

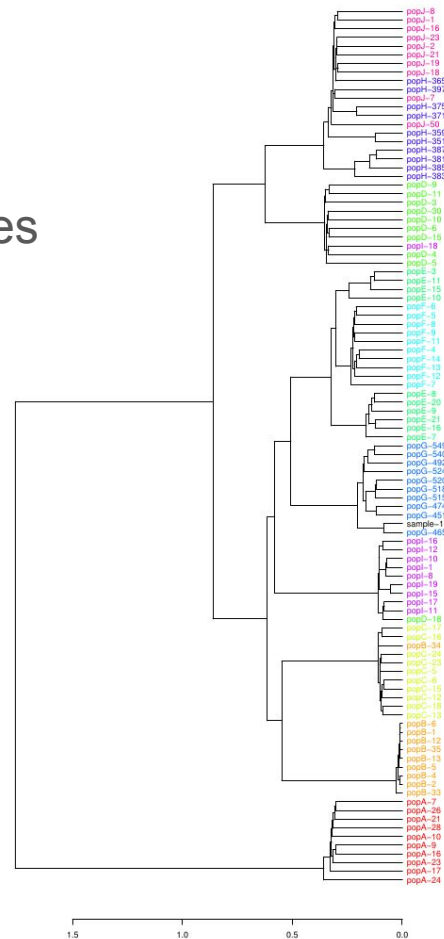
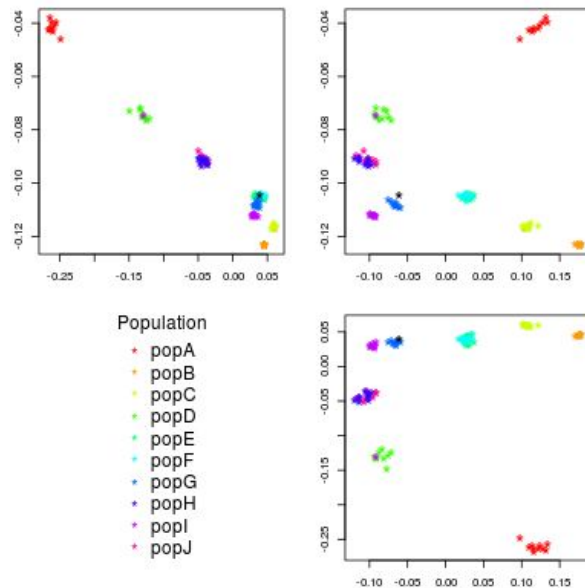
11 April, 2016:

Visualisation of genomic data and Admixture

Population structure

We used PCA and clustering based on IBS

- neither is ideal: PCA has no resolution, clustering tree does not reflect reality
- a single tree ignores:
 - recombination
 - migration
 - introgression

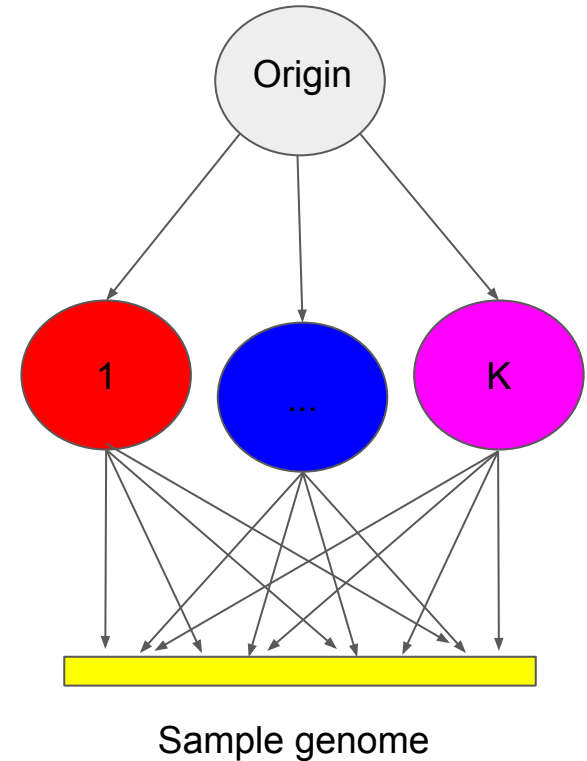


Population structure

Software: STRUCTURE / fastSTRUCTURE /

Admixture

- ancestral population split into K populations
- our sample populations are mixtures of these populations
- we want to estimate contribution of each ancestral population to our sample genomes



Population structure

Human population structure with $K=7$ using HGDP (Human Genome Diversity Project) data (Raj et al., 2013)

