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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

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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**

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Key Words:	Allen's rule, Bergmann's rule, Microcebus, cryptic species, sexual size dimorphism
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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.

1		the power of subsequent statistical procedures.	
2		Therefore, we propose to use the generic but	
3		powerful Hampel identifier (Davies & Gather,	
4		1993; Pearson, 2002) to exclude outliers of any	
5		kind. It uses the median and the median absolute	
6		deviation (MAD; Hampel, 1985) to define	
7		breakpoints below/above which measurements	
8		are identified as outliers (Pearson, 2002).	
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11	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.
12			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).
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32	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.
33			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 $\geq 3$ 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.
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55	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,
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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

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



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## 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.

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### 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.

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### 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.

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### 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.

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

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## 98 Introduction

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

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

121 Different approaches can be taken to ensure dataset reliability and to counteract confounding effects of  
122 inter- or intra-observer biases. Although transparency about measurement routines for morphological  
123 traits (e.g., information on how many researchers were involved, how training was conducted, how  
124 precise measurements were conducted) would be useful, it is remarkably rare in the literature. Yet,  
125 detailing which measurement definitions were used is rather common, either by citing other sources or  
126 by directly defining morphological variables (Chornelia et al., 2022; Michaloudi et al., 2018; Radespiel et  
127 al., 2008, 2012). Using these definitions and measuring individuals by only one researcher is occasionally  
128 stated to dispel doubts about the reliability of a dataset (e.g., Macdonald et al., 2018; Benites et al.,  
129 2020), even though intra-observer bias can still exist. If more than one researcher is taking  
130 measurements, the researcher's experience is sometimes reported (e.g., Pilloud et al., 2019), while joint  
131 researcher trainings are considered particularly useful by others (e.g., Morrison, 2015). Further  
132 approaches include taking measurements of each individual by different researchers and calculating an  
133 agreement or mean value for later analyses (e.g., Shirley et al., 2014). Such measures are typically  
134 applied in studies that require a high sampling effort and are designed prior to any data collection. In  
135 reality, however, huge datasets are often compiled after data collection has taken place. In these cases,  
136 *a posteriori* methods for reducing observer biases are needed but largely absent in the literature  
137 (Burghardt et al., 2012). A standardized framework of how to assess the quality of compiled  
138 morphological data and how to improve data quality has not been defined so far.

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

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3 141 interacting factors (Hallgrímsson & Hall, 2005). These factors could be phylogenetic signals with  
4 142 relevance to species delimitation studies (e.g., Cadena et al., 2018; Chornelia et al., 2022; Schüßler et al.,  
5 143 2020), large scale ecological adaptation to different environments or small scale niche differentiation  
6 144 (e.g., Agostini et al., 2017; Meachen et al., 2015; Santini et al., 2018). Variation can further be attributed  
7 145 to mechanisms of sexual selection acting differently on males and females (e.g., Jennions et al., 2001) or  
8 146 natural selection for sex-dependent environmental niches (Kamilar & Pokempner, 2008; Williamson et  
9 147 al., 2021). An established principle in the context of sexual size dimorphism is Rensch's rule (Rensch,  
10 148 1950), which predicts that at the genus level "the ratio of female to male size is larger the smaller the  
11 149 body size of a species" (Meiri & Liang, 2021). Regardless of sex, ecogeographic relationships such as  
12 150 those formulated in Allen's and Bergmann's rules (Mayr, 1942), could also be the underlying forces of  
13 151 morphological variation. According to both, thermoregulatory constraints in endothermic animals are a  
14 152 dominant driver in size variation, either in body size or in the proportions of appendages. In colder  
15 153 climates, body appendages like ears and a tail tend to be smaller (Allan's rule) and body size larger  
16 154 (Bergmann's rule; Mayr, 1942) than in warmer climates. Deviation from these "rules" can in turn provide  
17 155 insights into the evolutionary history of a lineage or relevant physiological processes (Maestri et al.,  
18 156 2016; Rodríguez et al., 2008; Webb & Freckleton, 2007).

19 157 This study aims to (1) develop and apply an objective multi-stage quality filtering pipeline to eliminate  
20 158 problematic data points and reduce the confounding effects of sampling, inter-observer bias and intra-  
21 159 observer variation, (2) evaluate the improvement of data quality across different filtering steps, and (3)  
22 160 use the filtered dataset to exemplarily test hypotheses concerning morphological variation in a genus of  
23 161 small, cryptic primates in Madagascar (i.e., *Microcebus*). Specifically, we test for (3a) the presence of  
24 162 sexual size dimorphism and predictions of (3b) Rensch's rule, (3c) Allen's rule and (3d) Bergmann's rule.  
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## 163 Methods

