Ecography

Supplementary material

Appendix 1: The putative effect of local species richness on the estimation of the activation energy of calling activity (E)

Here we show that there is no effect of local community richness on the estimation of the activation energy. Lets denote by S_a the number of species calling in each month. Then, according to the metabolic theory this should be

$$S_a \sim e^{\frac{-E}{kT}}$$

now, normalizing by S_{loc} or the total number of species that called at some moment of the year (in this work it is considered as the community species richness)

$$\frac{S_a}{S_{loc}} \sim \frac{e^{\frac{-E}{kT}}}{S_{loc}}$$

finally, linearizing the above equation we obtain

$$ln\left(\frac{S_a}{S_{loc}}\right) \sim ln\left(\frac{e^{\frac{-E}{kT}}}{S_{loc}}\right)$$

$$ln\left(\frac{S_a}{S_{loc}}\right) \sim \frac{-E}{kT} - ln(S_{loc})$$

$$ln\left(\frac{S_a}{S_{loc}}\right) \sim -E\frac{1}{kT} - ln(S_{loc})$$

where, E is the activation energy of the calling behavior, k is Boltzmann´s constant (8.62x10-5eV/K, Gillooly et al. 2001) and T is temperature in degrees Kelvin. The above development shows that species richness only affects the intercept estimation of the metabolic model and has no effects on the estimation of the activation energy. If you work with "$Ln(S_a)$" or "$Ln(S_a/S_{loc})$" the slope remains "E". Thus, there is no effect of species community richness (S_{loc}) on the slope E.

Appendix 2: Structural equation modelling

In order to evaluate the putative connection between environmental variables, local species richness (S_{loc}, total number of species that call at least once in the study period), community seasonality (S_{amp}, amplitude of the sinusoidal function), and the activation energy of the calling activity (E), we performed four Structural Equation Models (SEM) (Shipley 2000). In all of them we constructed a latent variable, Environment, with three components: NDVI (normalized difference vegetation index), PET (potential evapotranspiratio*n*) and Latitude. We performed alternative path models including a central role of local species richness (S_{loc}) connecting the environment with E (Fig. A1 and A2), an external role of S_{loc} on E which is also connected with the environment (Fig. A3), and the last SEM includes E, S_{loc} and S_{amp} affected by the environment with only a connection between the last two variables (Fig. A4).

