

Length – mass allometries in Amphibians.

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Abstract

Body mass is rarely recorded in amphibians, and other body measurements (e.g. Snout to vent length, SVL) are generally collected instead. However length measurements, when used as proxies of body mass in comparative analyses, are problematic if different taxa and morphotypes are included. We developed allometric relationships to derive body mass from SVL measurements. We fitted Phylogenetic Generalized Least Square models for frogs (Anura) and salamanders (Caudata) and for several families separately. We tested whether allometric relationships differed between species with different habitat preferences and between morphs in salamanders. Models were fitted with SVL-mass measurements for 88 frog and 42 salamander species. We assessed the predictive performance of the models by cross-validation. Overall, the models showed high explained variance and low forecasting errors. Models differed between semi-aquatic, terrestrial and arboreal frogs, and between paedomorphic and non-paedomorphic salamanders. Body mass estimates derived from our models allow for comparability of studies on multiple taxa and can be used for testing theories built upon evolutionary and ecological processes which are directly related to body mass.

Key-words: Anura, Caudata, Body length, Body mass, Body size, Body weight, Frog, Salamander, Snout to vent length, SVL

1 Introduction

2 Body mass is a fundamental parameter in ecology, as it is related to several key
3 ecological features such as species metabolic rates and energy-intake (Gillooly *et al.*,
4 2001; Brown *et al.*, 2004), population abundance (Peters & Wassenberg, 1983)
5 dispersal distance (Jenkins *et al.*, 2007; Hillman *et al.*, 2014) and reproductive output
6 (Blueweiss *et al.*, 1978). Among vertebrates, body mass is commonly recorded in birds
7 and mammals, whereas it is less often recorded in amphibians and reptiles (Meiri, 2010;
8 Feldman & Meiri, 2013). In amphibians body mass is highly variable within the same
9 species, but can also vary in the same individual over short time frames. In fact, body
10 mass in amphibians depends on the level of hydration of the animal, the physiological
11 state, the content of the bladder and the cloaca, as well as the reproductive state in
12 females (Dodd, 2010). As a consequence, amphibians' body masses are rarely reported
13 in ecological or taxonomic literature as compared to other morphometric measurements.
14 Among them snout to vent length (SVL) is the most common measure of body size in
15 amphibians (Dodd, 2010; Vitt & Caldwell, 2013). As a result, while SVL is available
16 for many species, body mass data are sparse in the literature and only available for a
17 minority of species.

18 Although SVL is undoubtedly preferable for many applications, information on
19 body mass is necessary for others. For example, the average body mass of a species is
20 needed to estimate the biomass of a population or of species assemblages (Watanabe,
21 Nakanishi & Izawa, 2005; Gibbons *et al.*, 2006; Deichmann, Duellman & Bruce
22 Williamson, 2008). In many comparative analyses, SVL is used as a proxy for body
23 mass, however this presents conceptual and comparability issues. As an example,
24 macroecological investigation has largely explored body mass variation along
25 environmental clines in several taxa (Arnett & Gotelli, 2003; Rodríguez, López-Sañudo
26 & Hawkins, 2006; Olson *et al.*, 2009), however studies focused on amphibians have
27 employed SVL measurements as a proxy of body mass (Ashton, 2002; Diniz-Filho *et al.*,
28 2004; Olalla-Tárraga & Rodríguez, 2007; Adams & Church, 2008; Cvetković *et al.*,
29 2009; Ficetola *et al.*, 2010; Guo & Lu, 2016). This is conceptually wrong because the
30 hypotheses proposed so far to explain the environmental clines in body size are based
31 on mechanisms related to body mass, not length (e.g., Bergmann's rule is often
32 explained by the heat conservation advantage of large body mass) (Blackburn, Gaston
33 & Loder, 1999; Meiri & Dayan, 2003).

34 Similarly, macroevolutionary studies focusing on body mass have often
35 employed mixed body size measurements for different taxa depending on data
36 availability (Harmon *et al.*, 2010), with unclear consequences for comparisons between
37 taxa. In comparative conservation analyses body mass is often considered a proxy of
38 extinction risk (Purvis *et al.*, 2000; Cardillo *et al.*, 2005). However, all comparative
39 analyses on extinction risk in amphibians have employed SVL as a proxy of mass
40 (Bielby *et al.*, 2008, 2009; Cooper *et al.*, 2008). This is problematic because SVL does
41 not account for different body structures (Meiri, 2010) and SVL and body mass
42 probably scale at different rates in frogs (Anura), salamanders (Caudata) and caecilians
43 (Gymnophiona), and between different morphotypes within these three taxonomic
44 orders. In fact, morphotypes represent adaptations to environments imposing divergent
45 selective forces (Vidal-García *et al.*, 2014; Vidal-García & Keogh, 2015), and
46 morphological parameters often show distinct relationships (Guo & Lu, 2016).