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### 165 Study system

166 Mouse lemurs (genus *Microcebus*) are among the most speciose genera of lemurs, containing >20 cryptic  
167 species (Zimmermann & Radespiel, 2014; Hotaling et al., 2016; Sgarlata et al., 2019; Schüßler et al.,  
168 2020). These small-bodied and omnivorous primates can be found in all major ecosystems across  
169 Madagascar (Mittermeier et al., 2010). Although subtle, morphological variation has often been used to  
170 support taxonomic decisions in mouse lemurs (e.g., Rasoloarison et al., 2000; Radespiel et al., 2012;  
171 Schüßler et al., 2020), genus-wide tests to assess morphological variability among mouse lemurs have  
172 not been conducted so far. Female-biased sexual dimorphism has been reported for *Microcebus murinus*  
173 body mass and head length (Jenkins & Albrecht, 1991; Kappeler, 1991; Schmid & Kappeler, 1998). Body  
174 mass variation, e.g., with heavier females, was also found in several other recent and extinct lemur  
175 species (Godfrey et al., 1993; Kappeler et al., 2022), and sex differences in canine length were found in  
176 *M. griseorufus* (Rasoazanabary, 2011). Mouse lemurs have been studied by various research groups over  
177 the years. Due to small distributions (i.e., micro-endemism) scattered across all forest habitats of the  
178 island, the high levels of endangerment of some species, the remoteness of their remaining forest  
179 habitats, and the difficulties of capturing larger numbers of mouse lemurs in various habitat types, it is  
180 not possible for one or a few researchers to generate a large morphological dataset encompassing all  
181 taxa. Consequently, the assembly of multiple datasets generated by multiple research groups, as it was  
182 done here, is the only way to study morphological variation in this genus. However, we believe that this  
183 problem is a general one and applies to a large variety of cryptic species worldwide.

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### 185 Dataset characteristics

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

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200 &lt;&lt;&lt; Figure 1 here &gt;&gt;&gt;

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## 203 Generalized quality filtering pipeline

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

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213 &lt;&lt;&lt; Table 1 here &gt;&gt;&gt;

214 &lt;&lt;&lt; Figure 2 here &gt;&gt;&gt;

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## 216 Assessment of data quality

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

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

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

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

247

## 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; Lüdecke 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).

## 288 Results

### 289 Assessment of data quality

290 After quality filtering, a total of 1,679 individuals (54.6%) remained in our dataset, while the number of  
291 individuals represented in the filtered dataset further differed among morphological variables (Figure  
292 3A). The sharpest decline in sample size was observed from step 1 to step 2, in which juvenile individuals  
293 and those captured outside of the reproductive season were dropped from the dataset. The consecutive  
294 steps then led to minor declines in sample size for certain variables, taxa and/or researchers. The highest  
295 decline was found for ear and third toe length (reduction of 43.3% and 42.1%, respectively; Figure 3A).  
296 Changes in the Shapiro 1-W' statistic, skewness and kurtosis across the five filtering steps were different  
297 among variables and across filtering steps (Figure 3). However, after applying our filtering pipeline, the  
298 distributions of most variables showed substantially improved quality, i.e., higher conformity to a normal  
299 distribution (Figure 3).

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301 <<< Figure 3 here >>>  
302  
303 After quality filtering, mean inter-observer reproducibility was  $CV < 0.1$  for most variables indicating very  
304 good quality (Figure 4), and  $CV < 0.2$  for the others (i.e., good quality): particularly reliable variables were  
305 head length and width, interorbital distance, lower leg length, hind foot length and tail length. Others  
306 like intraorbital distance, snout length and body mass were still associated with higher levels of variation  
307 across researchers (Figure 4).

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309 <<< Figure 4 >>>

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

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3 323 *Rensch's rule: Female-biased sexual size dimorphism increases with decreasing body size*

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5 324 The test for Rensch's rule revealed that the regressions between female (x-axis) and male (y-axis) body  
6 325 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-  
7 326 1.160), respectively (Figure 6). In both cases, the relationship was not significantly different from 1 (body  
8 327 length: test statistic  $r = -0.090$ ,  $df = 18$ ,  $P = 0.705$ ; body mass:  $r = 0.006$ ,  $df = 24$ ,  $P = 0.978$ ) and therefore  
9 328 our data does not support Rensch's rule. Female and male body length and body mass (investigated  
10 329 separately) were significantly and positively correlated with each other (body length:  $r^2 = 0.880$ ,  $P <$   
11 330  $0.001$ ,  $n = 20$ ; body mass:  $r^2 = 0.878$ ,  $P < 0.001$ ,  $n = 26$ , respectively), indicating that taxa with larger and  
12 331 heavier males also had larger and heavier females (Figure 6).

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17 333 <<< Figure 6 >>>

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21 335 *Allen's rule: The size of body appendices decreases in colder climates*

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23 336 Conformity with Allen's rule was found for tail length but not for ear size. The best model for tail length  
24 337 explained 68.3% of the variation by including different bioclimatic variables (Figure 7, Table S4). Tail  
25 338 length increased with increasing minimum temperature of the coldest month and decreased with  
26 339 increasing precipitation of the wettest and driest month (Figure 7A-C). The best model for ear size  
27 340 explained 45.0% of the variation but did not include temperature-related variables. Instead, ear size  
28 341 decreased with increasing precipitation of the driest month (Figure 7E). In both cases, null models  
29 342 received much larger  $\Delta AICc$  values and smaller Akaike weights than the preferred models (Table S4).  
30 343 Positive relationships were found for tail length with head length and for ear size with body length  
31 344 (Figure 7D, F; Table S4).

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36 346 <<< Figure 7 >>>

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40 348 *Bergmann's rule: Body size increases in colder climates*

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42 349 Body length and mass did not support Bergmann's rule. Variation in body mass was best explained by a  
43 350 positive relationship with minimum temperature in the coldest month together with precipitation of the  
44 351 driest month (Figure 8A-B; Table S4). Variation in body length was best explained by a positive  
45 352 relationship with maximum temperature of the warmest month and precipitation in the driest month  
46 353 (Figure 8C-D), contrasting predictions under Bergmann's rule. These models explained 23.9% and 20.6%  
47 354 of the variation, respectively (Table S4). For body mass, the null model was far worse than the preferred  
48 355 models, but for body length, the preferred model was only slightly better than the null model.