Appendix 3: Phylogenetic tree reconstruction

To reconstruct the phylogeny of the 361 species of Neotropical anurans found in our community datasets we began by finding the species in common with the molecular matrix of Pyron and Wiens (2011). Because some species were not represented in the molecular matrix, we used "surrogate" species of the same genus: *Dendrophryniscus* sp. was represented by *Dendrophryniscus minutus*; *Eleutherodactylus* sp. by *Eleutherodactylus abbotti*; *Chiasmocleis albopunctata* by *Chiasmocleis hudsoni*; *Flectonotus ohausi* by *Flectonotus fitzingeri*; *Megaelosia boticariana* by *Megaelosia goeldi*; *Pleurodema fuscomaculatum* by *P. diplolister* together with *Pleurodema bibroni*. In addition, Pyron and Wiens (2011) did not sample *Stereocyclops incrassatus*, which we added to the root of the family
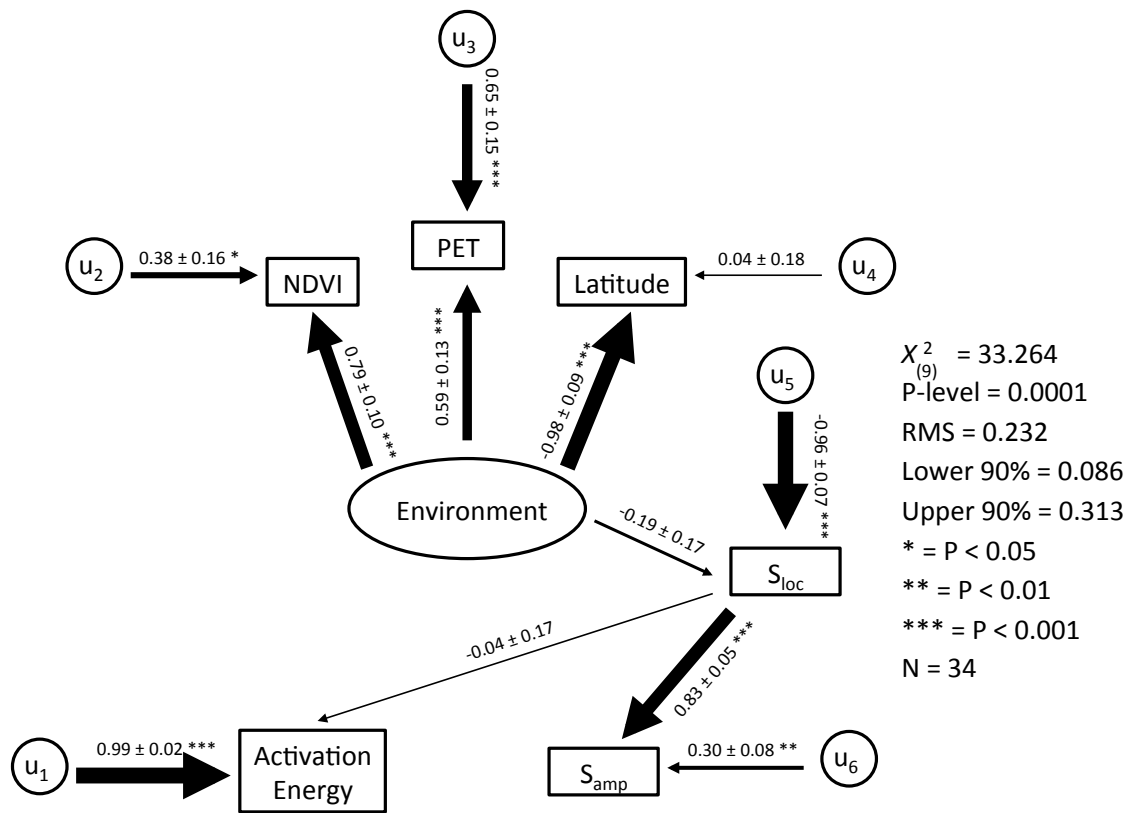
Microhylidae following Frost et al. (2006)*; Centrolenella* sp. registered by (Cardoso and Souza 1996) in our ecological matrix was considered a sister group of *Vitreorana* because it belongs to the family Centrolenidae. Finally, "Gen. sp." registered by Bernarde (2007) was included to the root of Centrolenidae (Bernarde com. pers.).

