Topic 8+9: Population genomics and plotting

Learning Goals

- Understand the basic principals, how to run and visualize F_{ST}, STRUCTURE and PCA analyses.

- Be able to list multiple methods for detecting selection in genomic data.

- Be able to list multiple methods for detecting hybrid ancestry.

Considerations for SNPs

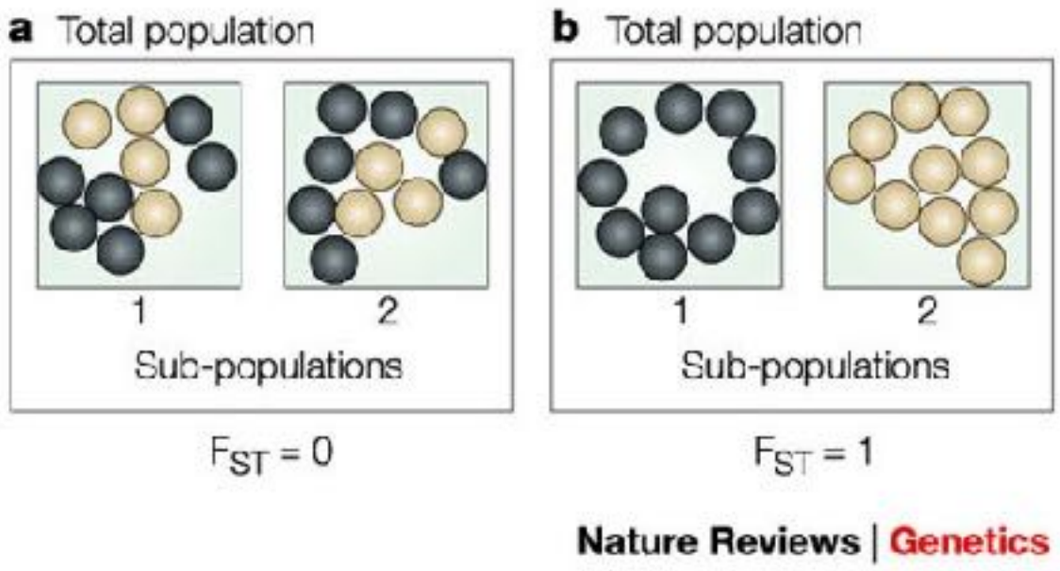
- Ascertainment bias
    - Typically only keep variable sites, can bias diversity estimates
- Linkage
    - With thousands of sites, some will be in close linkage.
- Quality filtering
    - You must filter your SNPs to remove false SNPs, sometimes difficult

