Topic 6+7: Population genomics and plotting

INTRO TO BIOINFORMATICS - MONASH SBS 2019

Learning Goals

- Understand the principals behind basic population genetic visualization methods
  - F_{ST}, STRUCTURE and PCA analyses.
- Be able to plot results of these programs

Considerations for SNPs

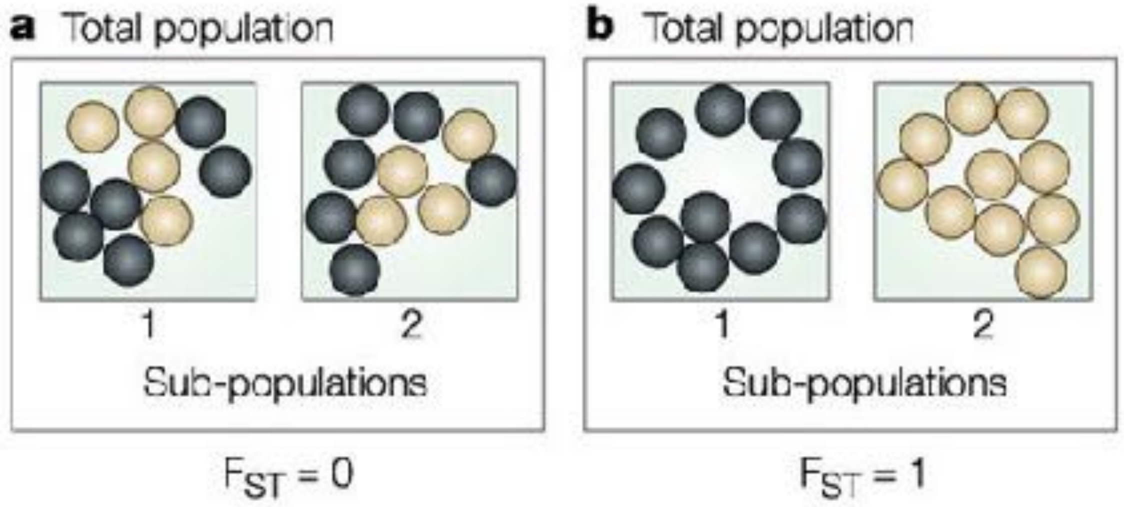
- Ascertainment bias
  - Typically only keep variable sites, can bias diversity estimates
- Linkage
  - With thousands of sites, some will be in close linkage.
- Quality filtering
  - You must filter your SNPs to remove false SNPs, sometimes difficult

Population structure

- F_{ST}
- PCA
- STRUCTURE

F_{ST}

- $F_{ST} = H_T - H_O / H_T$
  - H_T = Expected heterozygosity using global allele frequency based on Hardy-Weinberg
  - H_O = Average observed heterozygosity



