

Adequate statistical modelling and data selection are essential when analysing abundance and diversity trends

Marion Desquilbet, Pierre-André Cornillon, Laurence Gaume, Jean-Marc

Bonmatin

▶ To cite this version:

Marion Desquilbet, Pierre-André Cornillon, Laurence Gaume, Jean-Marc Bonmatin. Adequate statistical modelling and data selection are essential when analysing abundance and diversity trends. Nature Ecology & Evolution, 2021, 5 (5), pp.592-594. 10.1038/s41559-021-01427-x . hal-03191511v3

HAL Id: hal-03191511 https://hal.inrae.fr/hal-03191511v3

Submitted on 8 Dec 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Title page

Journal: Nature Ecology & Evolution, 2021 accepted version

Title. Adequate statistical modelling and data selection are essential when analysing abundance and diversity trends

Matters arising. Arising from Crossley *et al.*, No net insect abundance and diversity declines across US Long Term Ecological Research sites, *Nature Ecology & Evolution* (2020) doi:10.1038/s41559-020-1269-4.

Authors. Marion Desquilbet^{1*†}, Pierre-André Cornillon^{2†}, Laurence Gaume³, Jean-Marc Bonmatin⁴

Affiliations

¹ Toulouse School of Economics, INRAE, University of Toulouse Capitole, Toulouse, France.

² Univ Rennes, CNRS, IRMAR - UMR 6625, F-35000 Rennes, France.

³ AMAP, University of Montpellier, CNRS, CIRAD, INRAE, IRD, Montpellier, France.

⁴ Centre de Biophysique Moléculaire, CNRS, 45071 Orléans, France.

*Correspondence to: marion.desquilbet@inrae.fr.

[†]These authors contributed equally to this work.

Acknowledgments

Doyle McKey and Emmanuelle Jousselin (University of Montpellier) made suggestions to improve the paper. This work was publicly funded by the French National Research Agency (grants ANR-17-EURE-0010 to M. D. and ANR-16-IDEX-0006 to L. G. under the "Investissements d'avenir" program and grant ANR-15-CE21-0006 to M.D.).

Author contributions

M.D. and P-A.C. performed both the detailed and overall analysis of the article and wrote the original draft. P-A.C. examined and re-programmed the R code. L.G. contributed to the argumentation and extensively edited the manuscript. J-M.B. contributed to the analysis of data selection in the article. All authors contributed to the general comment and reviewed the manuscript.

Title. Adequate statistical modelling and data selection are essential when analysing abundance and
 diversity trends

Matters arising. Arising from Crossley *et al.*, No net insect abundance and diversity declines across
US Long Term Ecological Research sites, *Nature Ecology & Evolution* (2020) doi:10.1038/s41559020-1269-4.

6

7 Abstract

In an analysis of a large number of time series on arthropod abundances in natural and managed areas of the United States, Crossley et al. reported no evidence of an overall decline in insect abundance and diversity¹. We identified major concerns in the statistical analysis and inconsistencies in the selection of data, which, we argue, invalidate their conclusions. We call for a rigorous methodology in analyses of biodiversity trends because relevant information is crucial for stakeholders and policy makers.

14

15 Matters arising

The extent of the decline of insect populations worldwide is much debated²⁻⁵, with major implications for public policy investment in biodiversity protection. Crossley et al. conducted a statistical analysis of 5,375 geographically and taxonomically varied time series on arthropod abundance during 4 to 36 years across the United States¹. They concluded that there was no significant change in insect populations. However, we argue that issues in the statistical analysis and inconsistencies in data selection invalidate their conclusions.