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



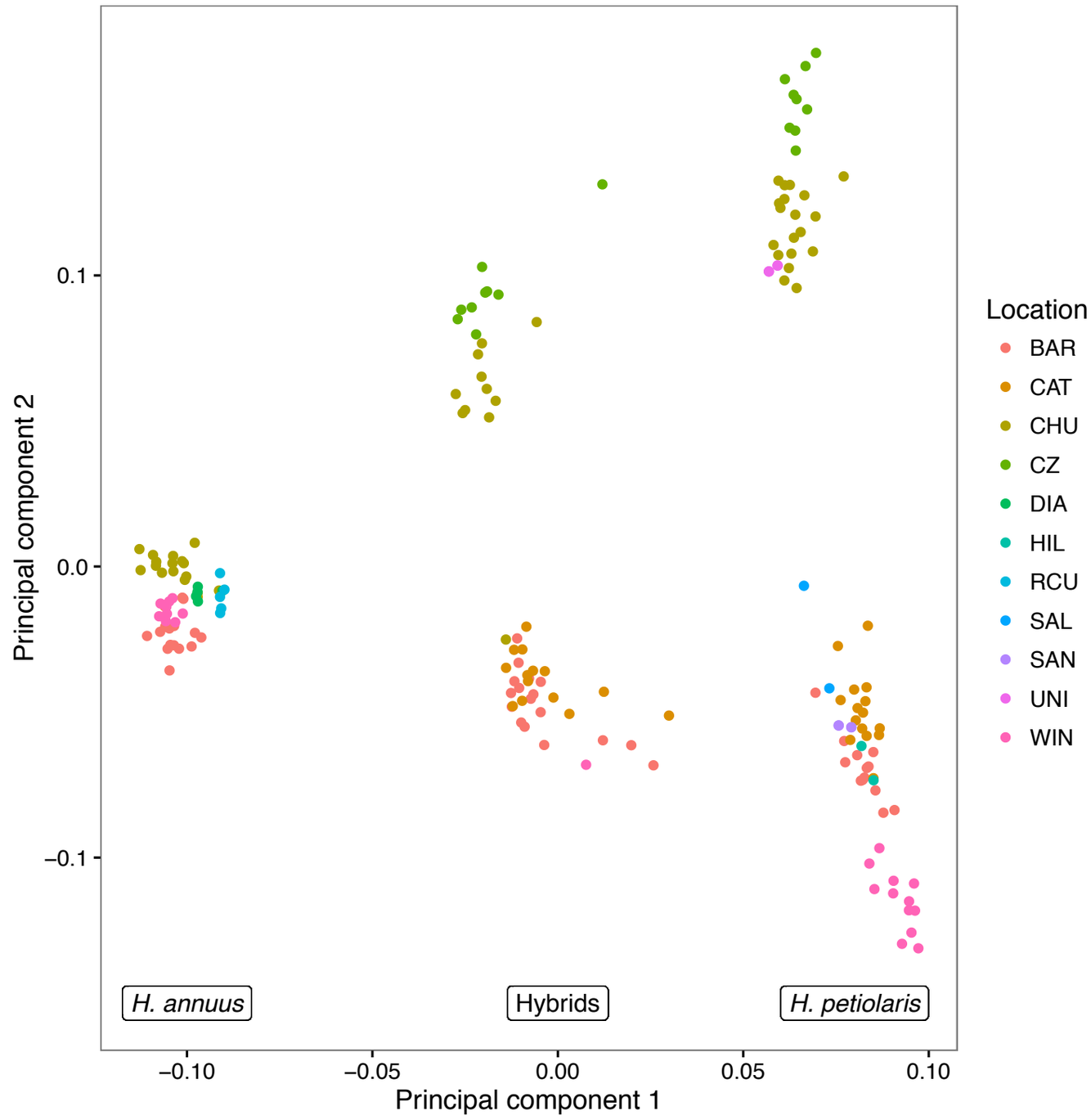
F_{ST} Programs

- hierfstat (R)
- **SNPrelate (R)**
- FSTAT
- Arlequin
- vcftools

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

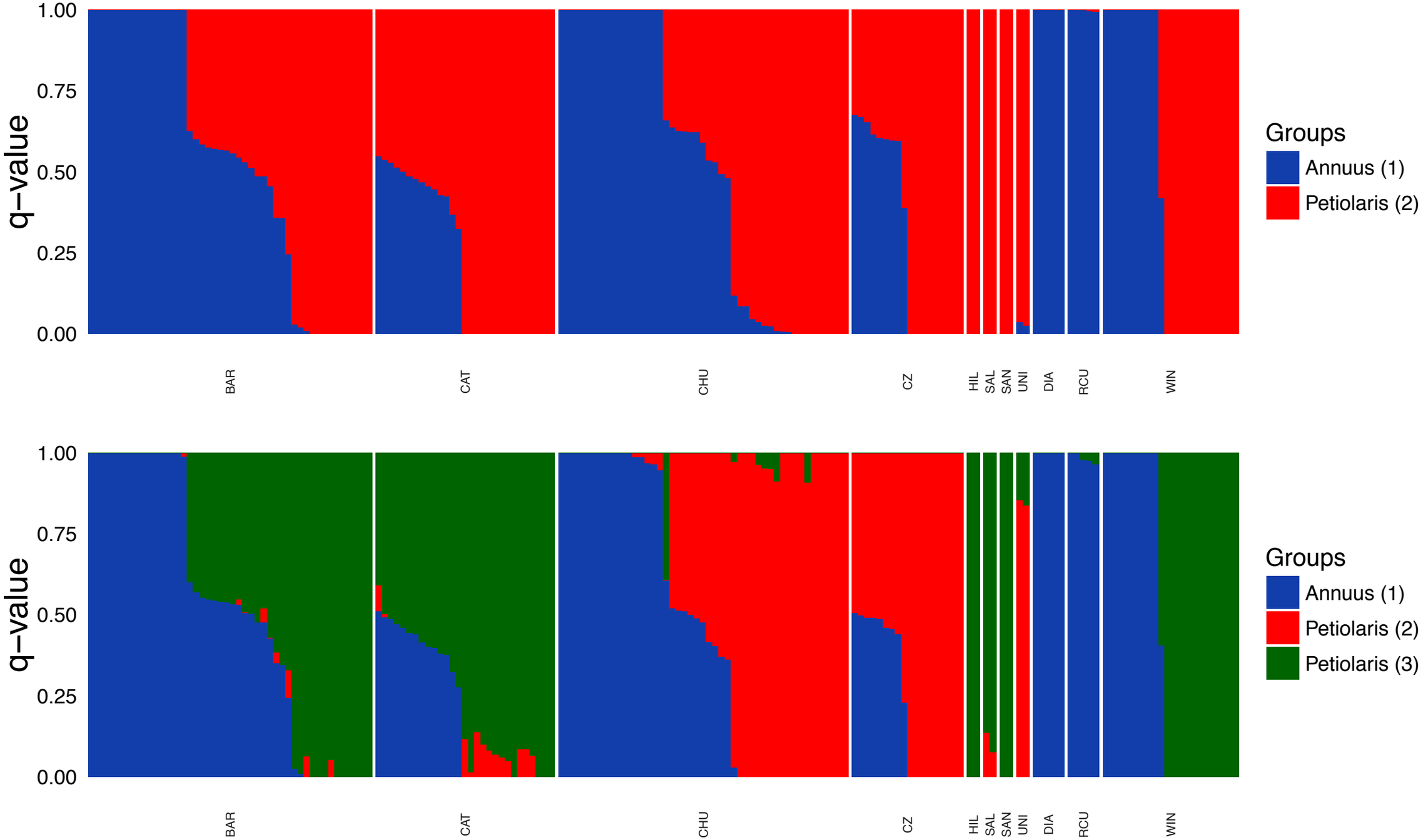
STRUCTURE

- 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


1.00
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BAR
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CHU
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HIL
SAL
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UNI
DIA
RCU
WIN
Groups
Annuus (1)
Petiolaris (2)
Petiolaris (3)

