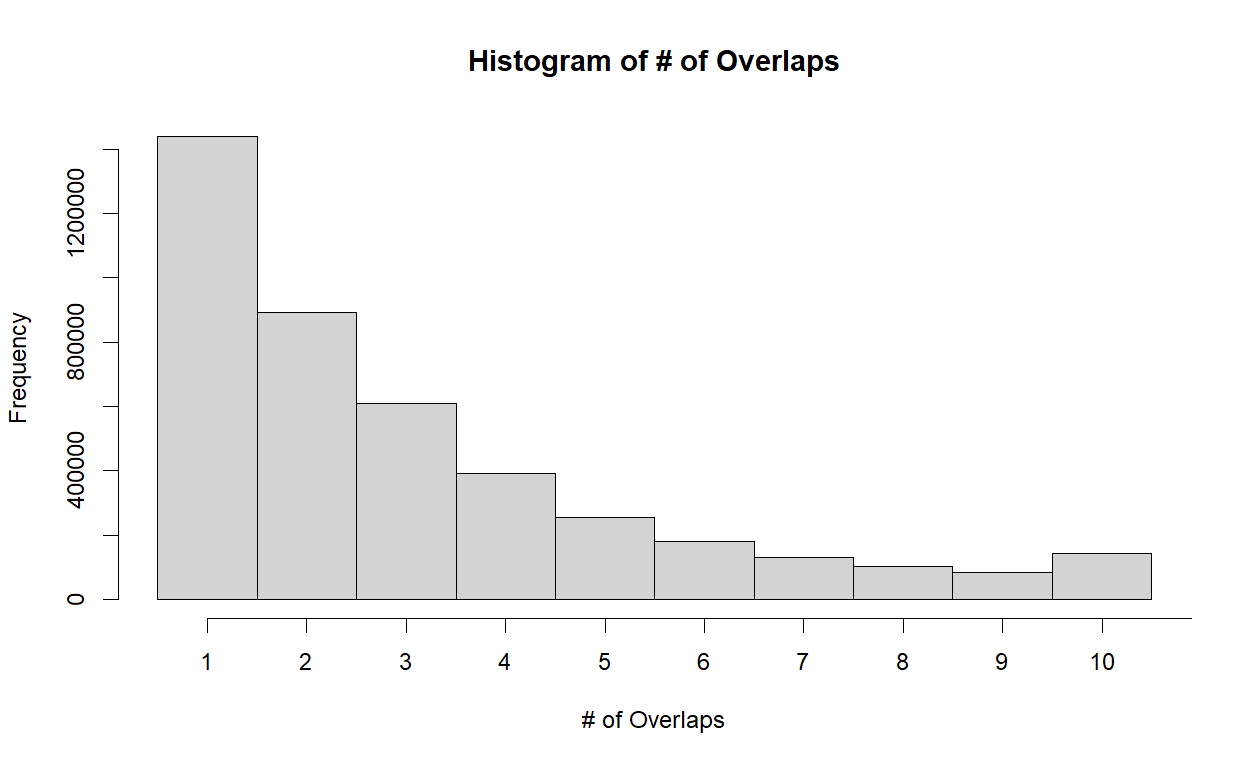
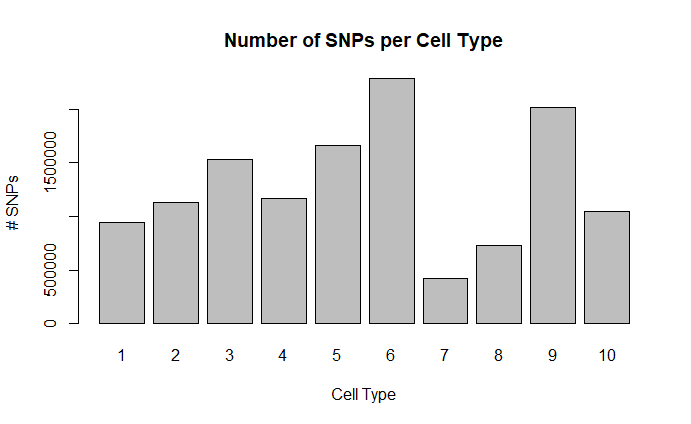
1/4/2022