47 The development of length-mass allometric relationships for amphibians would
48 contribute to overcome the above-mentioned issues. However, while length-mass
49 allometric relationships are available in scientific literature for a number of taxa (e.g.
50 Silva, 1998; Meiri, 2010; Feldman & Meiri, 2013), to our knowledge the only available
51 allometric models for anurans and salamanders date back to the 80's (Pough, 1980).
52 These are based on a limited number of species (Anura: n=15; Caudata: n=16),
53 including multiple individuals for the same species whilst not controlling for
54 phylogenetic autocorrelation. Additionally, the raw data used for these relationships
55 were never published, therefore it is impossible to know the identity of the species
56 underlying these relationships. Finally, allometric models that are meant to be used for
57 predictions should be evaluated for prediction accuracy, yet this is rarely done.

58 In this study we developed allometric relationships in amphibians to derive body
59 mass from SVL measurements. We fitted different models for frogs and salamanders,
60 and tested whether the relationships were different among morphotypes (Moen, Irschick
61 & Wiens, 2013; Moen, Morlon & Wiens, 2016) and between paedomorphic and non-
62 paedomorphic species. We hypothesized that:

- 63 1) allometric relationships between length and mass were different among species
64 with different habitat preferences (Vidal-García & Keogh, 2015), considering
65 that gravity exerts a different effect on aquatic, terrestrial and arboreal species,
66 and body mass is likely selected accordingly. Specifically we predicted that at
67 equal SVL arboreal frogs would be lighter than terrestrial and fossorial frogs,
68 and terrestrial and fossorial frogs would in turn be lighter than aquatic frogs.
69 Similarly, we predicted that at equal SVL terrestrial salamanders would be
70 lighter than aquatic salamanders.
- 71 2) paedomorphic species would display different relationships between length and
72 mass than species undergoing a full development, as metamorphosis implies a
73 major restructuring of the body's morphology, anatomy and physiology
74 (Brown & Cai, 2007).

75 We also fitted allometric models for all families having a sufficient sample size, in order
76 to evaluate the heterogeneity of the length-mass relationship across the different
77 lineages. Finally we used cross-validation to assess the predictive abilities of our
78 models, and thus to evaluate whether they can be successfully used to predict mass for
79 species for which this parameter is not available.

80

81 **Methods**

82 Data collection

83 We searched the Web of Science database in August 2016 using the following search
84 string: (body length OR body mass OR SVL OR length OR weight OR mass OR
85 allometr*) AND (amphibian OR anur* OR caecilian OR urodel* OR caudat*). We
86 saved the first 500 returned hits ordered by relevance. Additionally, we
87 opportunistically searched Google Scholar and Google using different combination of
88 the search terms "length", "mass", "SVL", "weight", "amphibian", "Anura", "frog",
89 "Gymnophiona", "caecilian", "Urodela", "Caudata", "salamander". After removing
90 duplicates, titles and abstracts were scanned by LS and AB for relevance. We recorded

91 the mean, ranges and individual mass (g) and length (SVL, mm) data of adult male and
92 female individuals, when possible, or for adults when there was no distinction between
93 sexes. These data were extracted from tables or graphs using WebPlotDigitizer 3.1
94 Desktop (<http://arohatgi.info/WebPlotDigitizer/>; Rohatgi, 2010). We recorded mass and
95 SVL data reported together for the same animals. We supplemented the data found in
96 publications with data collected in the field by one of the authors (GFF), and several
97 specialized websites (MVZ Herp Collection, AmphibiaWeb and CaliforniaHerps). For
98 those species for which we only found SVL data we performed additional searches
99 using the search string (Species name) AND (SVL OR mass OR length OR weight).
100 Besides morphometric measurements, we recorded information on the species' ecology
101 (habitat preference) and family. We categorized habitat as aquatic/semi-aquatic,
102 fossorial/terrestrial, and arboreal in frogs, and as terrestrial/fossorial and aquatic/semi-
103 aquatic in salamanders. Insufficient data were found for caecilians and therefore we
104 restricted our analyses to frogs and salamanders. In all our analyses we used one value
105 of SVL and mass per species by taking an average from multiple individuals and studies
106 weighted by sample size. All raw data collected are available in the supplementary
107 materials of this manuscript (Table S1).

