



Morphological variability or inter-observer bias? A methodological toolkit to improve data quality of multi-researcher datasets for the analysis of morphological variation

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Tables

Table 1: Quality filtering pipeline for the reduction of inter-observer bias in multi-observer datasets.

Step	Aim	Description	Example
1	Define geographic and taxonomic units	Hierarchical levels in the dataset (e.g., species or population level) must be defined. Individuals should be grouped accordingly for the next steps.	The taxonomy of mouse lemurs is still a topic of ongoing debate (e.g., Poelstra et al., 2021; Tiley et al., 2022), and geographic variation in morphological traits for taxa with wide distributions are possible (e.g., Schüßler et al., 2020). We defined populations per taxon as our units of investigation.
2	Exclude certain individuals from the population	It must be clarified whether there is strong sexual size dimorphism or intra-annual variability of certain variables (e.g., body mass, girth, fat deposits) in any of the study taxa. Can adults/juveniles or pregnant/non-pregnant females be distinguished from each other? Is there strong seasonal variation in the composition of the population? In these cases, the dataset may be split into male/female sub-categories, some individuals may be excluded completely (e.g., juveniles), or certain variables set to NA (e.g., body mass of pregnant females).	Mouse lemurs are fast-growing seasonal breeders with high population turnover rates and a relatively high mortality of young individuals (Radespiel et al., 2001; Lutermann et al., 2006; Kraus et al., 2008; Blanco et al., 2015; Evasoa et al., 2018). To remove the confounding effect of age, juveniles were excluded from the dataset. Furthermore, we excluded measurements of individuals from the nonbreeding season (as indicated by the lack of males with enlarged testes per species; Evasoa et al., 2018) to control for the high proportion of not yet fully-grown individuals in the population before the reproductive season starts. For pregnant females (identified during capture or as numerical outliers, i.e., if heavier than heaviest male), body mass was set to NA.
3	Exclude outliers	Outliers are data points that are inconsistent with the majority of data and their statistical distribution (Pearson, 2002; Liu et al., 2004). These may stem from methodological errors or may be actual biological variation. We argue that for the analysis of interspecific differences both kinds of outliers should be excluded. Biological outliers are of low value, because they do not contribute much to the statistical distribution of a certain measurement. Instead, their inclusion may impair	We set this breakpoint to the median $\pm 3 \times \text{MAD}$ (Davies & Gather, 1993; Pearson, 2005), and identified outliers were replaced with NA.

		the power of subsequent statistical procedures. Therefore, we propose to use the generic but powerful Hampel identifier (Davies & Gather, 1993; Pearson, 2002) to exclude outliers of any kind. It uses the median and the median absolute deviation (MAD; Hampel, 1985) to define breakpoints below/above which measurements are identified as outliers (Pearson, 2002).	
4	Exclude researchers that contribute too high variation	It should be assessed whether some researchers were less consistent than others in measuring. Such an observer effect introduces additional noise that may dilute subtle differences among the units of investigation, particularly in small-sized and cryptic species. We propose the use of the coefficient of variation (CV) as a measure of variability in a sample in relation to its mean (e.g., Pélabon et al., 2020). It is often applied to quantify the plasticity in a phenotypic trait and to compare it across different traits (Houle, 1992; Pélabon et al., 2020). To distinguish between actual phenotypic plasticity of species and high measurement variation of certain researchers, we assumed that (1) CV values per species-researcher combination follow a normal distribution, and (2) researchers with high CV values generate a long right tail in the distribution. In practice, the CVs for all researchers per unit of investigation were calculated separately for each variable.	We determined the upper limit of the Hampel identifier (see above) and used it as a truncation value, above which variables measured by the respective researchers were replaced with NA (Figure 2B).
5	Exclude systematic deviations among researchers	If there are several researchers who contributed to measurements of the same unit of investigation (i.e., species or population), variable-wise comparisons may help to identify systematic measurement errors. For this, we recommend visualizing the distributions of specific variables across all units of investigation via boxplots, with researchers represented as color-coded boxes.	For example, certain researchers measured mouse lemur hind foot length consistently different from others across different populations, which may indicate a different application of calipers (Figure 2A). We applied the following rules to exclude such inter-observer biases from our dataset: (1) If < 3 researchers contributed measurements, it is not possible to assess which measurements were more accurate; (2) if ≥ 3 researchers contributed measurements, boxes that do not overlap with each other and represent the smaller number of researchers (e.g., one deviating from the others) indicate a researcher whose values for this variable should be set to NA. Examples are illustrated in Figure 2A.
6	Define the dataset for	By replacing filtered values with NA (see previous steps), we aimed at retaining as much information as possible. Depending on the analysis of interest,	

downstream analyses	it is possible to use the whole dataset (e.g., for univariate analyses) or one that omits all individuals containing NA values (i.e., for multivariate analyses). In the latter case, it should be assessed whether remaining variables are still sufficient for testing the question under study.
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Morphological variability or inter-observer bias?

A methodological toolkit to improve data quality of multi-researcher datasets for the analysis of morphological variation

Running title: Quality filtering of morphological data

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Research highlights

- Morphological variation is commonly used to infer environmental adaptations and phylogenetic relationships in animal taxa, but multi-researcher datasets can hamper analyses due to inter-observer biases.
- Our filtering pipeline markedly improved data quality for downstream analyses and highlighted key steps in data quality assessment for generating reliable results.
- Across species, mouse lemurs are sexually dimorphic (with larger females), they follow neither Rensch's rule for sexual size dimorphism nor Bergmann's rule (larger mouse lemur taxa live in warmer and wetter climates), but are concordant with Allen's rule with regard to having shorter tails in colder environments.

Abstract

Objectives

The investigation of morphological variation in animals is widely used in taxonomy, ecology, and evolution. Using large datasets for meta-analyses has dramatically increased, raising concerns about dataset compatibilities and biases introduced by contributions of multiple researchers.

Materials and Methods

We compiled morphological data on 13 variables for 3,073 individual mouse lemurs (*Cheirogaleidae*, *Microcebus* spp.) from 25 taxa and 153 different sampling locations, measured by 48 different researchers. We introduced and applied a filtering pipeline and quantified improvements in data quality (Shapiro-Francia statistic, skewness, and excess kurtosis). The filtered dataset was then used to test for genus-wide presence of sexual dimorphism and the applicability of Rensch’s, Allen’s and Bergmann’s rules.

Results

Our filtering pipeline helped to reduce inter-observer bias (i.e., increased normality of data distributions). Inter-observer reliability of measurements was notably variable, highlighting the need to reduce data collection biases. Although subtle, we found a consistent pattern of sexual dimorphism across the genus *Microcebus*, with females being the larger sex in 6 of 13 variables. Sexual size dimorphism was isometric, providing no support for Rensch’s rule. Variations in tail length but not in ear size were consistent with the predictions of Allen’s rule. Body mass and length followed a pattern contrary to predictions of Bergmann’s rule.

Discussion

We highlighted the usefulness of large multi-researcher datasets for testing ecological hypotheses, after correcting for inter-observer biases. Using genus-wide tests, we outlined generalizable patterns of morphological variability across all mouse lemurs and generated a set of new hypotheses for further investigation.

Keywords: Allen’s rule, Bergmann’s rule, *Microcebus*, cryptic species, sexual size dimorphism

Introduction

Morphological variation is central to the quantification of within- and between-species diversity and thus at the heart of evolutionary biology and ecology (Darwin, 1859; Mayr, 1963; Wright, 1984). In times of increasing computational power that allows the analyses of large genomic datasets, combining morphological data from multiple sources will become an increasingly important task, for example, when aiming to combine multiple lines of evidence to derive conclusions in taxonomy (i.e., integrative taxonomy; de Queiroz, 2007; Padial et al., 2010; Leaché et al., 2019). In this and other contexts, distinguishing between biologically meaningful signals and methodological biases arising from the compilation of multi-observer datasets is of utmost importance (Burghardt et al., 2012; Howard, 2002; Morrison 2015).

