(ldsc) Irenes-MacBook-Pro:ldsc irenecho$ python /Users/irenecho/Desktop/final/ldsc/ldsc.py \

> --rg /Users/irenecho/Desktop/final/ldscstep/step1/bald/baldness.step1.sumstats.gz,/Users/irenecho/Desktop/final/ldscstep/step1/smoke/step1.sumstats.gz \

> --ref-ld-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_h2/eur\_w\_ld\_chr/ \

> --w-ld-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_h2/eur\_w\_ld\_chr/ \

> --out /Users/irenecho/Desktop/final/ldscstep/corr \

>

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

\* LD Score Regression (LDSC)

\* Version 1.0.1

\* (C) 2014-2019 Brendan Bulik-Sullivan and Hilary Finucane

\* Broad Institute of MIT and Harvard / MIT Department of Mathematics

\* GNU General Public License v3

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Call:

./ldsc.py \

--ref-ld-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_h2/eur\_w\_ld\_chr/ \

--out /Users/irenecho/Desktop/final/ldscstep/corr \

--rg /Users/irenecho/Desktop/final/ldscstep/step1/bald/baldness.step1.sumstats.gz,/Users/irenecho/Desktop/final/ldscstep/step1/smoke/step1.sumstats.gz \

--w-ld-chr /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_h2/eur\_w\_ld\_chr/

Beginning analysis at Tue May 3 21:19:56 2022

Reading summary statistics from /Users/irenecho/Desktop/final/ldscstep/step1/bald/baldness.step1.sumstats.gz ...

Read summary statistics for 1167696 SNPs.

Reading reference panel LD Score from /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_h2/eur\_w\_ld\_chr/[1-22] ... (ldscore\_fromlist)

Read reference panel LD Scores for 1293150 SNPs.

Removing partitioned LD Scores with zero variance.

Reading regression weight LD Score from /Users/irenecho/Desktop/BMI/HW4-selected/ldsc\_inputs/for\_h2/eur\_w\_ld\_chr/[1-22] ... (ldscore\_fromlist)

Read regression weight LD Scores for 1293150 SNPs.

After merging with reference panel LD, 1139643 SNPs remain.

After merging with regression SNP LD, 1139643 SNPs remain.

Computing rg for phenotype 2/2

Reading summary statistics from /Users/irenecho/Desktop/final/ldscstep/step1/smoke/step1.sumstats.gz ...

Read summary statistics for 1217311 SNPs.

After merging with summary statistics, 1139643 SNPs remain.

1121211 SNPs with valid alleles.

/Users/irenecho/Desktop/final/ldsc/ldscore/sumstats.py:532: FutureWarning: Method .as\_matrix will be removed in a future version. Use .values instead.

ref\_ld = sumstats.as\_matrix(columns=ref\_ld\_cnames)

/Users/irenecho/Desktop/final/ldsc/ldscore/irwls.py:161: FutureWarning: `rcond` parameter will change to the default of machine precision times ``max(M, N)`` where M and N are the input matrix dimensions.

To use the future default and silence this warning we advise to pass `rcond=None`, to keep using the old, explicitly pass `rcond=-1`.

coef = np.linalg.lstsq(x, y)

Heritability of phenotype 1

---------------------------

Total Observed scale h2: 0.3418 (0.0339)

Lambda GC: 1.4926

Mean Chi^2: 2.5685

Intercept: 1.1874 (0.0437)

Ratio: 0.1195 (0.0278)

Heritability of phenotype 2/2

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Total Observed scale h2: 0.0693 (0.0024)

Lambda GC: 1.5035

Mean Chi^2: 1.7598

Intercept: 0.8866 (0.0096)

Ratio < 0 (usually indicates GC correction).

Genetic Covariance

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Total Observed scale gencov: 0.0054 (0.0025)

Mean z1\*z2: 0.0379

Intercept: 0.0136 (0.0068)

Genetic Correlation

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Genetic Correlation: 0.0349 (0.0164)

Z-score: 2.1313

P: 0.0331

Summary of Genetic Correlation Results

p1 p2 rg se z p h2\_obs h2\_obs\_se h2\_int h2\_int\_se gcov\_int gcov\_int\_se

/Users/irenecho/Desktop/final/ldscstep/step1/bald/baldness.step1.sumstats.gz /Users/irenecho/Desktop/final/ldscstep/step1/smoke/step1.sumstats.gz 0.0349 0.0164 2.1313 0.0331 0.0693 0.0024 0.8866 0.0096 0.0136 0.0068

Analysis finished at Tue May 3 21:20:11 2022

Total time elapsed: 14.97s