

## Population structure corrections

- Analyze within each population
- OR
- include structure information in the statistical model.
  - instead of:  $\text{amylose} \sim \text{SNPgenotype}$
  - use:  $\text{amylose} \sim \text{SNPgenotype} + \text{population\_membership}$
- Often it is best to include BOTH population membership and a kinship matrix (genetic relatedness). We will not use that method today (but checkout GAPIT)