In general, processing of large datasets should involve the following steps: 1) contextualization of the dataset, 2) assessment, and 3) improvement of data quality (Van den Berghe 2017). In morphological studies, in particular, data quality can be severely constrained and impaired by intra- and inter-observer biases. These biases can principally arise from a differential use of measurement definitions, variable care or stringency while handling an animal, and the use of different tools by different researchers (Howard, 2002; Roitberg et al., 2011). A similar problem may arise if one researcher collects data over longer time periods and slowly and unconsciously shifts the measurement technique by developing routines (Roitberg et al., 2011). Particularly for small-bodied species, small measurement errors can introduce large relative biases. A problematic case in this respect is the study of cryptic species that display only subtle phenotypic variation by definition (Bickford et al., 2007), which may become easily masked when such biases are strong (Howard, 2002). Therefore, the detection and reduction of intra- and inter-observer biases should be a priority for studies aiming to investigate species- or population-specific morphological variability.

Different approaches can be taken to ensure dataset reliability and to counteract confounding effects of inter- or intra-observer biases. Although transparency about measurement routines for morphological traits (e.g., information on how many researchers were involved, how training was conducted, how precise measurements were conducted) would be useful, it is remarkably rare in the literature. Yet, detailing which measurement definitions were used is rather common, either by citing other sources or by directly defining morphological variables (Chornelia et al., 2022; Michaloudi et al., 2018; Radespiel et al., 2008, 2012). Using these definitions and measuring individuals by only one researcher is occasionally stated to dispel doubts about the reliability of a dataset (e.g., Macdonald et al., 2018; Benites et al., 2020), even though intra-observer bias can still exist. If more than one researcher is taking measurements, the researcher's experience is sometimes reported (e.g., Pilloud et al., 2019), while joint researcher trainings are considered particularly useful by others (e.g., Morrison, 2015). Further approaches include taking measurements of each individual by different researchers and calculating an agreement or mean value for later analyses (e.g., Shirley et al., 2014). Such measures are typically applied in studies that require a high sampling effort and are designed prior to any data collection. In reality, however, huge datasets are often compiled after data collection has taken place. In these cases, *a posteriori* methods for reducing observer biases are needed but largely absent in the literature (Burghardt et al., 2012). A standardized framework of how to assess the quality of compiled morphological data and how to improve data quality has not been defined so far.

After data compatibility and quality of a dataset have been secured, patterns of morphological variation among taxa can be investigated. Variation itself can then be attributed to a variety of potentially

interacting factors (Hallgrímsson & Hall, 2005). These factors could be phylogenetic signals with relevance to species delimitation studies (e.g., Cadena et al., 2018; Chornelia et al., 2022; Schüßler et al., 2020), large scale ecological adaptation to different environments or small scale niche differentiation (e.g., Agostini et al., 2017; Meachen et al., 2015; Santini et al., 2018). Variation can further be attributed to mechanisms of sexual selection acting differently on males and females (e.g., Jennions et al., 2001) or natural selection for sex-dependent environmental niches (Kamilar & Pokempner, 2008; Williamson et al., 2021). An established principle in the context of sexual size dimorphism is Rensch’s rule (Rensch, 1950), which predicts that at the genus level “the ratio of female to male size is larger the smaller the body size of a species” (Meiri & Liang, 2021). Regardless of sex, ecogeographic relationships such as those formulated in Allen’s and Bergmann’s rules (Mayr, 1942), could also be the underlying forces of morphological variation. According to both, thermoregulatory constraints in endothermic animals are a dominant driver in size variation, either in body size or in the proportions of appendages. In colder climates, body appendages like ears and a tail tend to be smaller (Allan’s rule) and body size larger (Bergmann’s rule; Mayr, 1942) than in warmer climates. Deviation from these “rules” can in turn provide insights into the evolutionary history of a lineage or relevant physiological processes (Maestri et al., 2016; Rodríguez et al., 2008; Webb & Freckleton, 2007).

This study aims to (1) develop and apply an objective multi-stage quality filtering pipeline to eliminate problematic data points and reduce the confounding effects of sampling, inter-observer bias and intra-observer variation, (2) evaluate the improvement of data quality across different filtering steps, and (3) use the filtered dataset to exemplarily test hypotheses concerning morphological variation in a genus of small, cryptic primates in Madagascar (i.e., *Microcebus*). Specifically, we test for (3a) the presence of sexual size dimorphism and predictions of (3b) Rensch’s rule, (3c) Allen’s rule and (3d) Bergmann’s rule.

Methods

Study system

Mouse lemurs (genus *Microcebus*) are among the most speciose genera of lemurs, containing >20 cryptic species (Zimmermann & Radespiel, 2014; Hotaling et al., 2016; Sgarlata et al., 2019; Schüßler et al., 2020). These small-bodied and omnivorous primates can be found in all major ecosystems across Madagascar (Mittermeier et al., 2010). Although subtle, morphological variation has often been used to support taxonomic decisions in mouse lemurs (e.g., Rasoloarison et al., 2000; Radespiel et al., 2012; Schüßler et al., 2020), genus-wide tests to assess morphological variability among mouse lemurs have not been conducted so far. Female-biased sexual dimorphism has been reported for *Microcebus murinus* body mass and head length (Jenkins & Albrecht, 1991; Kappeler, 1991; Schmid & Kappeler, 1998). Body mass variation, e.g., with heavier females, was also found in several other recent and extinct lemur species (Godfrey et al., 1993; Kappeler et al., 2022), and sex differences in canine length were found in *M. griseorufus* (Rasoazanabary, 2011). Mouse lemurs have been studied by various research groups over the years. Due to small distributions (i.e., micro-endemism) scattered across all forest habitats of the island, the high levels of endangerment of some species, the remoteness of their remaining forest habitats, and the difficulties of capturing larger numbers of mouse lemurs in various habitat types, it is not possible for one or a few researchers to generate a large morphological dataset encompassing all taxa. Consequently, the assembly of multiple datasets generated by multiple research groups, as it was done here, is the only way to study morphological variation in this genus. However, we believe that this problem is a general one and applies to a large variety of cryptic species worldwide.

Dataset characteristics

We assembled a morphological dataset comprised of 3,073 individual mouse lemurs belonging to 25 different taxa (Hotaling et al., 2016; Schüßler et al., 2020; Sgarlata et al., 2019) that were captured and measured by 48 researchers in 153 study sites across Madagascar (Figure 1). Representation of the different taxa was highly variable with a maximum of 748 individuals for *M. ravelobensis* and only two or four individuals for *M. marohita* and *M. manitatra*, respectively (Table S1). We collected measurements for the 13 most widely used morphological variables (ear length, ear width, head length, head width, inter- and intra-orbital distance, snout length, lower leg length, hind foot length, third toe length, body length, tail length, body mass; Hafen et al., 1998; Zimmermann et al., 1998) as defined in Table S2. However, these were not available for all individuals. We carefully checked which definitions were applied by different researchers and excluded all measures that did not conform to the most common definitions (Table S2). Most researchers provided additional data for each individual: sex was available for 99.5%, stage of maturity for 100.0%, GPS location for 99.6%, capture date for 79.4%, and reproductive state for 40.2% of all individuals.

