convert p-values to Z-scores by using the LDSC script munge\_sumstats.py

input = SNP A1 A2 N SIGN P

conda activate ldsc

Trait 1

./ldsc/munge\_sumstats.py --sumstats *v1/MUNGE\_INPUT1.txt* --n-min 4155 --signed-sumstats SIGN,1 --merge-alleles ldsc/w\_hm3.noMHC.snplist --out *v1/MUNGE\_OUTPUT1*

Trait2

./ldsc/munge\_sumstats.py --sumstats *v1/MUNGE\_INPUT2.txt* --n-min 4155 --signed-sumstats SIGN,1 --merge-alleles ldsc/w\_hm3.noMHC.snplist --out *v1/MUNGE\_OUTPUT2*

This will generate the following files for each trait:

* *MUNGE\_OUTPUT*.log
* *MUNGE\_OUTPUT*.sumstats.gz

I usually convert the \*.sumstats.gz file to a text file, because I got an error when I use this file directly as input to LDSC

mv MUNGE\_OUTPUT.sumstats.gz MUNGE\_OUTPUT.txt

# run LDSC

./ldsc/ldsc.py --rg *v1/MUNGE\_OUTPUT1.txt,v1/MUNGE\_OUTPUT2.txt* --ref-ld-chr ldsc/eur\_w\_ld\_chr/ --w-ld-chr ldsc/eur\_w\_ld\_chr/ --out *v1/GC\_1\_2*

This will generate the following files for each pair of traits

* *GC\_i\_j*.log

I have written a bash script to loop through all pairwise combinations (see Step3\_RunLDSC and Step3\_RunLDSC\_pub) in onder to compute genetic correlations within segments are between segments and publicly available traits. (I still have to move the latter to the SHARED folders)

To read the \*.log files, use the following script in Matlab: ReadGCResults.m