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☐ Initial submission ☐ Revised version ☒ Final submission

# Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

## Experimental design

1. Sample size

Describe how sample size was determined.

For our analysis, we extracted datasets from the BIOFRAG database only using datasets that measured abundance of vertebrates in at least nine plots per landscape. We subsequently analysed the abundance responses of all unique species measured in a total of 22 landscapes. Sample size is given as n. Sample sizes are described in the relevant text sections in the manuscript (Lines 223,225,244,248,249, 274), in the legends of Figures (1 to 3) and of Extended Data (Tables 1 and 4 and Figures 1 to 3). We used non-parametric tests for pair-wise comparisons. To test whether body size predicts species responses to edges, we used general additive models implemented in the mgcv package of the R statistical software.

2. Data exclusions

Describe any data exclusions.

In the analyses of threatened versus non-threatened species, we excluded species that have not been assessed for IUCN Red Lists or that were listed as data deficient (Extended Data Table 3, Lines 200-203). In the gam models linking body size of amphibians to their edge sensitivity, we excluded two species of the order Gymnophiona, as their body shape resembles that of worms or snakes (Fig. 3 Legend and Lines 223-224). When modelling edge sensitivity as a function of multiple predictors, we excluded highly inter-correlated predictors (V > 0.5, R2 > 0.5, P > 0.6) from these models using Pearson's Chi-squared test with Yates' continuity correction and Cramer's V measure of association to test for correlations among categorical predictors (lsr package), Pearson's product-moment correlation P for associations between numeric predictors and the coefficient of determination R2 of linear models for relationships between numeric and categorical predictors (Extended Data Table 4, see Methods for details - Lines 777-782, 791). When comparing edge sensitivities among edge response types, we excluded species that could not be classified (n = 113).

3. Replication

Describe whether the experimental findings were reliably reproduced.

Experimental replication was not attempted.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

Samples were not randomized for the experiments.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

We did not use techniques to blind the investigators to the experimental groups.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

| n/a | Confirmed |
|---|---|
| ☐ | ☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.) |
| ☒ | ☐ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| ☒ | ☐ A statement indicating how many times each experiment was replicated |
| ☐ | ☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section) |
| ☐ | ☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons |
| ☐ | ☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted |
| ☐ | ☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range) |
| ☒ | ☐ Clearly defined error bars |

*See the web collection on statistics for biologists for further resources and guidance.*

## Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.

We used R 3.2.1 statistical software for all our analyses: proportion tests, multiple pairwise comparisons between groups, general additive models (mgcv package), multi-model averaging (MuMin package and lsr package). We used in house generated software for analyses central to the manuscript. Details on these analyses are described in the Methods section of the manuscript. The software itself is accessible at https://github.com/VeroL/BioFrag (see reference 29 in the manuscript).

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

## Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

NA

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

NA

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

NA

b. Describe the method of cell line authentication used.

NA

c. Report whether the cell lines were tested for mycoplasma contamination.

NA

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

NA

## Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

| | |
|---|---|
| Provide details on animals and/or animal-derived materials used in the study. | NA |

Policy information about studies involving human research participants

12. Description of human research participants

| | |
|---|---|
| Describe the covariate-relevant population characteristics of the human research participants. | NA |