

Introduction to Genome-wide Association Studies (GWAS)

Practical

Part 3: Sex dimorphism

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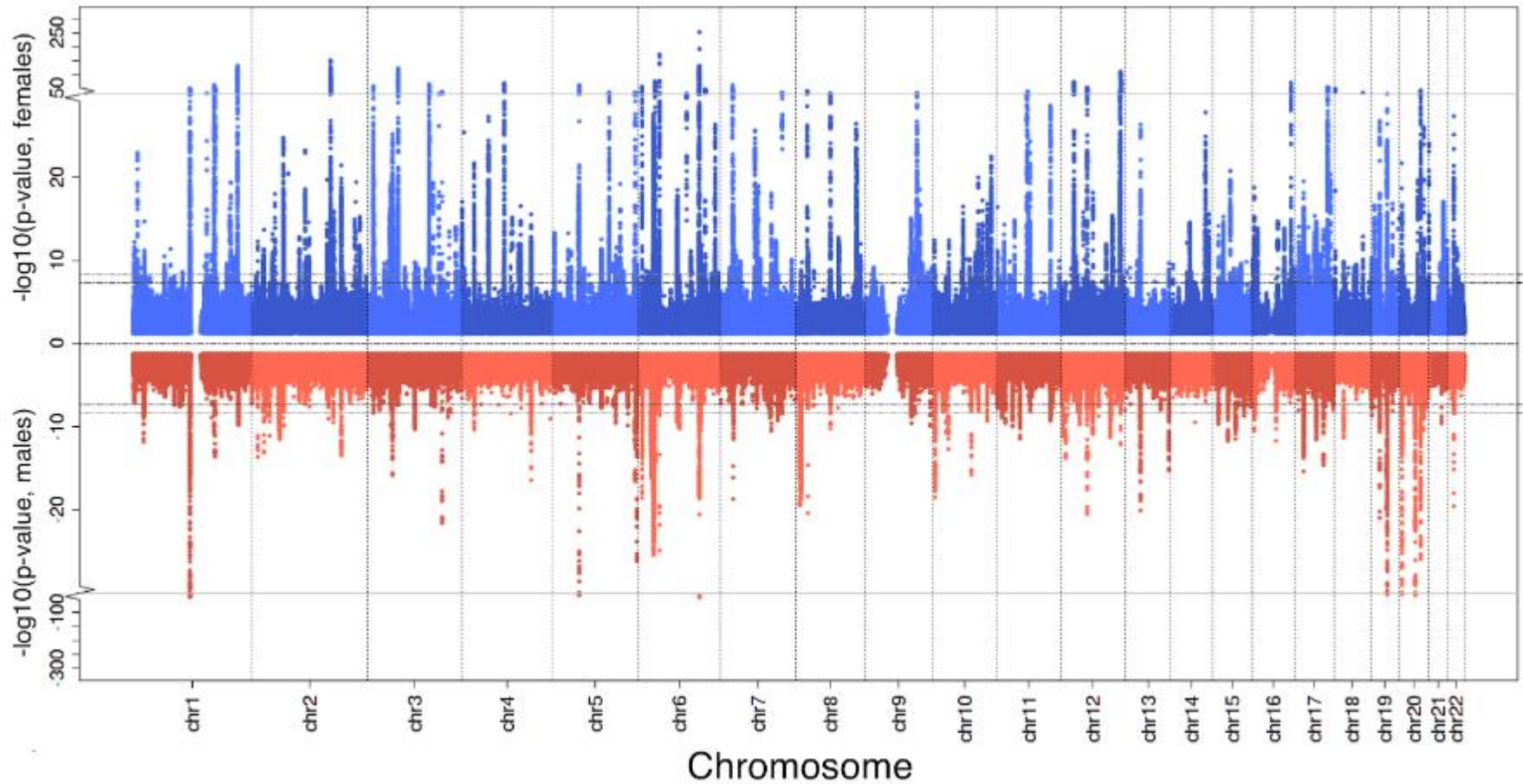
Wellcome Centre for Human Genetics/Big Data Institute

Sex dimorphism

WHRadjBMI

max N_{females} = 379,501

max N_{males} = 315,284



Sex dimorphism test

- Test signals for a sex-dimorphism effect
 - Estimate test statistic

$$t = \frac{\beta_{females} - \beta_{males}}{\sqrt{se_{females}^2 + se_{males}^2 - 2r * se_{females} * se_{males}}}$$

where se is the standard error and r is the genome-wide Spearman rank correlation coefficient between SNP effects in females and males.

- Calculate p-value (P_{diff}) from a t-distribution

$$p = 2 * pnorm(-abs(z))$$

- Implemented in the EasyStrata software

<https://www.uni-regensburg.de/medizin/epidemiologie-praeventivmedizin/genetische-epidemiologie/software/>

EasyStrata

- `library(EasyStrata)`
 - Not installed?
 - `install.packages("/path2tarball/EasyStrata_8.6.tar.gz")`
 - `library(EasyStrata, lib.loc = "/path2library")`
- `EasyStrata("/path2ecffile/sexdiff.ecf")`
 - Note: update paths and file names in the .ecf file

https://homepages.uni-regensburg.de/~wit59712/easystrata/EasyStrata_8.6_Commands_140615.pdf

Sex-dimorphism test

- Input
 - Female specific association summary statistics
https://portals.broadinstitute.org/collaboration/giant/images/9/97/Whradjbmi.giant-ukbb.meta-analysis.females.23May2018.HapMap2_only.txt.gz
 - Male specific association summary statistics
https://portals.broadinstitute.org/collaboration/giant/images/7/71/Whradjbmi.giant-ukbb.meta-analysis.males.23May2018.HapMap2_only.txt.gz
 - SNPs
`snps.for.sexdiff.lst`
 - Combine, female and male signals
 - Only index signals (556) considered for demonstration purposes

- Significance level?
- How many signals with evidence for sex dimorphism?

