Hi Prof. Degui,

For the final project for Statistical Analysis of Genomic Data, I would like to use the data and 3 of the differential co-expression ("DC") methods from this paper: <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-019-1851-8>

The (simulated) data used in the paper is available "in the University of Melbourne figshare repository", and 8 of the 11 DC methods used in the paper are available as an

R/Bioconductor.

Last year, I did a small pathway project for BMI 5330 (attached), so I want to continue in that kind of area for BMI 5332.

-Ben

I would like to recreate the benchmark F1 results in figure 3 of the paper:

