From: **Kyle Hernandez** kmhernan84@gmail.com
Subject: Re: FVT manuscript
Date: March 25, 2020 at 11:03 AM
To: Grey Monroe greymonroe@gmail.com
Cc: David Des DesMarias dldesmar@mit.edu, Haoran Cai hrcai@mit.edu

Nice to meet you too Grey! This is a cool project. One of the people I manage is a "research programmer" and has degrees in mathematics. I poked his mind about that phenotypic plasticity quantification section and I think he says it seems like you did kind of the best you could do in this situation and doesn't fundamentally have an issue with it. One thing he said was, "I don't think they're losing much/any information there, but probably someone could come up with a method which gives a finer approximation of plasticity, maybe by using some qualities of the curve itself like averaging absolute value of rate of change over all values of soil moisture, or looking at second or third degree derivatives of the trait curve with respect to soil moisture". So, maybe that makes you feel better about it. I do think at least referencing some attempts at quantifying these things may help with reviewers.

Some other things I thought about last night:

- WRT to the evolutionary constraints stuff, it seems ok to me, but I don't think I'm the best person to give advice on it
- Did y'all see what it looks like when you fit species in the model? Would probably be better to get into mixed effects though, and that may get exponentially complicated
- Thinking more about template functions… the opposite of plasticity is canalization, which would basically be a flat line… theoretically you could come up with a way to measure the deviation from canalization in all reaction norms… but again will get very complicated and doesn't solve the multiple trait stuff and you don't really have expectations of the intercept
- Math guy did find some of the multivariate trait plasticity stuff to be kind of confusing. He said, "one thing that's not clear to me is how they calculate the "total plasticity score" per species"… that isn't very clear… also he interpreted it as you getting means from discrete soil moisture for each trait and each species… but its actually soil moisture - trait - genotype - species right? And he also said, "probably it's just a weighted sum of the plasticity scores of all the traits, but they don't say that, or at least I can't tell by my reading of their stuff. if it is just a weighted sum like that, then that makes sense to me as well, and the t-test between species' plasticity score for each soil moisture value is okay. one thing that might be interesting and a finer-grain analysis though would be a trait-by-trait comparison between the two species"
- Brings me to the point about why you don't talk about univariate trait stuff very much here? I mean I think its actually ok, but maybe a bit more word smithing to convince reviewers why you are focusing on multivariate trait plasticity as a whole?
- Fig 2. It's kind of wild how little variation there is in 2a/2h for B distachyon, at first I thought it was missing lines or maybe I just misread something
- Fig 3. Is a beast. I think I like it. But I think its a lot to take. I think you will need to do a better job in the figure caption to make it more clear. I had to read it many times over.

Finally, if I was a reviewer I may press on why you didn't do mixed effect models (lm only does fixed effects right? I could be wrong, I'm more of a lmer guy). I'm not sure if you need to talk about it in the paper but something to keep in mind.

I think that's about all I can do for now. Having the code there is helpful as someone who does a lot of code review these days, I do have some suggestions for the code which you can take it or leave it, but I'm always for scientists striving to have production quality and community/reproducibility friendly code:

- Better comments. Roxygen or whatever its called makes it simple to document your code.
- Make more functions which can be sourced and reused without hard-coded paths.
- Use some better code spacing and styling. I suggest Hadley's R style. (I'm very glad you use the appropriate assignment operator "<-" I get angry when people use "=" as assignment operator in R)
- If you want to get super reproducible look into using packrat for the package version/env management and even possibly adding a Dockerfile to containerize it.

I hope this is helpful for you as I have been a bit removed from this world for a bit!

Best,
Kyle

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> On Mar 25, 2020, at 1:24 AM, Grey Monroe <greymonroe@gmail.com> wrote:
>
> Dear Kyle.
>
> Nice to meet you and thank you very much for taking the time to look through our paper.
>
> I will put together an experimental design diagram for sure. Indeed, it is a bit complicated with the multiple collections. Your questions on the multivariate plasticity part make a lot of sense to me. It is a bit tricky taking Euclidean distances from trait space because of covariance so I like the idea of the distance matrix approach and will try it out.
>
> Good luck with the reappointment package.

Thanks!
Grey

On Mar 24, 2020, at 3:27 PM, Kyle Hernandez <kmhernan84@gmail.com> wrote:

So I hunted down the plasticity quantification paper I went through during my PhD
https://besjournals.onlinelibrary.wiley.com/doi/full/10.1111/j.1365-2745.2006.01176.x

They too propose a distance matrix approach, but I think it's singular trait… anyways, may be worthwhile to peek through.

Kyle

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On Mar 23, 2020, at 9:00 PM, Kyle Hernandez <kmhernan84@gmail.com> wrote:

Hello all

I still need more time to go through this more deeply. But a couple comments.

- The design was really hard for me to picture with all your staggered collections etc. It's probably just me being rusty from these designs but I was wondering if a supplementary figure that was more of a flow chart of sub setting, measuring, etc over time would help?

- The one thing I'm still stuck on is the plasticity through multidimensional trait space method. I remember spending a lot of time in my PhD pouring over all the methods to "quantify" plasticity and it was pretty back then (are several review papers on this topic I think too... I would have to dig them up) So I think your choice of distance is really important here (just Euclidean is what you did?). I feel like there is a loss of non-linearity or the covariance structure across time here. But I also don't have a solution for you to look at the multidimensional trait space haha. But I may be weary of reviewers in this part. Can you cite other papers maybe?

- back as postdoc I also explored some R package that would use genetic algorithms for model selection, maybe not worth your effort here given you already did this stuff

- I keep wanting to suggest a template function approach to test deviation from an expected function but as you mention you don't really have an expected trend (except maybe in SLA?)

I think that's it from my first quick look (didn't get in the weeds of the interpretation yet). Also I will look at the code which I saw linked. More to come in the next couple days. Im working on my reappointment package that is due Wednesday.

Best

Kyle

Kyle Hernandez, PhD
https://kmhernan.github.io/

On Mar 23, 2020, at 1:10 PM, Dave Des Marais <dldesmar@mit.edu> wrote:

Thanks, Kyle! I look forward to hearing your thoughts (and please be critical!!!).

Dave

On Mar 23, 2020, at 10:15 AM, Kyle Hernandez <kmhernan84@gmail.com> wrote:

Hello,

AJ is used to it as someone who works from home regularly, but we are making it work! I'm sure it's not easy with kids etc. (our dogs are enough haha). I would love to look at this. I'll look over it today and depending on how much I have to say, I can better know if I can get you some comments in a day or two or if it will be more towards the end of the week. If you don't hear from me by tomorrow morning please feel free to send a reminder (things get buried).

Best,
Kyle

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On Mar 21, 2020, at 9:09 AM, Dave Des Marais <dldesmar@mit.edu> wrote:

Hi Kyle,

I hope that you and A.J. have settled into the new normal of our bizarre lives. I'm sure that you, like me, are working to find a balance between taking care of yourself, getting some work done, and maintaining sanity! But, if you have a little time to spare I'd love to hear your comments on our nascent manuscript on modeling soil drying responses as an FVT. The manuscript is on biorxiv, and is attached to this message. If things are just too crazy, and time is too precious, I certainly understand.

All the best,
Dave
<Monroe et al Brachy FVT.pdf>