<<< Figure 1 here >>>

Generalized quality filtering pipeline

We designed a six-step data quality filtering pipeline to reduce inter-observer bias and illustrate its use with examples stemming from our dataset (Table 1). Steps 1, 2 and 6 were used to contextualize the dataset (Van den Berghe et al., 2017). For this, geographic and taxonomic units were defined first, characteristics of the study taxon were acknowledged second, and the data were defined for downstream analyses. In steps 3-5, we aimed at improving overall data quality (i.e., to reduce inter-observer biases; see Van den Berghe et al., 2017) by excluding outliers, researchers who contributed unusually high variation in their measurements, and those who deviated systematically from the majority of measurements per taxon (Table 1).

<<< Table 1 here >>>

<<< Figure 2 here >>>

Assessment of data quality

Morphological variation among individuals of the same species or taxon should theoretically follow a normal distribution (Templeton, 2006; Cadena et al., 2018) if the sample is drawn at random from a randomly mating population and if the inheritance of a polygenic phenotypic trait is close to Hardy-Weinberg equilibrium (Templeton, 2006). Furthermore, cryptic species are per definition characterized by a similar and non-diverging morphology (Bickford et al., 2007), consistent with the idea of a unimodal normal distribution. This basic assumption for the distribution of measurements of a specific trait for a certain taxon should hold irrespective of the researcher. Accordingly, biases originating from multiple researchers should produce a deviation from a normal distribution for the trait under study. Any assessment of data quality should be based on well-founded and comprehensible metrics (Heinrich et al., 2018).

To test the effectiveness of the data quality filtering pipeline, we first quantified the deviation from a normal distribution by subtracting the Shapiro-Francia test statistic W' from 1 (i.e., deviation from normality = $1 - W'$; “nortest” package in R; Gross & Ligges, 2015) for each filtering step and variable separately. This modification of the widely used Shapiro-Wilk test for assessment of data normality represents the squared correlation between the ordered data values and the expected normal order statistics (i.e., the theoretical quantiles in a qqplot; Shapiro & Francia, 1972, Royston, 1991). In contrast to the typical Shapiro-Wilk test statistic W (Royston 1991), W' has been shown to powerfully capture the deviation from a normal distribution (Mbah & Paothong, 2014), while making the test statistic directly interpretable without relying on a P-value. Values of $1 - W'$ range from 0 (perfectly normally distributed data) to 1 (no normal distribution).

Second, we calculated the skewness, which measures asymmetry or horizontal deviation from a normal distribution, and excess kurtosis of the distribution, which measures “tailedness” or vertical deviation from normality (Hopkins & Weeks, 1990) for each filtering step and variable separately. We used absolute values for both measures to establish comparability across metrics, with 0 indicating perfect fit to a normal distribution. For both measures, deviations of 0 - 2 units are considered acceptable for a normal distribution (Trochim & Donnelly, 2006; Gravetter & Wallnau, 2014).

Finally, we assessed the inter-observer reproducibility of measures for each variable after the last quality filtering step: we used the coefficients of variation (CV) calculated for each population-researcher combination and compared them across the 13 different morphological variables. CV-values < 0.1 were defined as very good quality and CV = 0.1-0.2 as good quality (Aronhime et al. 2013).

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248 Testing hypotheses of morphological variation

249 Using the quality-filtered dataset, we tested for (1) the presence of sexual size dimorphism, as well as
250 predictions of (2) Rensch's, (3) Allen's and (4) Bergmann's rule in the genus *Microcebus*:

251 (1) Genus-wide sexual size dimorphism was tested in all 13 morphometric variables using linear mixed
252 effects models, including each variable individually as the response variable, sex as a fixed effect and
253 taxonomic affiliation (i.e., population of a species) as a random effect. Modelling was done using the
254 "lme4" and "lmerTest" packages in R, while the "performance" package was used to check the
255 assumptions of the models (Bates et al., 2015; Kuznetsova et al., 2017; Lüdtke et al., 2021). Variables
256 were standardized prior to analysis to improve comparability.

257 (2) Support for Rensch's rule (i.e., female-biased sexual size dimorphism is larger the smaller the body
258 size) is usually inferred if the slope of an allometric line is significantly >1 (i.e., male size on the y-axis and
259 female size on the x-axis, using standardized major axis regression; Meiri & Liang, 2021; Webb &
260 Freckleton, 2007). A slope equal to 1 would instead indicate an isometric relationship in which sexual size
261 dimorphism does not change in magnitude when overall size of the taxon changes. This effect was tested
262 first by regressing, for each species, female and male mean body length and mean body mass separately.
263 Statistical deviation from regression slopes of 1 was then tested by a standardized major axis regression
264 method as implemented in the "smatr" R package (Warton et al., 2011). For comprehensive illustration
265 purposes, we further estimated a linear model for both variables (i.e., body length and body mass).

266 (3) Conformity with Allen's rule (i.e., body appendages are smaller in colder climates) was tested for ear
267 size (= ear width * ear length) and tail length by taking the mean of the respective variable for each
268 population and extracting six different bioclimatic variables (i.e., mean annual temperature, minimum
269 temperature of the coldest month and maximum temperature of the warmest month, mean annual
270 precipitation, precipitation of wettest and driest month; CHELSA 2.1, Karger et al., 2017). Means per
271 population for each bioclimatic variable were calculated to reduce spatial autocorrelation. We followed
272 the proposed methodology by Alhajeri et al. (2020) who conducted a global test for Allen's rule in
273 rodents. As temperature and precipitation are known to covary across latitudes, including both allows to
274 disentangle purely thermoregulatory aspects from other climatic factors. Mean annual temperature and
275 annual precipitation were not used due to high correlations with other variables ($r \geq 0.84$). Linear models
276 (LMs) were then fitted using tail length and ear size separately as response variables and the log-scaled
277 bioclimatic variables as explanatory variables. To control for body size effects on appendage length, we
278 included head and body length as further explanatory variables (Alhajeri et al., 2020). We also computed
279 a null model excluding the bioclimatic variables. All possible variable combinations were calculated using
280 the "MuMIn" package in R (Barton, 2022), which ranks the best models based on their AIC (Akaike
281 Information Criterion). Only models with $\Delta AIC < 2$ and the null model are reported here. Akaike weights
282 (Wagenmakers & Farrell, 2004) were further calculated using the "qpcR" R package (Spiess, 2018).

283 (4) Conformity with Bergmann's rule (i.e., body size is larger in colder climates) was tested by using body
284 mass and body length separately as response variables and the bioclimatic variables as explanatory
285 variables following the same modeling approach as described above for the test of Allen's rule (Alhajeri
286 et al., 2020; Alhajeri & Steppan, 2016).

Results

Assessment of data quality

After quality filtering, a total of 1,679 individuals (54.6%) remained in our dataset, while the number of individuals represented in the filtered dataset further differed among morphological variables (Figure 3A). The sharpest decline in sample size was observed from step 1 to step 2, in which juvenile individuals and those captured outside of the reproductive season were dropped from the dataset. The consecutive steps then led to minor declines in sample size for certain variables, taxa and/or researchers. The highest decline was found for ear and third toe length (reduction of 43.3% and 42.1%, respectively; Figure 3A). Changes in the Shapiro 1-W' statistic, skewness and kurtosis across the five filtering steps were different among variables and across filtering steps (Figure 3). However, after applying our filtering pipeline, the distributions of most variables showed substantially improved quality, i.e., higher conformity to a normal distribution (Figure 3).

<<< Figure 3 here >>>

After quality filtering, mean inter-observer reproducibility was $CV < 0.1$ for most variables indicating very good quality (Figure 4), and $CV < 0.2$ for the others (i.e., good quality): particularly reliable variables were head length and width, interorbital distance, lower leg length, hind foot length and tail length. Others like intraorbital distance, snout length and body mass were still associated with higher levels of variation across researchers (Figure 4).