STRUCTURE

- You should prune dataset to unlinked SNPs

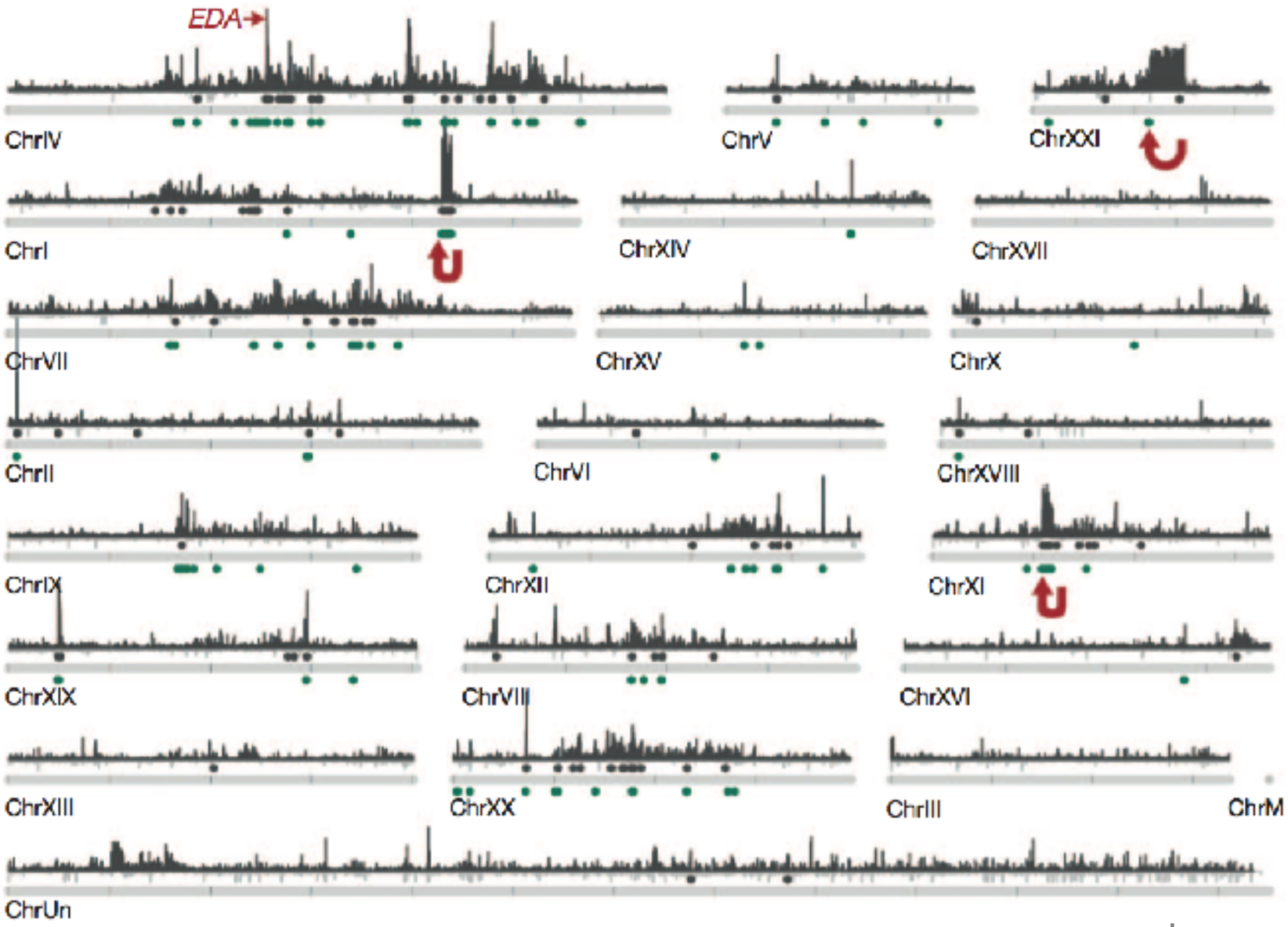
- Run multiple times to confirm consistency