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## 359 Discussion

### 360 A new methodological toolkit to assess data quality

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

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

390

### 391 Guidelines for future morphological studies

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

- 396 1) Multi-observer studies should be designed in such a way that larger sample sizes (morphometric  
397 measurements for > 30 individuals; Yusoff & Wah 2012) are collected by several researchers ( $n >$   
398 3) for each taxon in the dataset, so that inter-observer biases can be reliably identified and  
399 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

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3 440 flexibility with respect to individualized or sex-dependent feeding habits. Detailed studies comparing the  
4 441 feeding ecology of both sexes across mouse lemur species are needed to further test these hypotheses.

6 442 Interestingly, males had significantly larger ears than females, which may also have biological relevance,  
7 443 since mouse lemurs rely extensively on acoustic communication in addition to olfaction (Glatston et al.  
8 444 1993; Zimmermann 2018). Sensory experiments with mouse lemurs in in Mandena, SE Madagascar, and  
9 445 in captivity showed that auditory cues can initiate and guide insect hunting besides its relevance for  
10 446 intraspecific communication such as during mate localization and advertisement (Buesching et al., 1998;  
11 447 Goerlitz & Siemers, 2007; Piep et al., 2008; Siemers et al., 2007; Zimmermann & Lerch, 1993). Whether  
12 448 the detected differences in ear size are responsible for different acoustic perceptions of males and  
13 449 females needs to be investigated in future studies.

16 450 The slight female-biased sexual size dimorphism was uniform across the whole genus as indicated by its  
17 451 isometric relationship (slope  $\approx 1$ ). Rensch's rule, according to which the ratio of female to male size is  
18 452 expected to be larger the smaller the body size of the species (slope  $> 1$ ), was not supported for mouse  
19 453 lemurs. This finding is in line with the absence of Rensch's rule across a larger set of strepsirrhine  
20 454 primates (Kappeler, 1990) and with the results of a large-scale study in birds (Webb & Freckleton 2007).  
21 455 This deviation from Rensch's rule in mouse lemurs rather suggests an equal selection pressure on male  
22 456 and female body size within the genus, as already proposed by Schmid & Kappeler (1998).

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#### 27 458 *Climate-related morphological patterns*

29 459 Climatic constraints are dominant factors shaping the morphology of organisms (Mayr 1942).  
30 460 Bergmann's and Allen's ecogeographic rules state that body size and appendages are shaped by  
31 461 thermoregulatory principles. Small-bodied endothermic animals like rodents (Alhajeri et al. 2020) and  
32 462 birds (Symonds & Tattersall 2010) largely conform to Allen's rule, while showing a more complex  
33 463 association with but general conformity to Bergmann's rule (Alhajeri & Stepan 2016; Meiri & Dayan  
34 464 2003; Salewski & Watt 2016).

37 465 In mouse lemurs, climatic niche separation has been shown for a few taxa (Kamilar et al., 2016). We  
38 466 found statistical support for an influence of climate on morphology: tail length in mouse lemurs followed  
39 467 the predictions of Allen's rule. Animals living in warmer and drier environments (i.e., higher  
40 468 temperatures during the coldest months, lower precipitation in the driest and wettest months) had  
41 469 longer tails than those living in habitats of opposite characteristics. Prevention of heat loss via shorter  
42 470 tails is a likely explanation for this observation (Serrat, 2014; Sgarlata et al., 2019). As more than 68% of  
43 471 the variation in tail length was explained by climate, this adaptation appears to have a close evolutionary  
44 472 link to the surrounding environment.

47 473 Ear size could also be explained by climatic variables but to a much lesser degree than tail length.  
48 474 Temperature-related variables, however, were not included in the best performing models. Instead, we  
49 475 found that large-eared mouse lemurs were more likely to occur in areas of low amounts of rainfall during  
50 476 the dry season. This relationship most likely echoes the divide between the western dry deciduous and  
51 477 the eastern rain forests of Madagascar. These two macro-habitats differ in many aspects: dry forests are  
52 478 subject to stronger seasonal changes in climatic conditions as well as resource availability and differ in  
53 479 vegetation structure and composition from rain forests (Blanco et al., 2015; Génin, 2008). Acoustic  
54 480 communication may be particularly constrained in rain forest habitats where high precipitation and high  
55 481 vegetation density may lead to sound attenuation and diffusion (Luther & Gentry, 2013; Rasoloharijaona

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3 482 et al., 2010; Taylor et al., 2022). Whether mouse lemur ear sizes are causally linked to the relevance of  
4 483 intraspecific acoustic communication in different habitat types or show other adaptations, e.g., to  
5 484 different foraging habits, cannot be tested with our dataset but warrants further investigation. The  
6 485 difference between small- and large-eared mouse lemurs may further indicate an ancestral phylogenetic  
7 486 constraint associated with an ancient split between dry and rain forest taxa (Yoder & Heckman, 2006;  
8 487 Vences et al., 2009) and may not necessarily be driven by or highly interlinked with climatic adaptations.