22 The modelling proposed by Crossley et al. relied on the following steps: i) collecting data, ii)

23 separating each species of each locale of each LTER (in the R script, a locale could be an arthropod

- 24 group, a location or a collection method), iii) pre-processing data (Box 1), iv) running a different
- 25 autoregressive linear model for each species of each locale of each LTER (hereafter, LLS),

v) combining all estimated slopes into a "sample", vi) analysing this "sample" using violin plots, T26 27 tests and confidence intervals (Fig. 1). The statistical analysis carried out in this last step relied on 28 the assumption that the observations in the sample were independent and identically distributed 29 (iid). This assumption was violated for two reasons. First, the pre-processing step included a time 30 scaling to change the minimum year of each LLS time series to 0 and its maximum year to 1. As the 31 time length varied from 4 to 36 years depending on LLS, the scaled time x varied across LLS time 32 series. Therefore, the estimated slopes did not represent abundance trends per year, but per time 33 units x varying over time series and without a clear meaning. Second, according to the linear 34 regression theory, the expectation and variance of the estimated slopes depend on the number of 35 measures of the x variable (i.e. the length of the time series) and the distances of y measures to the 36 model (i.e. the quality of the model approximation). Among LLS time series, there are different time lengths, and different qualities of approximation. Therefore, the slopes cannot be iid, and 37 38 estimations and tests used in step vi) are not reliable. To circumvent this problem, it would be more 39 appropriate to use a hierarchical model to analyse the whole dataset.

40 Insert Box 1 and Figure 1.

41 Other problems are as follows. First, most individual time series were too short to provide reliable 42 estimations of the four unknown parameters specific to each LLS (Box 1). Indeed, 44% of LLS time 43 series only had 4 to 9 years of data. While no simple threshold exists, we do not see how to reliably 44 estimate four parameters with less than ten data points, which will only provide a very imprecise 45 estimation. Some limited sensitivity analysis was provided with a stricter data subset involving a minimum of 15 years of data, but this strict dataset only included less than 6% of the time series. It 46 47 represented a much more limited variety of situations than the total sample and was therefore much 48 less representative. This is another argument in favour of a global modelling approach, which would improve the precision of the trend estimate of any given LLS by using data from other LLS. 49 50 Second, the analysis was performed at a very fine taxonomic level, implying that a high proportion 51 of abundance counts was equal to zero (the full dataset contained 49% of zeros and the strict

dataset, 30.5%; moreover, 71% of the series in the full dataset, and 84% in the strict dataset,
contained at least a zero). As the logarithm of 0 is undefined, all zero abundance values were shifted
upwards before being log-transformed by adding an arbitrary value. Such rudimentary logtransformation of count data is to be avoided because results depend on the chosen value and
coefficient estimates are inaccurate^{6,7}. Zero-inflated models would have dealt appropriately with the
problem of high occurrence of zeros in the dataset⁸.

58 Third, the model corrected for scale differences between abundance series without accounting for 59 imperfect detection, which can be of particular concern for rare species. This problem may be illustrated by the case of Aphis asclepiadis, NEPAC locale, Midwest STN LTER (external database 60 S1⁹). In the ten years of records, its abundance was 0 for the nine first years, and 1 for the last year. 61 62 This time series (like the others in the dataset) was not composed of abundance levels, but 63 estimations of abundance. Due to imperfect detection, a shift from an estimated abundance from 0 to 1 provides poor information on the real abundance trend. After scaling log-abundances (Box 1). 64 65 this uninformative A. asclepiadis data series was erroneously modelled as having the highest abundance increase of all the time series (external database $S2^9$), while it could just reflect the rarity 66 67 of the species or its poor detection. The same slope could have been obtained with a time series reflecting a significant abundance change, with for example a hundred insects in all years except the 68 last year with a thousand insects. In total, 16% of time series included only abundance values of 0 69 70 and 1, and 27% of time series included only abundance values of 0, 1 and 2. Simple models of 71 occurrence and abundance have already been developed to cope with the problem of imperfect detection.¹⁰ 72

As all analyses of diversity (richness, evenness and β diversity) in the article relied on these
estimations of abundance and on the same modelling, they shared similar methodological problems.
We also point out that we had to re-program the R script provided by the authors using their
external databases S1 and S2⁹ to make it run.