STRUCTURE programs

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

Signatures of adaptation

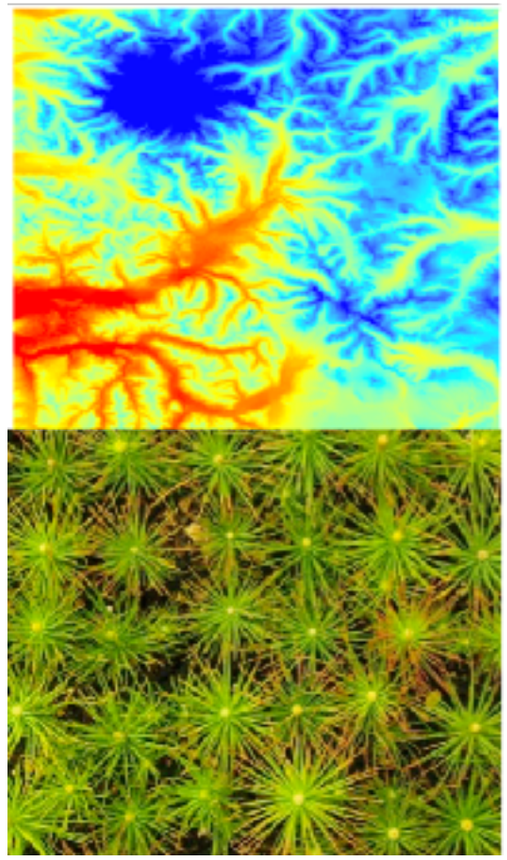
- Which loci are contributing to local adaptation?



Jones et al. (2012; Nature)

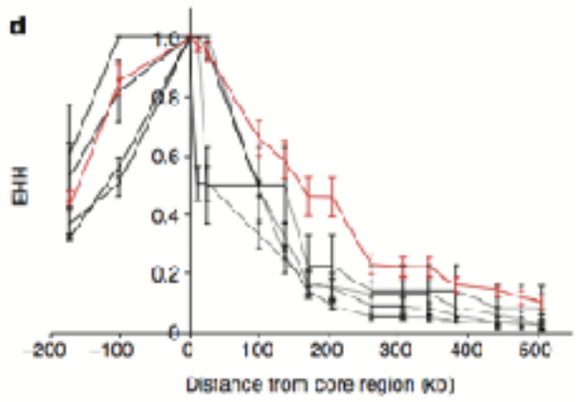
Outlier tests and signatures of selection

- Landscape level: differences in allele frequency among populations or environments



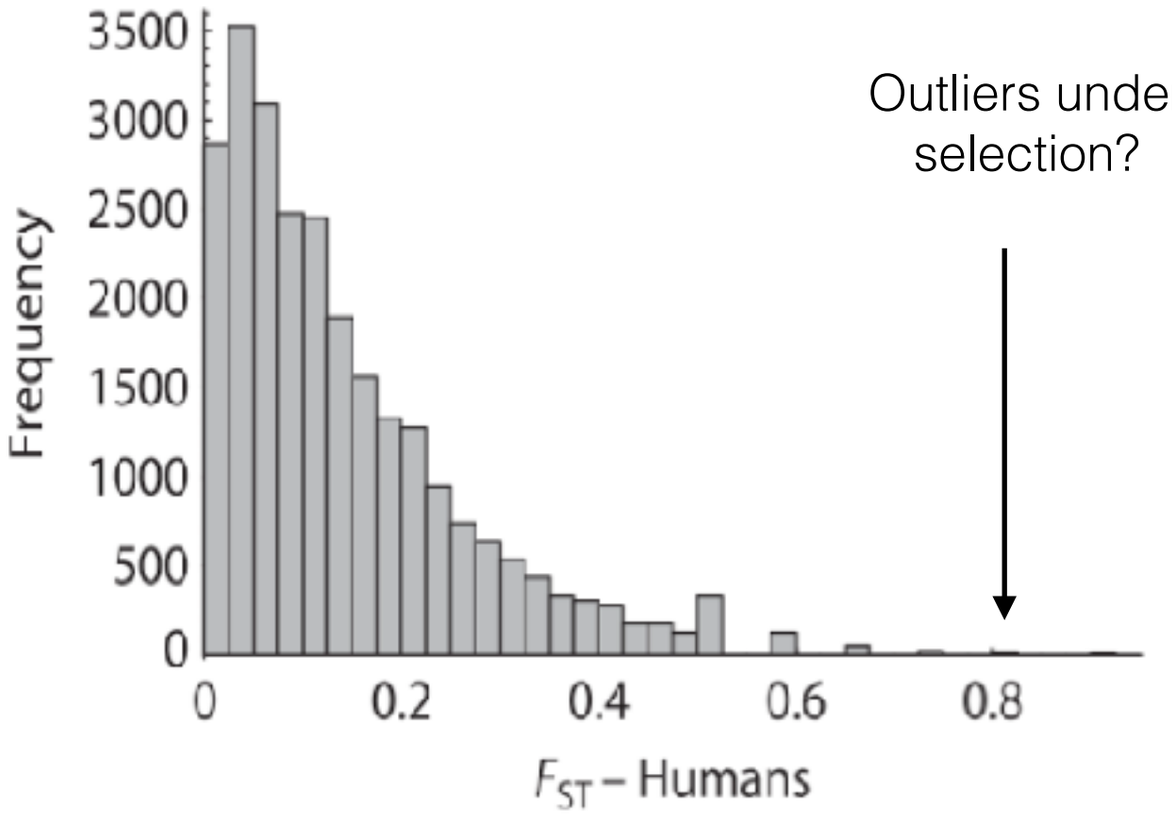
- Phenotypic level: associations between alleles and locally adapted phenotypes

- Sequence level: Changes in allelic diversity along a chromosome



F_{ST} outlier tests

F_{ST} - outlier tests



- Compare the outliers to some background distribution expected under a null model to evaluate significance

