

A meta-GWAS reanalysis of twenty years of quantitative traits in maize

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Zoom room password: **maize**

Hypotheses

1. The regulatory architecture of quantitative traits in maize is shared across mapping populations
2. Pleiotropy is widespread in maize with moderate sharing of functional loci in climinally adapted traits.

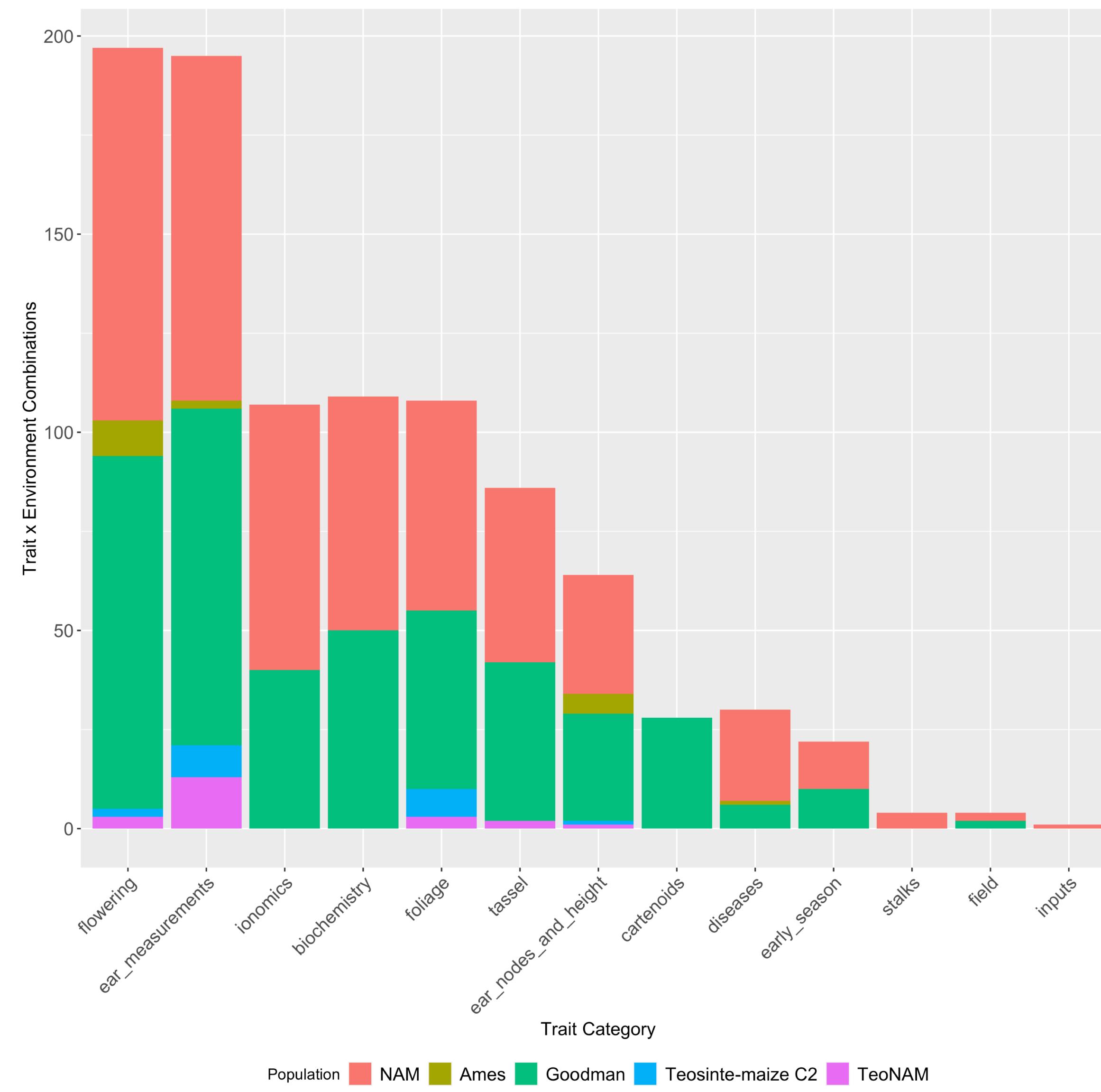
Development Goal

Database that summarizes the effect and interaction that each genomic site has on the genetic architecture of complex traits

