Hi Miriam

Thanks for all. It's all fixed now. My report is thus the following:

Data with metadata and script are accessible, a readme file is present. The script is well commented and understandable. It runs well on the data and produce the same results as in the article.

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

Best

Thomas

Le 20/02/2024 à 09:06, Miriam Be a écrit :

> Hi,
> great, thank you for the last remarks, I will update the script accordingly.
> And thank you generally for taking the time to actually test the script, I honestly was not expecting it when submitting but clearly do appreciate this procedure!
>
> Best wishes,
> Miriam
>
> Le lun. 19 févr. 2024 à 11:18, Thomas Guillemaud <thomas.guillemaud@inrae.fr> a écrit :
>
> > Hi Miriam
> >
> > I think we 're close to the end. I could run the whole script and obtain the expect outputs. :-)
> >
> > I had to correct the following issues:
> >
> > Plot in lines 247-262 Fails
> > ==> "object 'Level N' not found"
> > ==> I assume that we need a
> > "stoichios_long<- stoichios_long %>% rename('Level N' = stat_N)"
> > before running the plot
> >
> > line 456
> > write.csv(test, file = "commstoichios_classweighted_pred.csv", row.names=FALSE)
> > ==> object 'test' not found
> > ==> I assumed to use commstoichios_pred instead of test
> >
> > Error in line ~577-580
> > #_____
> > #plot
> > #_____
> > props_long<- props_long %>% rename('Level N' = stat_N)jpeg(paste("propclasses_waterPXstatN", ".jpg", sep=""), width=2800, height=900, res=300)
> > ==> I assumed I should replace this latest line by
> > props_long<- props_long %>% rename('Level N' = stat_N)
> > jpeg(paste("propclasses_waterPXstatN", ".jpg", sep=""), width=2800, height=900, res=300)
> >
> > If it's ok, could you correct these lines?
> >
> > Thank you!
> >
> > Thomas
> >
> > Le 16/02/2024 à 19:22, Miriam Be a écrit :
> >
> > > Hi again,
> > >
> > > I modified and copy/pasted most of the replications.
> > > There remain 1, 2 commands notably in the calculation of group-wise community stoichio and in plotting where one still has to decide for 'class' or 'food_cat', but I also made it clearer/ easier to do so. (I considered also copy-pasting those, but I honestly think that this will make it way more difficult to keep the overview about the script)
> > >
> > > I hope it runs well & easy now!
> > >
> > > Best wishes,
> > > Miriam
> > >
> > > Le ven. 16 févr. 2024 à 09:19, Thomas Guillemaud <thomas.guillemaud@inrae.fr> a écrit :
> > >
> > > > Dear Miriam

It's me again, sorry ... :-)

I'm again stucked in the script, lines 162-163, for almost the same reason:

#group-wise calculation:
#-> modify the object name (L. 168, e.g. lm_biv, lm_gas...), include the 'filter' (L.128) and modify group name in L. 140

Because you changed the script to answer me (thanks), the actual line numbering does not match with the sentence above. I could make many tests to proceed, but I think it's more efficient if you modify the script (and maybe copy/past the code for each object, if I may suggest).

Thanks for your effort to answer me.

Cheers

Thomas

Le 15/02/2024 à 19:52, Miriam Be a écrit :