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11 488 In our test of Bergmann's rule, we found a relationship between body mass and length and climatic  
12 489 variables, with larger/heavier individuals being more likely to live in warmer and wetter environments.  
13 490 This finding contrasts the prediction of Bergmann's rule that individuals from colder environments  
14 491 should be larger (Salewski & Watt, 2016). Although the association between the variables was relatively  
15 492 low ( $R^2 \leq 0.213$ ), its direction agrees with results from other studies on small mammals in tropical  
16 493 environments (Maestri et al., 2016; Rodríguez et al., 2008; Sgarlata et al., 2022). In all cases, body size  
17 494 appeared to increase in warmer environments (e.g., at lower altitudes) probably due to an increase in  
18 495 resource availability, suggesting that Bergmann's rule may only apply to animals in colder regions but not  
19 496 in the tropics (Rodríguez et al. 2008). This also conforms to general patterns of ecogeographic size  
20 497 variation across lemurs of all sizes, both living and recently extinct (Albrecht et al., 1990).

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24 498 Several mouse lemur species (e.g., *M. berthae* and *M. murinus* at Kirindy, Schmid, 2000; *M. griseorufus*,  
25 499 Génin, 2008; *M. lehilahytsara*, Randrianambinina et al., 2003, Andriambelason et al., 2020; *M.*  
26 500 *ravelobensis*, Thorén et al., 2011; *M. rufus*, Atsalis, 1999, Ramananjato et al., 2022) can cope with  
27 501 thermoregulatory challenges under low temperatures using torpor or even hibernation (Blanco et al.  
28 502 2018; Salewski & Watt 2016). However, more than 78% of the variation in body mass and body length  
29 503 could not be explained by climatic factors. It is known that resource availability, seasonality and most  
30 504 likely also phylogeny are additional drivers of mouse lemur body mass variation (Atsalis 1999; Génin  
31 505 2008; Randrianambinina et al. 2003). Phylogenetic constraints on body size of mouse lemurs are  
32 506 indicated by the observation that several smaller taxa (*M. berthae*, *M. myoxinus*, *M. lehilahytsara*, *M.*  
33 507 *rufus*) form a distinctive clade of small-bodied mouse lemur species (Louis & Lei 2016) that can occur not  
34 508 only in sympatry with other larger species but also across a variety of environments in eastern and  
35 509 western Madagascar. These include the highly seasonal western dry deciduous forests with their clear  
36 510 separation into a 4–6 month hot rainy season and a 6–8-month cooler dry season lacking precipitations  
37 511 almost entirely, the central highlands that undergo substantial seasonal temperature fluctuations, and  
38 512 the eastern lowland rainforests that exhibit the least climatic variations across the year (Andriambelason  
39 513 et al. 2020; Blanco et al. 2015, Evasoa et al. 2018). A comprehensive evaluation of the relative impact of  
40 514 environmental variables and phylogenetic constraints on the morphology of mouse lemurs is currently  
41 515 hampered by a lack of a fully resolved phylogeny of all currently described mouse lemur lineages.

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## 47 48 517 **Conclusions**

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50 518 Our new filtering pipeline was developed in order to enable analyzing a large multi-researcher dataset.  
51 519 We detailed on the six different filtering steps and illustrated their usefulness for reducing potential  
52 520 inter-observer biases. With our generalized suggestions for future morphological studies, we aim to  
53 521 improve data collection procedures and overall quality in these kind of studies. Using this pipeline, we  
54 522 filtered the largest currently available dataset of morphometric measurements for the species-rich genus  
55 523 of mouse lemurs and generated a consolidated dataset with which four biologically meaningful  
56 524 hypotheses were tested.

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3 525 Morphometric variation was partly explained by sexual size dimorphism and by various bioclimatic  
4 526 variables which were partly in agreement with the predictions of Allen's rule (tail length) but not with  
5 527 those of Rensch's or Bergmann's rule. The remaining unexplained variation could be due to yearly and  
6 528 monthly variations in resource availability, possible differences in resource use across lineages and  
7 529 between the sexes, variation in intraspecific acoustic communication patterns and sociality, as well as  
8 530 phylogenetic constraints. Our genus-wide analysis could therefore outline general patterns of  
9 531 morphological variation in mouse lemurs. We further generated hypotheses for later testing in order to  
10 532 fully understand the drivers of morphological variation within a genus of nocturnal, cryptic and small-  
11 533 bodied primates.  
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## 553 CONFLICT OF INTEREST STATEMENT

554 The authors declare no conflict of interest.

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## 557 DATA AVAILABILITY STATEMENT

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

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## 886 Figure captions

887  
888 **Figure 1:** Distribution of *Microcebus* spp. populations sampled across Madagascar. Overlapping symbols  
889 were rarified to improve display. Minimum temperature of the coldest month according to Karger et al.  
890 (2017) is shown in shadings from white to black.

891  
892 **Figure 2:** Illustration of steps 4 and 5 of the generalized data filtering pipeline. A: Boxplots per lineage  
893 and researcher for one variable (hind foot length), boxes encircled in red indicate examples outlined in  
894 Table 1. B and C: Histograms for ear length and interorbital distance, respectively, with truncation  
895 threshold (median + 3 \* median absolute deviation) introduced as vertical dashed red line. Truncation  
896 (i.e., the exclusion of measurements for this variable for the respective researcher) takes place in B but  
897 not in C.

