**variation can be introduced through shape variation that is unique to one species and not attributable to patterns of co-variation, which is what this manuscript’s question was. It is rare for any variable to explain as much as 36% of shape variation in a dataset of overall homogenous shapes and very unusual for more than half of overall variation to be explained in any study of 3D GMM. For example, accounting for size, geography and climate still resulted high amounts of unexplained variation in northern quolls (76%), a species complex of *Antechinus* (79%), and the genus of Rock Wallabies (61%) – all samples with low overall shape variation.**

**It is equally conceivable that there is no consistent pattern at all – for example, if the cranium was not integrated or modular after removal of size – or that we are looking at such small variation that the remaining variation is just noise.**

**We have clarified this now on p. X, line Y: “”**

**Note also that the percentage of variation explained in a dataset does not necessarily relate to high absolute amounts of variation. In this group of rodents with famously homogenous shapes, it is conceivable that what little variation exists is indeed explained by allometry and little else. In addition, GMM datasets naturally have a large amount of unexplained variation (compared to linear measurements) because Procrustes superimposition relates the variation in the x,y and z coordinates to that variation in all other landmarks during the Procrustes superimposition (discussed in Viacava et al. 2023).**

Literature:

Barbero et al. 2023 discuss sigmodontines but the dataset is a little different (just a few linear measurements) and our patterns (larger, robust skulls in folivores) don’t really match well.

as well as several species that consume sedges or dicotyledons such as the stick-nest rat genus *Leporillus* (Kraehe et al., in prep.), *Rattus lutreolus* (Driessen, 1999), *Pseudomys desertor* (Read et al., 1999), *P. shortridgei* (Cooper et al., 2003), and to a lesser degree *Pseudomys oralis* (*Pyke & Read, 2002).*

Note that the probabilities from *Phytools* are given as Akaike Information Criterion (AIC), which are a special case of and similar to the GICs given by the mvMORPH package (Cavanaugh & Neath, 2019).

A caveat here is that all cases where integration is significantly different between the full and the residual dataset include comparisons with the cranial vault, which could be an effect of the vault having the largest number of landmarks; however, variation in the vault is a feature of the first two PCs in the residual dataset (see below), suggesting that these significances accurately reflect the residual variation. This is particularly the case for the increased strength of integration between the vault and the basicranium, which features in the heatmap visualisations of both residual PC1 and PC2 and is discussed further below.