> Hi,
> I apologise for the inconveniences...
> 1) First of all, I added the 'extended' code to obtain results of all the 6 variables (c, n, p, cn, cp, np) without copy/pasting (and did so also throughout the manuscript).
>
> 2) You're right, we do not report the p values for the decision between including the interaction (or not), since the reported results are those of the best model. From the table structure and the figure it should become clear whether it was the interaction/non-interaction model (i.e. without interaction it is stated 'ns' in the interaction column (PXN) and also one slope is indicated as indicated in the table description)
> (we'd be happy to re-think this representation of results if any reviewer has a nice/efficient suggestion)
>
> 3) It was indeed meant to be 'stochio_long', I fixed this
> I actually was faced with the same error re-running the script now. It seemed to be some change in the package; it should be fixed now.
>
> Best wishes (and thank you for reviewing!),
> Miriam
>
> Le jeu. 15 févr. 2024 à 11:25, contact PCI <contact@peercommunityin.org> a écrit :
>
> > Dear Miriam
> >
> > Thanks. It helps.
> >
> > **in line 45 of the R script:** commstoichios<- rbind(commdata_c, commdata_n, commdata_p, commdata_cn, commdata_cp, commdata_np)
> >
> > ==> it looks like commdata_n, commdata_p, commdata_cn, commdata_cp, commdata_np are not defined before. Only commdata_c and _t are defined before. I had to copy paste and change the text for each mean_*.
> >
> > commdata_np<- commdata_t %>% #*adapt stoichio here*
> > #to exclude taxa for which corresponding stoichio is not available:
> > filter(!is.na(mean_np)) %>% # *adapt stoichio here*
> > #log(x+1) abundance data:
> > mutate_at(vars(2:1308), funs(log1p(.))) %>%
> > #group_by(class) %>% #-> 'class' or 'food_cat' to calculate within major taxa group/feeding type
> > #relative frequency:
> > mutate_at(vars(2:1308), funs(./sum(.))) %>%
> > mutate_at(vars(2:1308), funs(.*log(mean_np))) %>% # *adapt stoichio here*
> > summarise_at(vars(2:1308), sum, na.rm=TRUE) %>%
> > mutate(index="comm_np")# *adapt stoichio here*
> >
> > ==> I think it is was what you explained in the R file, but I'm not sure. It is not very convenient. Could copy-paste it yourself in the R file?
> >
> > **lines 133-138 :**
> >
> > ==> I don't find the interaction p-value in the manuscript, so I couldn't check the congruence between the script result and the MS. Is that intended?
> >
> > **line 143:** lm_stoichios<- indices_long %>%
> >
> > ==> it looks like indices_long is not defined before
> >
> > ==> I tried to ("randomly") replace indic_long by stoichios_long, but it failed:
> >
> > > Error in `unnest()`:
> > > ! In row 1, can't recycle input of size 4 to size 0.
> >
> > I could not continue. Can you check what's wrong?
> >
> > Best
> >
> > Thomas

Le 15/02/2024 à 09:51, Miriam Be a écrit :

> Hello Thomas,
> thank you for the message.
> You're right, we didn't put the stoichio file into the repository, because it is online available.
> However, to facilitate the use I now added it to the repository (version3). Considering your further remarks, also added modified the readme to add a small description of the code.
>
> Best wishes,
> Miriam
>
> Le mer. 14 févr. 2024 à 15:42, contact PCI <contact@peercommunityin.org> a écrit :
>
> > Hello Miriam,
> >
> > I'm going to play the role of data and script editor of your preprint #677 submitted to PCI Ecol.
> >
> > PCI Ecol indeed wants to ensure as best as possible the reproducibility of the analyses carried out in the reviewed articles. Readers of articles eventually recommended by PCI should be able to reuse the data and scripts from these articles. A "naive" outside eye is useful to ensure that this reuse is effective in an environment different from that of the authors. Hence, I'll be an additional reviewer and will send my report as a review of the 1st round of peer review. Before writing my report I'll probably have to have Email contacts with you (such as the present Email).
> >
> > **==> The goal is to get a YES for all the following questions** deriving from the instructions for authors before the end of the 1st round of review:
> >
> > 1- Can we get the data and script from the links indicated in the submission form or from the article itself? Yes/no/not applicable (if not applicable, the next questions should not be replied)
> >
> > 2- Is there a readme file. Yes/no
> >
> > 3- Are there metadata for the data and comments for the scripts? Yes/no
> >
> > 4- Are the readme, and data files understandable by a normal reader? Yes/no
> >
> > 5- Do the scripts run on the data? Yes/no
> >
> > 6- Are the results the same as in the paper? Yes/no
> >
> > **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.
> >
> > I already tried to understand your code and data. Here is my temporary pre-report:
> >
> > - metadata of data : OK, thanks
> > - It would be good to have a rough description of the script and analysis in the readme file (even if in this case, it is straight forward because there is only 1 R file)
> > - The code is well commented, thanks
> > - I tried to run the code and I got this problem:
> >
> > > line 18
> > > reading the data
> > > stoichio_db <- read.csv2("stoichio.csv", header=TRUE, na.strings="NA", stringsAsFactors=FALSE, check.names=FALSE)
> >
> > ==> There is no such file in the Zenodo zip deposit
> >
> > ==> I'm not sure I can continue to run the code. it's maybe worth trying to solve this problem before we can proceed with the rest.
> >
> > Thanks for your help in getting this done and thanks again for submitting your preprint to PCI Ecol
> >
> > Thomas
> >
> > --
> >
> > --
> > **********
> >
> > Thomas Guillemaud
> > Peer Community in
> > peercommunityin.org
> >
> > **********
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