

# Summary

*Danfeng Chen*

*2020/2/25*

## Summary

We compared the performance of UNICORN method and the standard GWAS using the crohn's disease dataset from Inflammatory Bowel Disease Genetics Consortium. Here is a summary of the dataset.

## Procedure for standard GWAS

The crohn's disease cases were compared with its internal controls (controls that collected together with cases, *i.e.*, from same region, same date and etc). Related samples ( $PI-HAT > 0.025$ ) are removed from the analysis. All other standard filters for GWAS are also applied. A logistic regression with first 10 PCs are done to detected loci that are strongly correlated with the the disease status.

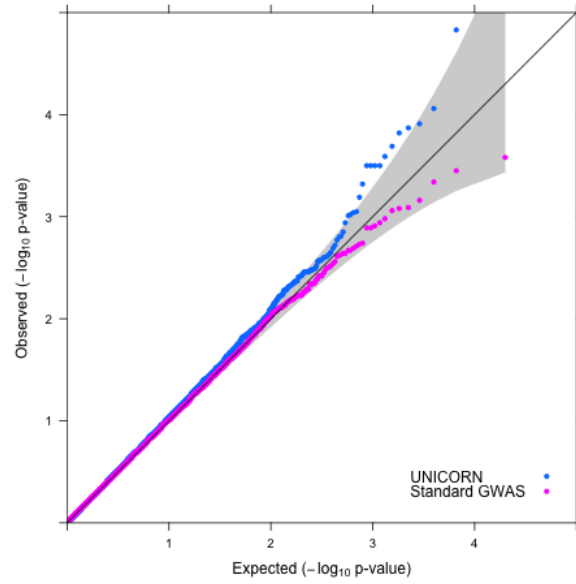
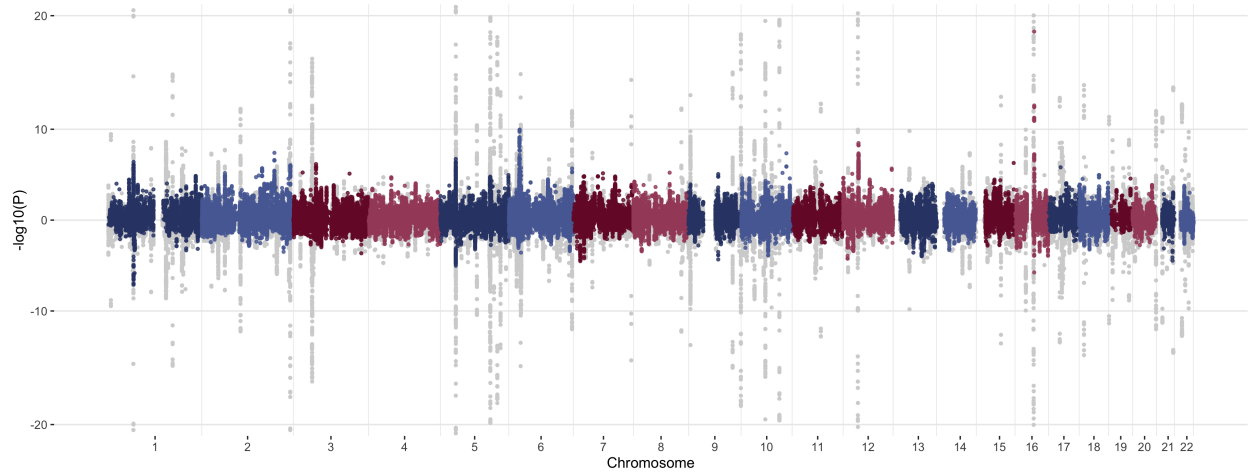
## Procedures for UNICORN

The crohn's disease cases were compared with the external UNICORN controls. The detailed method for UNICORN is described in the draft paper. All cases are going through the same QC procedure as UNICORN controls to ensure the quality of the data and to avoid batch effects.

