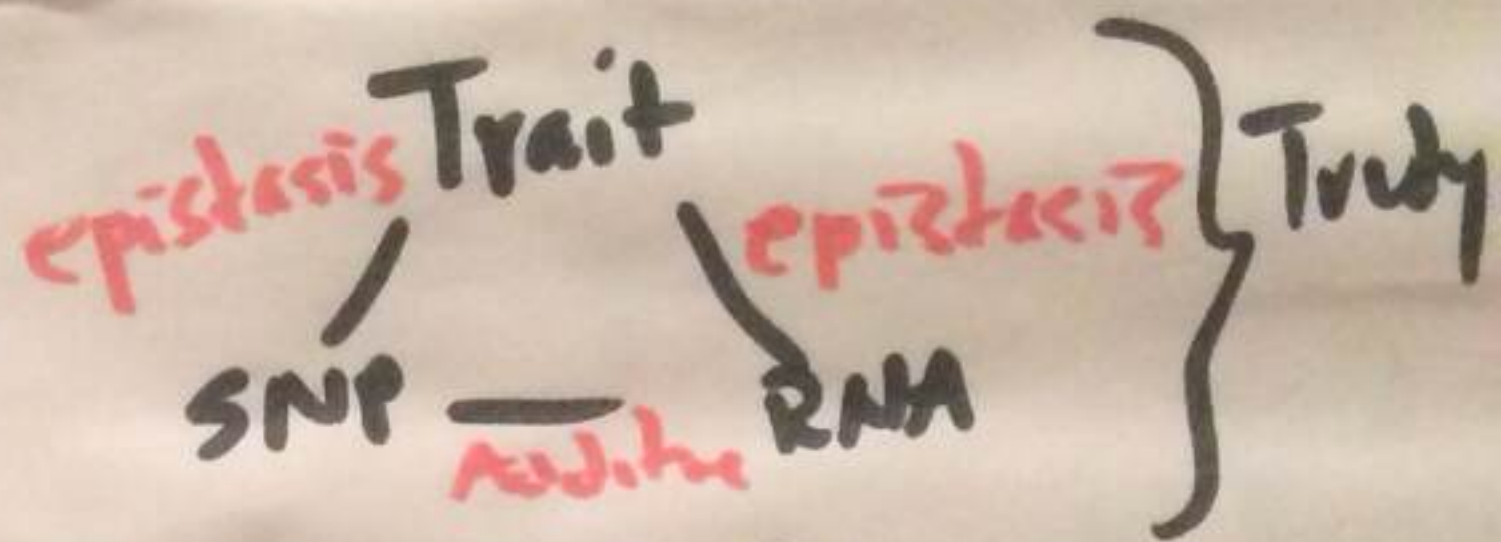


Day 1 - morning



- Trudy finds evidence of epistasis at RNA level
 - Why is epistasis between transcripts so much stronger than SNP-SNP epistasis in *Drosophila*?
 - hypothesis: correlation between transcripts may be strong enough to go across tissues.
 - Does data exist in humans to test these ideas?
 - SNPs + RNA \rightarrow trait
 - It is the genetic variation that creates the RNA-Trait relationships
 - Need to connect SNP-SNP interaction networks with RNA-RNA networks
 - How to bring in family info?
 - How do allele freqs from sample to sample or pop. to pop influence results?
 - We need to change our approach from replication to prediction. (Trudy)
 - multiple traits can be leveraged.

Day 1 - Afternoon + Day 2

- Deliverable ideas
- 1) joint paper — PNAS (indy)? — brief? → high impact 2? papers
easy to review read
 - 2) joint JLES-ASMB ed. session for Baltimore 2015
 - 3) reference data for methods
 - 4) Power not just n? paper?
 - 5) Review of classic quant. genetics
 - 6) Paper on 'How many genes'
- is gene even the right level or unit of inference