108 Analyses

110 Data were log₁₀-transformed prior to the analyses to meet the assumptions of
111 normality, linearity and homoscedasticity of regression models (Appendix S1).

112 We first ran a linear regression between SVL and body mass and tested the residuals for
113 Pagel's λ . Pagel's λ measures the phylogenetic autocorrelation, and ranges from 0 (no
114 phylogenetic autocorrelation) to 1 (phylogenetic autocorrelation as expected under
115 Brownian motion). Because Pagel's λ was always significantly higher than zero (Anura:
116 $\lambda = 0.873$, $p < 0.001$; Caudata: $\lambda = 0.486$, $p = 0.016$) we used Phylogenetic Generalized
117 Least Square model (PGLS) to develop the allometric models based on the phylogeny
118 developed by Pyron (2014).

119 Amphibians often show sexual dimorphism for body size (Kupfer, 2007). In
120 principle, in sexually dimorphic species we should expect a difference in the allometric
121 models for males and females only if the body shape changes between the two sexes
122 (Mass and SVL proportions remain constant). However, at a given SVL females might
123 be heavier because they carry eggs (or embryos). We evaluated this possibility in
124 preliminary analyses (Appendix S2). As we did not observe differences between the two
125 sexes, for the main analyses we pooled males and females. We only used averages that
126 included both males and females. When individual data were available, we averaged the
127 average mass for the two sexes to avoid sex-biased estimates due to differences in
128 sample sizes.

129 We used the primary habitat preference as a categorical fixed factor, in order to
130 account for differences among morphotypes. However the sample size of some
131 categories was small and the distinction between aquatic and semi-aquatic, and
132 terrestrial and fossorial species is often unclear. Therefore, we clumped aquatic with
133 semi-aquatic species, and terrestrial with fossorial species in the same categories (Semi-
134 aquatic and Terrestrial respectively). Additionally, we used paedomorphosis as an
135 additional categorical fixed factor to distinguish between morphs in salamanders. We
136 ran 4 PGLS models for frogs and 7 for salamanders, for a total of 11 models (i.e. 2 sets
137 of candidate models). For both frogs and salamanders, the first model included SVL
138 only as predictor, the second included SVL and habitat, the third included SVL and an

139 interactive term for habitat, and the fourth included SVL and an additive and an
140 interactive term for habitat. For salamanders, we also considered an additive, an
141 interaction only, and an additive and interaction model with the category paedomorphic
142 (Table 1). The two models with the interaction terms were considered as we can expect
143 that the difference between morphotypes increases/decreases with SVL.

144 For each order, models were ranked using the AIC corrected for small sample
145 sizes (AICc) (Burnham & Anderson, 2002). Models were compared using Akaike
146 weights (ω), indicating the relative weight of evidence of competitive models. Models
147 were considered unequivocally supported if $\omega > 0.9$. If no model showed unequivocal
148 support, we used model averaging, which produce model parameters that take into
149 account the uncertainty detected by the model selection procedure (Burnham &
150 Anderson, 2002). The average model was calculated by taking the average of models'
151 coefficients weighted by the models' Akaike weights, and assuming a weight of zero for
152 the models in which a given variable was not included. We also calculated the relative
153 importance of variables, by summing the weights of all models including that variable.
154 Then for each Family having $N \geq 5$, we ran a separate allometric model including only
155 SVL as a predictor since species belonging to the same family generally have the same
156 habitat preferences (see Table S1). Because in the Ambystomatidae family
157 measurements for the Axolotl (*Ambystoma mexicanum*) were particularly influential on
158 the slope, we ran an additional model excluding the Axolotl.