<<< Figure 4 >>>

Morphological variation in mouse lemurs

Sexual dimorphism

Significant and consistent size differences between the two sexes were found for eight out of 13 variables, with females being the larger sex concerning head length and width, as well as snout length, hind foot length, body length and tail length. Males exhibited larger ears (i.e., ear length and width). Most pronounced was the difference in ear dimensions, head and body length (Figure 5; Table S3). Significant differences were visible as a congruent direction in male vs. female means in 58.8-84.2% of the studied taxa (Table S3).

<<< Figure 5 >>>

323 *Rensch's rule: Female-biased sexual size dimorphism increases with decreasing body size*

324 The test for Rensch's rule revealed that the regressions between female (x-axis) and male (y-axis) body
 325 length and mass in log-scale had slopes of $\beta = 0.969$ (95% CI: 0.817-1.149) and $\beta = 1.002$ (95% CI: 0.865-
 326 1.160), respectively (Figure 6). In both cases, the relationship was not significantly different from 1 (body
 327 length: test statistic $r = -0.090$, $df = 18$, $P = 0.705$; body mass: $r = 0.006$, $df = 24$, $P = 0.978$) and therefore
 328 our data does not support Rensch's rule. Female and male body length and body mass (investigated
 329 separately) were significantly and positively correlated with each other (body length: $r^2 = 0.880$, $P <$
 330 0.001 , $n = 20$; body mass: $r^2 = 0.878$, $P < 0.001$, $n = 26$, respectively), indicating that taxa with larger and
 331 heavier males also had larger and heavier females (Figure 6).

332

333 <<< Figure 6 >>>

334

335 *Allen's rule: The size of body appendices decreases in colder climates*

336 Conformity with Allen's rule was found for tail length but not for ear size. The best model for tail length
 337 explained 68.3% of the variation by including different bioclimatic variables (Figure 7, Table S4). Tail
 338 length increased with increasing minimum temperature of the coldest month and decreased with
 339 increasing precipitation of the wettest and driest month (Figure 7A-C). The best model for ear size
 340 explained 45.0% of the variation but did not include temperature-related variables. Instead, ear size
 341 decreased with increasing precipitation of the driest month (Figure 7E). In both cases, null models
 342 received much larger $\Delta AICc$ values and smaller Akaike weights than the preferred models (Table S4).
 343 Positive relationships were found for tail length with head length and for ear size with body length
 344 (Figure 7D, F; Table S4).

345

346 <<< Figure 7 >>>

347

348 *Bergmann's rule: Body size increases in colder climates*

349 Body length and mass did not support Bergmann's rule. Variation in body mass was best explained by a
 350 positive relationship with minimum temperature in the coldest month together with precipitation of the
 351 driest month (Figure 8A-B; Table S4). Variation in body length was best explained by a positive
 352 relationship with maximum temperature of the warmest month and precipitation in the driest month
 353 (Figure 8C-D), contrasting predictions under Bergmann's rule. These models explained 23.9% and 20.6%
 354 of the variation, respectively (Table S4). For body mass, the null model was far worse than the preferred
 355 models, but for body length, the preferred model was only slightly better than the null model.

356

357 <<< Figure 8 here >>>

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Discussion

A new methodological toolkit to assess data quality

The application of our data quality filtering pipeline resulted in a marked decrease in available individuals and measurements per individual for downstream analyses. However, the process resulted in a strong increase in data quality through improved metrics of data normality after filtering. Excluding non-adult individuals and those from the non-breeding season resulted in the largest loss of available data points (step 1), but notably improved the overall quality as indicated by changes in skewness, kurtosis and Shapiro-Francia W' test statistic. In comparison, filtering steps 2-5 led only to minor changes in the sample size per variable, with the exception of ear length and third toe length. These two variables appeared to be difficult to measure accurately across researchers. Both measures measured particularly fragile structures of mouse lemurs and may therefore be particularly error-prone. For all other variables, steps 2-5 led only to the exclusion of single researcher-variable combinations due to unusually high variation in the measurements or to systematic deviations from measurements made by other researchers. It must be noted that biases could have remained undetected in cases where only one or two researchers provided data for a certain taxon or where inter-observer bias followed a normal distribution.

Inter-observer reproducibility differed notably between the 13 different morphological variables, but was within an acceptable quality range for most of them. Body mass, snout length and intraorbital distance had the smallest reproducibility among all variables. Body mass can be measured with high accuracy but is also well known to vary across individuals due to different reasons other than seasonality (e.g., body condition, resource availability; Randrianambinina et al., 2003; Schmid & Kappeler, 1998). Whether this variable is included in subsequent morphological analyses in species like mouse lemurs should be well considered and justified as it introduces a high amount of variation if treated like other variables. In contrast, snout length and intraorbital distance seem to be particularly difficult to measure in mouse lemurs, especially if taken on animals that are not anesthetized. Snout length is difficult to measure accurately since the proximal end point of this measure, the inflection near the inner corner of the eyes, is sometimes not easy to locate. The most reliable measures, i.e., those with low values of inter-observer variation, were head length and width, interorbital distance, lower leg length, hind foot length, and tail length (Figure 4). As morphological variation between cryptic species can be subtle (e.g., Radespiel et al., 2012; Schüßler et al., 2020; Sgarlata et al., 2019), methodological biases can easily dilute biological variation, especially in multivariate analyses.

Guidelines for future morphological studies

We have presented a pipeline to reduce inter-observer biases after data collection has been completed. Besides illustrating the usefulness of the pipeline for the improvement of data quality, we make the following suggestions for future data collection and a streamlined quality assessment based on our findings:

- 1) Multi-observer studies should be designed in such a way that larger sample sizes (morphometric measurements for > 30 individuals; Yusoff & Wah 2012) are collected by several researchers ($n > 3$) for each taxon in the dataset, so that inter-observer biases can be reliably identified and reduced.

- 2) Several measures to improve inter-observer reproducibility should be implemented before data collection (e.g., defining standard protocols, co-training of researchers)
- 3) We suggest calculating the inter-observer reproducibility before any further analyses, and to use only those measures that are most reliably measured by the set of researchers involved.
- 4) Measurements should be used that don't rely on ambiguous start or endpoints for caliper placement. Start and endpoints of measures must be clearly defined and identifiable across taxa.
- 5) Sampling protocols and measures undertaken for quality filtering must be transparently reported. Ideally, data quality and inter-observer reproducibility for every variable is briefly outlined to warrant reliability of the results in downstream analyses.

Morphological variation in mouse lemurs

Sex-related differences

Sexual size dimorphism in primates is most likely driven by sexual selection, by natural selection of niche differentiation and by differential growth patterns (Cassini, 2020; Kappeler et al., 2019; Plavcan, 2001; Thomas et al., 2015). Strepsirrhine primates and particularly the lemurs of Madagascar have generally been considered as sexually monomorphic compared to most other primate families (Jenkins & Albrecht, 1991; Kappeler, 1991; Plavcan, 2001). Counterexamples were only rarely reported but included few mouse lemur species like *Microcebus murinus* (Kappeler 1991; Kappeler et al., 2022), warranting further investigation. We found a consistent pattern of sexual size dimorphism across the whole genus that was visible in the majority of the studied mouse lemur species, with females being significantly larger in six of the 13 morphological variables investigated. In contrast, males had significantly larger ears than females, and no sexual dimorphism was detected in the remaining five variables.

