

1. Sex stratified GWAS
   1. Testosterone
   2. IGF1, creatinine, whole body fat mass
2. Relative heritability by genetic correlation
3. Mash mixture weights
   1. M<F - M>F Weights by Trait ---supplement
4. M<F - M>F Weights by M:F Variance
5. M<F - M>F Weights by M:F Heritability
6. R2 v Phenotype over 5 folds
7. Additive Both-sex R2 to mash R2 by Female to Male heritability –-supplement
8. Correlation between Mean and Testosterone -- supp
9. Mean/Var v Testosterone ---literature search to see if its well known –supplement?
   1. BMI, arm fat free mass L, protein level, calcium
10. Correlation between Pheno~PGS and Testosterone
11. Pheno~PGS Testosterone
    1. BMI, arm fat free mass L, protein level, calcium
    2. One positive, one negative results
    3. 10 and 11 side by side to each other
    4. \*\*\* make corr pgs~pheno and testosterone plot by with slope instead of correlation
       1. Order by concordance of sign
       2. Significance
       3. Genetic correlation
       4. M-F difference magnitude
12. Simulation - Grid of Mixture Names (male, equal, female) by parameters

Literature search: Testosterone -> estrogen affect phenotype

Increase testosterone increase estrogen – more female side of the trait?

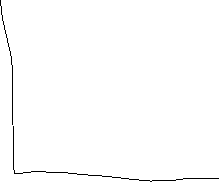
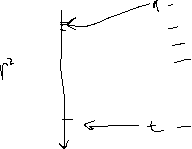
Labels

* Add both, mash, add
  + Additive
  + independent gwas – sex specific additive
  + Covariance aware

1. How effects covary in polygenic sense
   1. Figure 1: pipeline – Miami to mash mixture heat
      1. Flowchart figure: ‘Miami (mini figure)’ to ‘model polygenic covariance between males and females (text)’ to ‘Large covariance matrix (figure (below))’
      2. Actual covar matrix popping out from the large heat map one (couple of them)
      3. Then take big section of large heat map to show what goes into a box in the small heat map
      4. Show a few interesting examples (1 uninteresting case) – small
      5. Mash for binary

Relative heritability by genetic correlation

* Write correlation next to label
* Flip coordinates
* or log scale



* Arrow with more genetically correlation (correlation in parenthesis)

Next Meeting

* New iteration of figure outline – sketch out some
* Simulation
* Other stuff (above)

More questions

* Variation within age group for testosterone? -research
* Ukbb estrogen –
* Evolutionary analysis, F\_ST by mash effect size? Working with Matt

Conference???

* Submit abstract -> oral presentation
* Summary stats one site at a time for the simulation – sample and gwas then take together to put into mash
* Corr plot – line to divide every trait
* Manhattan plot – drop text, cut white spaces
* Mash plots
  + Infer weights of hypothesis matrices
  + Summarize qualitative covariance matrices
  + No effect weight (on bottom)
  + Remove color bar
  + Testosterone and calcium on right side, Manhattan plot on top
    - Have calcium as the walkthrough
    - Testosterone later plays as mediator for genetic effects
    - Whole body fat mass
  + Show simpler covariance matrice
  + M and F to m and f, also on side of covariance matrice
* Mash weights for each variant – 3 traits
  + Cell type annotation
  + For all variants in certain annotation, look at average weight (where those weights are)
  + Testosterone, whole body fat mass, calcium

11/12/21

-- error bars on pgs plot -- correct

-- why is R and L armfatmass different ---- handedness

-- rerun wth bmi adj 5 times again (diff seed please) -- done

11/24

arm\_fat\_free -- handedness, trait distribution

- gene to env variance ratio: phenotype variance

- mash weights

- first draft done by december

start with results

**12/1/2021**

* Getting null effect because not getting any causal snps
* Sample causal snps for i
  + Use the 100/1000/10000 i causal snps, add snps till have 20,000 snps then do gwas/mash on them



* Thin out Manhattan plot – take out the ones at the bottom (non interesting)
  + Subsample



* Genotype variance to environmental variance
  + Genetic variances usually correlated between males and females (ldsc)
    - p(1-p)B^2
    - Assume male and female p(1-p) are very similar (allele frequencies very close)
    - So differences in genetic variances are due to effect size B^2
  + Alpha is the effect size difference factor
  + B(m) = alpha \* B(f) Vg(m) = alpha^2 Vg(f)
  + Environment (m) = environment (f) Ve(m) = alpha^2 Ve(f)
  + 1:1 line
  + Error bars (horizontal and vertical error bars)
    - Method to get standard error of ratio
    - Taylor approximation OR better is to resample (bootstrapping)
      * Calculate pheno variance and h2
      * Have B (10) bootstrap samples (sample with replacement for individuals)
        + All males out of all males
        + Calculate pheno variance 🡪 gwas then calculate h2
    - When have all bootstrap samples, calculate ratio in each
      * Then calculate standard error of the 10 samples
    - Interquartile bars based on bootstrap samples

A picture containing diagram

Description automatically generated

12/20/2021

mash partition - use LD block subset?

weights look the same across groups

dig more on creatinine

use color sim/distinct to 1:1 line

rename title (broader context) (m/f)

more numbers for testosterone

rename axis titles (M/F)

bootstrapping

overlapping annotations? - plot

why similar across cell types

are weights similar

LD blocks?