

Hello

I think it's ok like that.

Here is my report (I will paste it as a small review in the PCI Ecol website)

The data are available with a readme file. The article uses basic stats (no test) but there is a "hierarchical clustering (group-average link) based on the Bray-Curtis similarities". The next version of the article will include the description of this treatment.

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) <== only the data are available, but it's ok because there is no statistical analysis except a hierarchical clustering described in the text

2- Is there a readme file. <== YES

3- Are there metadata for the data and comments for the scripts? <== YES there are metadata for data

4- Are the readme, and data files understandable by a normal reader? <== YES

5- Do the scripts run on the data? <== there is no script, but it's ok because there is no statistical analysis except a hierarchical clustering described in the text

6- Are the results the same as in the paper? <== a treatment of the data using R for the hierarchical clustering described in the text produces the same clustering as in the MS.

==> it's ok from the side of the data and script editor

Thanks

Thomas

Le 15/02/2024 à 16:59, Aline Migne a écrit :

In fact, after answering and checking the function using "vegan", I remembered that I did not use R for this analyse but the software Primer...

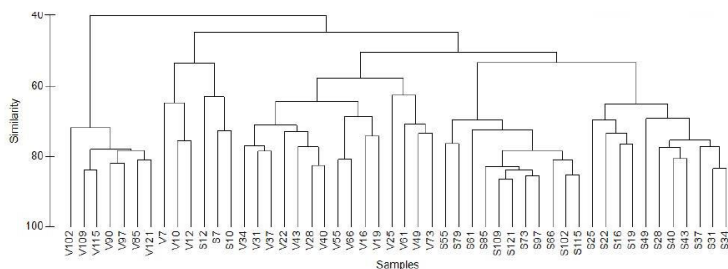
I thought you wanted to be sure that the result of the analyse can be obtained using the data available in Zotero and that is the case! I don't know how to obtain a figure with branches of the same size using R, but I hope you don't need this detail... Otherwise, I could replace the actual figure by the one obtain with R in a next version of the article.

Le 15/02/2024 à 15:13, Thomas Guillemaud a écrit :

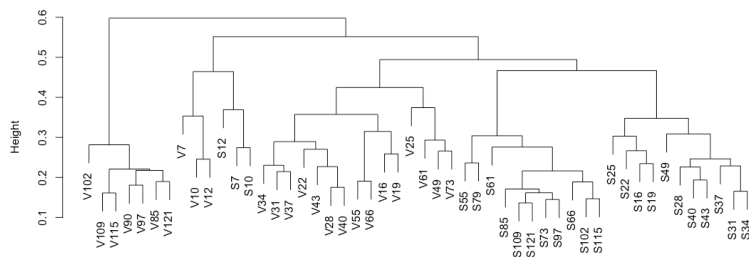
Thanks

A detail: The branches all have the same size in your MS, but not when using the code. Could you indicate the option of hclust that would produce the exact figure of the MS?

your MS:



What the code produces



Thanks for your help

Best

Thomas

Le 15/02/2024 à 14:42, Aline Migne a écrit :

Thomas,

Please find attached the table with the occurrence data (from hal-04347756 raw data, sheet "occurrences") and the R script using the vegan library to perform the hierarchical clustering.

Aline

Le 15/02/2024 à 11:32, contact PCI a écrit :

Hello Aline

Thanks for your message. It helps.

Could you send me, by replying to this Email, the R code for your use of vegdist and hclust on your data?

What do you call the next version? Should I add this section after the first round of review only if the paper is not rejected?

==> Yes, this is what I mean

Again, should I add this description after the first round of review only if the paper is not rejected?

==> Yes, and please send me the R code by replying to this Email.

Thanks a lot,

Thomas

Le 15/02/2024 à 10:51, Aline Migne a écrit :

Hello Thomas,

Below are the answers (and also questions) regarding the different points of your pre-report.

Thanks

Aline

Le 12/02/2024 à 15:07, contact PCI a écrit :

Here is my pre-report

The article use basic stats (no test) but there is a "hierarchical clustering (group-average link) based on the Bray-Curtis similarities". How was that done? by hand?

The hierarchical clustering was done on R 3.4.1 with the library "vegan" using the function "vegdist" to calculate the Bray-Curtis similarities and the function "hclust" to perform the hierarchical clustering.

Data are in zenodo in an excel file. thanks
A readme is in the same excel file with metadata. thanks

There is no data and script section in the paper. Please add 1 in the next version of your article at least for the data with the zenodo link

What do you call the next version? Should I add this section after the first round of review only if the paper is not rejected?

There is no script but a hierarchical clustering (group-average link) based on the Bray-Curtis similarities that would deserve at least the description of the software or a library in R. Please provide such a description in plain text, or provide a script, and include it in the next version of the article.

Again, should I add this description after the first round of review only if the paper is not rejected?

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) <== only the data are available

2- Is there a readme file. Yes/no <== YES

3- Are there metadata for the data and comments for the scripts? Yes/no <== YES there are metadata for data, but no script

4- Are the readme, and data files understandable by a normal reader? Yes/no <== YES

5- Do the scripts run on the data? Yes/no <== NO script, please provide one and/or add a description in plain text in the article

6- Are the results the same as in the paper? Yes/no <== NO script

Please could you check the points above in the pre-report, send me your replies and modify your article accordingly? Thanks a lot

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

Thomas

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