- **BayeScan**: uses a Dirichlet distribution, akin to assuming no migration nor mutation since common ancestry

- **FDIST**: assumes an island model, uses IM to estimate demography

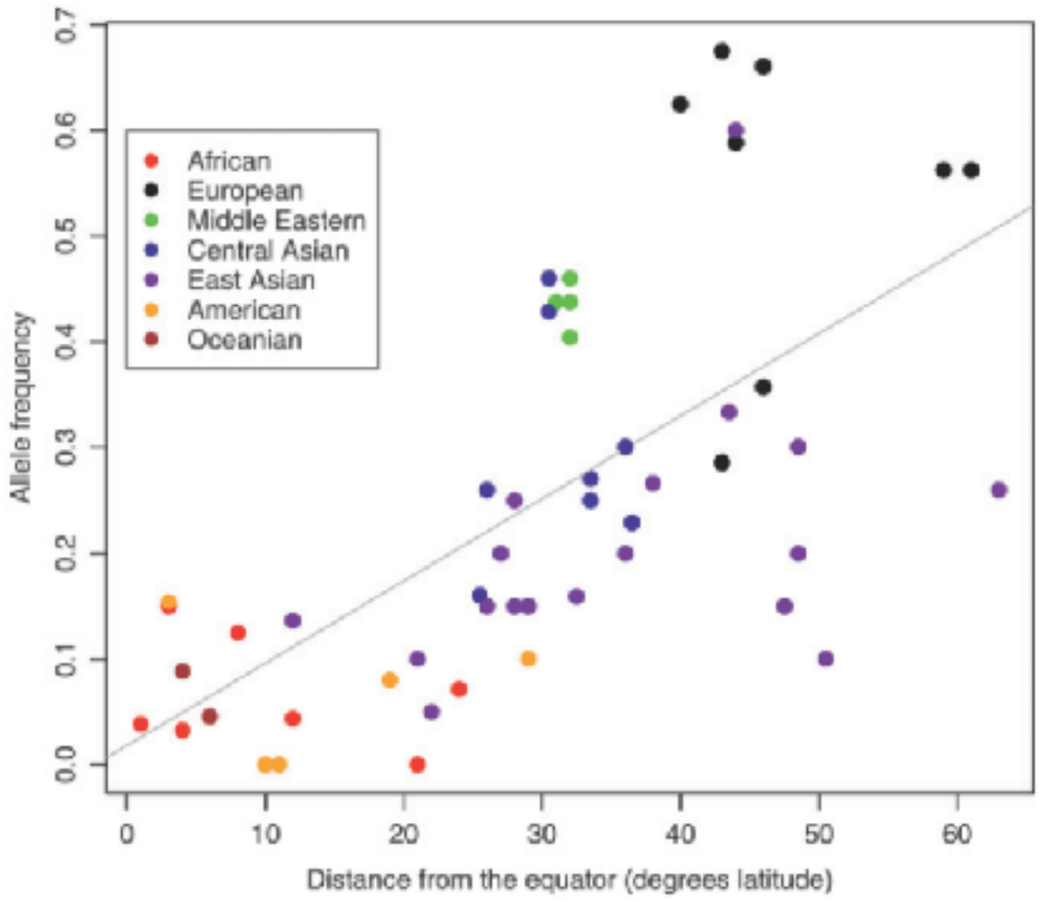
- BayENV

- OUTFLANK

Other causes of F_{ST} outliers

- Background selection against deleterious mutations.
- Cryptic hybrid zones involving multiple loci involved in reproductive isolation.
- Stochastic effects at wave-edge of an expanding population.
- Species-wide selective sweep.

Environment-allele associations



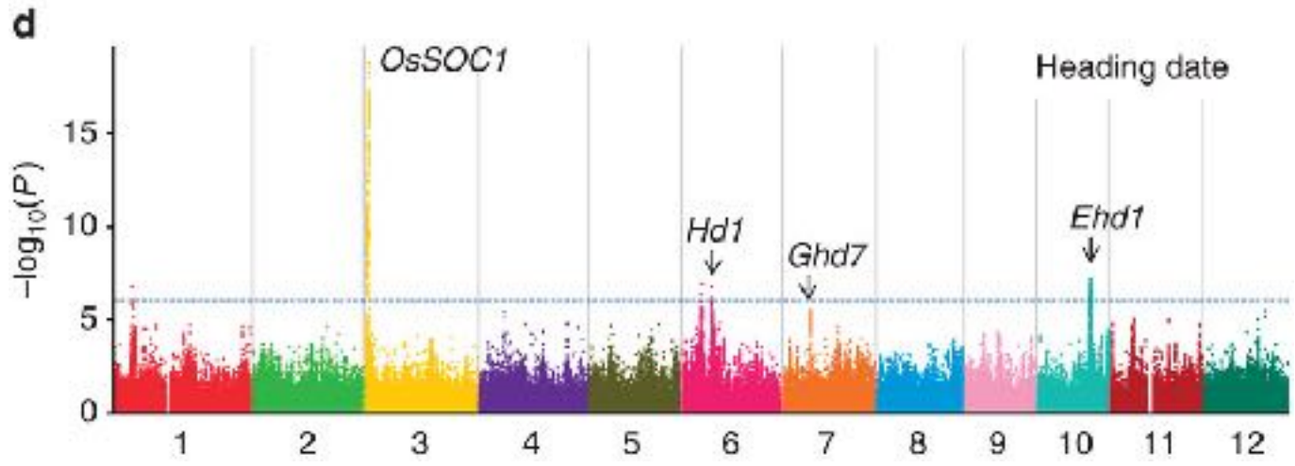
- Tests correlation between SNP and environment after controlling for population structure