With all of these sequences we estimated a new tree of 164 species; including *Homo sapiens* as outgroup, with the program RAXML using the same concatenated sequences and models of Pyron and Wiens (2011). To this tree of 164 species we added the remaining taxa of the ecological matrix that did not have genetic information using a taxonomic criterion. The added species were collapsed to the ancestral node of the genus in order to avoid any assumptions about their affinity with other species in their respective genera. Those species that were assigned by authors to other species (i.e. "affinis" and conferred), were collapsed to them. This method did not modify the known relationships between other species already in the tree. In order to estimate the node ages of the 164 species tree, we used eight nodes shared with the tree dated by Wiens (2011, Fig. 2) and the software r8s 1.8 (Sanderson 2012). These eight fixed nodes were those which clustered *Homo sapiens* with *Pipa carvalhoi* (400 My), *Pipa carvalhoi* with *Lithobates catesbeianus* (250 My), *Lithobates catesbeianus* with *Leptodactylus fuscus* (200 My), *Leptodactylus fuscus* with *Dendrophryniscus minutus* (159.8 My), *Thoropa miliaris* with *Scinax ruber* (152.5 My), *Flectonotus fitzingeri* with *Oreobates quixensis* (133.6 My), *Phyllomedusa tomopterna* with *Scinax.nasicus* (125.4 My), *Flectonotus fitzingeri* with *Gastrotheca fissipes* (114.7 My), *Pseudis paradoxa* with *Scinax fuscovarius* (107.4 My), *Leptodactylus fuscus* with *Leptodactylus mystacinus* (54.1 My), *Dendrophryniscus minutus* with *Rhinella marina* (39.3 My), *Trachycephalus venulosus* with *Osteocephalus taurinus* (39.3 My). Using the BLADJ module of PHYLOCOM software (Webb et al. 2008), we estimated
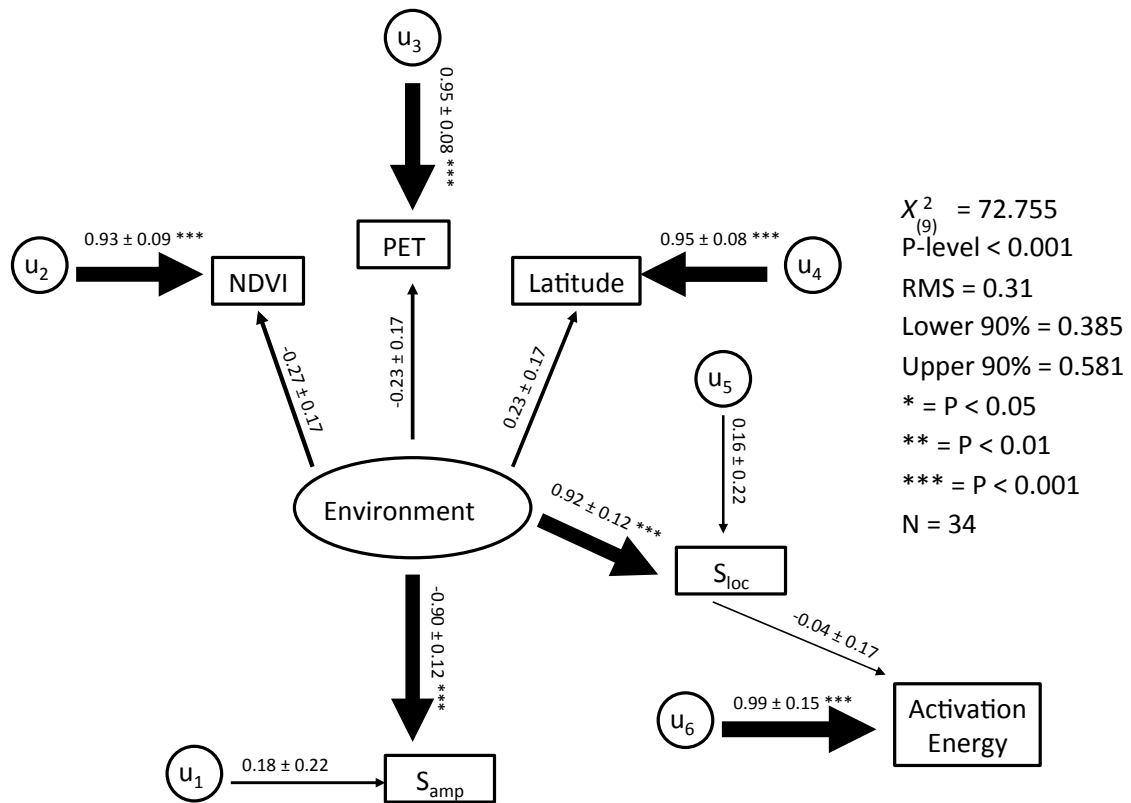
the branch lengths of the tree of 361 anuran species (Fig. A5). The anuran taxonomy used in this article follows Frost (2015).

