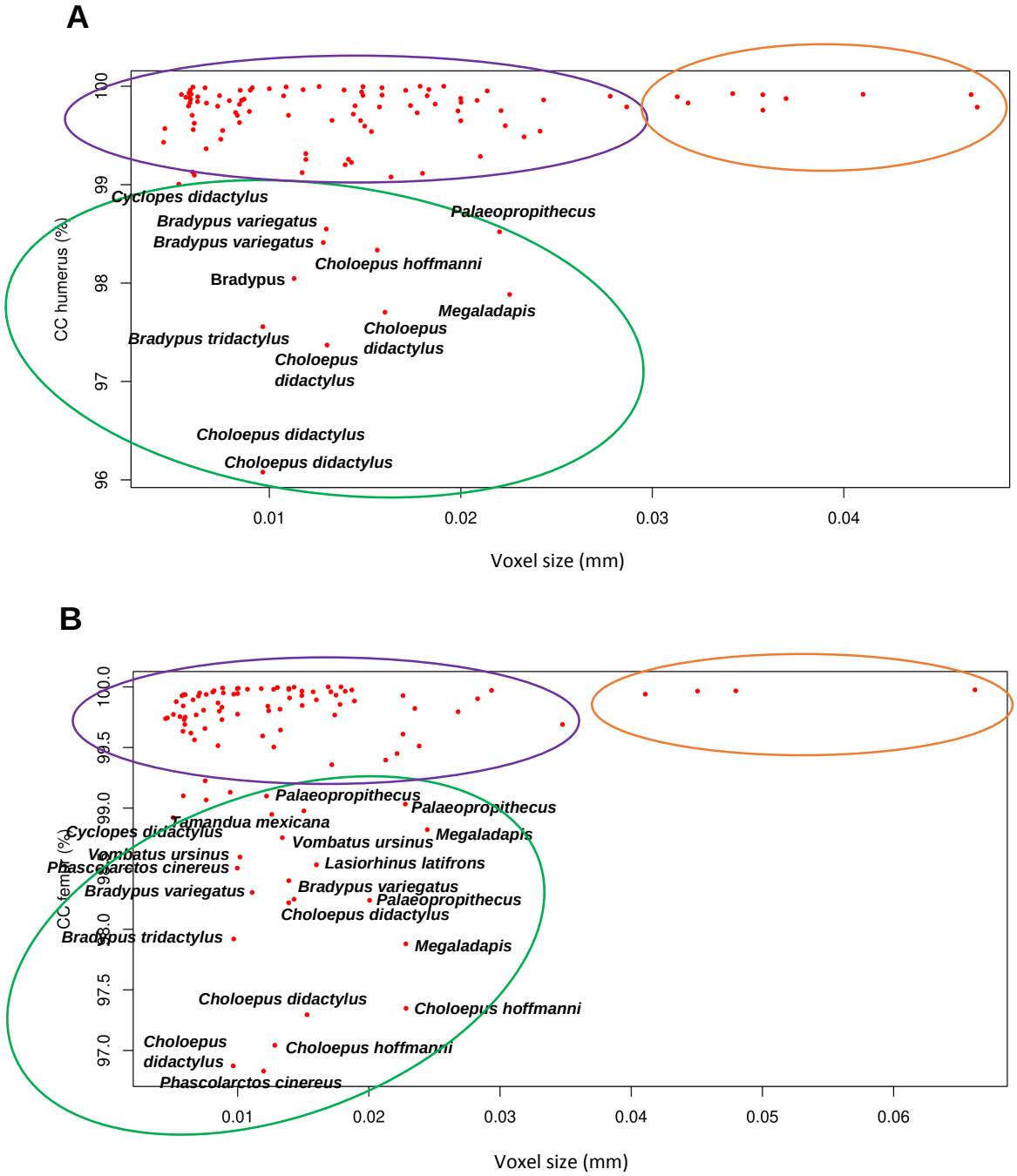

Additional methods

Plot S1. Humeral (A) and femoral (B) cortical compactness (CC) are plotted against CT spatial resolution (i.e. voxel size), for each analysed specimen. The resolution is proportional to bone size (and, in turn, to body mass), since larger specimens requires higher source-specimen distances during CT scanning, increasing voxel size and decreasing resolution. As shown with green ellipses, specimens yielding rather low CC (99% or less) are mainly 'tree sloths' (*Bradypus* and *Choloepus*), subfossil lemurs (*Palaeopropithecus* and *Megaladapis*) and *Cy. didactylus*, generally found with convergent low CC in the study. Only in the femur, specimens of *Tamandua mexicana* and marsupials (*Phascolarctos cinereus*, *Vombatus ursinus* and *Lasiorhinus latifrons*) resulted in low CC as well (Discussed in the Unexpected patterns section). Importantly, all these bones were CT-scanned in the same voxel size range of specimens of comparatively same sizes which, conversely, yielded high CC (shown with purple ellipses). It allows to exclude biases related to the tendency of CTscans with higher resolutions (low voxel size) to preferentially capture additional features (e.g. osteocyte lacunae). It would have resulted in smaller bones (acquired with higher resolutions) consistently yielding low CC, which is not supported by the two plots. The same result would have been expected if biases related to higher number of osteocytes in small species (reported for mammals, Mullender et al., 1996) had acted. Since the same voxel size range (0-0.03 mm) brought to high CC (purple ellipses) and low CC (green ellipses), we can exclude a role of resolution in causing such discrepancies in CC. Moreover, high CC was obtained for specimens covering the entire resolution (and body size) range, as shown by additional orange ellipses.

The resolution is also affected by the presence of bony processes in the diaphysis (e.g. third trochanter in the femur of Cingulata). This forces a longer specimen to X-ray source distance, resulting in lower resolution. For one specimen (femur of *Priodontes maximus* ZSM 1931-293) the resolution was purposely increased excluding the process from the acquired field of view. Since its CC falls within the Cingulata' range (Table S2), we assume that the associated bias is minor.