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

905  
906 **Figure 4:** Inter-observer reproducibility quantified as coefficient of variation (CV) across the 13 different  
907 morphometric parameters. Only data after quality filtering was included. The horizontal line indicates  
908 the upper limit of the CV values interpreted as very good reproducibility (CV=0.0-0.1, Aronhime et al.,  
909 2013).

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

914  
915 **Figure 6:** Relationship between female and male body length (A) and body mass (B). Rensch's rule is not  
916 supported in both cases ( $P \geq 0.705$ ). Red line: linear model for observed data (including 95% confidence  
917 interval), dashed line: slope = 1. Note: model estimates slightly differ between the standardized major  
918 axis and the linear model; the former was used for hypothesis testing and the latter for visualization.

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920 **Figure 7:** Partial regression plots for the linear model best explaining the variation in tail length (A-D,  $R^2 =$   
921 0.683) and ear size (E-F,  $R^2 = 0.450$ ) across mouse lemur taxa. Note: the y-axis represents the marginal  
922 impact of the response variable on the explanatory variable.

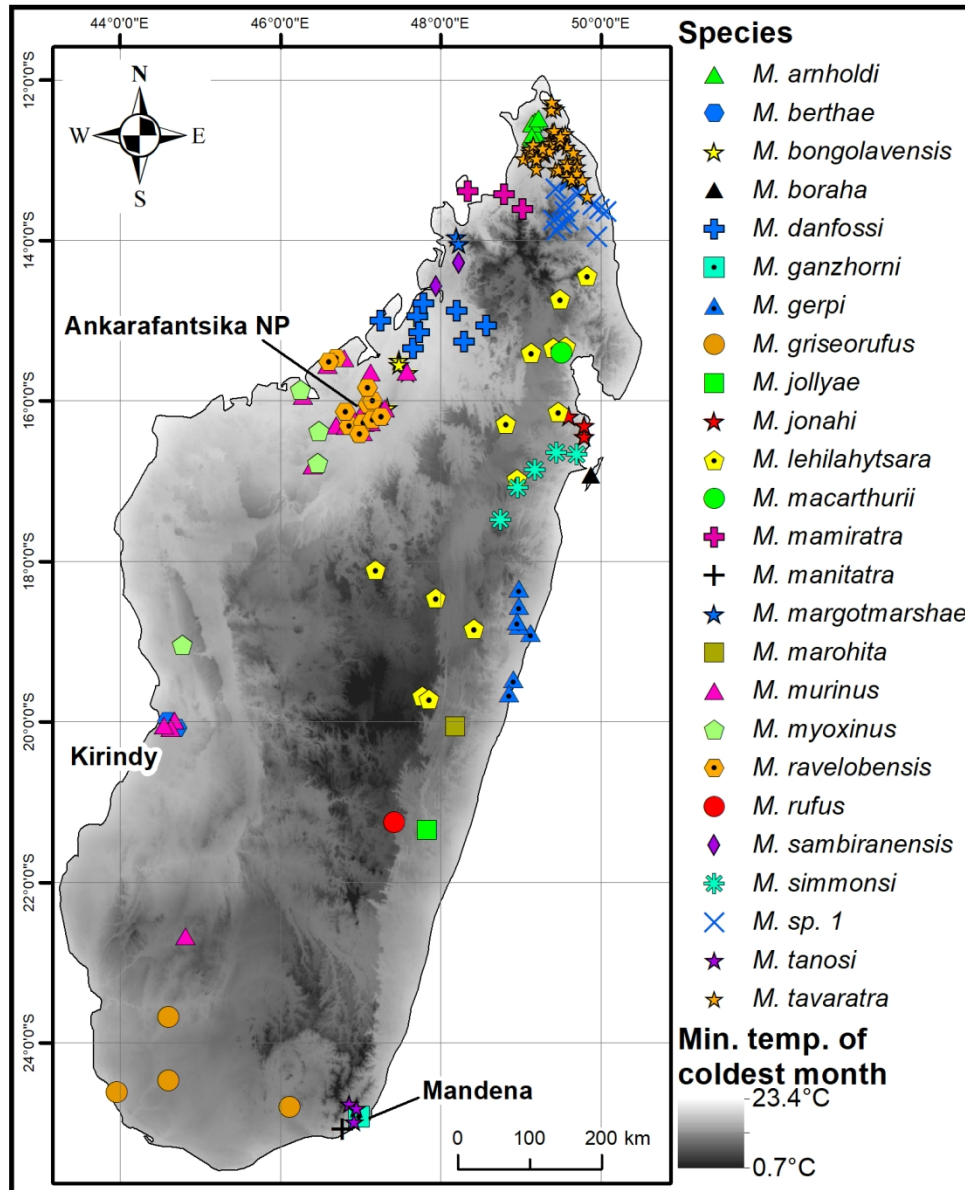


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924 **Figure 8:** Partial regression plots for the linear models best explaining the variation in body mass (A-B,  $R^2$   
925 = 0.239) and body length (C-D,  $R^2 = 0.206$ ) across mouse lemur taxa. Note: the y-axis represents the  
926 marginal impact of the response variable on the explanatory variable.

