Homework 2

Interpreting interaction results

Important dates:

- Presentation date: 18 April 2017

Marks:

- 20 points

Instructions:

- In Homework 1 you have read and discussed the Bessonov et al. 2015 paper. By addressing the questions and discussing them further in class, you now have a basic understanding about the analysis work flow of a genome-wide association interaction analysis (epistasis analysis). However, it is only the beginning …. What do the findings mean? Can they be impactful?
- In this homework, we are asking to dwell upon a single approach that can increase your understanding of a statistical epistasis finding. To help you in looking for relevant material, we have included some guiding thoughts below. Following up on a single thought is sufficient to achieve the goals of this homework, as long as you can fill a 20 min presentation with it.
- As before, you can work in groups, but everyone should present. The final score is a group score. Please submit your slides presentation to Kris Chaichoompu.

Guiding thoughts

1) Results do not mean anything if they cannot be replicated? What does replication mean or involve in the context of interaction studies? Do you find information about this in the literature? Were there some strategies implemented in the Bessonov et al. 2015 or Evans et al. 2013 paper towards replicability?
2) What is the meaning of a biological interaction? Does it always need to involve genetic markers? Can it also refer to other omics? Can knowledge about biological interactions (such as via the STRING data base - http://string-db.org/) be useful BEFORE / AFTER performing a genome-wide association interaction study (GxG)? See also Gusareva et al. 2014 (course website).
3) What type of knowledge data bases about biological interactions exist? Can you name a few and describe them? How would you use them in the context of an interaction study? Have you heard from the tool “Biofilter” from the Ritchie lab? Could this be useful? See also Gusareva et al. 2014 (course website).
4) In an eQTL study, the aim is to find those SNPs that regulate gene expression. Such a study involves carrying out many GWAs, one for each gene transcript in your data. For a main effects GWAs (relating a disease trait to SNPs, one by one), eQTL follow-up studies help in giving a functional interpretation to GWA findings. By extension, one can also perform a study to identify those SNP x SNP interactions that regulate gene expressions. Could such a study be helpful as well in interpreting statistical epistasis findings for your disease trait of interest? See also Clyde 2017 (course website).