159 We used a 5-fold cross-validation to test the accuracy of the allometric models
160 by splitting the dataset into training (random 80% of the data) and testing dataset
161 (remnant 20% of the data), where the former was used to fit the model, and the latter to
162 validate it. For each validation we calculated two forecasting error estimates: the Root
163 Mean Square Error (RMSE) and the Mean Absolute Percentage Error (MAPE). RMSE
164 is a scale-dependent measure, in which the errors are squared before the average.
165 Therefore, RMSE penalizes more large errors and it is more sensitive to outliers than
166 MAPE. Conversely, MAPE is scale-independent and provides an intuitive measure for
167 interpretation (Hyndman, 2006). The cross-validation procedure was repeated 10 times
168 and the forecasting errors averaged. For the allometric models for each family, we used
169 a jackknife cross-validation instead by removing 1 observation at a time. This was
170 necessary as the sample size of some families did not allow for conducting a 5-fold
171 cross-validation.

172 Our main analyses were limited to species for which paired measurements of
173 body mass and SVL were available from the same individuals. However, in
174 interspecific allometric models on traits and taxa for which a limited amount of data are
175 available, it is not unusual to derive data for the dependent and the independent
176 variables from separate sources to increase sample size and taxonomic coverage
177 (Gittleman & Harvey, 1982; Pagel & Harvey, 1988; Swihart *et al.*, 1988; White &
178 Seymour, 2003; Hendriks *et al.*, 2009; Santini *et al.*, 2013). Therefore, we repeated
179 the analyses presented in the main text using a larger dataset that also included mass-length
180 measurements collected from different sources for species for which paired
181 measurements were not available, and compared the results with those in the main text
182 (Appendix S3).

183 All analyses were conducted in R 3.0.3 (R Core Team, 2016) using the packages
184 'ape' (Paradis, Claude & Strimmer, 2004), 'caper' (Orme, 2013) and 'phytools' (Revell,
185 2012).

186

187

188 **Results**

189 Data were gathered from 207 different sources including peer-reviewed articles, PhD
190 and MSc theses, and specialized websites (see Table S1). We found body mass data on
191 190 frog species and 88 salamander species, but for 111 and 49 species only paired SVL
192 measurements calculated on the same individuals were available. Because not all
193 species in our datasets were included in the phylogeny, we excluded from the analyses
194 23 species of frogs, and 3 species of salamanders. The final dataset included 88 species
195 of frogs and 46 species of salamanders. Frog species ranged between 15.99-262 mm
196 SVL and 0.32-1907 g body mass, whereas salamanders ranged between 23.99-542 mm
197 SVL and 0.23-912.7 g body mass.

198 In frogs, the best AICc model suggested an interactive effect between habitat
199 and SVL, but no model was unequivocally supported ($\omega > 0.9$) so we averaged all
200 models weighting by Akaike ω (Table 1). In the average model, the slope of the length-
201 mass relationship was steeper for semi-aquatic and terrestrial species than for arboreal
202 species, partly supporting our first prediction (Fig. 1). The importance of habitat as
203 additive or interactive term was not very high (Table 2), yet the average model that
204 accounts for the weight of evidence of the models suggests different estimates (Table
205 3).

206 In salamanders, we found one highly supported model that included an additive
207 and an interaction term with the factor 'paedomorphic' (Fig. 1, Table 1), in accordance
208 to our second prediction. Paedomorphic animals displayed a less steep relationship
209 indicating longer and lighter bodies. The variance explained by the models was high
210 ($\text{adj. } R^2 > 0.9$; Table 3). The models on frogs showed good predictive performances with
211 RMSE ranging between 0.12 and 0.15 and MAPE ranging between 17.97% and
212 31.01%. The supported model on salamanders had lower predictive performances with
213 $\text{RMSE}=0.28$ and $\text{MAPE}=44.79\%$ (Table 3). Complete model outputs are presented in
214 the Table S7.

215 We ran allometric models for 5 Anura and 3 Caudata families (Table 3-S7, Fig.
216 2). The slopes for the individual families slightly differed from the models at the order
217 level, yet the differences were not significant. The intercepts of the relationships
218 between families were similar with the exception of true toads (Bufonidae) that were
219 systematically heavier. These models performed better than the models at the order
220 level in terms of forecasting errors and variance explained (Table 3).

221 Although the sample size of the dataset including unpaired mass-length
222 measurements was almost twice as large as the dataset including only paired
223 measurements, the resulting models had lower explained variance and predictive
224 performances (Appendix S3).