Nature Reviews | Genetics

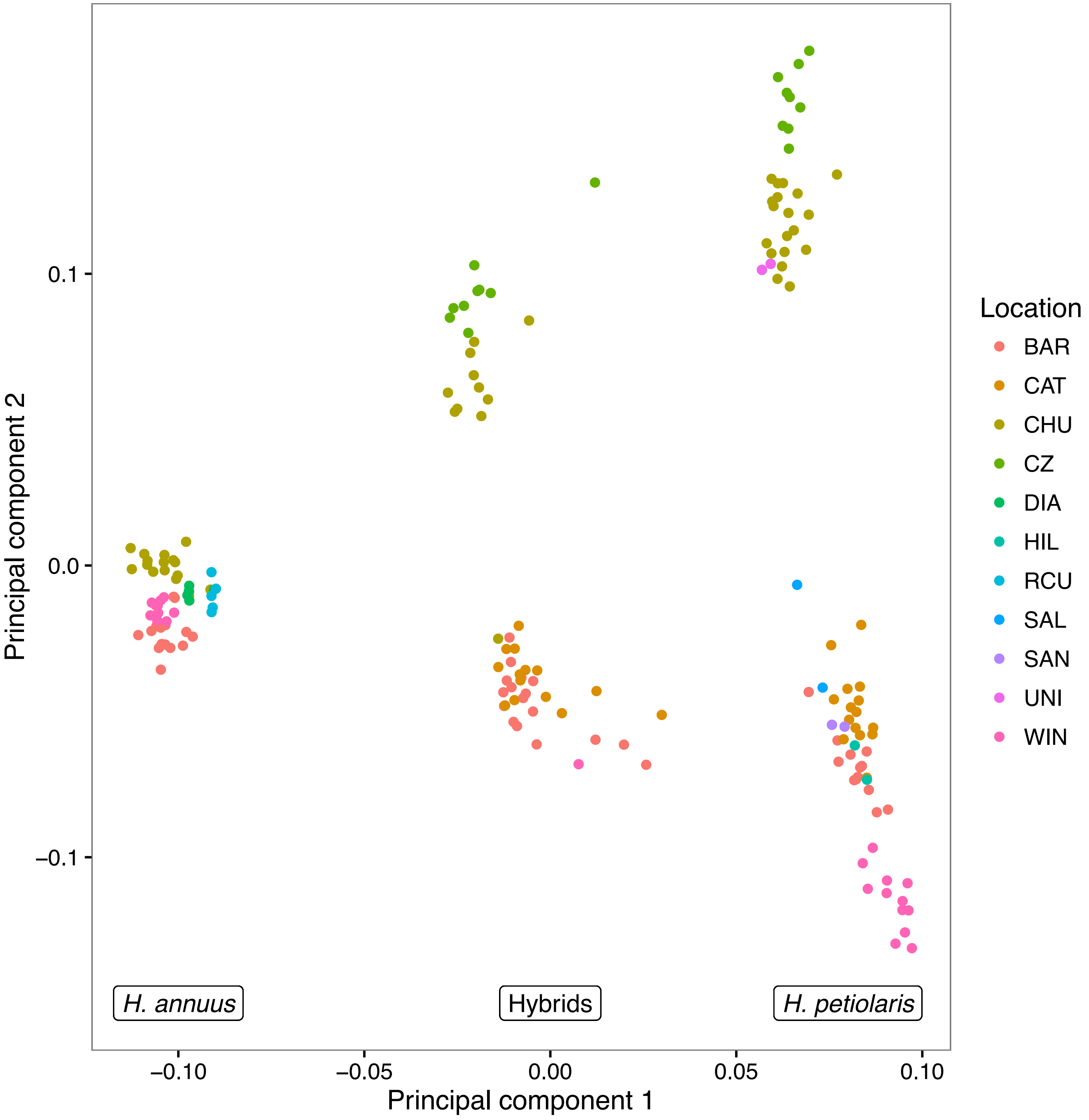
F_{ST} Programs

- hierfstat (R)
- **SNPrelate (R)**
- FSTAT
- Arlequin
- vcftools
- scikit-allel (python)

Principal Component Analysis

- Converts a set of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.

Principal Component Analysis



Principal Component Analysis

- Converts a set of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.

