Context:

* Trans eqtl
  + Currently few identified trans eQTLs
  + Lack of power to find them
  + Trans eQTL strength no more than cis eQTLs and potential number of trans eQTLs, transcript combinations is huge
* Epistasis
  + Number of tests is number of snps choose 2

Innovation

* Switch from many single gene x gene or snp x transcript test to single global tests of a snp being a trans eQTL for one or more transcript or a snp being in epistasis with some other snp for a particular phenotype
* non-local levels methods:
  + Variance components methods: Crawford et al 2017 for epistasis, find ref using for eqtl
  + cpma
* Incorporating Local levels
  + What local levels are?
  + Alternative: Non-equivalent local levels methods
    - KS method is current common method
    - HC
    - BJ
  + Equivalent local levels:
    - Gnull independent case
    - My extension ggnull for correlation
* Estimate correlation
  + Trans eqtl: For any dataset estimate the correlation in Z-scores between transcript level assuming it is the same from one snp to another
  + Epistatis: tbd
* Estimate eta
  + Method 1: monte carlo
  + Method 2: sun and lin method
    - Discuss implications of markov assumption
    - Flesh out alternative assumptions
* Data sets
  + GTEx, GEUVADIS
* Simulation studies:
  + If time, power analysis across detectable region of eps and mu between many stats to see where each has strong and weak power