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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)

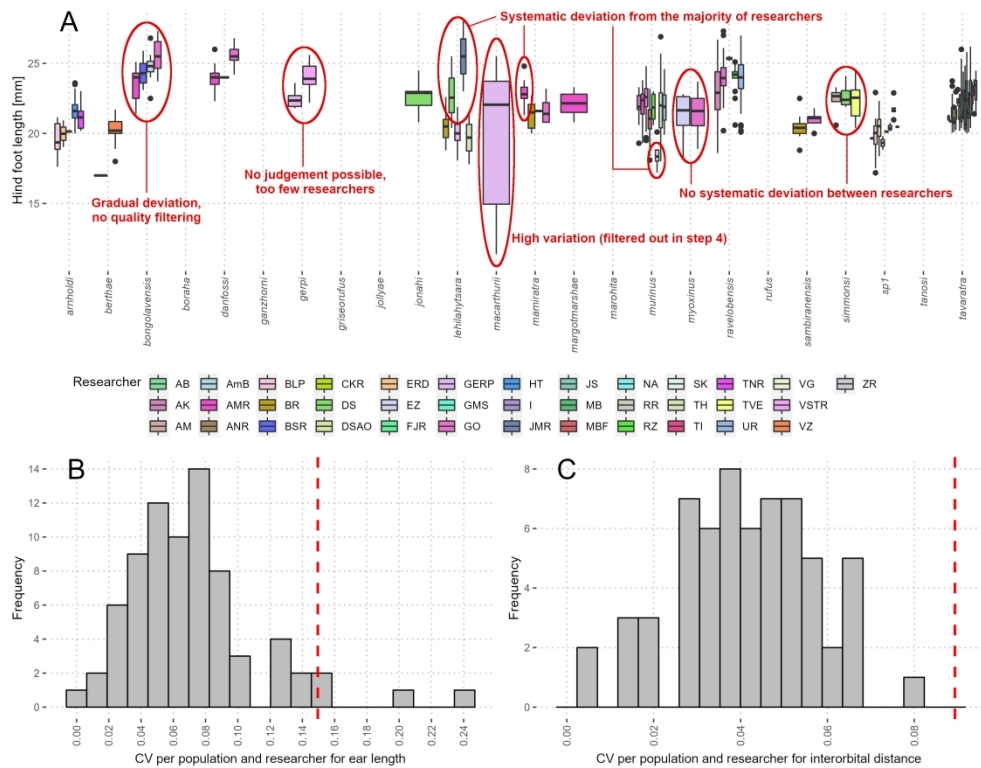
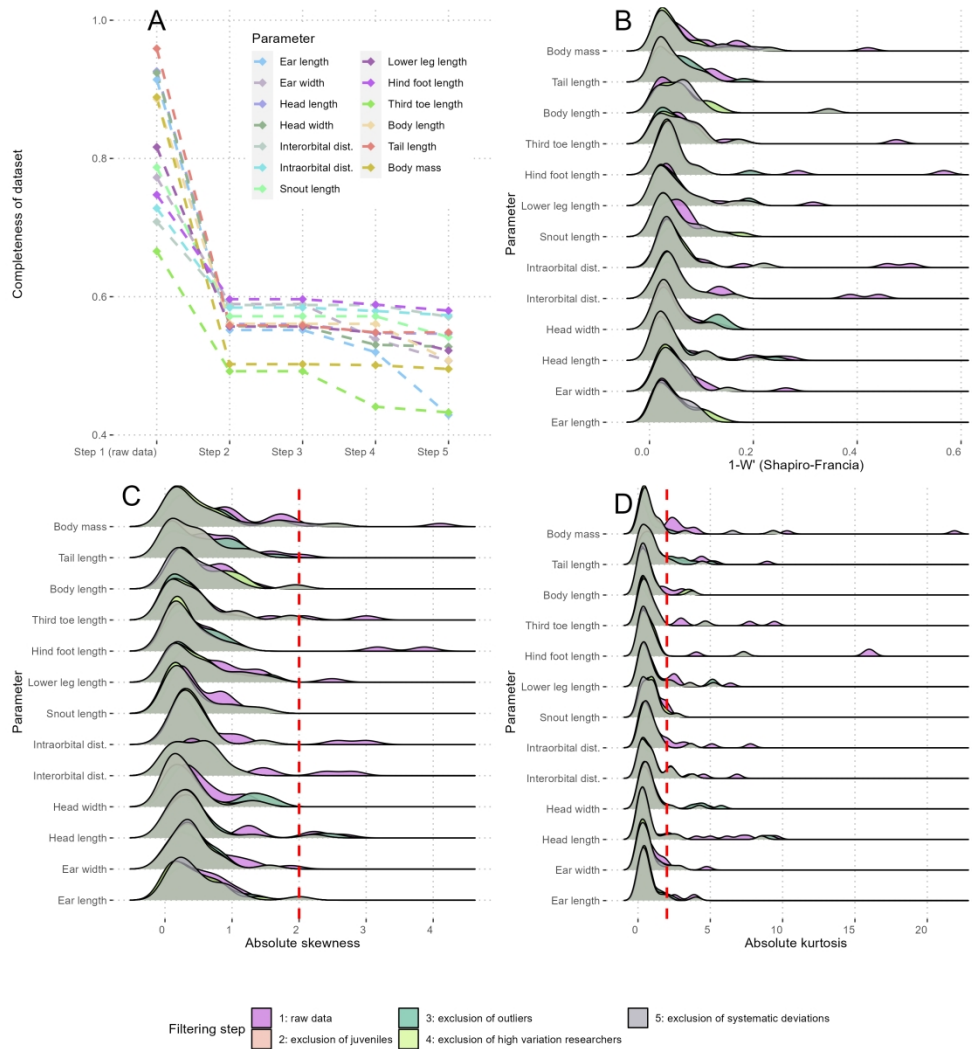


