

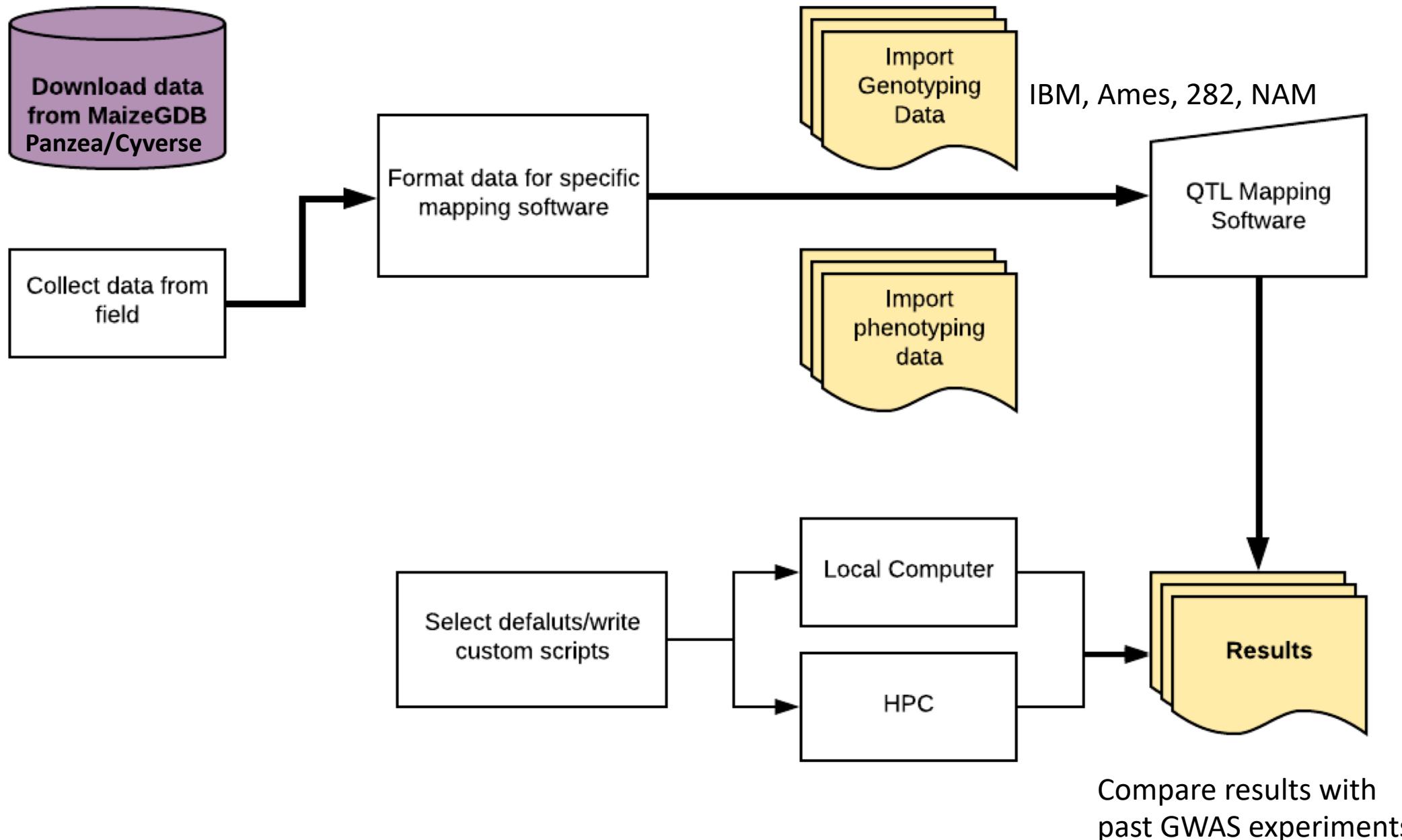
SNP-GWAS/Haplotype-GWAS in Maize

Merritt Burch

Buckler Lab Presentation

2019-06-06

R-Shiny (or similar) based web-based GWAS tool



Maize-GWAS mapping tool

- R/Shiny (or similar) web-based mapping interface
- Perform SNP-GWAS and test haplotype-GWAS using PHG
 - Collect phenotypes from past experiments

Hypotheses

- Haplotype GWAS will still produce similar significant loci/haplotypes associated with traits as compared to the 80M SNP-GWAS but:
 - “New” haplotypes will be uncovered as being associated with complex phenotypes that previously in SNP-GWAS, were masked due to: surrounding SNP effects (synthetic associations, rare-alleles, etc)
 - Significant haplotypes will be highly conserved as inferred by GERP
 - Haplotypes will be associated with changes in expression as inferred from 282 expression data, NAM parents, and B73 data

Collecting past phenotypes

- QTL/GWAS data for IBM, NAM, 282, and Ames populations spanning 30+ years
- Prior data collection efforts: MaizeGDB, Wallace 2014, Hung 2011, Panzea/Cinta
- Currently have: 5481 individuals, ~<60 phenotypes
- Phenos: flowering time, chlorophyll a&b, leaf length, glucose, metabolites, total AA, total protein, disease resistance

Ongoing questions

- Should we collect data on other populations?
 - Landrace and teosinte common garden (n=4000 teos; n=4000 LRs)
 - Zea synthetics & DHs (n=1000s)
 - European and Chinese NAM (n=?)
 - Magic population, NAM and Ames hybrids, Genomes to Fields data?
- How far back should we go?
 - IBM phenotypes date back to 1990's