Appendix 4: Association between temperature range (T_{range}) with the activation energy estimation (E) and with standard error of E (SE of E)
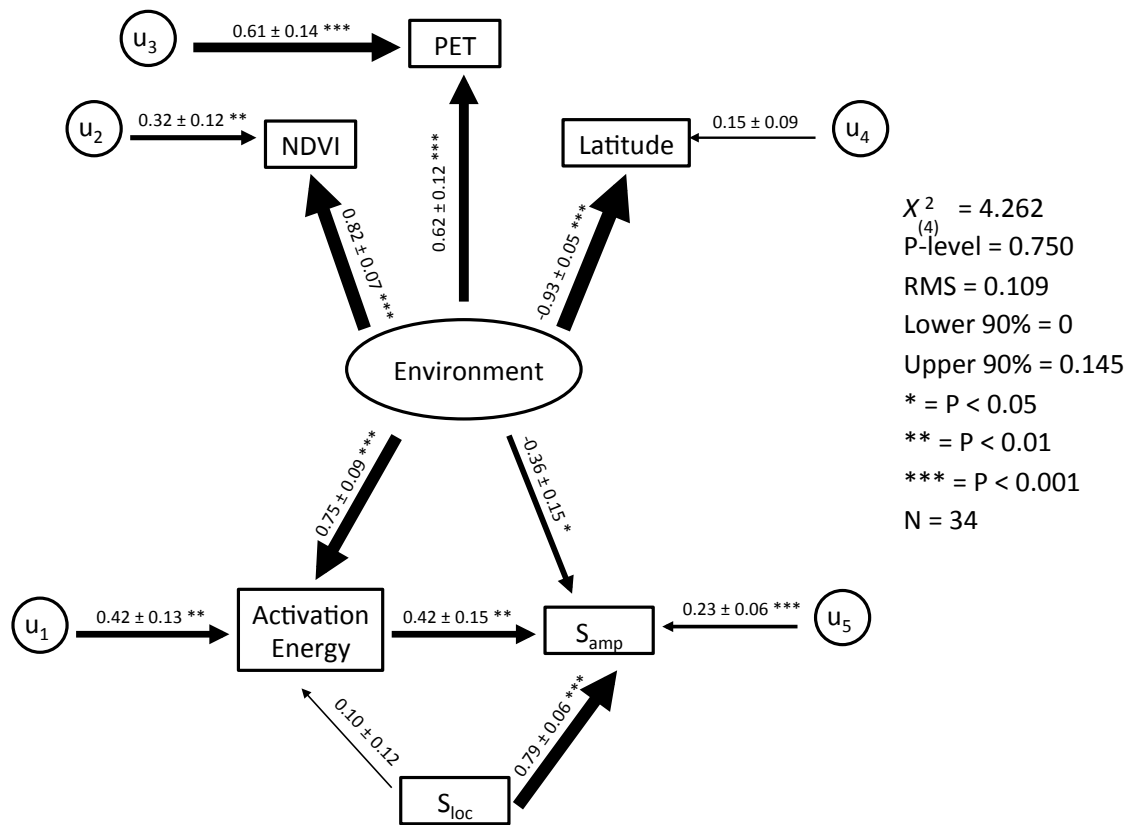
We explore a statistical artifact related to the range of temperatures from which activations energies (E) were estimated (Pawar et al. 2016). The source of an overestimation of E is the potential nonlinear association between log(S) and 1/KT (see Pawar et al. 2016). This non-linearity was not observed in our dataset, where the probability of the linear model is close to 1.0 in comparison to its alternatives. Discarding non-linearity, the relatively narrow range of temperatures experienced by amphians' communities could determine an over dispersion of estimated E—large standard errors (Pawar et al. 2016). It should be highlighted that the present dataset follows the opposite trend, with an increase in standard errors within the temperature range (Fig. A6).