Jason's thoughts

- Get away from pairwise
 - ↳ network analysis
 - ↳ Gene action

Modeling strategies

- ↳ lots of methods - pick a few

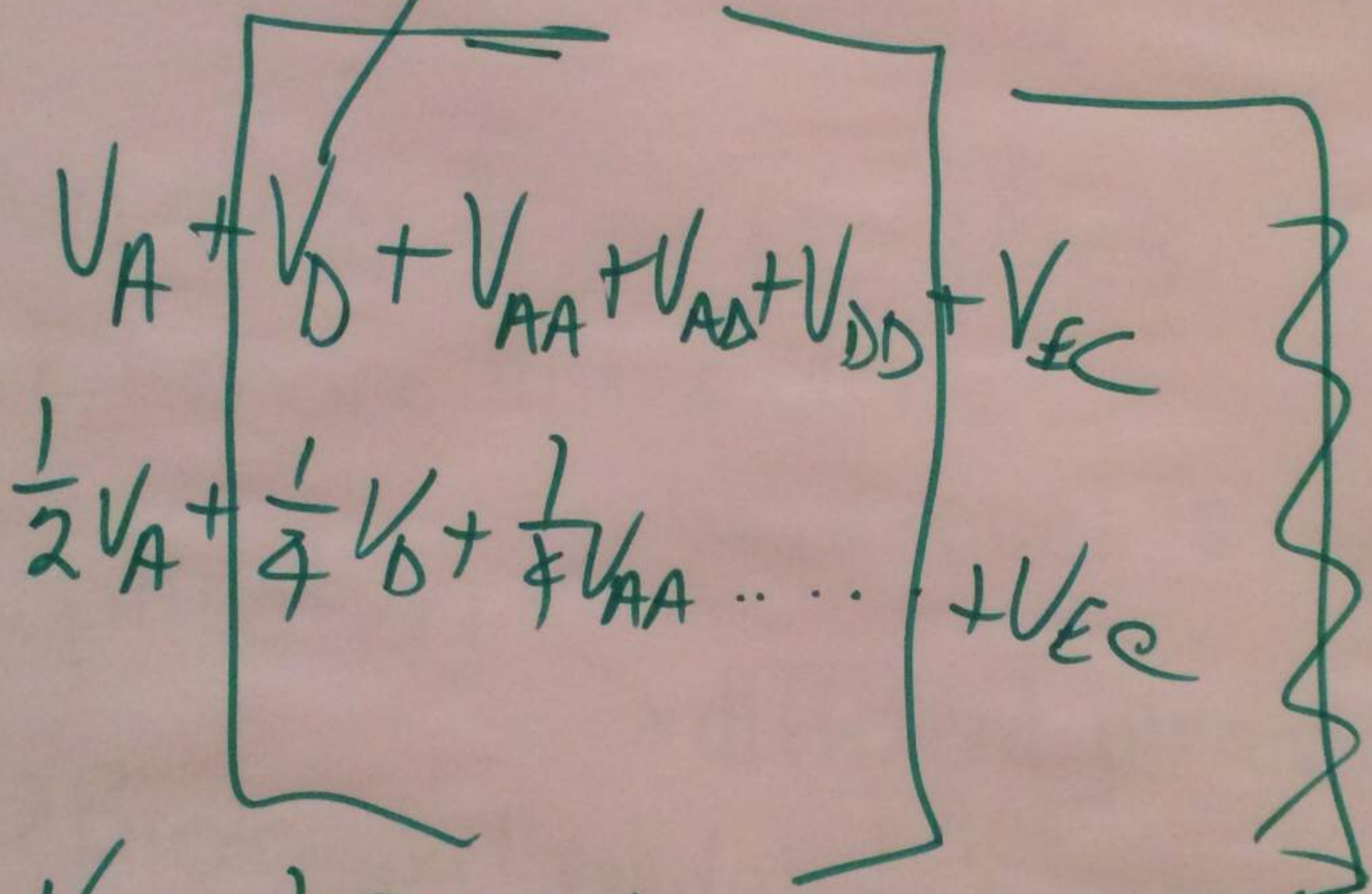
- Run away from p-values

- LD more to be done

- Replication
 - ↳ what level is replication
 - ↳ different pieces of evidence

↳ Biological validation is ^{DICE} where we need to go

$$2(r_{MZ} - r_{DZ})$$



$$V_A + 1.5V_D + 1.5V_{AA} + 1.75V_{AD} + 1.87V_{DD}$$