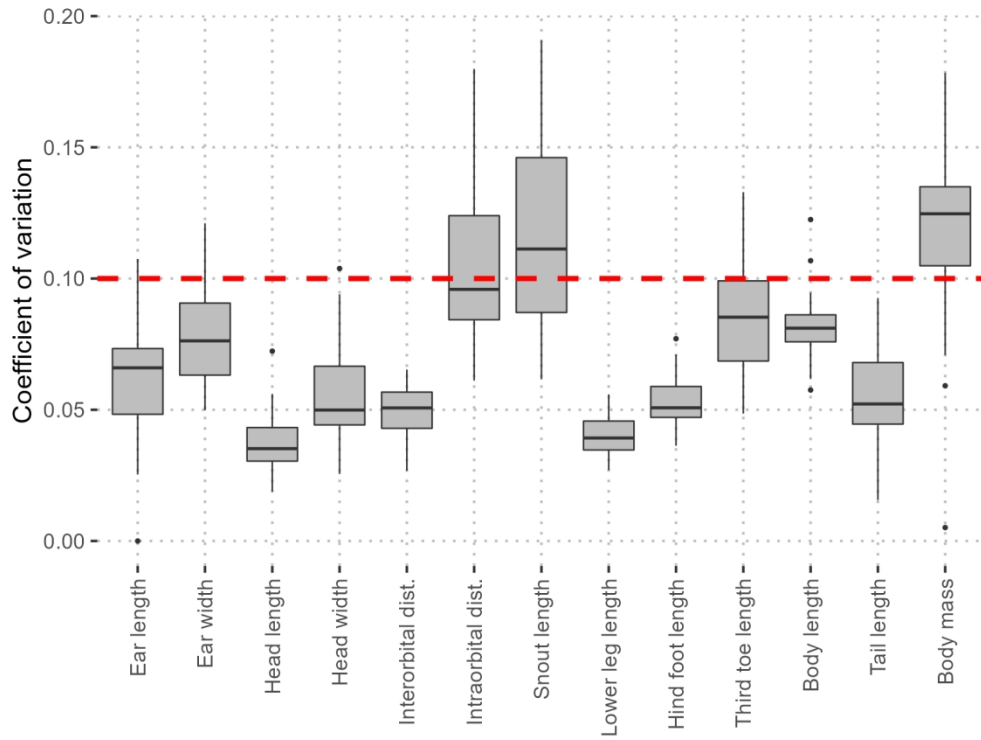
Illustration of steps 4 and 5 of the generalized data filtering pipeline. A: Boxplots per lineage and researcher for one variable (hind foot length), boxes encircled in red indicate examples outlined in Table 1. B and C: Histograms for ear length and interorbital distance, respectively, with truncation 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.

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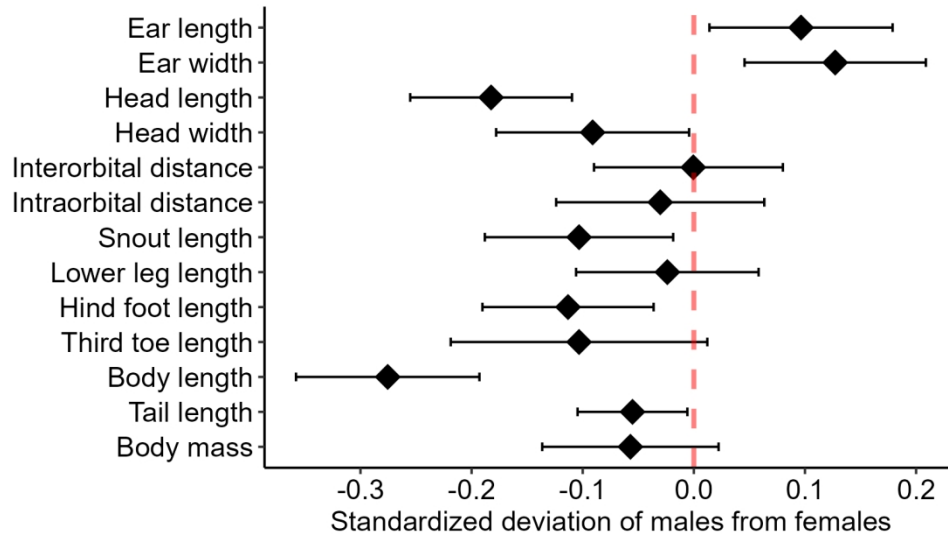
Quality assessment following the five data filtering steps indicated by different color code in B-D. A: Completeness of the dataset refers to the number of available values per variable compared to the number of individuals in the raw data (n = 3,073). B: 1-W' measure of normality, C: absolute skewness, 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)



