SIDE PROJECTS

6/23/2021

* Create table / plots to summarize information of top hits from GWAS Manhattan plot
  + Just table of top hits – no need to annotations yet

6/30/2021

* Partitioned correlation
  + Not available with bulik LDSC

7/15/2021

* Heritability plot: scale the x-axis (genetic correlation) so distance proportional to correlation

7/27/2021

* ~~GWAS vs mash -> PGS -> prediction~~

7/28/2021 (Nasa Meeting)

* GCTA (relatedness matrix) or REMML as another way to measure heritability
* Glycine
* Partitioned mash, use SNPs in subset of tissue
  + Read Spence’s paper (6/6/22)
  + SLDXR (?) – possible method to partition by tissue
* Sex chromosomes – X chromosome androgen receptor

8/18/2021

* ~~Decide outline and format for figures we want in a paper~~

9/1/2021

* ~~Conduct multiple simulations to test p-value thresholds and MAF selections for mash step 3 (random subset).~~
  + MAF – negative selection, more frequent alleles tend to have smaller effect and vice versa
  + sensitivity check: random SNPs from different allele freq and diff p-value thresholds to see if they change our weight estimates

9/22/2021

* put pre-processed files on corral
* Jonathan's question on Bernabeu’s paper - gene pathway of hormones, see if enriched with sex-specific variants
  + Look more into the Science Paper: gene expression

2/22/2022

* want biological hook for amplification section
  + differences of effect size estimates – do partitioned heritability
  + current results limited for genome wide, want to look with annotations

4/5/2022

* method of taking random subset for mash
  + use most common variants (high allele frequency)
* Shared amplification: currently using 90% CI, check if distance from 1:1 is normally distributed
  + Distances not normally distributed (6/6/2022)

4/22/2022

* Scatterplot for table 1 to compare effect sizes – help explain
* Male and female effect estimate comparison
  + Resend PowerPoint, revisit what was going on when we left off
  + Compare raw and posterior effect estimates
  + Alpha represents weight in females over weight in males

5/2/2022

* Sex-specific intercepts
  + grab them and compare standard error information as well
    - Intercept when 0 causal effects are tagged –> structure

5/17/2022

* Why use those specific hypothesis covariance matrices
  + Need to do more sensitivity analysis, can get early start – talk through design with Arbel
    - Ex. Grid further/closer from 1 , denser/less dense grid

6/6/2022

* Keeping summary statistics on Box or move it to different platform (Dryad, or Figshare)
  + Look through Cell website to make sure that they accept Dryad as repository
  + See largest we can get for free (otherwise ask Sandra)