77	Regarding data selection, the article is intended to analyse insect abundance trends in US Long		
78	Term Ecosystem Research (LTER) sites, but it departs from this description in two ways. First,		
79	39.5% of time series are from the Suction Trap Network (STN). One suction trap of the STN is		
80	located in the Kellogg LTER site, and all STN data, encompassing ten US states, were incorporated		
81	into the Kellogg LTER dataset up to 2014 ¹¹ . But the dataset used in the analysis		
82	(https://suctiontrapnetwork.org), spanning up to 2019, is not linked to a LTER. Its inclusion may		
83	bias results by minimising the damages of intensive farming, because the STN exclusively provides		
84	data on aphids, and primarily aims to document pest aphids ¹¹ , which benefit from intensive		
85	agriculture ^{12,13} , unlike most insects (e.g. aphid natural enemies ¹³ or bees ¹⁴).		
86	Second, the reference to insects in the title of the article is confusing as almost 10% of time series		
87	were of non-insect arthropods or included insects and other arthropods. In Fig. 2, three of the 22		
88	violin plots concerned or involved crustaceans. Unlike the rest of the dataset, the violin plot from		
89	the Coweeta LTER related to aquatic invertebrate communities in terms of functional feeding		
90	groups, and not individual species. These inconsistencies add to other criticisms of this article ¹⁵		
91	regarding unaccounted-for changes in sampling location and sampling effort at LTER sites and the		
92	unaccounted-for impact of experimental conditions on insect populations.		
93	As a conclusion, the methodology chosen in this article is very approximate with several identified		
94	problems likely to substantially bias the results. The analysis would have required an adequate		
95	global model for all data, considering all our criticisms and those of ref. ¹⁵ . We call for the		
96	application of rigorous standards for analyses on global change, especially because results could		
97	have a significant impact on policy decision-making and the fate of biodiversity.		
98			
99	References		
100	1 Crossley, M. S. <i>et al.</i> No net insect abundance and diversity declines across US Long Term		
101	Ecological Research sites. Nat Ecol Evol 4, 1368-1376, doi:10.1038/s41559-020-1269-4		

102 (2020).

103	2	Cardoso, P. et al. Scientists' warning to humanity on insect extinctions.
104		Biological Conservation 242, doi:10.1016/j.biocon.2020.108426 (2020).
105	3	van Klink, R. et al. Meta-analysis reveals declines in terrestrial but increases in freshwater
106		insect abundances. Science 368, 417-420, doi:10.1126/science.aax9931 (2020).
107	4	Desquilbet, M. et al. Comment on "Meta-analysis reveals declines in terrestrial but increases
108		in freshwater insect abundances". Science 370, eabd8947, doi:10.1126/science.abd8947
109		(2020).
110	5	Jähnig, S. C. et al. Revisiting global trends in freshwater insect biodiversity. WIREs Water,
111		doi:10.1002/wat2.1506 (2020).
112	6	O'Hara, R. B. & Kotze, D. J. Do not log-transform count data. Methods in Ecology and
113		<i>Evolution</i> 1 , 118-122, doi:10.1111/j.2041-210X.2010.00021.x (2010).
114	7	St-Pierre, A. P., Shikon, V. & Schneider, D. C. Count data in biology-Data transformation or
115		model reformation? <i>Ecol Evol</i> 8 , 3077-3085, doi:10.1002/ece3.3807 (2018).
116	8	Lambert, D. Zero-inflated Poisson regression, with an application to defects in
117		manufacturing. Technometrics 34, 1-14, doi:10.2307/1269547 (1992).
118	9	Crossley, M. et al. No net insect abundance and diversity declines across US Long Term
119		Ecological Research sites, Dryad, Dataset, https://doi.org/10.5061/dryad.cc2fqz645 (2020).
120	10	Royle, J. A., Nichols, J. D. & Kéry, M. Modelling occurrence and abundance of species
121		when detection is imperfect. Oikos 110, 353-359, doi:10.1111/j.0030-1299.2005.13534.x
122		(2005).
123	11	Lagos-Kutz, D. and D. Voegtlin. Midwest Suction Trap Network. Iowa State Research Farm
124		Progress Reports, 2203, http://lib.dr.iastate.edu/farms_reports/2203 (2015).
125	12	Simon, J. C. & Peccoud, J. Rapid evolution of aphid pests in agricultural environments.
126		Curr. Opin. Insect Sci. 26, 17-24, doi:10.1016/j.cois.2017.12.009 (2018).