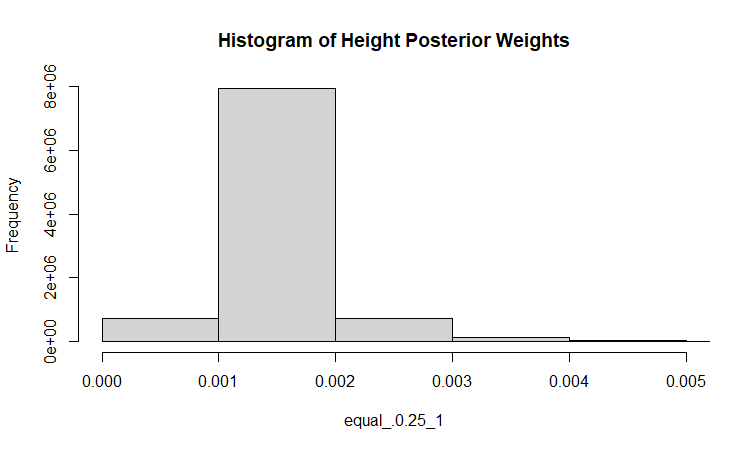
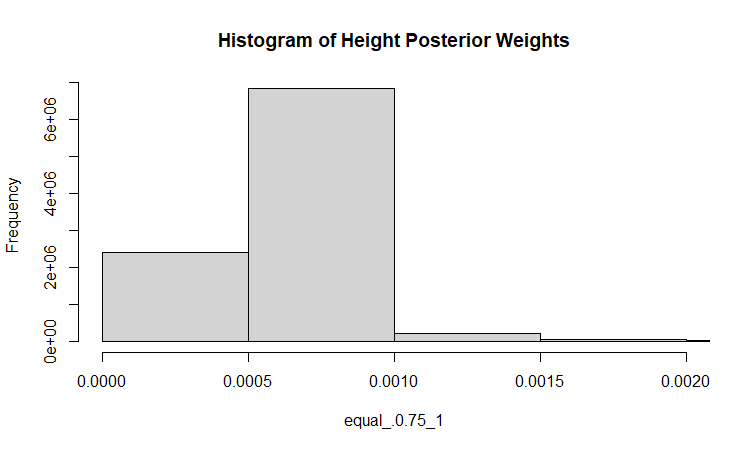
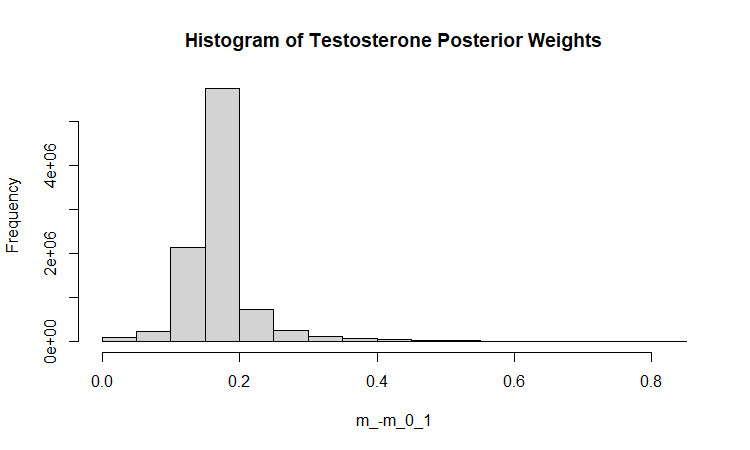
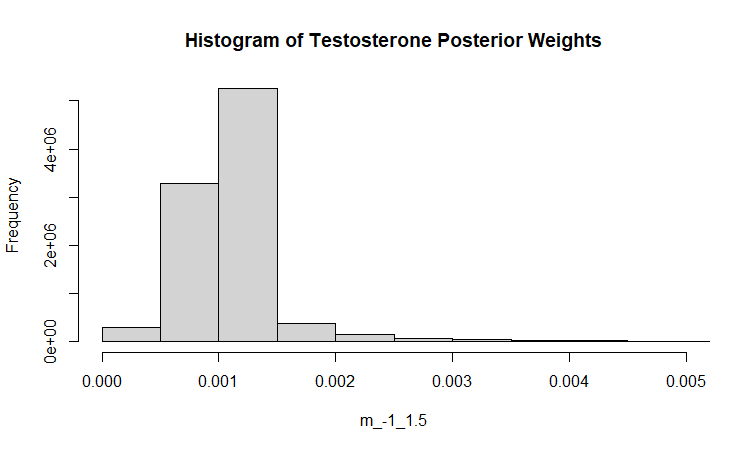
**Partitioned mash Weights**

* Weight proportions (from each individual snps in the posterior step) similar, but not exactly the same as the mixture proportions mash generates (from average of 100 trials)