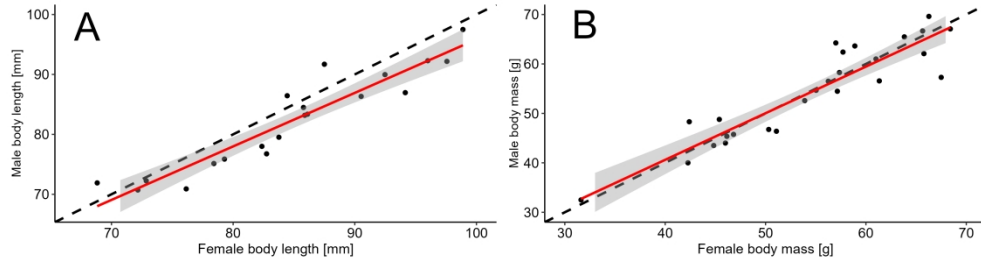
Inter-observer reproducibility quantified as coefficient of variation (CV) across the 13 different morphometric parameters. Only data after quality filtering was included. The horizontal line indicates the upper limit of the CV values interpreted as very good reproducibility (CV=0.0-0.1, Aronhime et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

143x111mm (300 x 300 DPI)



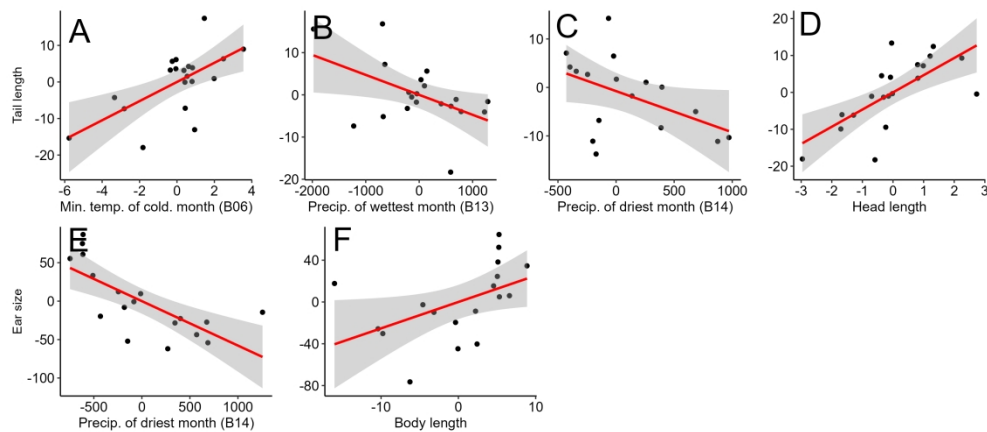
Sexual size dimorphism across all *Microcebus* taxa displayed via model estimates with 95% confidence intervals. The differences in all variables except inter- and intraorbital distances, lower leg length, third toe length, and body mass were statistically significant ( $P \leq 0.029$ ; Table S3).

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.

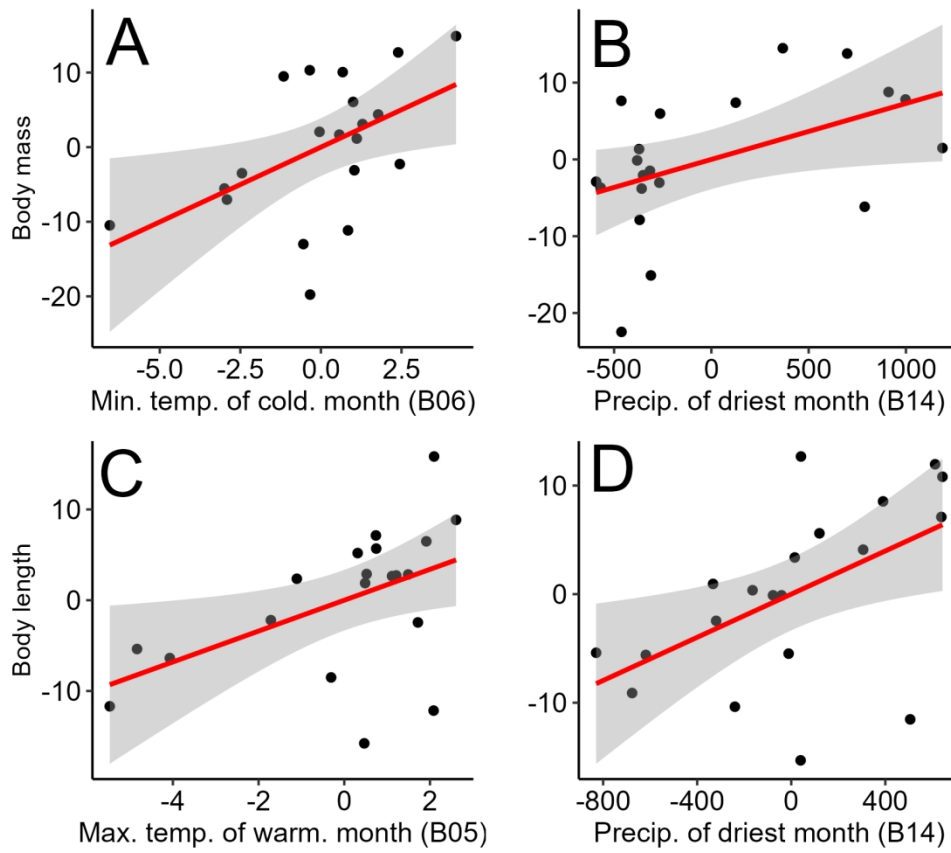
305x84mm (300 x 300 DPI)



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)