## Manhattan plot and QQ plot

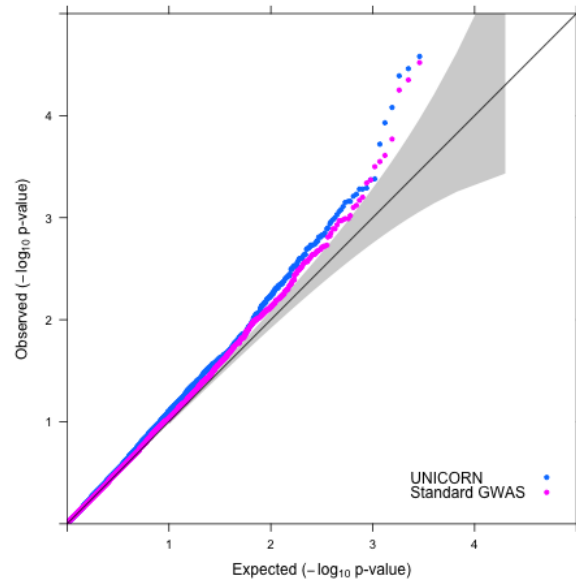
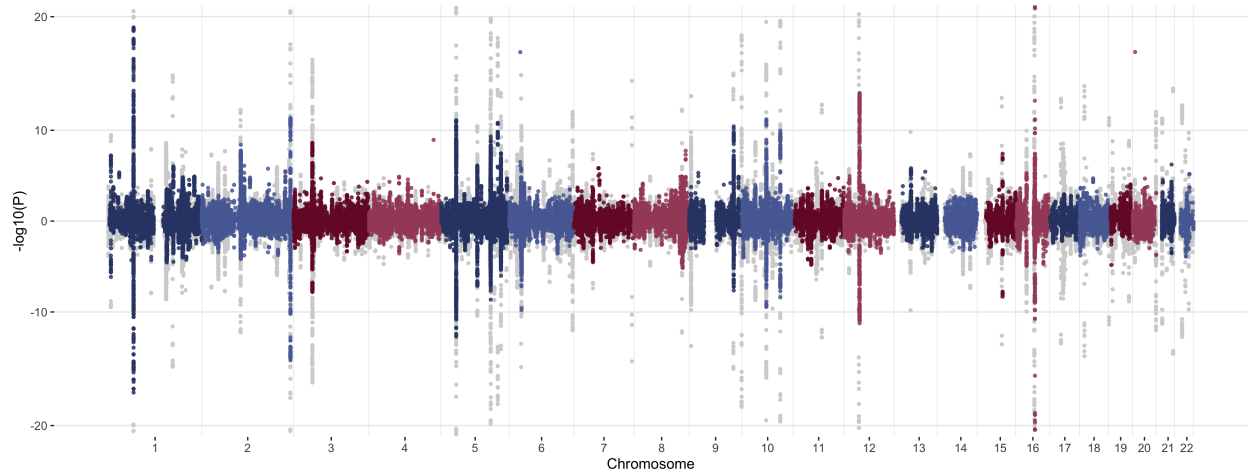
The resulting manhattan plots and QQ plots are as follows:

## Belgium Cohort



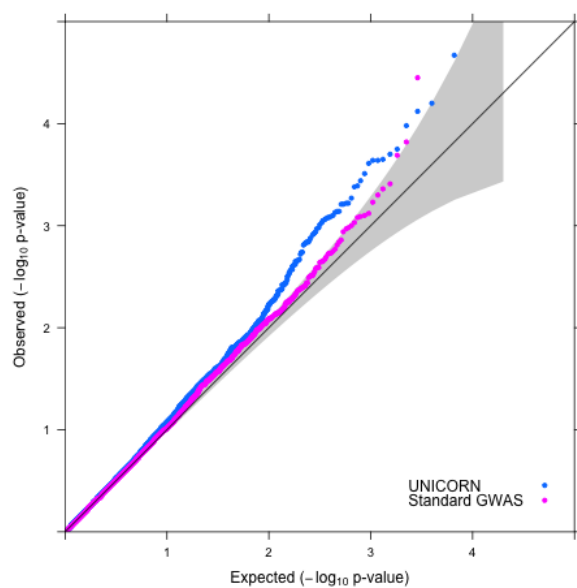
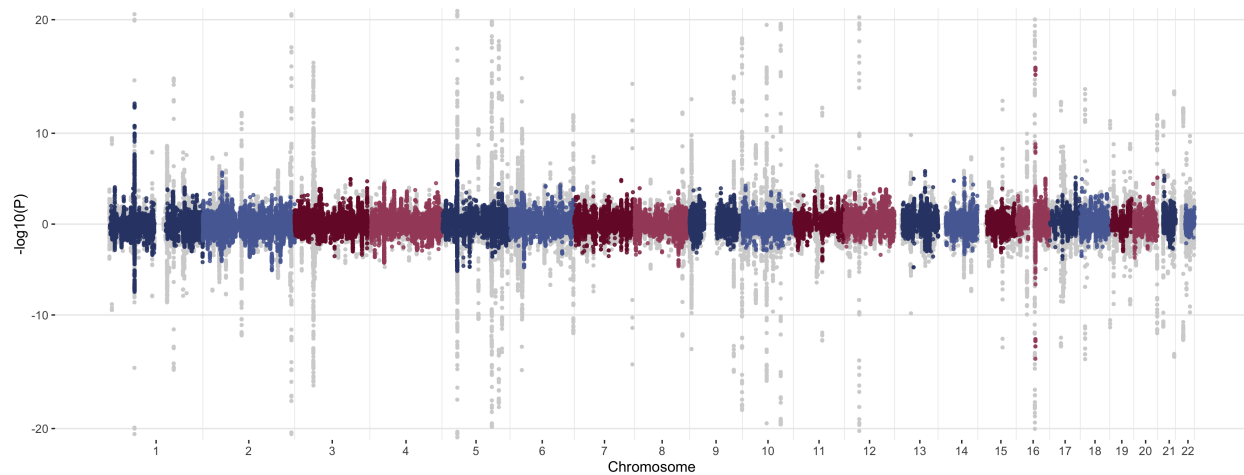
The manhattan plot and QQ plot (tail not shown) for two methods. On the top is the manhattan plot for UNICORN. On the bottom is the manhattan plot for standard GWAS. Lambda GP are 1.0535 and 1.014.

# CHOP Cohort (samples from North America including USA, Canada)



The manhattan plot and QQ plot (tail not shown) for two methods. On the top is the manhattan plot for UNICORN. On the bottom is the manhattan plot for standard GWAS. Lambda GP are 1.0605 and 1.0439.

## German Cohort



The manhattan plot and QQ plot (tail not shown) for two methods. On the top is the manhattan plot for UNICORN. On the bottom is the manhattan plot for standard GWAS. Lambda GP are 1.0476 and 1.0223.