



A matter of weight: Critical comments on the basic data analysed by Maestri et al. (2016) in *Journal of Biogeography*, 43, 1192–1202

Abstract

Recently, Maestri, Luza, et al. (2016) assessed the effect of ecology and phylogeny on body size variation in communities of South American Sigmodontinae rodents. Regrettably, a cursory analysis of the data and the phylogeny used to address this question indicates that both are plagued with inaccuracies. We urge “big data” users to give due diligence at compiling data in order to avoid developing hypotheses based on insufficient or misleading basic information.

We are living a great time in evolutionary biology, where the combination of the increased power of systematics, coupled with the use of ever more inclusive datasets allows—heretofore impossible—questions in ecology and evolution to be addressed.

Frequently, the main source of these datasets are specimens deposited in natural history collections and taxonomic publications accumulated over 300 years of scientific exploration. These data are crucial for biodiversity research and thus, it is imperative that they are as accurate and precise as possible (Hortal et al., 2015). Data used in “big data” publications must be verified against primary sources in order to avoid introducing unwelcome biases in the analyses.

The amazing extant diversity of sigmodontine, the largest subfamily within the rodent family Cricetidae, invites a wide array of evolutionary inquiries; thus, it is not surprising that the evolution of body size—a crucial and recurrent topic in biology—was assessed in this clade of New World mammals. Maestri, Luza, et al. (2016) recently approached this question by applying a large battery of statistical techniques on a dense database of body masses, phylogeny, and environmental variables. The authors concluded, “... environment alone was not sufficient to explain body size variation in sigmodontine assemblages. Rather, environmental gradients interacted with historical processes to determine body size variation in the Neotropical assemblages” (Maestri, Luza, et al., 2016; p. 1192). To achieve this understanding Maestri, Luza, et al. (2016) started from two kinds of basic data: (1) a matrix of the mass, in grams, of 245 species of sigmodontines, and (2) a molecular-based phylogenetic hypothesis for the subfamily. Both datasets are provided as Appendix S1 in the Supporting Information of the mentioned article. The following comments are mostly derived from our scrutiny of these basic data; therefore, we are not re-analysing here the specific study nor commenting on the results or conclusions obtained by

Maestri, Luza, et al. (2016), although we believe that an exploration of the quality of the original data informs both. Ultimately, we submit that the matrix of body size and the phylogeny used by these authors were plagued with major inaccuracies.

The matrix of body sizes used by Maestri, Luza, et al. (2016, p. 1194) was obtained from two secondary or tertiary sources: Rodríguez, Olalla-Tárraga, and Hawkins (2008) and Bonvicino, Oliveira, and D’Andrea (2008). The former study derived cricetid mass data from Smith et al. (2003), an ambitious project focused on the compilation of “body mass information for all mammals on Earth” where the basic data were derived from “primary and secondary literature ... Whenever possible, we used an average of male and female body mass, which was in turn averaged over multiple localities to arrive at our species body mass values ... although we relied heavily on a data set for ... the CRC handbook of Mammalian Body Mass ($N = 688$), and a data set compiled for South America by P. Marquet ($N = 505$), these represent less than half the records in the current database. The remainder are derived from more than 150 other sources” (Smith et al., 2003; p. 3403). In turn, Bonvicino et al. (2008) include external measurements and body mass data derived, mostly, from primary sources (i.e. measured specimens). Summarizing, the list of body sizes analysed by Maestri, Luza, et al. (2016) is—prima facie—a very complex set of data extracted from several, sometimes “grey,” sources (e.g. compilation by P. Marquet).

The data matrix of Maestri, Luza, et al. (2016) encompasses 72 genera; if we consider that at last count there were 84 genera of living sigmodontines in South America, we conclude that the taxonomic coverage at this level is adequate (86%). However, the coverage to specific level is—at best—moderate; Maestri, Luza, et al. (2016) included 245 of the 382 species (c. 64%) registered in South America (all our numbers following Patton, Pardiñas, & D’Elía, 2015; a source also mentioned by Maestri, Luza, et al., 2016). A minor issue is that about 5% of forms included by Maestri, Luza, et al. (2016) are currently considered synonyms. For example, they listed *Juscelinomys huanchacae* and *J. guaporensis* as separate species, but the latter is considered a junior synonym of the former (Emmons & Patton, 2012). It is clear that these authors updated the taxonomy of several forms; for example, they used *Neomicroxus* as the genus to allocate *bogotensis*, an action that reflects a recent taxonomic change (see Alvarado-Serrano & D’Elía, 2013). However, they missed the change in the generic affiliation of *Phyllotis wolffsohni* to *Tapetomys*. These aspects highlight two main issues not clarified by



