

We ask for a minor revision

Dear Ainhoa Magrach,

Your preprint, entitled Interaction network structure maximizes community-level plant reproduction success via niche complementarity, has now been reviewed again. The referees' comments and the recommender's decision are shown on PCI site. As you can see, the recommender found your article interesting, but suggests a few (minor) revisions.

We shall, in principle, be happy to recommend your article as soon as it has been revised in response to the points raised by the referees, and in particular the second one. Once the recommender has read the revised version, he/she may decide to recommend it directly, in which case the editorial correspondence (reviews, recommender's decisions, authors' replies) and a recommendation text will be published by PCI Ecology under the license CC-BY-ND.

Alternatively, other rounds of reviews may be needed before the recommender reaches a favorable conclusion. He/she also might decide not to recommend your article. In this latter case, the reviews and decision will be sent to you, but they will not be published or publicly released by PCI Ecology. They will be safely stored in our database, to which only the Managing Board has access. You will be notified by e-mail at each stage in the procedure.

Thanks in advance for submitting your revised version. Yours sincerely, The Managing Board of PCI Ecology.

We would like to thank once again the Editor and the Reviewer for taking the time to provide all this useful feedback which has again allowed us to improve our paper.

Reviews

Reviewed by Nicolas Deguines, 2019-10-02 16:01

General comments

I would to thank the authors for their work on the revisions and for the clear Responses to reviewers file provided. Following previous reviews, the revised version is very much improved indeed.

Thank you for your helpful suggestions.

My comments were mostly all considered, so I'll only focus on a few remaining points that I think need to be addressed. Specifically, I have three main remaining concerns:

- are results qualitatively similar when using the same max(NODF) 'uncorrected' measure for all sites (instead of a new version for 13 sites but an uncorrected version for 3 sites)?

Yes, the results do not change qualitatively when using one approach or the other. This is now stated in methods.

P12/L245-249: “To calculate max(NODF) we used a recently corrected version of the algorithm (Simmons et al 2019) in all but three sites, where the condition that the number of links > number of species was not met and thus precluded us from using this new version. Results did not change qualitatively when using the uncorrected version of the algorithm for all sites.”

- I don't understand how GLMM Poisson models with response variables 'average values of fruit and seed weight' that are (most likely) continuous (and not count-like data) can be used?

Following the Reviewer's advice we have now changed this and used a normal distribution in both cases. This does not change any of our results, only the fact that model 1 is now best in both cases but still none of the variables included is able to explain the variability observed. This change is now reflected in the Methods and Results section as well as in Tables S5 and S6 in the Supplementary material section:

P13/L270-273: “At the species level, response variables included the fruit set for different individuals of each species analyzed using a binomial distribution and the average number of seeds per fruit, the average fruit and seed weight fitted using normal distributions.”

P17/357-359: “For all other measures of reproductive success considered (i.e., fruit and seed weight), model 1 showed the best fit. However, none of the variables included within our model explain the differences observed (Tables S5-S6).”

- is the effect of pollinator richness on Fruit weight and Seed weight (Figure 4) still positive and is it statistically significant (or what's the confidence intervals for the estimates) when removing the site of maximum pollinator richness?

Following the reviewer's advice we have now repeated these analyses but removing the site with the large pollinator richness value. Our results remain robust to this removal and pollinator richness still shows a positive effect in both cases. Results for this new analyses are available in the Supplementary material section (Tables S7 and S8, Fig S5). And this has now been referenced in the main text.

P18/L380-381: “Here, we find a consistent positive effect of site-level pollinator richness for both weight descriptors (Tables S7A-S8A, Fig. 4). This effect is maintained even after removing a site that has a particularly large pollinator richness value (Tables S7B-S8B, Fig. S5).”

More details are for these main points are provided below, along with minor comments.

Also, I again had no access to the supplementary materials.

We did upload the Supplementary material so we are not sure why this is the case. Sorry again for this inconvenience.

Detailed comments

Abstract

I feel like the abstract is lacking a sentence of conclusion or perspective.

We agree with the Reviewer and so we have now modified the abstract slightly to reduce the number of words and added a conclusion sentence.

P3/L23-26: “Declines in pollinator diversity and abundance have been reported across different regions, with implications for the reproductive success of plant species. However, research has focused primarily on pairwise plant-pollinator interactions, largely overlooking community-level dynamics. Here, we present one of the first efforts linking pollinator visitation to plant reproduction from a community-wide perspective using a well-replicated dataset encompassing 16 well-resolved plant-pollinator networks and data on reproductive success for 19 plant species from Mediterranean shrub ecosystems. We find that models including simple visitation metrics are sufficient to explaining the variability in reproductive success observed. However, insights into the mechanisms through which differences in pollinator diversity translate into changes in reproductive success require additional information on network structure. Specifically, we find a positive effect of increasing niche complementarity between pollinators on plant reproductive success. This shows that maintaining communities with a diversity of species but also of functions is paramount to preserving natural ecosystems.”

Introduction

L89: change “these potential pathways” (i.e. nestedness and complementary specialisation) to “these potential attributes”?

Changed

L109: delete ‘of’ in ‘requires of the delivery’

Deleted

Methods

L199: perhaps change ‘Here’ to ‘With this method,’?

