Comments from the Data and script Editor (09/02/2024 16:30)

It's now all perfect. The authors solved all the issues I raised in my previous comments.
As a consequence, every question below has a “yes” as a reply

1- Can we get the data and script from the links indicated in the submission form or from the article itself? ==> YES
2- Is there a readme file? ==> YES
3- Are there metadata for the data and comments for the scripts? ==> YES
4- Are the readme, and data files understandable by a normal reader? ==>YES
5- Do the scripts run on the data? ==> YES
6- Are the results the same as in the paper? ==> YES

In summary, data and scripts are available, clear and understandable. Scripts properly run on data. Results obtained from the scripts are the same as in the article.

I thank the authors for their very clear, detailed and precise work..

Author's response (09/02/2024 10:20)

We have now addressed all your comments (see details in the attached answer). In a nutshell: the updated version of the supplementary materials is now available on Zenodo under the same DOI as before: https://zenodo.org/doi/10.5281/zenodo.10371863.

Best regards,

Eric

Answers to comments on Supplementary Information for preprint #633 “Habitat structural complexity increases age-class coexistence and population growth rate in fish”, authored by Eric Edeline, Yoann Bennevault and David Rozen-Rechels.

Comments in grey, answers below in black.
==

Hello Eric,

My (naive) attempts to run your scripts on your data

****
Summary:
-very clear scripts, very well commented, helpful readme file.

-the scripts requires the installation of JAGS on the computer (not only in R) <== it should be indicated
We have now specified in the Readme file that JAGS must be installed on the computer.

-the script run ok on data.

-the script could be completed to obtain the output from the models (summary, plots, etc.)

-I could not find the way to generate SAMPLES_Gaussian_mixture_treatment_random_effects.txt" from by model 3.
We have now added into to all model codes the command lines needed to save posterior samples and model summary from JAGS models.

-I did not find the code to generate figures of the MS and p-values of table 2.
Sorry, it was not clear to us from instructions that figure codes were also needed. We now provide codes to generate the figures in the supplement. Note that Figure 1 does not require coding, and the supplement concerns Figs. 2-4. Additionally, how to obtain MCMC p-values from posterior samples is now explained in the Readme file.

The links in the PCI Ecol submission form are ok but the link provided in biorxiv and in the pdf (https://entrepot.recherche.data.gouv.fr/dataset.xhtml?persistentId=doi:10.57745/KKITFP) does not seem to work. Why did you indicate this second link?
We initially used the INRAE dataverse, but they were very slow to open access due to review delays. So as not to slow the review process down, François Massol urged us to rather use Zenodo, which we did. To avoid duplicates, we asked the deletion of our INRAE dataverse submission. Therefore, the manuscript was submitted with an INRAE dataverse DOI, which is now down. The next manuscript version will use the correct Zenodo link (https://zenodo.org/doi/10.5281/zenodo.10371863).

Could you please amend the scripts and the readme to solve the issues raised in the summary above? and send me a reply with the corrected files? It may also be useful to update the supplementary files in Zenodo in case the other reviewers want to use them. It is crucial that we swiftly come to a point where every question is answered with a "yes", as my report will play a pivotal role in the recommender's decision during the first round of peer review.
W have now uploaded on Zenodo a revised version of the supplement that accounts for all of your comments, downloadable at https://zenodo.org/doi/10.5281/zenodo.10371863.

Comments from the Data and script Editor (07/02/2024 18h35)

Hello Eric,

My (naive) attempts to run your scripts on your data

****
Summary:
-very clear scripts, very well commented, helpful readme file.
-the scripts requires the installation of JAGS on the computer (not only in R) <== it should be indicated
-the script run ok on data
-the script could be completed to obtain the output from the models (summary, plots, etc.)
-I could not find the way to generate SAMPLES_Gaussian_mixture_treatment_random_effects.txt" from by model 3
-I did not find the code to generate figures of the MS and p-values of table 2.
-it would be nice to have these missing details

****
Model 1
had to do write simple code to get output (summary(m))
OK same stats as in MS
could not get script for fig 2

****

Model 2 requires package Jagsui
runs ok until

```
> mod <- jags(data = jags.data, parameters.to.save = parameters, model.file =
"Model_codes/Ricker_POISSON_full_interaction.jags", n.chains = nc, n.thin = nt, n.iter = ni,
n.burnin = nb, n.adapt = 2000, parallel = TRUE)
Error: .onLoad failed in loadNamespace() for 'rjags', details:
  …
```

==> requires the installation of JAGS on my computer (not only in R)
runs ok
of course requires
"summary(mod) "
to obtain table 2 model 2 ok, not last colomne p-value
I don't have script to get figures, etc.

****

Model 3
runs ok
same stats as in table 2 model 3, no last colonne p-value
I don't see how SAMPLES_Gaussian_mixture_treatment_random_effects.txt" is produced by model 3

****

Model 4
runs ok
same stats as in table 2 model 4, no last colonne p-value

****

Model 5
runs ok
same stats as in table 2 model 5, no last colonne p-value

****

My temporary list of answers:

1- Can we get the data and script from the links indicated in the submission form or from the article itself? *YES. The links in the PCI Ecol submission form are ok but the link provided in biorxiv and in the pdf (https://entrepot.recherche.data.gouv.fr/dataset.xhtml?persistentId=doi:10.57745/KKITFP) does not seem to work. Why did you indicate this second link?
2- Is there a readme file. ***YES***
3- Are there metadata for the data and comments for the scripts? *YES
4- Are the readme, and data files understandable by a normal reader? *YES
5- Do the scripts run on the data? ***YES but see details above***
6- Are the results the same as in the paper? ***YES but see details above***
*==> Could you please amend the scripts and the readme to solve the issues raised in the summary above? and send me a reply with the corrected files? It may also be useful to update the supplementary files in Zenodo in case the other reviewers want to use them
*

It is crucial that we swiftly come to a point where every question is answered with a "yes", as my report will play a pivotal role in the recommender's decision during the first round of peer review.

Thanks for your help in getting this done and thanks again for submitting your preprint to PCI Ecol

Thomas