- Great first step to visualize data

- You should prune dataset to unlinked SNPs

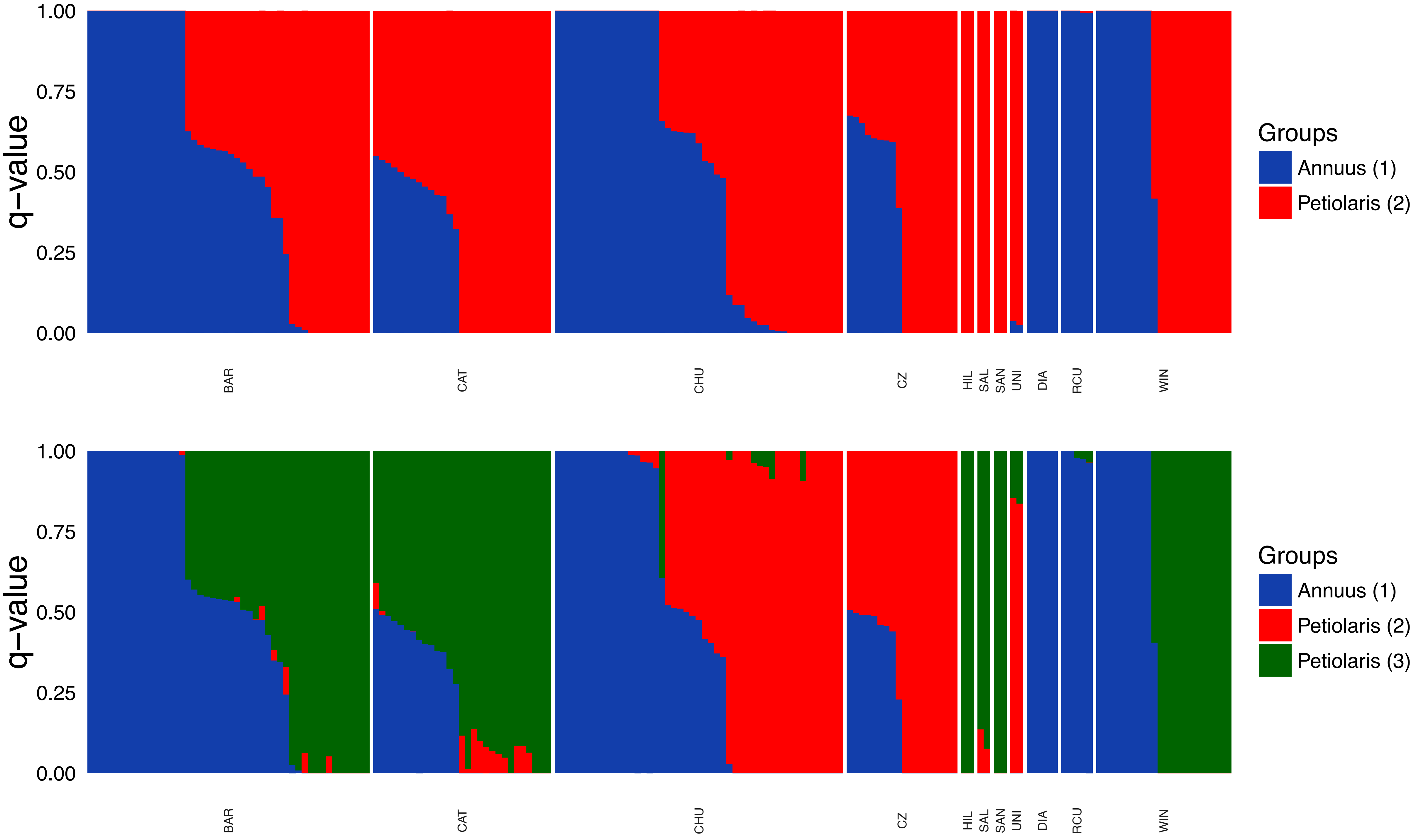
PCA Programs

- **SNPrelate (R)**
- adegenet (R)
- SPSS

STRUCTURE

- Models *K* populations with a set of allele frequencies at each locus.
- Individuals are assigned to one or more populations based on their genotype
- Can pick the best *K* based on your data

STRUCTURE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Groups
Annuus (1)
Petiolaris (2)
1.00
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Groups
Annuus (1)
Petiolaris (2)
Petiolaris (3)

STRUCTURE

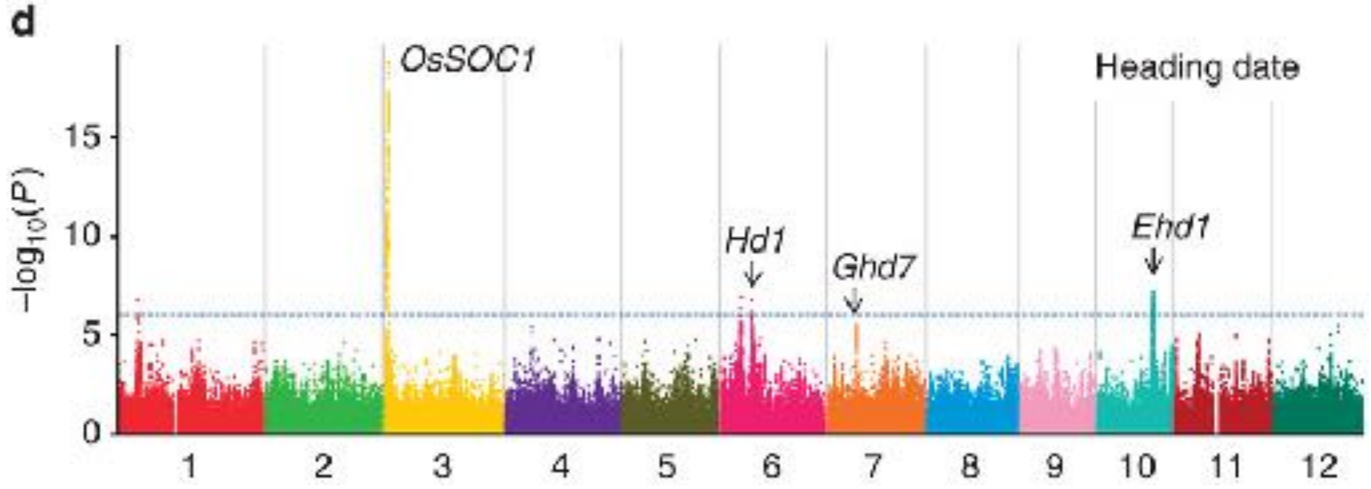
- You should prune dataset to unlinked SNPs
- Run multiple times to confirm consistency

STRUCTURE programs

- STRUCTURE
- Admixture
- **FASTstructure**
- NGSadmix

SNP-phenotype associations (GWAS): one allele at a time

- Regression of phenotype on SNP
- Use PCA or STRUCTURE as a covariate in a linear model or a kinship matrix of relatedness in a mixed effect model
- Yields an estimate of the association between SNP and phenotype beyond what would be expected due to population structure



Huang et al., 2015; Nat. Com.

GWAS programs

- Tassel
- ANGSD
- GWAStools (R)
- GenABEL (R)
- GCTA

Plotting

- dplyr for data manipulation
- ggplot2 for plotting