- **Bayenv**: estimates covariance matrix representing population structure from separate set of “neutral” loci

- **LFMM**: Latent-factor mixed model; estimates the population structure from SNPs in test panel

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.

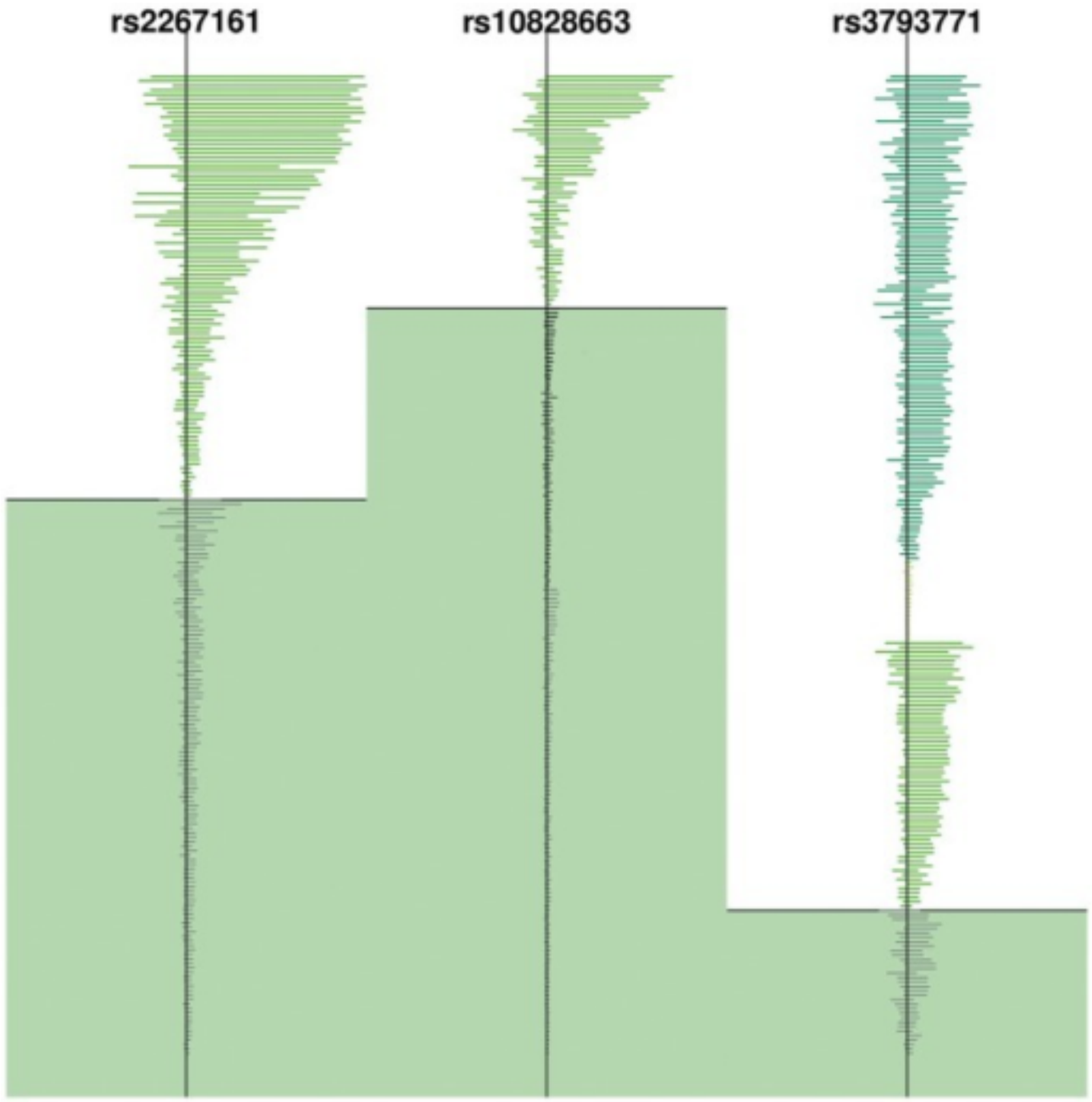
GWAS programs

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

Haplotype length

- Integrated Haplotype Score (iHS)
  - Measures levels of LD surrounding a derived allele compared to an ancestral allele at the same position.
- Extended Haplotype Homozygosity (EHH)
  - Measures the length of haplotypes in a region.