TABLE 1 Comparison of body mass data (in grams) between selected species of sigmodontine rodents analysed by Maestri, Luza, et al. (2016) and data retrieved from primary sources. The column “%” reports the percentage difference between the values listed in both contributions

Maestri, Luza, et al. (2016)		This paper		
Species ^a	Mass	Mass	%	Source
<i>Abrothrix lanosus</i>	32.5	21.5	33.8	Feijoo, D'Elía, Pardiñas, and Lessa (2010)
<i>Akodon azarae</i>	25	22.5	10.0	CNP ^b collections
<i>Akodon^c serrensis</i>	28.3	25.8	8.8	Pardiñas, Geise, Ventura, and Lessa (2016)
<i>Akodon cursor</i>	39.9	54.2 (males)	35.8	Geise (2012)
<i>Akodon cursor</i>	39.9	43.2 (females)	8.3	Geise (2012)
<i>Akodon montensis</i>	44.1	32.6	26.1	CNP collections
<i>Akodon toba</i>	51.2	35	31.6	Massoia (1971b)
<i>Calomys musculinus</i>	20.1	11.5	42.8	CNP collections
<i>Chelemys^d macronyx</i>	73.3	49	33.2	CNP collections
<i>Chinchillula sahamae</i>	169.8	151	11.1	Aliaga-Rossel, Ríos-Uzeda, and Salazar-Bravo (2009)
<i>Deltamys kempi</i>	26.4	24	9.1	CNP collections
<i>Eligmodontia morgani</i>	16.5	18.2 (males)	10.3	Pearson, Martin, and Bellati (1987)
<i>Eligmodontia morgani</i>	17.5	21.7 (females)	24.0	Pearson et al. (1987)
<i>Euneomys petersoni</i>	83	34.1	58.9	CNP collections
<i>Holochilus brasiliensis</i>	155	308.5	99.0	Massoia (1971a)
<i>Holochilus sciureus</i>	163.5	155.4	5.0	Voss (1992)
<i>Holochilus chacarius</i>	204	165.4	18.9	Massoia (1971a)
<i>Ichthyomys stolzmanni</i>	84.7	140	65.3	Brito, Tenecota, and Pozo-Zamora (2016)
<i>Juscelinomys huanchacae</i>	97.3	85	12.6	Emmons and Patton (2012)
<i>Kunisia tomentosus</i>	115.6	448	287.5	Bezerra et al. (2007)
<i>Loxodontomys micropus</i>	72.7	57.6	20.8	Pearson (1983)
<i>Necromys lasiurus</i>	39.9	28.8	27.8	CNP collections
<i>Neusticomys monticolus</i>	39.5	32	19.0	Zeballos et al. (in press)
<i>Neusticomys peruviensis</i>	40	37	7.5	Zeballos et al. (in press)
<i>Neusticomys venezuelae</i>	47.1	62.5	32.7	Voss, Lunde, and Simmons (2001)
<i>Notiomys edwardsii</i>	21.3	21.3	0.0	Pardiñas, Udrizar Sauthier, Teta, and D'Elía (2008)
<i>Oecomys trinitatis</i>	73.4	45.8	37.6	Carleton et al. (2009)
<i>Oecomys superans</i>	73.4	85	15.8	Carleton and Musser (2015)
<i>Oligoryzomys flavescens</i>	21.3	24.1	13.1	Massoia (1973)
<i>Oligoryzomys microtis</i>	22.5	15.2	32.4	Massoia (1973)
<i>Oligoryzomys magellanicus</i>	25.2	41	62.7	Massoia (1973)
<i>Oligoryzomys longicaudatus</i>	27	33	22.2	Massoia (1973)
<i>Oligoryzomys delticola^e</i>	29.4	39	32.7	Massoia and Fornes (1964)
<i>Oligoryzomys eliurus^e</i>	30	20.4	32.0	CNP collections
<i>Oxymycteris inca</i>	35	120	242.9	Hinojosa et al. (1987)
<i>Oxymycteris paramensis</i>	42	63	50.0	Jayat, D'Elía, Pardiñas, Miotti, and Ortiz (2008)
<i>Oxymycteris rufus</i>	75.4	54.6	27.6	CNP collections
<i>Phyllotis bonaeriensis^f</i>	42.5	47.8	12.5	CNP collections
<i>Pseudoryzomys simplex</i>	51.2	42	18.0	Massoia (1976)
<i>Reithrodont auritus</i>	70.9	80	12.8	Guthmann, Lozada, Monjeau, and Heinemann (1997)
<i>Rhagomys rufescens</i>	21.2	16	24.5	Passamani, Cerboncini, and de Oliveira (2011)
<i>Salinomys delicatus</i>	12.5	11.4	8.8	Rodríguez et al. (2012)
<i>Scapteromys tumidus</i>	146	103	29.5	CNP collections