Adjustements to the Maximum Clade Credibility (MCC) DNA-only node-dated mammals phylogeny taken from the related posterior distribution of the work of Upham et al. (2019)

- Two extant species (*Dasypus septemcinctus* and *Tamandua mexicana)* not present in Upham et al. (2019) were added following recently published phylogenetic positioning and divergence times: *Dasypus novemcinctus* and *Dasypus septemcinctus* are sister taxa diverging 5.14 Mya (Feijó et al. 2019), *Tamandua mexicana* and *Tamandua tetradactyla* are sister taxa diverging 1,6 Mya (Casali et al. 2020).
- Santacrucian sloths' families position in respect to *Choloepus* and *Bradypus* and all node ages of Folivora (extinct + extant sloths) were constrained on the tree provided by Delsuc et al. (2019). However, since none of the extinct sloths we studied were present in this tree, infra-familiar relationships followed the morphological phylogeny built by Varela et al. (2019). First Appearance Datum (FAD) and Last Appearance Datum (LAD) are respectively 17.5 and 16.3 Mya for the analysed extinct sloths, which all come from the Santa Cruz Formation (Bargo et al. 2012). Divergence times between *Hapalops* and *Eucholoeops* and between *Analcitherium* and *Nematherium* could only be placed in a period ranging from the previous node to the FAD. In such cases, the divergence time was arbitrarily set halfway between these two corresponding ages.
- *Mesopropithecus* and *Babakotia*, not present in the tree from Upham et al. (2019), were added following the phylogeny of Herrera and Dávalos (2016). This phylogeny was used to set topology and date nodes for the ('Indriidae'+Palaeopropithecidae) clade, with 'Indriidae' being paraphyletic (Herrera and Dávalos 2016). Indeed, constraining ages only for palaeopropithecids would have resulted in a lack of consistency with the tree from Upham et al. (2019), concerning their temporal relationships with 'Indriidae'.

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Additional results

Models comparison, to choose the best fitting for Ancestral Lifestyle Reconstruction: 0= 'non- slow arboreal'; 1= 'slow arboreal'. Models: *ER*, Equal Rates, rate of slow arboreality acquisition being equal to rate of reversion from slow arboreality; *UNR_1*: Unequal Rates 1, reversion rate from slow arboreality half the rate of acquisition; *UNR 2*: Unequal Rates 2, reversion rate from slow arboreality one third the rate of acquisition.