225

226 **Discussion**

227 Snout to vent length is the most frequently available morphometric measure reported for
228 amphibians (Dodd, 2010; Vitt & Caldwell, 2013), yet body mass - although variable
229 between populations and within individuals (Dodd, 2010) - is necessary for some
230 applications (Watanabe *et al.*, 2005; Gibbons *et al.*, 2006). In this work we developed
231 allometric relationships that can be used for estimating body mass from SVL
232 measurements. The allometric models performed well both in terms of explained
233 variance and forecasting errors, and can therefore provide reliable predictions for
234 species for which average body mass measurements are unavailable. Our allometric

235 model for frogs provides predictions comparable to those derived from the model in
236 Pough (1980). Specifically, the model developed by Pough (1980) provides similar
237 predictions to our model on arboreal species at small SVLs, and similar to our model on
238 semi-aquatic and terrestrial at larger SVLs (Fig. S4). In contrast, Pough's model for
239 salamanders provides different results, consistently underestimating the mass of non-
240 paedomorphic species, and overestimating the mass of paedomorphic species with SVL
241 > 63 mm while underestimating the mass of larger paedomorphic species (Fig. S4).

242 Two main hypotheses (so-called similarity hypotheses) describe how anatomical
243 structures would be affected by increasing body size (Schmidt-Nielsen, 1984). The
244 geometric similarity hypothesis predicts body length to scale with body mass to the
245 power of 0.33, whereas the elastic similarity hypothesis predicts body length to scale
246 with body mass to the power of 0.25. Our results seem to support the geometric
247 similarity hypothesis better, but do not strictly conform to that, and are in line with
248 previous length-mass allometries in vertebrates that generally range between 0.25 and
249 0.32 (Green, 2001).

250 As expected, the relationship between SVL and body mass is somehow
251 heterogeneous among frogs with different habitat preferences (Moen *et al.*, 2013, 2016),
252 with arboreal species being lighter than terrestrial and semi-aquatic species at a given
253 SVL. Furthermore, body mass increases more rapidly with increasing SVL for
254 terrestrial and semi-aquatic species, suggesting that for arboreal frogs limiting body
255 mass is particularly important in larger species. Conversely, contrary to our predictions,
256 we did not find differences between terrestrial and semi-aquatic species. In frogs, body
257 length and body mass are key determinants of locomotor performance: longer body
258 length is often associated with longer legs, and heavier body generally determines
259 higher muscle mass and acceleration (Wassersug & Sperry, 1977; Ficetola & De
260 Bernardi, 2006). Overall, larger and heavier frogs tend to have better locomotor
261 performance, and heavy body mass is not disadvantageous, even when taking into
262 account leg length (Emerson, 1978; Semlitsch *et al.*, 1999; Ficetola & De Bernardi,
263 2006). However, arboreal frogs often move on small branches, which may deform
264 substantially under heavy loads (Astley, Haruta & Roberts, 2015). Therefore a limited
265 body mass likely improves the possibility of movement in the tree canopy. Furthermore,
266 after hopping arboreal frogs often land by attaching with toes to small branches. Forces
267 acting on toes at landing may be up to fourteen times the mass of the animal (Bijma,
268 Gorb & Kleinteich, 2016), and this might additionally impose limits to body mass.
269 Conversely, these are probably less important for terrestrial and semi-aquatic frogs.

270 Contrary to our predictions, the allometric models for salamanders were not
271 different between terrestrial and semi-aquatic species. As predicted, however,
272 paedomorphic species exhibited lower slopes than non-paedomorphic species. This
273 difference is likely associated with the restructuring of body morphology and anatomy
274 taking place during metamorphosis (Brown & Cai, 2007). Nonetheless, caution on the
275 interpretation of this difference is needed as the number of paedomorphic species in our
276 sample was low. A comparison between metamorphosed and paedomorphic adults in
277 species with facultative paedomorphosis could shed more light on these differences.

278 The allometric models for the individual families showed different coefficients,
279 and generally better predictive performances, than models fitted across all families.
280 Consequently, allometric relationships for families are preferable for predictions when
281 possible. An exception is given by the Pelobatidae family (spadefoot toads), for which
282 the predictive power was lower than that of models including all families. This is

283 probably because Pelobatidae in our dataset had a very limited range of SVL variation
284 (SVL range: 49-74 mm) that hampers obtaining relationships with high determination
285 coefficients and predictive value.