Haplotype length



Haplotype length programs

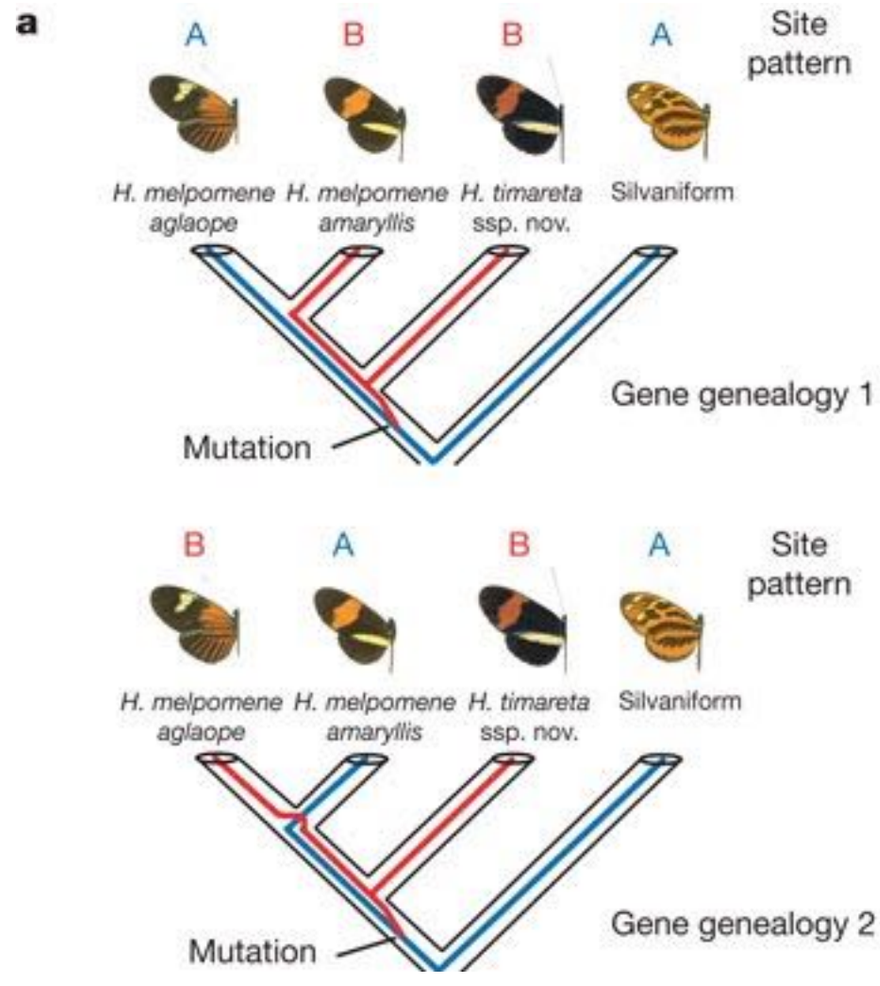
- selscan
- hapbin
- sweep

Hybrid ancestry

- Are genotyped samples hybrids?
- What generation hybrid?
- Where does each loci come from?

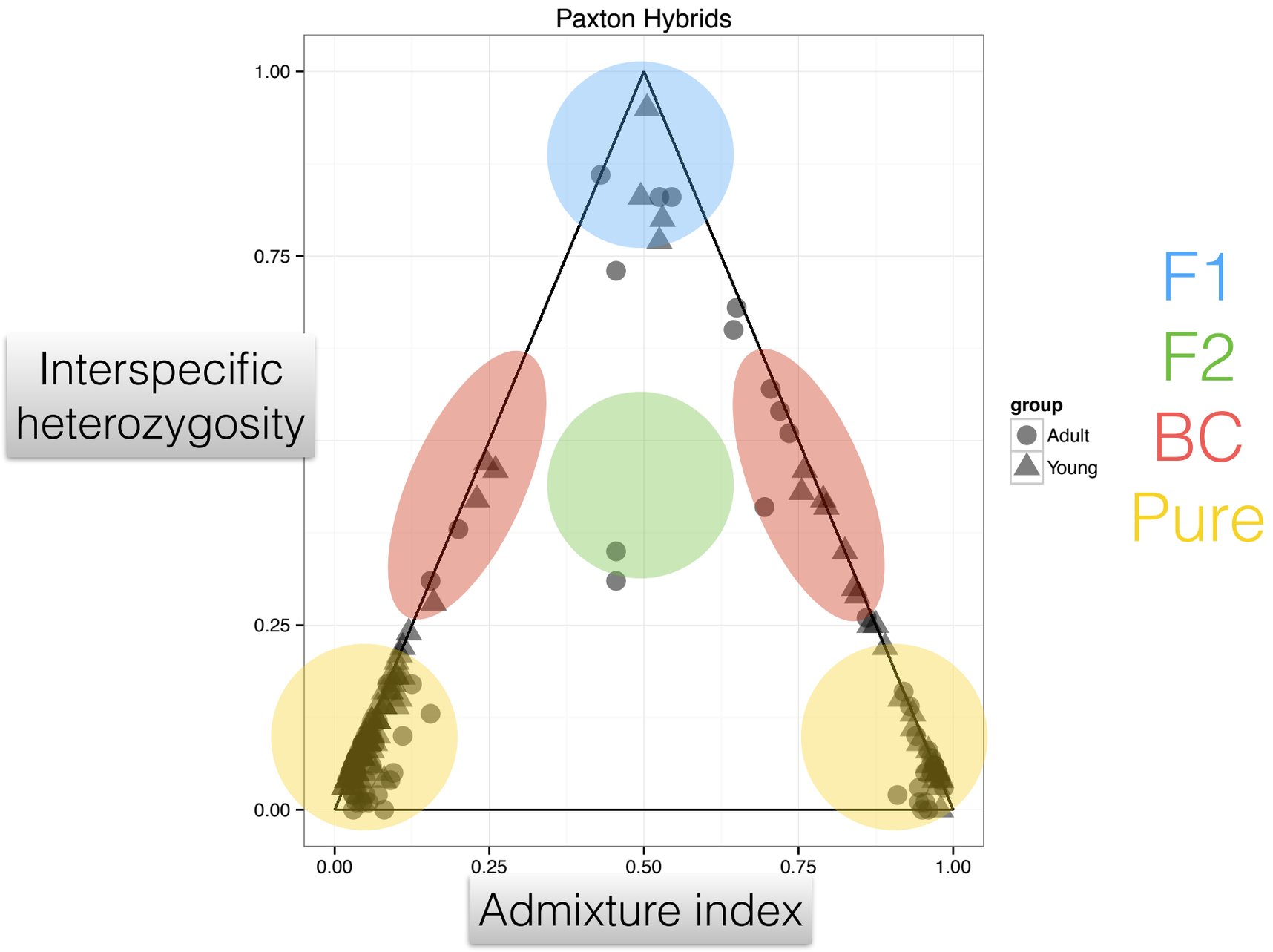
Are genotyped samples hybrids?

