SIDE PROJECTS: MENTIONED BUT NOT DONE 😊

6/23/2021

* Create table / plots to summarize information of top hits from GWAS Manhattan plot

6/30/2021

* Partitioned correlation
  + Not available in 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 (has paper)
* Partitioned mash, use SNPs in subset of tissue
  + 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 Bernabea’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
  + diff of effect size estimates – do partitioned heritability
  + current results limited for genome wide, want to look with annotations