

## Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

### Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a | Confirmed

- The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
- An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted  
*Give  $P$  values as exact values whenever suitable.*
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's  $d$ , Pearson's  $r$ ), indicating how they were calculated
- Clearly defined error bars  
*State explicitly what error bars represent (e.g. SD, SE, CI)*

*Our web collection on [statistics for biologists](#) may be useful.*

### Software and code

Policy information about [availability of computer code](#)

Data collection

No software was used for data collection.

Data analysis

We used R version 3.4.0. The source code of a program "SLOUCH" is available at (<https://github.com/kopperud/slouch>) and as a supplementary data file.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

### Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

All data and source code that support the finding of our study are available either as supplementary materials or as an archived dataset in Dryad.

## Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences  Behavioural & social sciences  Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

## Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Our research is a phylogenetic comparative study based on existing data. Our data consist of 20,293 observations of brain and body mass across 4,587 species and dated molecular phylogenies.
Research sample	Our study is based on existing datasets and a lab population of the guppy ( <i>Poecilia reticulata</i> ). The data is brain mass (gram) and body mass (gram). The source of datasets are briefly described in the manuscript and a complete description (taxa, measurements, sample size, standard deviation, original source, sex, age and notes) is supplied in dataset deposited in Dryad.
Sampling strategy	We used all available data and no attempts were made to predetermine sample size.
Data collection	Brain and body size of the guppy were collected by one person (Alexander Kotrschal) using a digital weight. All the rest of our data were obtained from existing datasets.
Timing and spatial scale	Since our goal is to gain a global view on how brain-body allometry within- and across-species are related, we collected all available data relevant to our question irrespective of timing and spatial scale.
Data exclusions	From all published datasets that we have examined, we exclusively included the data that meets the following criteria: 1) data are taken from sexually-mature adult individuals evaluated either by direct description in the source or inferred from body size, ii) data represent original measurements of samples recorded by authors of the data source, and iii) brain mass are reported with body mass collected from the same individual(s). These initial screenings were made to ensure that we estimate allometries at a comparable life stage and that the data will be reported with full transparency. In addition, in our assessment of the static allometry, we excluded 1.34 % of the relevant subset of the data based on model residuals and cook's distance with pre-established exclusion criteria, as described in the text.
Reproducibility	We performed no experiments to reproduce.
Randomization	Our study does not have groups to allocate samples. Thus, randomization is not relevant to our study.
Blinding	The majority of our study is based on existing data, thus blinding is not applicable for this subset of the data. With respect to the data collected from a lab population of the guppy, the data were collected blindly to our study question.
Did the study involve field work?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> No

## Reporting for specific materials, systems and methods

### Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique biological materials
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

### Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals

Wild animals

The study does not involve wild animals.

Field-collected samples

The study does not involve field-collected samples.