286 The dataset supplemented with unpaired length-mass measurements allowed us
287 to use information on a larger number of species and families, but increased the error
288 associated to the models (Appendix S3). In fact, amphibians show strong intraspecific
289 variation in body size, with differences among individuals within populations, and
290 among populations within the species (Morrison & Hero, 2003; Adams & Church,
291 2008; Cvetković *et al.*, 2009; Ficetola *et al.*, 2010; Guo & Lu, 2016). The better
292 performance of the model based exclusively on paired measurements suggests that,
293 when analyzing macroecological relationships among morphological traits with high
294 intraspecific variability, it is better to improve data quality at the expenses of quantity.

295 Although our models showed consistently high predictive performance, the
296 accuracy and the generality of the allometric relationships is limited by sample size,
297 especially in salamanders. For example, more complex models also including habitat,
298 might have been selected for salamanders if a sufficient sample size was provided.
299 Similarly, within frogs, the three supported models suggest that both the intercepts and
300 the slopes probably differ between semi-aquatic, terrestrial and arboreal species, but
301 sample size limited model complexity penalizing the most complex model (additive and
302 interactive term for habitat). Therefore, although our models show good predictive
303 performances, additional data on body mass for frogs and salamanders would contribute
304 to develop even better allometric models, and, more importantly, to increase the number
305 of families and species for which family- and species-specific models can be fitted
306 (Deichmann *et al.*, 2008). All data used for the modelling are available in the
307 supplementary materials of this paper providing a good basis for further data collection
308 and studies on amphibians' morphometric measurements and their intra-specific
309 variability.

310 The high predictive power of our models suggests that they can be used in
311 macroevolutionary and macroecological analyses that require information on species
312 body mass, especially when these data are not available for some species, or the
313 available values do not seem to be representative of the species as coming from a few
314 individuals. Predictions from our models allow estimating body masses that are
315 comparable between frogs and salamanders, and between different morphotypes in
316 frogs. Our models would clearly be inappropriate for predictions on single individuals,
317 because body weight in a specific period strongly depends on the body condition of the
318 animal. Nevertheless, they will provide a good approximation of the average mass of a
319 species, provided that representative averages of the species SVL are available. In
320 conclusion, our models can contribute to uniform conservation, macroecological and
321 macroevolutionary analyses by employing a single measurement of body size that
322 increases comparability among taxa and is more directly related to the underlying
323 ecological processes for which it is used as a proxy.

324
325

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Commenté [FF1]: C'è qualche non scientifico nei riferimenti che non è in corsivo (in Ficetola et al. 2010, Bijma et al., Cvetković et al. ...)

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Table 1. PGLS models' selection results ordered by AICc. M = Mass; SVL = Snout-to-Vent length; H = Habitat preference; P = Paedomorphic; : = interaction term; * = additive and interaction term; AICc = Akaike Information Criterion corrected for small sample sizes; Δ AICc = Difference in AICc from the most supported model; ω = Akaike weights; df = degrees of freedom.

Taxon	Formula	AICc	ΔAICc	ω	df
Anura	<i>M~SVL:H</i>	-129.201	0	0.532	4
	<i>M~SVL+H</i>	-128.216	0.985	0.325	4
	<i>M~SVL*H</i>	-126.567	2.634	0.142	6
	<i>M~SVL</i>	-116.141	13.060	0.001	2
Caudata	<i>M~SVL*P</i>	-25.831	0	0.925	4
	<i>M~SVL:P</i>	-20.304	5.527	0.058	3
	<i>M~SVL+P</i>	-16.672	9.159	0.009	3
	<i>M~SVL*H</i>	-14.000	11.831	0.002	4
	<i>M~SVL:H</i>	-13.311	12.520	0.002	3
	<i>M~SVL</i>	-13.217	12.614	0.002	2
	<i>M~SVL+H</i>	-12.504	13.327	0.001	3

Table 2. Variable importance estimate based on Akaike weights.

Taxon	Variable	Importance
Anura	SVL	1.000
	Habitat (interaction)	0.674
	Habitat (additive)	0.467
Caudata	SVL	1.000
	Paedomorphic (interactive)	0.983
	Paedomorphic (additive)	0.934
	Habitat (additive)	0.003
	Habitat (interaction)	0.004

Table 3. Power laws for predicting body mass (g) from SVL (mm) for anurans, caudates and families with $N \geq 5$. All models' coefficients, associated standard errors and statistical significance are presented in Table S7. H = Habitat preference; A = Arboreal; SA = Semi-Aquatic and Aquatic; T = Terrestrial; P = Paedomorphic; adjR^2 = Adjusted R²; n = sample size; RMSE = Root Mean Square Error; MAPE = Mean Absolute Percentage Error.

