**General Instructions for Obtaining Statistics**

Given a list of weighting files and a tab-delimited phenotype file, where the second column determines the type of phenotype (0 = don’t analyse, 1 = case-control outcome, 2 = continuous covariate, 3 = categorical covariate, 4 = continuous outcome), use the following command:

parallel --tag PRSstats -g phenotype -w {} --pheno phenotype\_file.txt ::: method\_phenotype\_weighting\_files > method\_phenotype\_statistics.txt

**For Cross-Validation (CV) Analysis**

1. To analyse with missing CV numbers:
2. parallel --tag PRSstats -g phenotype\_cvnum\_missing -w {} --pheno phenotype\_file.txt ::: method\_phenotype\_weighting\_files > method\_phenotype\_cvnum\_missing\_statistics.txt
3. To analyse with only CV numbers:
4. parallel --tag PRSstats -g phenotype\_cvnum\_only -w {} --pheno phenotype\_file.txt ::: method\_phenotype\_weighting\_files > method\_phenotype\_cvnum\_only\_statistics.txt

**Choosing the Best Result**

Select the best result from the cvnum\_missing analysis and evaluate its performance on the cvnum\_only analysis. Sum the results for all CV numbers.

**To perform this analysis using R rather than on the command line**

Use a similar method as in pgs\_bootstrap, but do not bootstrap.