Changed

L220-223: Are results qualitatively similar when using the uncorrected version of $\max(\text{NODF})$ for all sites (not only the three not meeting the assumption of number of links > number of species)? I’m concerned about not using the same calculation for all sites.

Yes, the results do not change when using one approach or the other.

L239-240: given GLMs were used for site-level analyses and GLMMs were used for species-level analyses, I suggest the following change at L239: “we used generalized linear mixed models (GLMMs) and generalized linear models (GLMs) respectively.”

Changed

L247-248: authors mentioned in their response that there had been an error in the first version of the MS and have corrected it. However, I still don't see how ‘the average values of fruit and seed weight [which would almost inevitably produce decimal values, or am I missing something?] fitted to Poisson distributions’ could work.

Looking at R scripts provided by the authors (e.g. L324-330 in ‘removing out obs.R’), I see the use of package glmmTMB when modeling the response variable ‘mean.seedw’ but Poisson distribution should only work with so-called count data (i.e. positive integer), as stated for example in a glmmTMB related paper: <https://journal.r-project.org/archive/2017/RJ-2017-066/RJ-2017-066.pdf>.

This is an important concern here as I don't understand how this could work and this requires a clarification.

L258-259: conversely to ‘species-level models’, here, average fruit and seed weight were modeled using a Normal distribution and I agree with this. If it was an error above, did the R code also include an error then (i.e. are the results presented from a Poisson model as in the R code or a Gaussian model?)

Following the Reviewer's advice we have now changed this and used a normal distribution in both cases. This does not change any of our results, only the fact that model 1 is now best in both cases but still none of the variables included is able to explain the variability observed. This change is now reflected in the Methods and Results section as well as in Tables S5 and S6 in the Supplementary material section:

P13/L270-273: “At the species level, response variables included the fruit set for different individuals of each species analyzed using a binomial distribution and the average number of seeds per fruit, the average fruit and seed weight fitted using normal distributions.”

P17/357-359: “For all other measures of reproductive success considered (i.e., fruit and seed weight), model 1 showed the best fit. However, none of the variables included within our model explain the differences observed (Tables S5-S6).”

Results

L347-349: Was the positive effect statistically significant? I could not access Tables S7-8 (no access to supplementary materials). However, when looking at Figure 4, I am concerned about the influence of a single site on the overall relationships (panel A and B). Indeed, the site with scaled pollinator richness at ~2 appears well above and apart from all others and I am worried that any significant effect would disappear without this site (or even become negative in case of effect of pollinator richness on Fruit Weight).

I strongly suggest running again both models (1 and 2) for both response variables without that extreme site and check if results are robust.

Following the reviewer's advice we have now repeated these analyses but removing the site with the large pollinator richness value. Our results remain robust to this removal and pollinator richness still shows a positive effect in both cases. Results for this new analyses are available in the Supplementary material section (Tables S7 and S8, Fig S5). And this has now been referenced in the main text.

P18/L380-381: "Here, we find a consistent positive effect of site-level pollinator richness for both weight descriptors (Tables S7A-S8A, Fig. 4). This effect is maintained even after removing a site that has a particularly large pollinator richness value (Tables S7B-S8B, Fig. S5)."

Tables

Table 1: I read answers of authors to my previous comment on including or not p-values (especially from mixed-effects models) and confidence intervals. Taking the example of Centrality, the 'large effect' (0.46) seems also associated with large variation (SE = 0.25), and a confidence interval would help to interpret how likely the effect is (especially because SE are not so easily interpretable for non-Gaussian model).

Also, I suspect grey bands in Figure 2-4 represent confidence intervals (they often do as it's easily interpretable). If so, if used in these figures, I think CIs could be added to tables showing model results. This was recently suggested in Conservation Letters (Fidler et al. 2018) to improve statistical transparency. So I still suggest to add 95% confidence intervals.

We have now included two additional figures in the Supplementary material representing forest plots of confidence intervals for all models considered. See Fig. S3 and S4, which we have also now referenced in the main text.

Figures

Figure 2:

Relative to my previous comment on panel A: points don't go over 1 but the prediction line does. I see two issues with this panel:

1) what is the grey band surrounding the black line? I understand it describes uncertainty around the predicted effect, but is it a confidence interval and at which level (95% or 99%)?

2) given these are results from a glmm based on a binomial distribution (L245-247), neither the estimated effect (the black line) nor its uncertainty (grey band) should be predicted at values >1. For example, when using function predict() or add_ci() (package ciTools) in R on a binomial gl(m)m model, predicted values stay within the boundaries of the its associated distribution.

We thank the Reviewer for pointing this out. We have now amended this.

Reference used above

Fidler, F. et al. 2018. Improving the transparency of statistical reporting in Conservation Letters. - Conserv. Lett. 11: e12453.

Reviewed by anonymous reviewer, 2019-09-04 21:23

The revised version has successfully addressed all of my concerns. I especially enjoyed reading the added discussion of the challenges in linking network and function empirically. I believe this paper presented important advancements on an important topic.

We thank the Reviewer for such positive comments.

One last suggestion is to expand the figure captions. The current captions are too brief to be understood by someone skipping the papers.

Following the Reviewer's suggestion we have now expanded figure captions when necessary.