#1a. with equal lifestyle transition rates (Equal Rates, ER)

```
logLikER<-make.simmap(time_tree,LifestyleGen,model="ER")$logL
make.simmap is sampling character histories conditioned on the transition matri
x

Q =
              0            1
0 -0.005465982  0.005465982
1  0.005465982 -0.005465982
(estimated using likelihood);
and (mean) root node prior probabilities
pi =
  0   1
0.5 0.5
Done.
> logLikER
[1] -26.262
attr(,"df")
[1] 1
```

#1b. with NonSlowArb-SlowArb transition rate twice SlowArb-NonSlowArb transition rate (unequal Rates, UNR_1)

```
> trans_mat_1<- matrix(c(-0.005465982,1,2,-0.005465982),2)
> colnames(trans_mat_1)<- c(0,1)
> rownames(trans_mat_1)<- c(0,1)
> logLikUNR_1<-make.simmap(time_tree,LifestyleGen,Q=trans_mat_1)$logL
make.simmap is sampling character histories conditioned on the transition matri
x

Q =
              0            1
0 -0.005465982  2.000000000
1  1.000000000 -0.005465982
(specified by the user);
and (mean) root node prior probabilities
pi =
  0   1
0.5 0.5
Done.
> logLikUNR_1
[1] -54.97134
attr(,"df")
[1] 2
```

#1c. with NonSlowArb-SlowArb transition rate three times SlowArb-NonSlowArb transition rate (unequal Rates, UNR_2)

```
> trans_mat_2<- matrix(c(-0.005465982,1,3,-0.005465982),2)
> colnames(trans_mat_2)<- c(0,1)
> rownames(trans_mat_2)<- c(0,1)
> logLikUNR_2<-make.simmap(time_tree,LifestyleGen,Q=trans_mat_2)$logL
```

```
make.simmap is sampling character histories conditioned on the transition matri
x

Q =
             0            1
0 -0.005465982  3.000000000
1  1.000000000 -0.005465982
(specified by the user);
and (mean) root node prior probabilities
pi =
  0   1
0.5 0.5
Done.
> logLikUNR_2
[1] -66.34417
attr(,"df")
[1] 2
```

#compute AIC, AIC_c and AIC_c weights for the three models (k=1, n=59)

```
> k<-1
> n<-59
>
> AIC_ER<- (2*k)-(2*logLikER)
> AIC_UNR_1<- (2*k)-(2*logLikUNR_1)
> AIC_UNR_2<- (2*k)-(2*logLikUNR_2)
>
>
> AIC_ER_c<-AIC_ER+(((2*k)*(k+1))/(n-k-1))
> AIC_UNR_1_c<-AIC_UNR_1+(((2*k)*(k+1))/(n-k-1))
> AIC_UNR_2_c<-AIC_UNR_2+(((2*k)*(k+1))/(n-k-1))
>
> AIC_c_scores<- c(AIC_ER_c, AIC_UNR_1_c, AIC_UNR_2_c)
> names(AIC_c_scores)<- c("AIC_ER_c", "AIC_UNR_1_c", "AIC_UNR_2_c")
>
> d.AIC_ER_c<- AIC_ER_c-min(AIC_c_scores)
> d.AIC_UNR_1_c<- AIC_UNR_1_c-min(AIC_c_scores)
> d.AIC_UNR_2_c<- AIC_UNR_2_c-min(AIC_c_scores)
```

#ER resulted to have the lowest AIC scores, thus the following analysis performed with such model

```
> d.AIC_ER_c
[1] 0
attr(,"df")
[1] 1
> d.AIC_UNR_1_c
[1] 57.41867
attr(,"df")
[1] 2
> d.AIC_UNR_2_c
[1] 80.16433
attr(,"df")
[1] 2
```

Summary results for Ancestral Lifestyle Reconstruction through Stochastic Character Mapping, using the *make.simmap* R function (ER, 1000 simulations, 'phytools' package; Revell 2012). 0='Non Slow Arboreal' Lifestyle, 1 ='Slow Arboreal Lifestyle.

```
> summary(mtreeER)

1000 trees with a mapped discrete character with states:
```

```
 0, 1

trees have 10.044 changes between states on average

changes are of the following types:
       0,1   1,0
x->y 7.435 2.609

mean total time spent in each state is:
                0          1    total
raw  1596.8279269 252.1409443 1848.969
prop    0.8636316   0.1363684    1.000
```