- STRUCTURE
- PCA
- ABBA-BABA



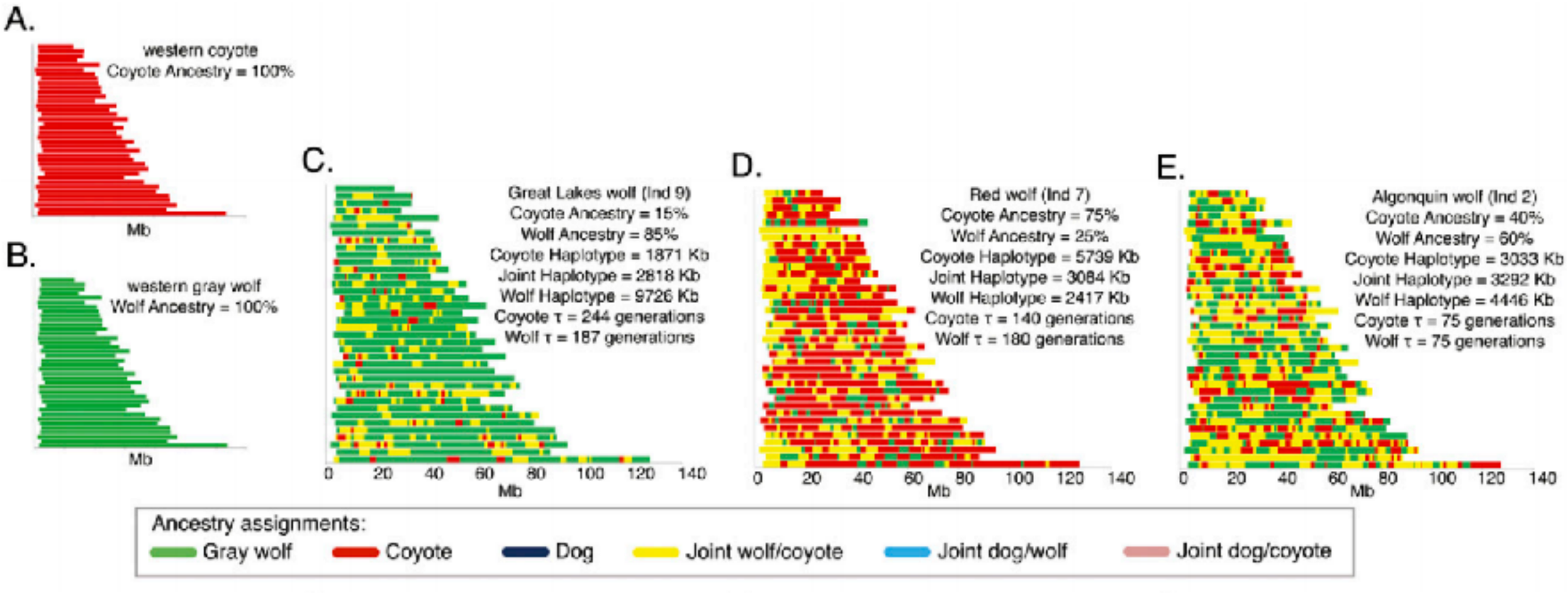
What generation hybrid?

- **Hlest**
- Hindex



Where does each loci come from?

- SABER
- STUCTURE linkage model
- MSG
- Ancestry_HMM



Plotting

- dplyr for data manipulation

- ggplot2 for plotting