Taxon	Formula	Power law	adjR ²	n	RMSE	MAPE
Anura	<i>Average model</i>	<i>A</i> : $10^{-4.328} \times \text{SVL}^{3.098}$	0.949-0.966	88	0.119-0.150	17.969-31.010
		<i>SA</i> : $10^{-4.375} \times \text{SVL}^{3.215}$				
		<i>T</i> : $10^{-4.298} \times \text{SVL}^{3.181}$				
Bufo	<i>M-SVL</i>	$10^{-3.791(\pm 0.275)} \times \text{SVL}^{2.914(\pm 0.148)}$	0.980	9	0.081	5.731
Hylidae	<i>M-SVL</i>	$10^{-4.462(\pm 0.236)} \times \text{SVL}^{3.201(\pm 0.141)}$	0.938	35	0.207	18.856
Myobatrachidae	<i>M-SVL</i>	$10^{-4.586(\pm 0.357)} \times \text{SVL}^{3.372(\pm 0.228)}$	0.952	12	0.128	13.206
Ranidae	<i>M-SVL</i>	$10^{-4.862(\pm 0.749)} \times \text{SVL}^{3.492(\pm 0.425)}$	0.847	13	0.179	12.100
Caudata	<i>M-SVL*P</i>	<i>nP</i> : $10^{-4.709(\pm 0.255)} \times \text{SVL}^{3.045(\pm 0.134)}$	0.940	46		44.792
		<i>P</i> : $10^{-3.567(\pm 0.361)} \times \text{SVL}^{2.325(\pm 0.246)}$				
Ambystomatidae	<i>M-SVL</i>	$10^{-4.215(\pm 1.265)} \times \text{SVL}^{2.867(\pm 0.696)}$	0.727	7	0.199	19.070
Ambystomatidae (+A.m.)	<i>M-SVL</i>	$10^{-2.677(\pm 0.629)} \times \text{SVL}^{2.012(\pm 0.332)}$	0.836	8	0.836	11.178
Plethodontidae	<i>M-SVL</i>	$10^{-4.706(\pm 0.322)} \times \text{SVL}^{2.968(\pm 0.189)}$	0.925	21	0.184	19.331
Salamandridae	<i>M-SVL</i>	$10^{-4.744(\pm 0.414)} \times \text{SVL}^{3.073(\pm 0.237)}$	0.933	13	0.176	26.382

Figure legends

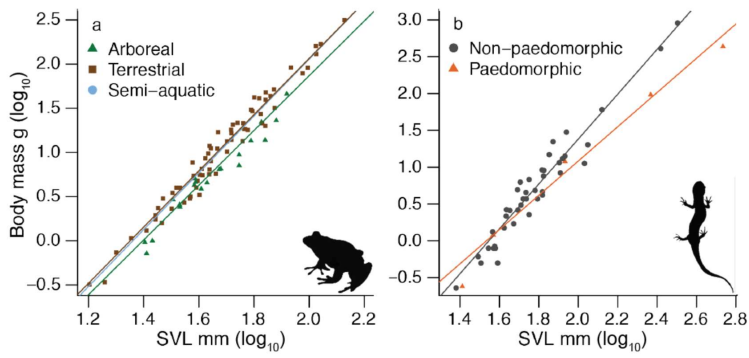


Fig. 1. Relationships between SVL and body mass for frogs (a) and salamanders (b).

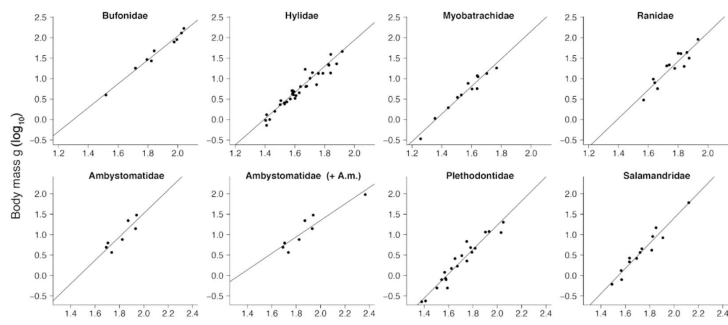


Fig. 2. Relationships between SVL and body mass for families with $N \geq 5$. + A.m. = Dataset including the Axolotl (*Ambystoma mexicanum*).