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Some results and questions

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Hi Chu,

Please, just Giovan. Doctor sounds me like a non-human being. I am your colleague since now!

Sorry for my late answer. I have been a little but busier than before. Replying your questions:

1. I have made some tables of allometry, discriminant analysis, and metric disparity. I see an allometric effect in 2/7 of my locations but all are the same species. Can I ignore this effect from my field collected mosquitoes here but should I consider this more closely when I work on my lab reared data that has temperature treatment that can affect the growth?

Allometric effect has been considered negligible at the same species level. It is considered an intrinsic attribute of the species and then, it is not necessary to correct (if possible) this effect. It will be different when you are comparing different species. Please, ignore this effect at population level.

Regarding your lab reared data, please see if is possible to correct the effect as I explained in the GM guide. Is it is possible you could compare the final data with and without the allometric effect. Anyway, I think that it should not change your results strongly.

2. How should I organize my lab reared data for CLIC analysis? I am thinking about having separate .txt files for my different comparisons, such as one male and one female when comparing sexes? I have attached my complete lab reared landmark .csv file.

It is depending on the way that you took the data. However, if you will do i.e. the sexual dimorphism analysis you will need to have a .txt file with first specimens belonging to one sex and after the other ones because when you are on MOG it will require knowing the number of specimens per group—in this case, two groups (F and M) with (n n) specimens. Understanding that, and having into account the question that you want to solve you can set the data as you want. Personally, I take the data per population, sex, etc... after I do scale (pixels to mm) and at this point, I have the full raw data--with that, I can do as many .txt files with the specific data that I need for the Procrustes analysis and going forward.

Please, review the TET module of CLIC (http://mome-clic.com/wp-content/dlic-ohelp/tet_start.txt)---you can concatenate several .txt files (and transform them) as you want to get new .txt for analyses.

3. I did the PCA in PAST3 and CLIC. I have it grouped by Biome and State and Locality. My PC1 for both is about 25% and about 17% for PC2. They both seem to be in agreement?

Yes, both analysis should be very similar or almost identical in the results no matter what software you used. Graphs look a little bit different but it is not relevant—the most important is to check the % of variation explained by each PC are the same on each software. Anyway, PCA is an exploratory analysis then it is useful to see the variation in the full dataset and check if i.e. some populations are grouped specifically in a separate “cloud” in the morphospace which will support the idea of relevant differences.

4. I'm not sure if I understand the results from the CLIC-PAD module for discriminant analysis. I have attached the file. I am not sure how to do the CVA from this information?

Chu, a discriminant analysis (DA) is applied when you just have two groups to compare. As you have more than 2 groups or pops, this DA is called in the literature CVA. CLIC does not have the way to do CVA. It applies a classification – the simple and cross-check classification. It is useful because you can know the % of specimens that based on wing shape are classified correctly. Simple classification does not have resampling, while cross check classification do that and you should take the last values (generally lower) as the more reliable. You can take the _PW data and paste them on PAST, label each pop and then go to the Multivariate menu to apply a CVA analysis. PAST also will show a jackknife classification similar to the %classification done on PAD.

Let me know how is going your current analysis.

PD: In the output of CLIC you will get Euclidian, Procrustes and Mahalanobis distances with statistical significances among pairwise comparisons. Please, check them to see if the significances are similar, regardless of distances used. As a brief summary of your results, could you do a short paragraph about the conclusions and statistics!analysis supporting them? It will be interesting to know if we require any additional analysis. It will be nice to have a ppt showing question-analysis-statistics-conclusion on each. In this way, I will realize what else I can recommend you.

Cheers,

Giovan

[Quoted text hidden]