Figure A1: Evaluation of the putative role of the environment and local community richness (S_{loc}) on the activation energy of anuran calling activity through local species richness. S_{loc}, total number of species that call at least once in the study period; NDVI, normalized difference vegetation index; PET, potential evapotranspiration; S_{amp} is a parameter of the sinusoidal function: $S=S_{mean}+S_{amp} \sin [2\times\pi\times(month + c)/12]$; S, number of species that call in a particular month; S_{amp}, amplitude of the sinusoidal function; S_{mean}, mean value of S estimated from the sinusoidal function. Path values are standardized effects ± 1 SE. Arrow width represents the strength of the causal link. u1 to u6 represent variances unexplained by the model, and the explained variance for endogenous variables is represented by one minus the path coefficient between its associated error variable. RMS, root mean square error.
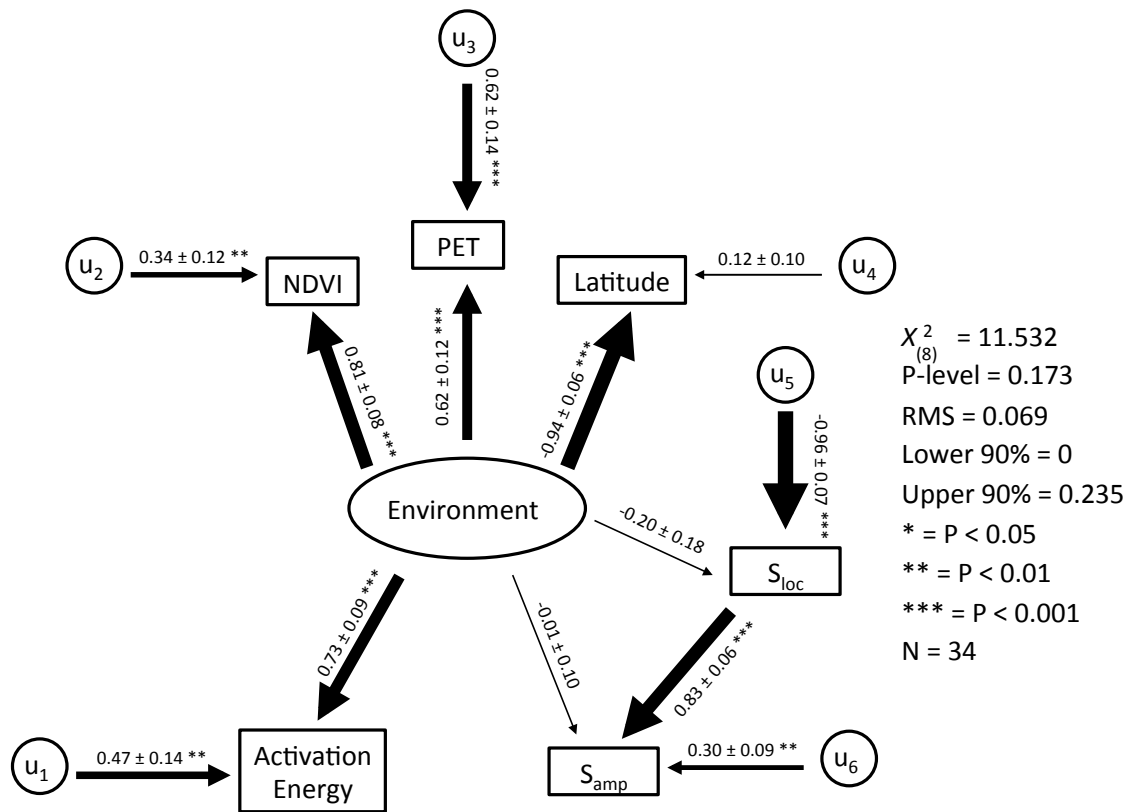
u_3

0.95 ± 0.08 ***

u_2 0.93 ± 0.09 *** NDVI

PET

Latitude 0.95 ± 0.08 *** u_4

-0.27 ± 0.17

-0.23 ± 0.17

0.23 ± 0.17

u_5

0.16 ± 0.22

$X^2_{(9)}$ = 72.755
P-level < 0.001
RMS = 0.31
Lower 90% = 0.385
Upper 90% = 0.581
* = P < 0.05
** = P < 0.01
*** = P < 0.001
N = 34