Female dominance is a trait found in a variety of species from all five extant lemur families (Evasoa et al., 2019; Kappeler et al., 2022). However, variation among species exists, suggesting some level of species divergence in this behavioral trait (Evasoa et al., 2019). Although a relationship between body mass dimorphism and female dominance was not supported in a recent review study on 37 lemur species (including nine mouse lemur species; Kappeler et al., 2022), subtle size differences between sexes may have gone undetected due to the non-exclusive confounding effects of small sample size, large error-to-measurement ratio in small animals, inter-observer bias and seasonal variations in body condition (making body mass a rather unreliable variable to assess sexual size dimorphism).

Sex differences in skull size may also be explained by sex differences in ecological niches. A larger head size has been empirically associated with increased bite force in *M. murinus* (Chazeau et al., 2012; Thomas et al. 2015). Together with differences in canine length, as found in *M. griseorufus* (Rasoazanabary 2011), this could indicate subtle niche differentiation between male and female mouse lemurs concerning feeding habits or preferred food items. Sex-dependent feeding and foraging strategies have so far not been reported for mouse lemurs. However, female *M. murinus* in Kirindy (W Madagascar) were observed in higher densities around gum trees than males, which was interpreted as a consequence of female dominance (Génin 2003). The solitary foraging mode of the omnivorous mouse lemurs (e.g., Dammhahn & Kappeler 2008; Radespiel et al. 2006) certainly conveys considerable

flexibility with respect to individualized or sex-dependent feeding habits. Detailed studies comparing the feeding ecology of both sexes across mouse lemur species are needed to further test these hypotheses. Interestingly, males had significantly larger ears than females, which may also have biological relevance, since mouse lemurs rely extensively on acoustic communication in addition to olfaction (Glatston et al. 1993; Zimmermann 2018). Sensory experiments with mouse lemurs in in Mandena, SE Madagascar, and in captivity showed that auditory cues can initiate and guide insect hunting besides its relevance for intraspecific communication such as during mate localization and advertisement (Buesching et al., 1998; Goerlitz & Siemers, 2007; Piep et al., 2008; Siemers et al., 2007; Zimmermann & Lerch, 1993). Whether the detected differences in ear size are responsible for different acoustic perceptions of males and females needs to be investigated in future studies.

The slight female-biased sexual size dimorphism was uniform across the whole genus as indicated by its isometric relationship (slope ≈ 1). Rensch's rule, according to which the ratio of female to male size is expected to be larger the smaller the body size of the species (slope > 1), was not supported for mouse lemurs. This finding is in line with the absence of Rensch's rule across a larger set of strepsirrhine primates (Kappeler, 1990) and with the results of a large-scale study in birds (Webb & Freckleton 2007). This deviation from Rensch's rule in mouse lemurs rather suggests an equal selection pressure on male and female body size within the genus, as already proposed by Schmid & Kappeler (1998).

Climate-related morphological patterns

Climatic constraints are dominant factors shaping the morphology of organisms (Mayr 1942). Bergmann's and Allen's ecogeographic rules state that body size and appendages are shaped by thermoregulatory principles. Small-bodied endothermic animals like rodents (Alhajeri et al. 2020) and birds (Symonds & Tattersall 2010) largely conform to Allen's rule, while showing a more complex association with but general conformity to Bergmann's rule (Alhajeri & Steppan 2016; Meiri & Dayan 2003; Salewski & Watt 2016).

In mouse lemurs, climatic niche separation has been shown for a few taxa (Kamilar et al., 2016). We found statistical support for an influence of climate on morphology: tail length in mouse lemurs followed the predictions of Allen's rule. Animals living in warmer and drier environments (i.e., higher temperatures during the coldest months, lower precipitation in the driest and wettest months) had longer tails than those living in habitats of opposite characteristics. Prevention of heat loss via shorter tails is a likely explanation for this observation (Serrat, 2014; Sgarlata et al., 2019). As more than 68% of the variation in tail length was explained by climate, this adaptation appears to have a close evolutionary link to the surrounding environment.

Ear size could also be explained by climatic variables but to a much lesser degree than tail length. Temperature-related variables, however, were not included in the best performing models. Instead, we found that large-eared mouse lemurs were more likely to occur in areas of low amounts of rainfall during the dry season. This relationship most likely echoes the divide between the western dry deciduous and the eastern rain forests of Madagascar. These two macro-habitats differ in many aspects: dry forests are subject to stronger seasonal changes in climatic conditions as well as resource availability and differ in vegetation structure and composition from rain forests (Blanco et al., 2015; Génin, 2008). Acoustic communication may be particularly constrained in rain forest habitats where high precipitation and high vegetation density may lead to sound attenuation and diffusion (Luther & Gentry, 2013; Rasoloharijaona

et al., 2010; Taylor et al., 2022). Whether mouse lemur ear sizes are causally linked to the relevance of intraspecific acoustic communication in different habitat types or show other adaptations, e.g., to different foraging habits, cannot be tested with our dataset but warrants further investigation. The difference between small- and large-eared mouse lemurs may further indicate an ancestral phylogenetic constraint associated with an ancient split between dry and rain forest taxa (Yoder & Heckman, 2006; Vences et al., 2009) and may not necessarily be driven by or highly interlinked with climatic adaptations.

In our test of Bergmann's rule, we found a relationship between body mass and length and climatic variables, with larger/heavier individuals being more likely to live in warmer and wetter environments. This finding contrasts the prediction of Bergmann's rule that individuals from colder environments should be larger (Salewski & Watt, 2016). Although the association between the variables was relatively low ($R^2 \leq 0.213$), its direction agrees with results from other studies on small mammals in tropical environments (Maestri et al., 2016; Rodríguez et al., 2008; Sgarlata et al., 2022). In all cases, body size appeared to increase in warmer environments (e.g., at lower altitudes) probably due to an increase in resource availability, suggesting that Bergmann's rule may only apply to animals in colder regions but not in the tropics (Rodríguez et al. 2008). This also conforms to general patterns of ecogeographic size variation across lemurs of all sizes, both living and recently extinct (Albrecht et al., 1990).

Several mouse lemur species (e.g., *M. berthae* and *M. murinus* at Kirindy, Schmid, 2000; *M. griseorufus*, Génin, 2008; *M. lehilahytsara*, Randrianambinina et al., 2003, Andriambeloson et al., 2020; *M. ravelobensis*, Thorén et al., 2011; *M. rufus*, Atsalis, 1999, Ramananjato et al., 2022) can cope with thermoregulatory challenges under low temperatures using torpor or even hibernation (Blanco et al. 2018; Salewski & Watt 2016). However, more than 78% of the variation in body mass and body length could not be explained by climatic factors. It is known that resource availability, seasonality and most likely also phylogeny are additional drivers of mouse lemur body mass variation (Atsalis 1999; Génin 2008; Randrianambinina et al. 2003). Phylogenetic constraints on body size of mouse lemurs are indicated by the observation that several smaller taxa (*M. berthae*, *M. myoxinus*, *M. lehilahytsara*, *M. rufus*) form a distinctive clade of small-bodied mouse lemur species (Louis & Lei 2016) that can occur not only in sympatry with other larger species but also across a variety of environments in eastern and western Madagascar. These include the highly seasonal western dry deciduous forests with their clear separation into a 4–6 month hot rainy season and a 6–8-month cooler dry season lacking precipitations almost entirely, the central highlands that undergo substantial seasonal temperature fluctuations, and the eastern lowland rainforests that exhibit the least climatic variations across the year (Andriambeloson et al. 2020; Blanco et al. 2015, Evasoa et al. 2018). A comprehensive evaluation of the relative impact of environmental variables and phylogenetic constraints on the morphology of mouse lemurs is currently hampered by a lack of a fully resolved phylogeny of all currently described mouse lemur lineages.