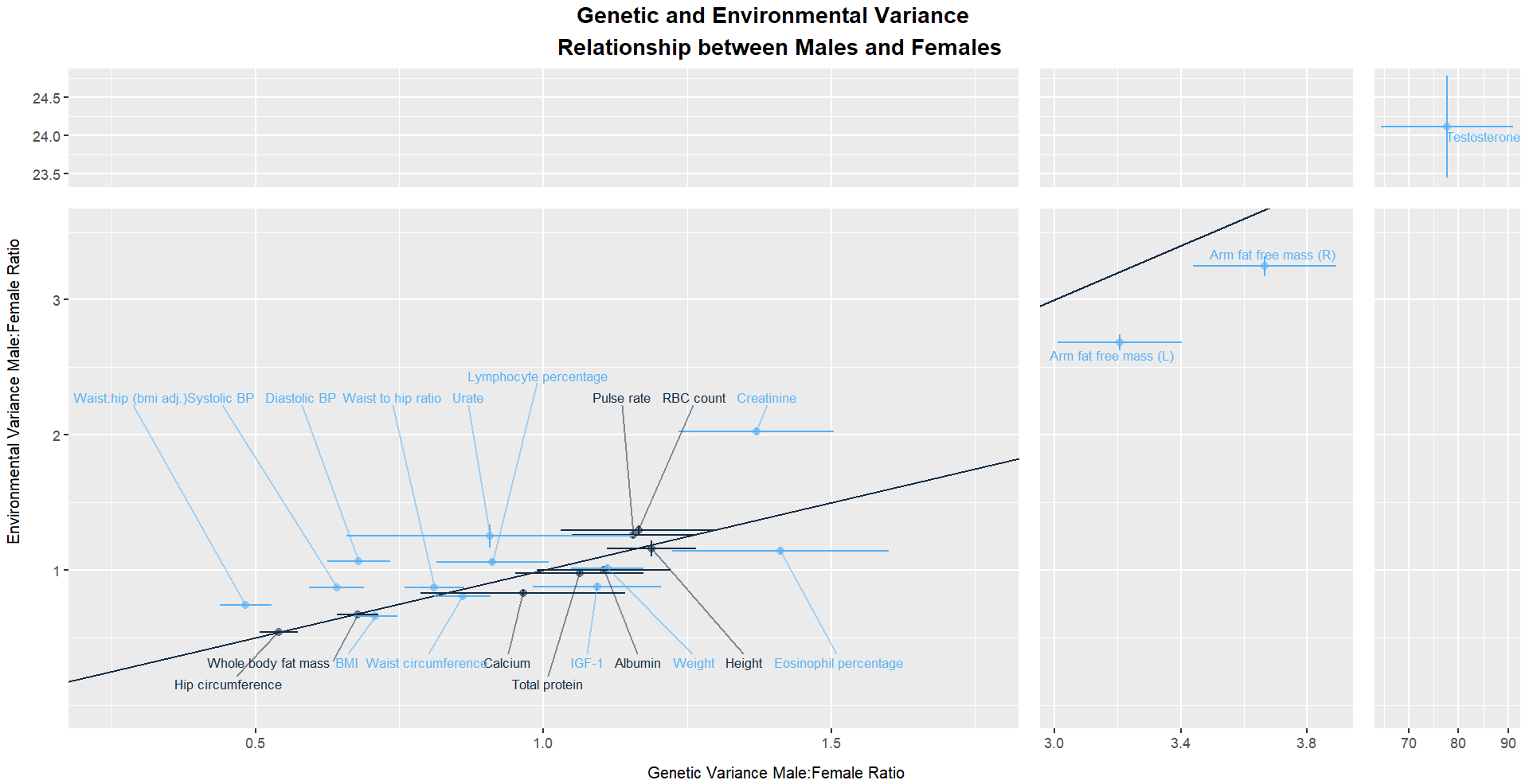






**Genetic v Environmental Variance**

Bootstrap



Non-bootstrap

Graphical user interface

Description automatically generated

* Plot errors to see difference
* Get schematic of cartoon of hypothesis to show what this is testing
* Illustrator – got the purchase
  + Do most in R, fine tuning in illustrator

Creatinine

* Waste product of muscles; filtered out by kidneys; exits in urine
* Serum kidney influenced by glomerular filtration rate, age, gender, skin color, ethnicity, illnesses, diet, etc
* CKD chronic kidney disease has strong genetic component
* Males, on average, have ~17% higher creatinine levels than females do
  + Reflect lean muscle mass
* Levels highly affected by dietary intake and muscle mass
* Usually measured to test how well kidneys are filtering, but known to vary with multiple factors across individuals
  + Filters at relatively steady rate within individual

Story that works for creatinine, but doesn’t say the same for other related traits