Environment

0.92 ± 0.12 ***

S_{loc}

-0.90 ± 0.12 ***

-0.04 ± 0.17

u_6 0.99 ± 0.15 *** Activation Energy

u_1 0.18 ± 0.22 S_{amp}

Figure A2: Evaluation of the putative role of the environment and local community richness on the activation energy of anuran calling activity through local species richness. For further references see Fig. A1.
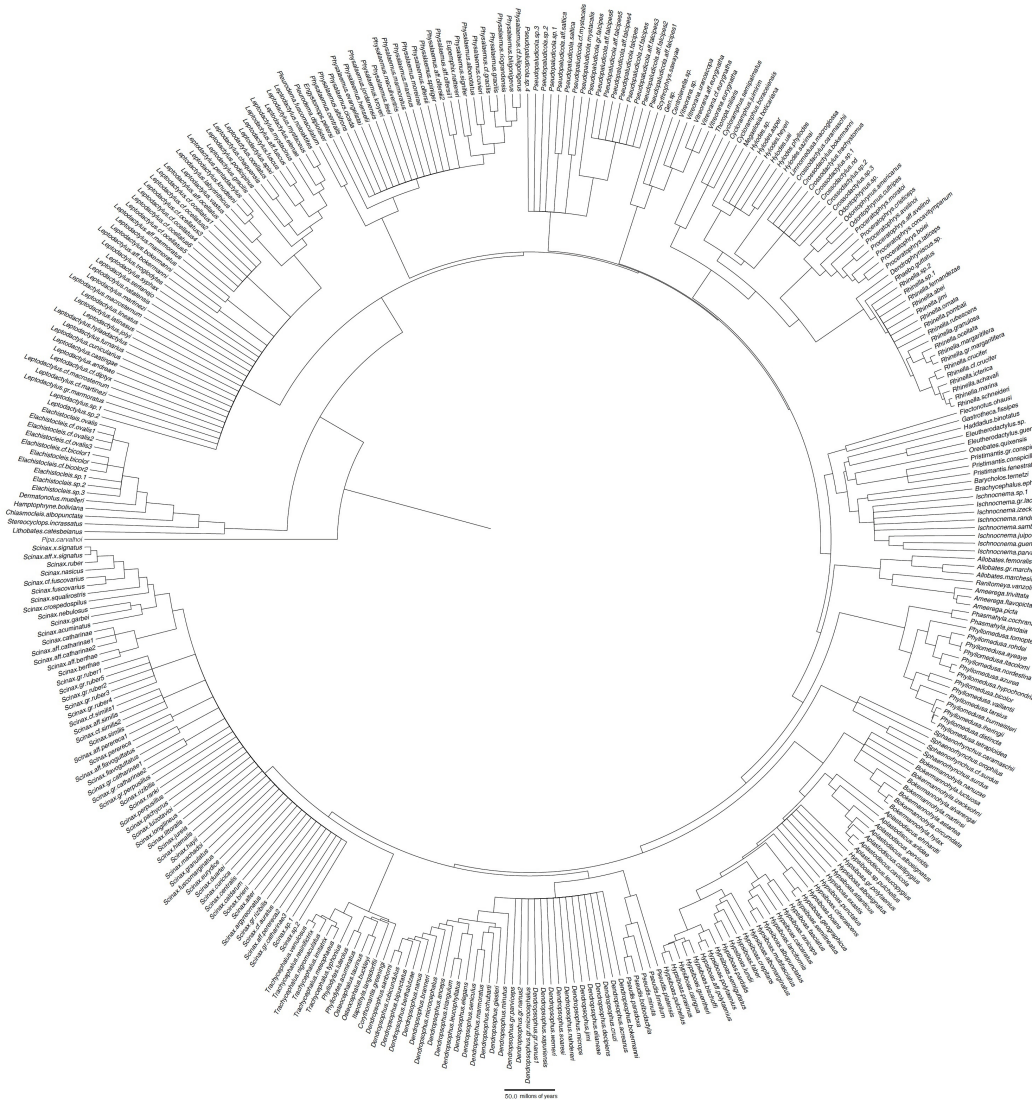
Figure A3: Evaluation of the putative role of the environment and local community richness on the activation energy of anuran calling activity with independent and direct effects of environment and local species richness. For further references see Fig. A1.
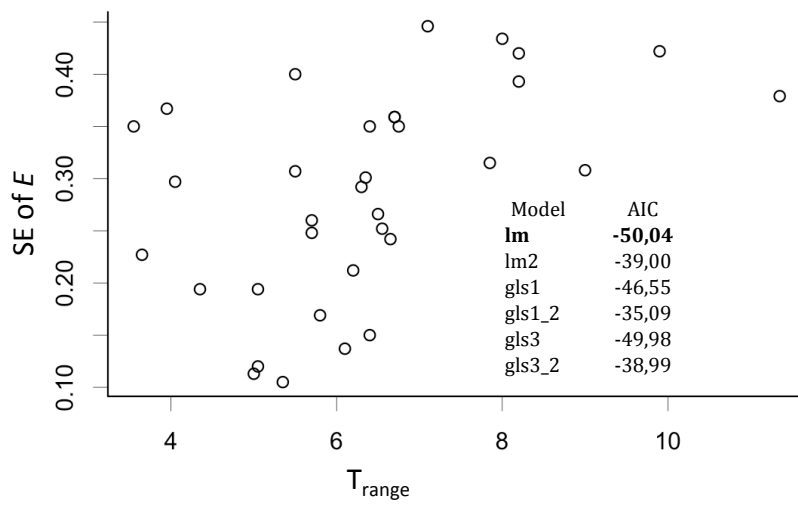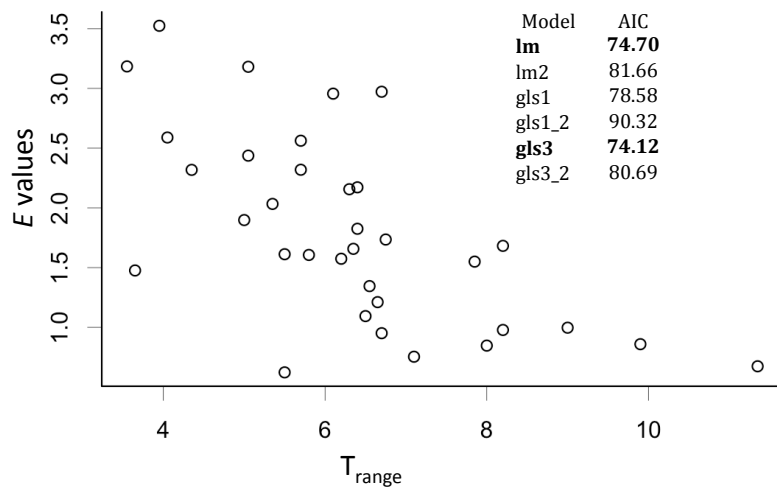
Figure A4: Evaluation of the putative role of the environment on the activation

energy of anuran calling activity. For further references see Fig. A1.

Figure A5: Reconstructed phylogenetic tree for the 361 species of Neotropical anurans found in our community datasets.

Model	AIC
lm	**-50,04**
lm2	-39,00
gls1	-46,55
gls1_2	-35,09
gls3	-49,98
gls3_2	-38,99

Figure A6: standard error (SE) of activation energy estimations (E) *vs.* temperature ranges (T_{range}). lm: lineal model, lm2: second order polynomic model, gls: linear model with error variance proportional to T_{range}, gls1_2: second order polynomic model with error variance proportional to T_{range}, gls3: linear model with error as a power function of T_{range}, gls3_2: polynomic model with error as a power function of T_{range}.

Figure A7: activation energy estimations (*E*) *vs*. temperature ranges (T_{range}). lm: lineal model, lm2: second order polynomic model, gls: linear model with error variance proportional to T_{range}, gls1_2: second order polynomic model with error variance proportional to T_{range}, gls3: linear model with error as a power function of T_{range}, gls3_2: polynomic model with error as a power function of T_{range}.

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