Conclusions

Our new filtering pipeline was developed in order to enable analyzing a large multi-researcher dataset. We detailed on the six different filtering steps and illustrated their usefulness for reducing potential inter-observer biases. With our generalized suggestions for future morphological studies, we aim to improve data collection procedures and overall quality in these kind of studies. Using this pipeline, we filtered the largest currently available dataset of morphometric measurements for the species-rich genus of mouse lemurs and generated a consolidated dataset with which four biologically meaningful hypotheses were tested.

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525 Morphometric variation was partly explained by sexual size dimorphism and by various bioclimatic
526 variables which were partly in agreement with the predictions of Allen’s rule (tail length) but not with
527 those of Rensch’s or Bergmann’s rule. The remaining unexplained variation could be due to yearly and
528 monthly variations in resource availability, possible differences in resource use across lineages and
529 between the sexes, variation in intraspecific acoustic communication patterns and sociality, as well as
530 phylogenetic constraints. Our genus-wide analysis could therefore outline general patterns of
531 morphological variation in mouse lemurs. We further generated hypotheses for later testing in order to
532 fully understand the drivers of morphological variation within a genus of nocturnal, cryptic and small-
533 bodied primates.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

The quality filtering pipeline, the assessment of data quality (R scripts), and all supplementary information are available at: <https://doi.org/10.25625/6EINJN>

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Figure captions

Figure 1: Distribution of *Microcebus* spp. populations sampled across Madagascar. Overlapping symbols were rarified to improve display. Minimum temperature of the coldest month according to Karger et al. (2017) is shown in shadings from white to black.

Figure 2: Illustration of steps 4 and 5 of the generalized data filtering pipeline. A: Boxplots per lineage and researcher for one variable (hind foot length), boxes encircled in red indicate examples outlined in Table 1. B and C: Histograms for ear length and interorbital distance, respectively, with truncation threshold (median + 3 * median absolute deviation) introduced as vertical dashed red line. Truncation (i.e., the exclusion of measurements for this variable for the respective researcher) takes place in B but not in C.

Figure 3: Quality assessment following the five data filtering steps indicated by different color code in B-D. A: Completeness of the dataset refers to the number of available values per variable compared to the number of individuals in the raw data ($n = 3,073$). B: 1- W' measure of normality, C: absolute skewness, D: absolute kurtosis. Values closer to zero in the ridge plots B-D indicate increased conformity to a normal distribution. For skewness (C) and kurtosis (D), the range of acceptable values is indicated with the vertical line at 2 units from 0.

Figure 4: Inter-observer reproducibility quantified as coefficient of variation (CV) across the 13 different morphometric parameters. Only data after quality filtering was included. The horizontal line indicates the upper limit of the CV values interpreted as very good reproducibility (CV=0.0-0.1, Aronhime et al., 2013).

Figure 5: Sexual size dimorphism across all *Microcebus* taxa displayed via model estimates with 95% confidence intervals. The differences in all variables except inter- and intraorbital distances, lower leg length, third toe length, and body mass were statistically significant ($P \leq 0.029$; Table S3).

Figure 6: Relationship between female and male body length (A) and body mass (B). Rensch's rule is not supported in both cases ($P \geq 0.705$). Red line: linear model for observed data (including 95% confidence interval), dashed line: slope = 1. Note: model estimates slightly differ between the standardized major axis and the linear model; the former was used for hypothesis testing and the latter for visualization.

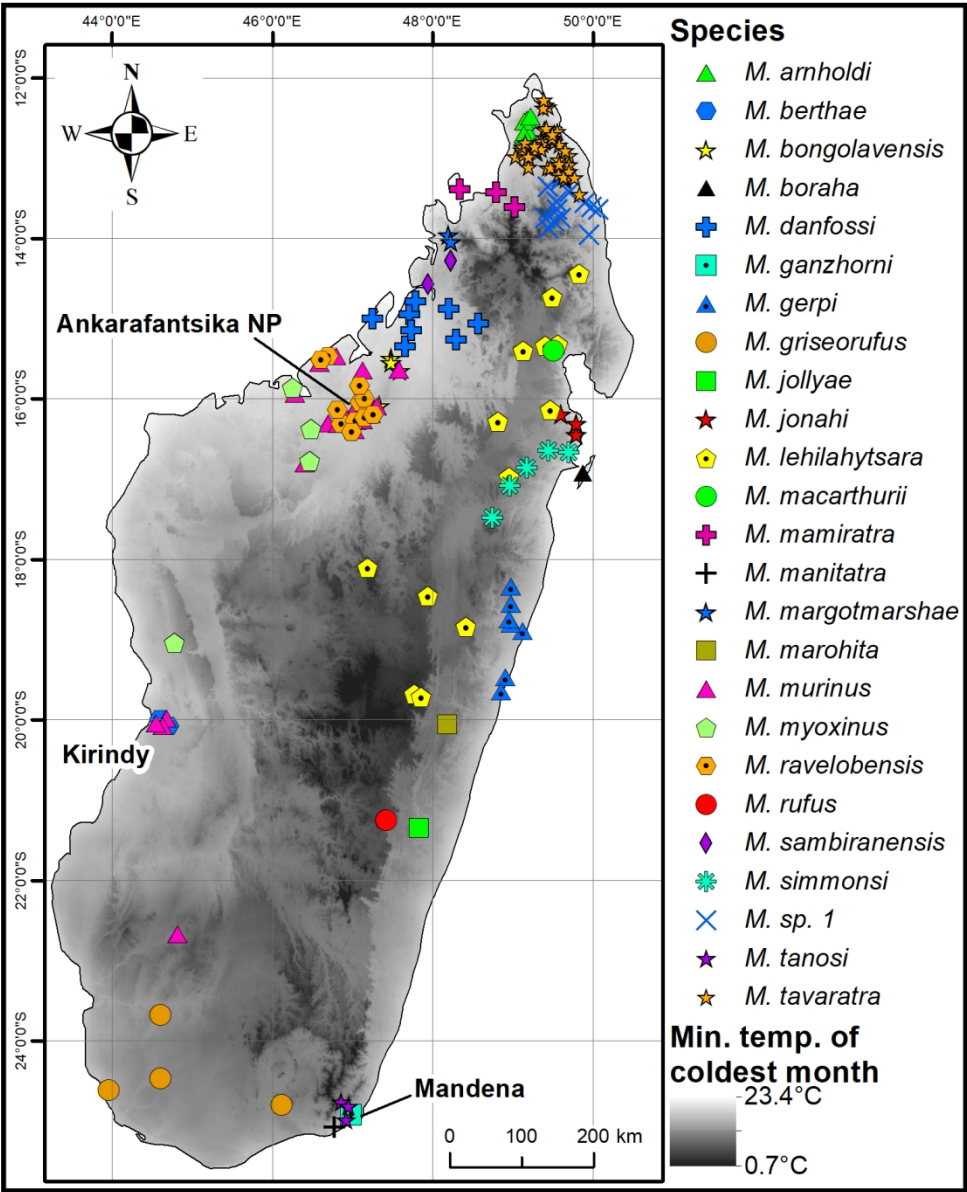
Figure 7: Partial regression plots for the linear model best explaining the variation in tail length (A-D, $R^2 = 0.683$) and ear size (E-F, $R^2 = 0.450$) across mouse lemur taxa. Note: the y-axis represents the marginal impact of the response variable on the explanatory variable.