(Continues)

**TABLE 1** (Continued)

Maestri, Luza, et al. (2016)		This paper		
Species ^a	Mass	Mass	%	Source
<i>Scolomys ucayalensis</i>	26.5	29.6	11.7	Brito and Arguero (2012)
<i>Sigmodon hispidus</i>	92.4	107.5	16.3	Voss (1992)
<i>Tapecomys primus</i>	71.5	85.2	19.2	Pardiñas et al. (2015b)
<i>Thomasomys baeops</i>	77	36	53.2	Voss (2003)
<i>Thomasomys hylophilus</i>	77	36	53.2	Voss (2003)
<i>Wiedomys pyrrhorhinos</i>	46.7	41	12.2	Sobral and Oliveira (2014)
<i>Wilfredomys oenax</i>	46.8	24	48.7	UFSC ^b one adult female
<i>Zygodontomys brevicauda</i>	52.2	56.7	8.6	Voss (1991)

^aSpecies names as originally reported by Maestri, Luza, et al. (2016).

^bCNP = Centro Nacional Patagónico (Puerto Madryn, Chubut, Argentina).

^cGenus *Castoria*, according to Pardiñas et al. (2016).

^dGenus *Paynomys*, according to Teta, Cañón, Patterson, and Pardiñas (2017).

^eActually, a junior synonym of *Oligoryzomys nigripes*.

^fActually, *bonariensis*.

^gUFSC = Universidade Federal de Santa Catarina (Florianópolis, Santa Catarina, Brasil).

Maestri, Luza, et al. (2016), that is, how did they select the sigmodontine species analysed and how were these species treated taxonomically. To answer these questions, we compared the list of species used by Maestri, Luza, et al. (2016) and that in appendix 1 of Rodríguez et al. (2008): there is a c. 90% correspondence. Clearly, the qualitative and quantitative structure of the database analysed by Maestri, Luza, et al. (2016) reflects the selection made by Rodríguez et al. (2008) and previously by Smith et al. (2003).

However, the most concerning aspect of the matrix used by Maestri, Luza, et al. (2016) is not the actual species representation but the masses reported for a number of them. Any student familiar with sigmodontines is aware that the sigmodontine *Kunisia tomentosus* is the heaviest living representative (*Megalomys desmarestii* or *Antillomys rayi* were probably heavier than *K. tomentosus*, but both are extinct Caribbean forms). Full-grown adult individuals of *K. tomentosus* exceed 500 or 600 g; a confident mean value from adult animals ($n = 8$, range 241–610 g) of this species derived from trapping data is 448 g (cf. Bezerra, Carmignotto, Nunes, & Rodrigues, 2007). *Kunisia tomentosus* is listed in the Maestri, Luza, et al. (2016) database with 115.6 g. Similar outstanding differences are detected elsewhere in the list. In many cases, the data used by Maestri, Luza, et al. (2016) are either below or above field-obtained body weights (Table 1). A second conspicuous issue derived from the scrutiny of the matrix of basic data analysed by Maestri, Luza, et al. (2016) is the series of repeated values for several species, ranging from 2 (e.g. *Bibimys chacoensis* and *Bibimys torresi*) to 19 (almost all *Thomasomys* included). We detected, among several remarkable examples, five species of *Oxymycterus* listed with 68 g (including *O. hiska* and *O. hucucha* which do not exceed 36 g according to the original description provided by Hinojosa, Anderson, & Patton, 1987), and 10 *Oecomys* all “weighting” 73.4 g (with species ranging from the small *O. trinitatis* to the large *O. superans*; see Carleton, Emmons, & Musser, 2009; table 4). The number of species with repeated masses

represents 34% of the total matrix of analysed species. Both issues, the erroneous reported masses and the repeated values, indicate that Maestri, Luza, et al. (2016) analysed a series of data that quite inaccurately represent the diversity of body masses of South American sigmodontine rodents.

