

Homework 3

Introduction

In this homework you will use the data from the previous homework to answer relevant questions in a family-based genetic association context. You should use the “FBAT” package as well as R (GenABEL package).

Specific questions

1. To be able to work with our data sets in FBAT, we need to create a phenotype file containing our continuous trait with the file extension phe, e.g., pedigree.phe. Use R to manipulate your original data files into the necessary structure and formats! When working with data, you will often encounter situations where you have to manipulate your data in order to work with a certain software.
2. After question 1, analyse the family data using the FBAT statistics/package on the continuous trait from the phenotype file (consider the default options). What do you observe? Can you detect a significant marker?
3. Perform a family-based association study using R (GenABEL with default options). Compare the results between R and FBAT! If the results differ between R and FBAT, discuss how this can be explained!
4. Are the results in question 2 and 3 corrected for multiple testing? If not, how can you correct for multiple testing?
5. Is it possible to correct the GenABEL analysis for population stratification? If so, and when implementing such a correction, do the results change? Is population stratification an issue in GenABEL / in FBAT? Why or why not?
6. Re-analyse the family data using FBAT and explore different settings
 - Modes
 - Models
 - Options `-o` and `-e`Compare your results to those from questions 2 and 3. What do you observe?

Write a small report, including some explanations about how you obtained the results. Send your answers to bmaus@ulg.ac.be.

Due date: 20 May 2013