Arm -fatfree mass also not on 1:1 line

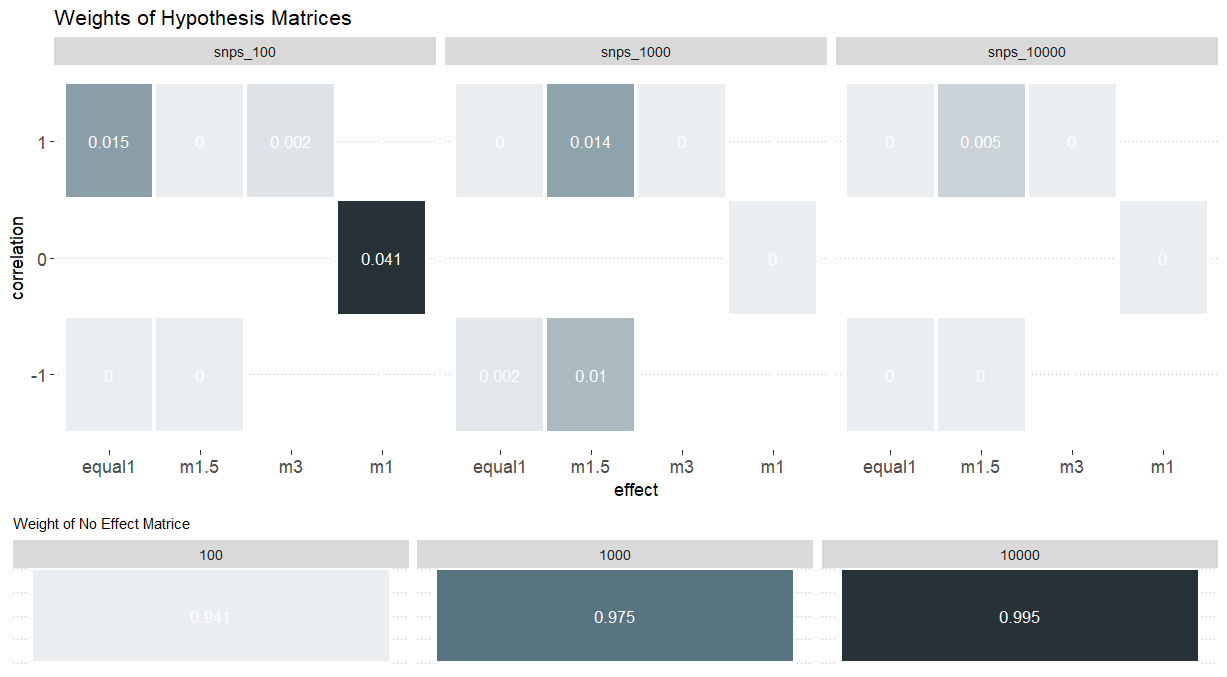
Are genetic effects and environmental effects being amplified in the same pathway???

<https://labs.selfdecode.com/blog/creatinine/>

Chart, bar chart

Description automatically generated

Simulation

****

* Increasing null value when increase number of snps? Should be opposite
* As increase # snps, also decrease heritability per snp
  + On average, less heritability can infer snp as null
* Another analysis
  + Change number of snps, but keep heritability the same
* Do multiple heritability per snp – 0.05, etc

**Figure outline**

* How would describe figures in the results section
* Self-explanatory figures

**Omicron can wfh**

**1/18/2022**

* Figure 1
  + Research paper is actually smaller
  + Smallest font size = 8
  + Too much white space, make it more compact
  + Consistency with font sizes across figures
    - Have important text be much larger
    - Have hierarchy
  + Need margin
  + Only need title if give useful information
  + Have overarching title to describe what you are showing
    - “Infering polygenic covariance structure between males and females in “testosterone””
  + Use white space for male and female label in miami plot
  + Don’t use orange for the annotations since it seems to link odd colored chromosomes
  + White font white box is eligible – maybe change entire palette or font color
  + Magnitude on x-axis
    - Bc effect size is linked to beta
  + If have room afterwards, have another covariance matrice explained
    - Don’t have arrow or have in other direction
    - Have dotted line
  + Perhaps when pointing to small heatmap, have funnel with dotted lines of both edges
  + For matrices – labels (“male-specific”, “female-specific”
  + No effect matrix
  + 2.25 matrix, confusing, maybe write out (0.75 x 3), instead of 9, write (3^2)
    - Or maybe written out in caption
* Figure 2
  + Change title to something more helpful
  + Genetic Correlation on y-axis; SNP Heritability relative to heritability of both-sex sample on x-axis
  + Arm fat free, weight, bmi; waist circ, whole body, sex specific heritability is sig higher than both-sex heritability
    - Highlight in figure text
    - Maybe add little asterisk next to those traits
  + Have larger legend in the empty space of the graph
    - Can have just the text be in color in the legend, can possible even link to one of the data points
* Missing figure?
  + Main takeaway – non-trivial correlation 🡪 mash shows difference in magnitude
  + Have figure showing across traits
    - Scatterplot
      * One axis show amplification signal (amplification M>F)
    - Overall weight on non-trivial correlation and magnitude differences
      * Trivial – perfect correlation, equal magnitude
      * Weight – proportion of traits ex. (1-marginal weight on perfect correlation)
    - People often analyze in variant specific way and miss signal, or look at genetic correlation and still may miss differences --- show up in mash as amplification signal
* Let him know if cant help with Lonestar