127	13	Zhao, Z. H., Hui, C., He, D. H. & Li, B. L. Effects of agricultural intensification on ability
128		of natural enemies to control aphids. Scientific Reports 5, 7, doi:10.1038/srep08024 (2015).
129	14	Woodcock, B. A. et al. Impacts of neonicotinoid use on long-term population changes in
130		wild bees in England. Nat. Commun. 7, 8, doi:10.1038/ncomms12459 (2016).
131	15	Welti, E. A. R. et al. Meta-analyses of insect temporal trends must account for the complex
132		sampling histories inherent to many long-term monitoring efforts, EcoEvoRxiv Preprints,
133		doi:10.32942/osf.io/v3sr2 (2020).

134

142

135 Box 1. Model used by Crossley et al. (2020)

Each time series *i* was composed of abundance levels A_{it} for LLS *i* and for years t_{i1} to t_{iT_i} .

137 The first step of data pre-processing consisted in log-transforming abundances. For LLS *i* in year *t*,

138 the abundance value A_{it} was replaced either by its logarithm, log A_{it} , or, if $A_{it} = 0$, by the logarithm

139 of a constant, $\log c_i$, where c_i was half the minimum non-zero abundance in time series *i*, to obtain a

140 series of log-transformed abundances *a*_{*it*}.

141 In a second step, log-abundances were scaled: the empirical mean \bar{a}_i of log-transformed abundances

of the series was subtracted to each ait and this difference was divided by the empirical standard

143 deviation s_i of log-transformed abundances. This yielded the scaled logarithm of abundance of LLS

144 *i* in year *t*, y_{it} , defined as $y_{it} = (a_{it} - \overline{a}_i)/s_i$.

145 In a third step, the authors transformed all time units using a common scale varying between 0 (the

146 first year of the LLS abundance time series) and 1 (its last year). The scaled year x_{it} was obtained by

147 transforming the first year of time series t_{i1} to 0, and its last year t_{iTi} to 1, and scaling all years

148 accordingly as $x_{it} = (t_{it} - t_{i1})/(t_{iT_i} - t_{i1})$.

149 The proposed modelling was a linear model with a Gaussian auto-regressive error of order 1:

150 $y_{it} = \beta_{i1} + \beta_{i2} x_{it} + \varepsilon_{it}$, where $\varepsilon_{it} = \rho_i \varepsilon_{i,t-1} + \eta_{it}$, with $\eta_{it} \sim N(0, \sigma_i^2)$.

For each individual LLS time series, this model implied the estimation of four parameters, β_{i1} , β_{i2} , ρ_i 151 and σ_i , the slope β_{i2} representing the abundance trend and therefore being the parameter of interest. 152 153

Figure 1. Modelling steps in Crossley et al. (2020) and arising problems. Time trends were 154 155 estimated separately for each species of each locale of each LTER (LLS). The time scaling was 156 performed on LLS of different time lengths and the quality of approximation varied across LLS. Therefore, the abundance time trends were not independent and identically distributed as assumed 157 when calculating the average abundance trends, confidence intervals and significance tests 158 associated with the violin plots of Fig. 2 in Crossley et al. (2020). A global hierarchical modelling 159 160 would have circumvented this problem.



- 163
- 164 **Competing interests.**
- 165 The authors declare no competing interests.