The second main topic that we want to highlight is the phylogeny used by these authors to explore body size variation. According to Maestri, Luza, et al. (2016), “The phylogenetic relationships among the 245 sigmodontine species . . . were reconstructed using the most recent and comprehensive phylogenetic hypothesis for rodents (Fabre, Hautier, Dimitrov, & Douzery, 2012). Species not treated by Fabre et al. (2012) were embedded in the phylogeny following Parada, Pardiñas, Salazar-Bravo, D’Elía, and Palma (2013).” Thus, they worked on the multigenic matrix constructed by Fabre et al. (2012) but focusing exclusively on sigmodontines and several species were manually “pasted” into large artifactual polytomies. Maestri, Luza, et al. (2016) overlooked the fact that the phylogeny obtained by these means is at odds with all molecular-based phylogenies produced in the last decade (Leite et al., 2014; Machado et al., 2015; Martínez, Ferro, Mollerach, & Barquez, 2012; Parada et al., 2013; Pardiñas, Teta, & Salazar-Bravo, 2015a,b; Salazar-Bravo, Pardiñas, & D’Elía, 2013; Salazar-Bravo, Pardiñas, Zeballos, & Teta, 2016; Schenk, Rowe, & Steppan, 2013; Steppan, Adkins, & Anderson, 2004; among others). In particular, the phylogeny used by Maestri, Luza, et al. (2016) has the following major spurious “clades” (the nomenclature of these “clades” according to Maestri, Luza, et al., 2016). Their “clade A,” including *Chinchillula*, *Euneomys*, *Irenomys*, *Juliomys*, *Punomys*, *Rhagomys* and *Wilfredomys*, is a mixture of members currently placed in the tribes Andinomyini (*Andinomys* plus *Punomys*), Euneomyini (*Euneomys*, *Irenomys* and *Neotomys*), Thomasomyini (*Rhagomys* plus several genera), Wiedomyini (*Phaeomys*, *Wiedomys* and *Wilfredomys*), plus two incertae sedis genera (*Chinchillula* and *Juliomys*). Furthermore, their “Clade B,” including *Abrothrix*, *Auliscomys*, *Chelemys*,



Delomys, *Geoxus*, *Notiomys*, *Pearsonomys*, *Reithrodon* and *Wiedomys*, is, again, a mixture of members of Abrotrichini (*Abrothrix*, *Chelemys*, *Geoxus*, *Notiomys* and *Pearsonomys*), Phyllotini (*Auliscomys* plus several genera), Reithrodontini (*Reithrodon*), Wiedomyini (*Wiedomys*, see above), whereas *Delomys*, an incertae sedis, is typically retrieved as sister to Phyllotini. Finally, their "Clade C" are all members of the Ichthyomyini; however, this tribe is sister to Sigmodontini and together form Sigmodontalia. Minor additional inaccuracies in the topology presented by Maestri, Luza, et al. (2016), including the position of *Abrawayaomys* within Akodontini or *Mindomys* as sister of the remainder Oryzomyini, do not deserve further comments.

Summarizing, Maestri, Luza, et al. (2016) analysed a large set of sigmodontine rodents to explore phylogenetic and geographical variation of body size. However, a moderate scrutiny of the basic data used by these authors highlights several inaccuracies.

Here, we do not dispute whether the issues of incomplete, redundant, or erroneous body masses and a poor hypothesis of relationships are enough to lead to erroneous general results in Maestri, Luza, et al. analyses we are data stewards. Methods in macroevolution and macroecology are evolving, like everything else. We personally are not sure whether the approaches currently available are robust enough to retrieve the correct answers despite potential biases and uncertainty in inputs.

We welcome the contribution by Maestri and collaborators and encourage these and other colleagues to retrieve data from the primary literature ("*nanos gigantium humeris insidentes*")—discovering truth by building on previous discoveries). We believe this is the most productive way to achieve a connection between the architects of the seminal knowledge on these rodents (such as Oldfield Thomas, Emmet Hooper, Philip Hershkovitz, Wilfred Osgood, Oliver Pearson, Elio Massoia, among many others) and the new promising generations.

Keywords

basic data, body mass, Cricetidae, error, phylogeny, South America

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