LDSC

# Environment

## Anaconda

Initialize conda:

source /home1/08005/cz5959/anaconda3/bin/activate

conda init

Activate conda and ldsc env:

conda activate /scratch1/08005/cz5959/ldsc/env

source activate ldsc

# Features

## LD Scores

* For European GWAS, no need to compute own LD scores and can instead use the pre-computed LD scores
  + This will create a eur\_w\_ld\_chr/ directory
  + Computed using 1000 Genomes European data

wget https://data.broadinstitute.org/alkesgroup/LDSCORE/eur\_w\_ld\_chr.tar.bz2

tar -jxvf eur\_w\_ld\_chr.tar.bz2

* Currently, bulik recommends using those same LD scores for both –w-ld-chr and –ref-ld-chr flags for non-partitioned ldsc

## Heritability and Genetic Correlation

<https://github.com/bulik/ldsc/wiki/Heritability-and-Genetic-Correlation>

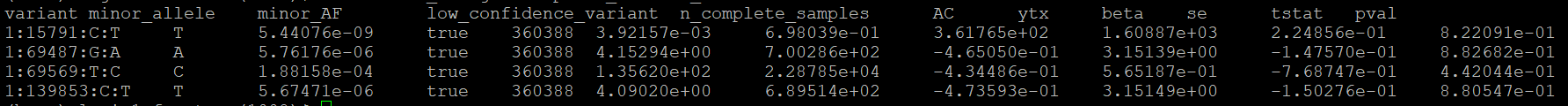
* Convert your results to .sumstats format using munge\_sumstats.py
  + Requires following information: rsid; effect allele; non-effect allele; sample size; p-value; signed summary statistic (ex. beta)
  + –merge-alleles makes sure that the alleles in your results match the alleles listed in the data used to estimate LD scores
  + Check log file for errors with: grep ‘WARNING’ \*log



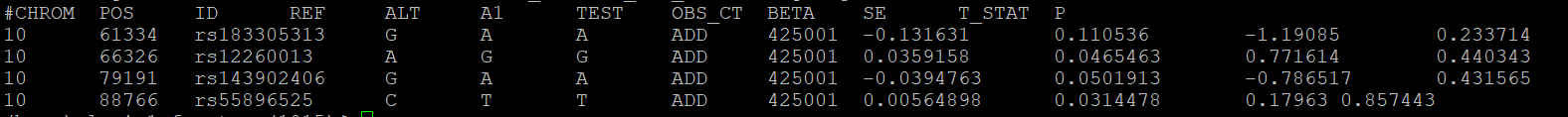
# Log

### 6/10/2021

* Set up environment by downloading anaconda for linux <https://github.com/bulik/ldsc#readme>
* Neale Lab Header



* + Neale doesn’t have rsid included; I can try to match with plink2 results
* Plink2 Header



### 6/11/2021

* Download LD scores and alleles used to compute LD scores
* Create sumstats file format from results



6/14/2021

* Calculate heritability and ldsc intercept for height
* Error: IndexError while reading LD Scores
  + Forgot to add the “/” after eur\_w\_ld\_chr
* H2 and intercept for height
  + What is lamda and ratio

