Re: Cancel chilling paper meeting

Bohrer, Anne-Sophie <bohreras@msu.edu>
Tue 1/11/2022 10:15 AM

To: Wang, Peipei <peipeiw@msu.edu>;Li, Xingxing <lixingxi@msu.edu>;Seguraaba, Kenia <seguraab@msu.edu>

Good morning all!

I just met with Hideki and have a few things to share:

- for the statistical analysis, we should perform a 2-way ANOVA to first determined if there is a difference between all the samples tested (difference between genotypes and differences between treatments and GxT differences) and then do an ad hoc test to see which samples/metabolites are significantly different.
- for your analysis Peipei, and the fact that you only have both datasets from "my leaf", it is fine to use the datasets for Xingxing's analysis as well. Considering the samples you got come from the same plants as the samples we used, it is fine to use the same transcriptome dataset for both Xingxing and I.

I hope it makes sense, but let me know if you have questions!

Anso

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From: Wang, Peipei <peipeiw@msu.edu>
Sent: Wednesday, January 5, 2022 1:53 PM
To: Li, Xingxing <lixingxi@msu.edu>; Bohrer, Anne-Sophie <bohreras@msu.edu>; Seguraaba, Kenia <seguraab@msu.edu>
Subject: Re: Cancel chilling paper meeting

Hi Xingxing,

Thanks for your reply. I am glad that you had some feedbacks before I move forward. For the gene co-expression clustering, what I did is just based on the expression profiles of genes. It would be the same for the metabolites. But I don't have much knowledge about the metabolites, and I am not sure whether it makes sense to do the clustering that way. What you mentioned makes sense to me. Do you have the information about which metabolites should be in the same class? Or I can share my preliminary results with you. You can have a look to see whether there is any useful information you can find out. Thanks!

Please check files in Switchgrass_chilling_project\Paper\Figures \Correlation_between_metablome_and_expression_XX_exp1.
"TPM_xingxing_Exp1_expressed_differential_median_WGCNA_exp_MEDissThres_0.1_zscore_profile.pdf" showing expression profiles of gene modules
"Correlation_between_metabolites_and_WGCNA_modules_median_MEDissThres_0.1.xlsx" showing the correlation of metabolite abundance with gene co-expression modules.
Let me know if you have any questions!

Peipei

From: Li, Xingxing <lixingxi@msu.edu>
Sent: Wednesday, January 5, 2022 1:42 PM
To: Wang, Peipei <peipeiw@msu.edu>; Bohrer, Anne-Sophie <bohreras@msu.edu>; Seguraaba, Kenia <seguraab@msu.edu>
Subject: Re: Cancel chilling paper meeting

Hi Peipei,

It's a good idea to group the metabolites first and perform the co-expression analysis. You mentioned to conduct the clustering for the metabolites. That will be grouping the metabolites according to the similarity in their abundances, right? If that's the case, I'm curious about what the criterions would be to say, for example, two metabolites are close enough in their abundances and thus should be grouped together. As a complementary approach, I will calculate the accumulative ion abundances for some specialized metabolite classes. That will help to simplify your co-expression analysis a little bit.

Thanks,
Xingxing

From: Wang, Peipei <peipeiw@msu.edu>
Sent: Wednesday, January 5, 2022 1:07 PM
To: Bohrer, Anne-Sophie <bohreras@msu.edu>; Seguraaba, Kenia <seguraab@msu.edu>; Li, Xingxing <lixingxi@msu.edu>
Subject: Re: Cancel chilling paper meeting

Happy New Year all of you!

I have gotten the gene co-expression modules and the correlation between the abundance of each metabolite and the gene co-expression modules. This was done for the exp1 data from Xingxing. Since there are thousands of metabolites in Xingxing's data, I am considering conducting the clustering for metabolome too. And then analysis the correlation between metabolite modules and co-expression modules. After that, I would share you guys with the figures and also seek helps from Xingxing for the interpretation of the results.

Another consideration is that, since we have the corresponding RNA-seq data from Xingxing for the exp1, I did the analysis using these RNA-seq data. But for the exp2, we only had RNA-seq data from Anne-Sophie. I am wondering if we should just use RNA-seq data from Anne-Sophie for both experiments? Because we may do the same analysis for the metabolome data from Anne-Sophie, right? Any thoughts?

Best,
Peipei

From: Bohrer, Anne-Sophie <bohreras@msu.edu>
Sent: Wednesday, January 5, 2022 12:52 PM
To: Wang, Peipei <peipeiw@msu.edu>; Seguraaba, Kenia <seguraab@msu.edu>; Li, Xingxing <lixingxi@msu.edu>
Subject: Cancel chilling paper meeting

Hi all and happy 2022!

We were supposed to meet today to discuss our progress on the chilling paper, but I have a conflict at that time today!

I propose we cancel this meeting and meet again as scheduled on January 19 at 4pm.

In the meantime, we can update the to-do list Peipei created on Trello and see where we are all at.
If you have any pressing news or updates, let's chat by email or Slack and schedule a meeting sooner if needed! 🙂

I hope you all had a great break!
Anne-Sophie

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