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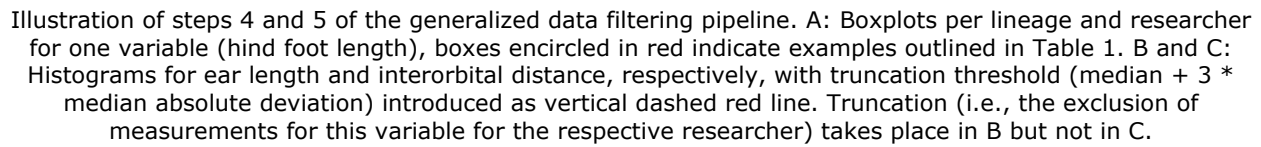
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Figure 8: Partial regression plots for the linear models best explaining the variation in body mass (A-B, $R^2 = 0.239$) and body length (C-D, $R^2 = 0.206$) across mouse lemur taxa. Note: the y-axis represents the marginal impact of the response variable on the explanatory variable.

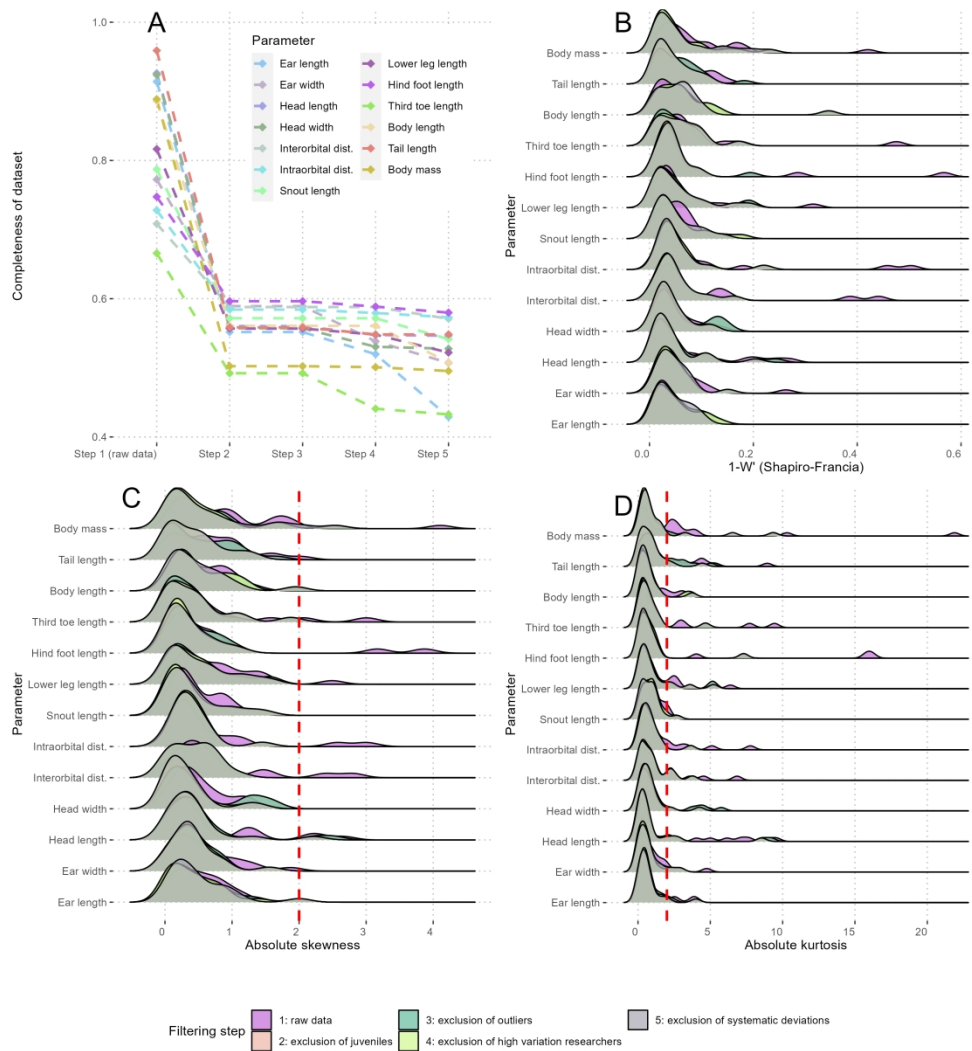


Distribution of *Microcebus* spp. populations sampled across Madagascar. Overlapping symbols were rarified to improve display. Minimum temperature of the coldest month according to Karger et al. (2017) is shown in shadings from white to black.

134x165mm (300 x 300 DPI)

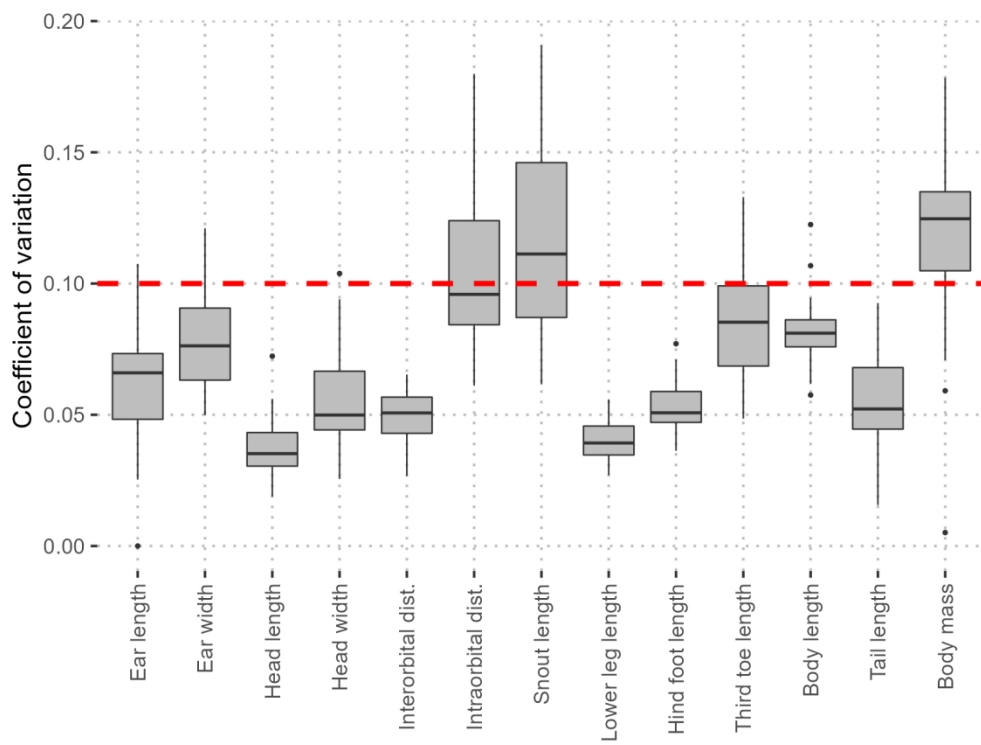


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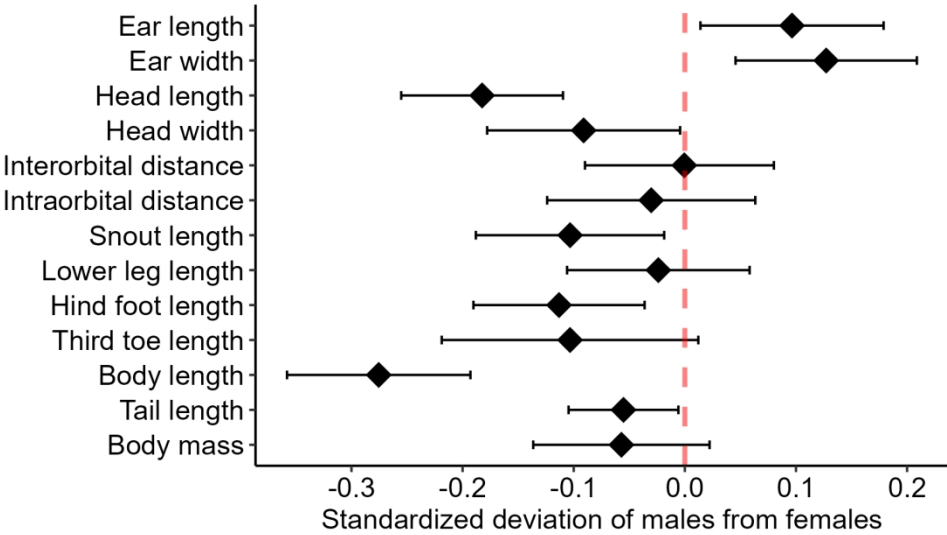
Quality assessment following the five data filtering steps indicated by different color code in B-D. A: Completeness of the dataset refers to the number of available values per variable compared to the number of individuals in the raw data ($n = 3,073$). B: 1-W' measure of normality, C: absolute skewness, D: absolute kurtosis. Values closer to zero in the ridge plots B-D indicate increased conformity to a normal distribution. For skewness (C) and kurtosis (D), the range of acceptable values is indicated with the vertical line at 2 units from 0.