Research Goals

1. Consistently remap 250k phenotypes across maize mapping populations
2. ID potential pleiotropic loci in genome
3. Prioritize causal sites using additional data

Collected Classical Phenotypes

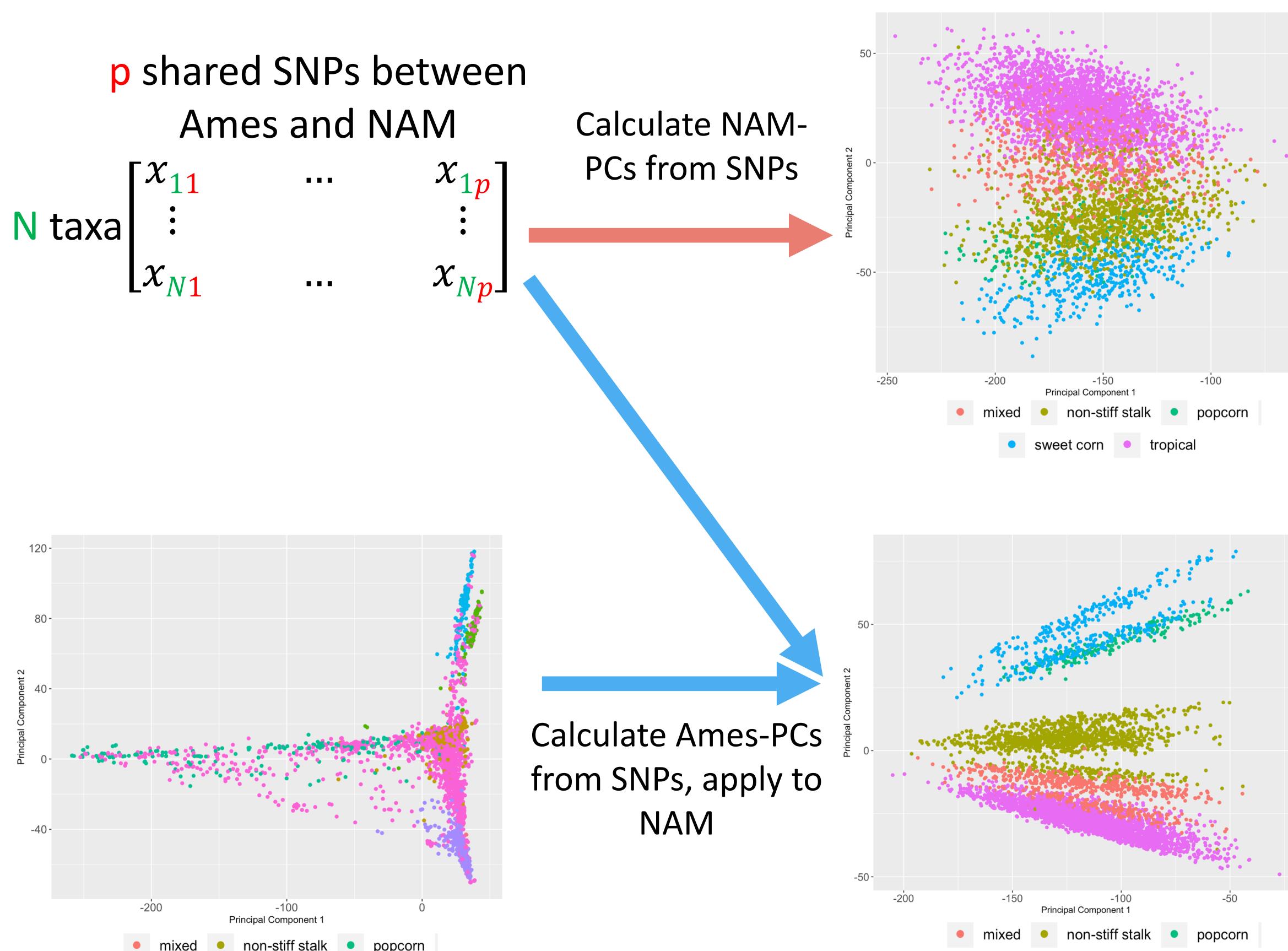


Remapping Strategy

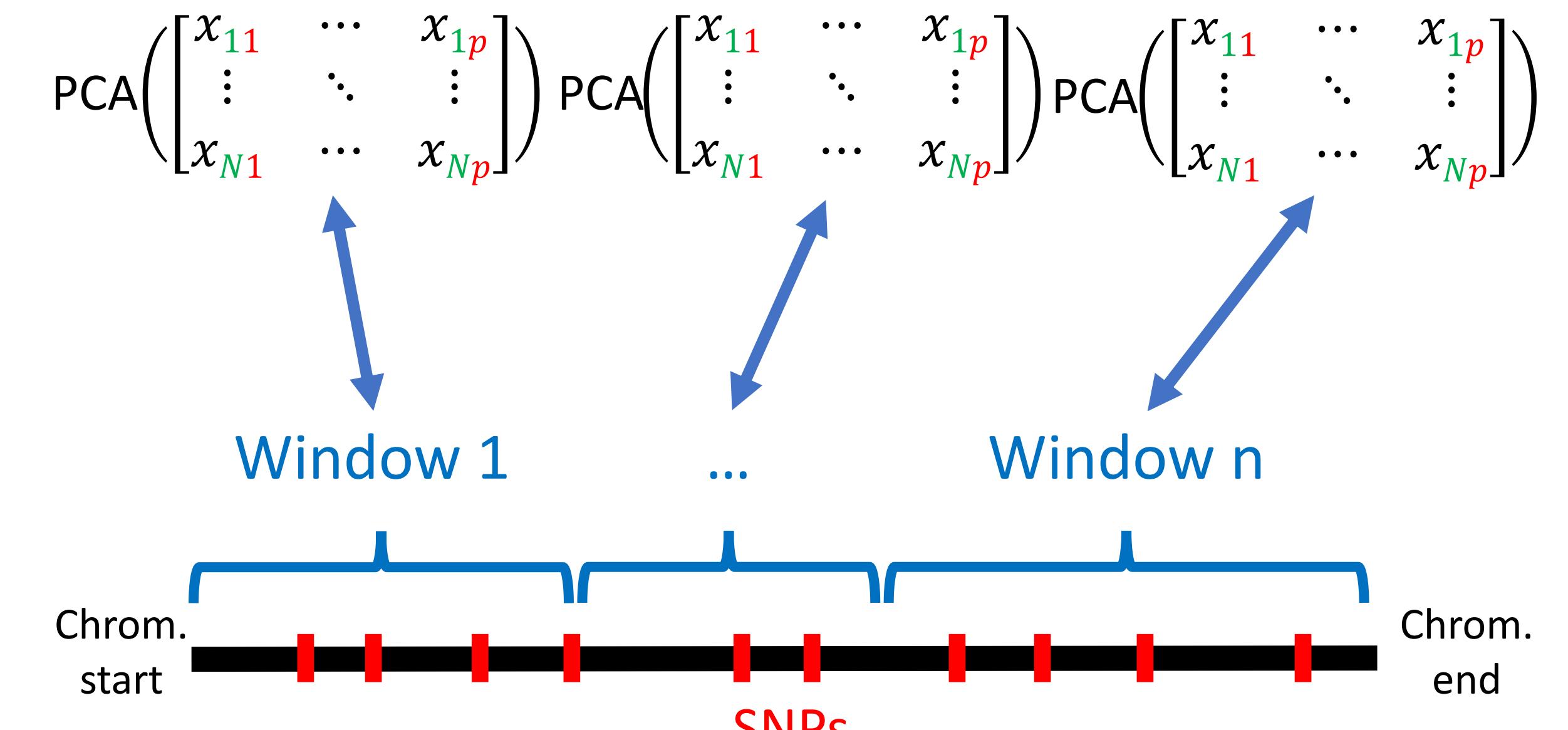
Model for NAM:

$$y \sim X\beta_1 + 3 \text{ global PCs} + \text{window PCs} + e$$

Where global principal components are:



Where window principal components are:



- PCs are calculated in 10 cM windows
- Enough PCs taken within a window explain equal amount of variance across the genome
- Models ran in TASSEL 5 using Fast Association

Preliminary Results

- Remapped ~3700 traits in NAM and the Goodman-Buckler Association Panel

Prediction 1

- Pleiotropic loci in maize are clustered into categories as being trait specific, trait-type specific, or being involved in multiple unrelated traits

Prediction 2

- Pleiotropy differs by the genomic resolution queried in (SNP vs gene vs haplotype)

Next Steps

- Categorize results into potential trait or trait-domain pleiotropic groups
- Test haplotype-GWAS approaches with the Practical Haplotype Graph (PHG)
- Train machine learning models given features of associated complex traits to identify additional functional sites