Summary results for Phylogenetic Generalized Least Square (PGLS) Regression of humeral cortical compactness (CC) against lifestyle (categorical binary variable, with states 'Slow Arboreal'/'Non Slow Arboreal). The cortical area (CA), body mass proxy, is added as a covariate to test for body mass influence on CC. R 'gls' function was applied with method "ML" ('nlme' R package; Pinheiro et al. 2020). Bold added by authors.

```
> summary(gls_CChumerusBM)
Generalized least squares fit by maximum likelihood
  Model: log(CChumerus) ~ Lifestyle + log(BMproxy)
  Data: humData_forPCM
        AIC       BIC   logLik
  -365.9434 -356.8002 187.9717

Correlation Structure: corPagel
 Formula: ~1
 Parameter estimate(s):
   lambda
0.7829458

Coefficients:
                           Value   Std.Error   t-value p-value
(Intercept)             4.601385 0.004060385 1133.2384  0.0000
LifestyleSlow Arboreal -0.007647 0.001446947   -5.2846  0.0000
log(BMproxy)            0.000462 0.000604663    0.7643  0.4489

 Correlation:
                       (Intr) LfstSA
LifestyleSlow Arboreal -0.031
log(BMproxy)           -0.479 -0.210

Standardized residuals:
        Min          Q1         Med          Q3         Max
-2.44348598 -0.07305843  0.17679381  0.35295197  1.67399616

Residual standard error: 0.006251489
Degrees of freedom: 46 total; 43 residual
```

Detailed resulting coefficients for PGLS: log(CChumerus) ~ Lifestyle + log(BMproxy). Bold added by authors

```
> coef(summary(gls_CChumerusBM))
                                Value    Std.Error      t-value      p-value
(Intercept)             4.6013848196 0.0040603855 1133.2384254 7.347365e-98
LifestyleSlow Arboreal -0.0076465684 0.0014469465   -5.2846241 3.966028e-06
log(BMproxy)            0.0004621189 0.0006046626    0.7642591 4.488866e-01
```

Summary results for Phylogenetic Generalized Least Square Regression of femoral cortical compactness (CC) against lifestyle (categorical binary variable, with states 'Slow Arboreal'/'Non Slow Arboreal). The cortical area (CA), body mass proxy, is added as a covariate to test for body mass influence on CC. R 'gls' function was applied with method "ML" ('nlme' R package; Pinheiro et al. 2020). Bold added by authors

```
> summary(gls_CCfemurBM)
Generalized least squares fit by maximum likelihood
  Model: log(CCfemur) ~ Lifestyle + log(BMproxy)
  Data: femData_forPCM
        AIC       BIC   logLik
  -320.0612 -311.3729 165.0306

Correlation Structure: corPagel
 Formula: ~1
 Parameter estimate(s):
   lambda
0.9115482

Coefficients:
                           Value   Std.Error  t-value p-value
(Intercept)             4.597075 0.005926167 775.7248  0.0000
LifestyleSlow Arboreal -0.007297 0.001828552  -3.9908  0.0003
log(BMproxy)            0.000614 0.000679803   0.9037  0.3717

 Correlation:
                       (Intr) LfstSA
LifestyleSlow Arboreal -0.101
log(BMproxy)           -0.412 -0.071

Standardized residuals:
       Min         Q1        Med         Q3        Max
-1.7375763  0.3195928  0.5413179  0.6549574  1.5660698

Residual standard error: 0.008894899
Degrees of freedom: 42 total; 39 residual
```

Detailed resulting coefficients for PGLS: log(CCfemur) ~ Lifestyle + log(BMproxy). Bold added by authors

```
> coef(summary(gls_CCfemurBM))
                              Value   Std.Error     t-value      p-value
(Intercept)             4.5970746096 0.005926167 775.7248310 2.693075e-83
LifestyleSlow Arboreal -0.0072973444 0.001828552  -3.9907770 2.815117e-04
log(BMproxy)            0.0006143083 0.000679803   0.9036564 3.717258e-01
```

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