287x319mm (300 x 300 DPI)



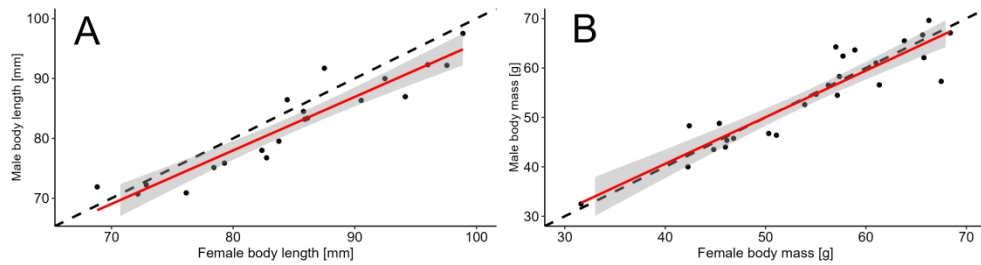
Inter-observer reproducibility quantified as coefficient of variation (CV) across the 13 different morphometric parameters. Only data after quality filtering was included. The horizontal line indicates the upper limit of the CV values interpreted as very good reproducibility (CV=0.0-0.1, Aronhime et al., 2013).

143x111mm (300 x 300 DPI)



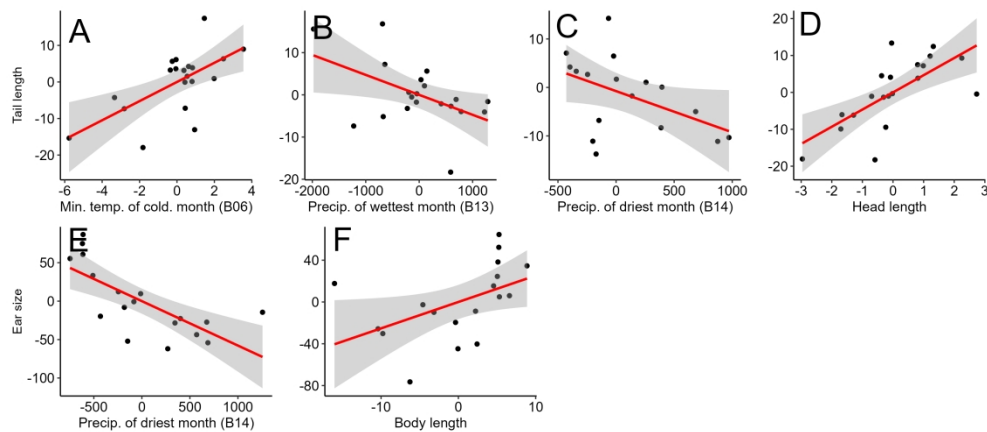
Sexual size dimorphism across all *Microcebus* taxa displayed via model estimates with 95% confidence intervals. The differences in all variables except inter- and intraorbital distances, lower leg length, third toe length, and body mass were statistically significant ($P \leq 0.029$; Table S3).

152x84mm (300 x 300 DPI)



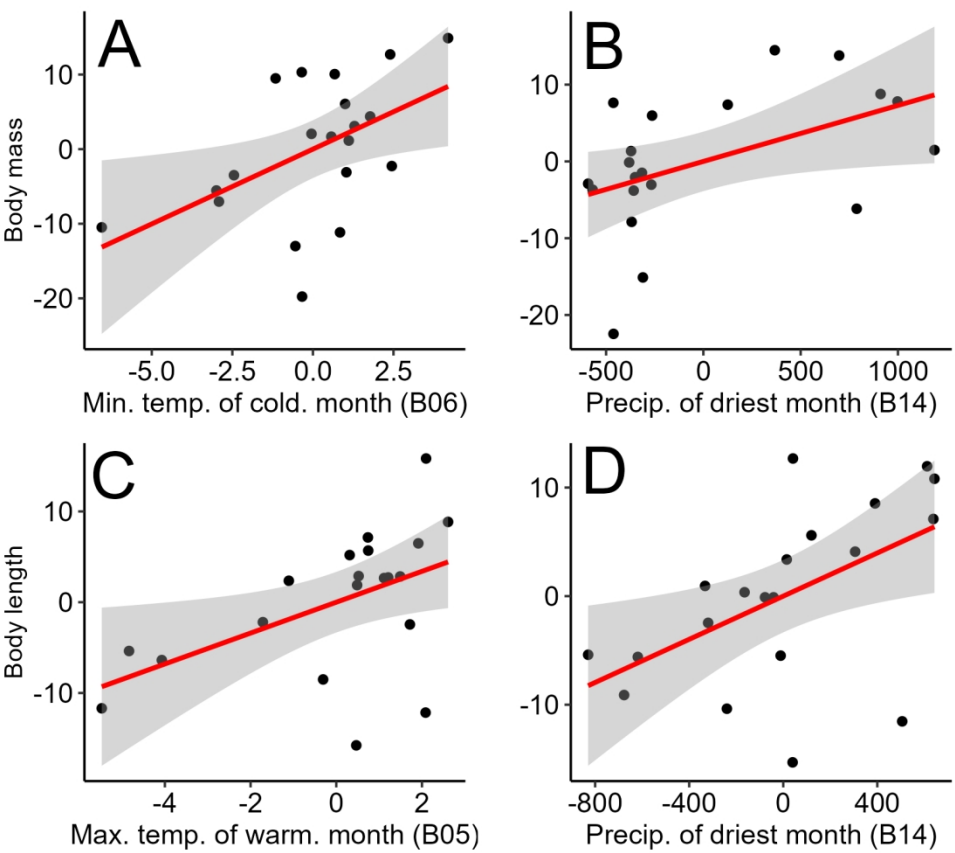
Relationship between female and male body length (A) and body mass (B). Rensch’s rule is not supported in both cases ($P \geq 0.705$). Red line: linear model for observed data (including 95% confidence interval), dashed line: slope = 1. Note: model estimates slightly differ between the standardized major axis and the linear model; the former was used for hypothesis testing and the latter for visualization.

305x84mm (300 x 300 DPI)



Partial regression plots for the linear model best explaining the variation in tail length (A-D, $R^2 = 0.683$) and ear size (E-F, $R^2 = 0.450$) across mouse lemur taxa. Note: the y-axis represents the marginal impact of the response variable on the explanatory variable.

305x135mm (300 x 300 DPI)



Partial regression plots for the linear models best explaining the variation in body mass (A-B, $R^2 = 0.239$) and body length (C-D, $R^2 = 0.206$) across mouse lemur taxa. Note: the y-axis represents the marginal impact of the response variable on the explanatory variable.

152x135mm (300 x 300 DPI)