

Exercises in Marine Ecological Genetics

07. Genetic clustering (pop. structure II)

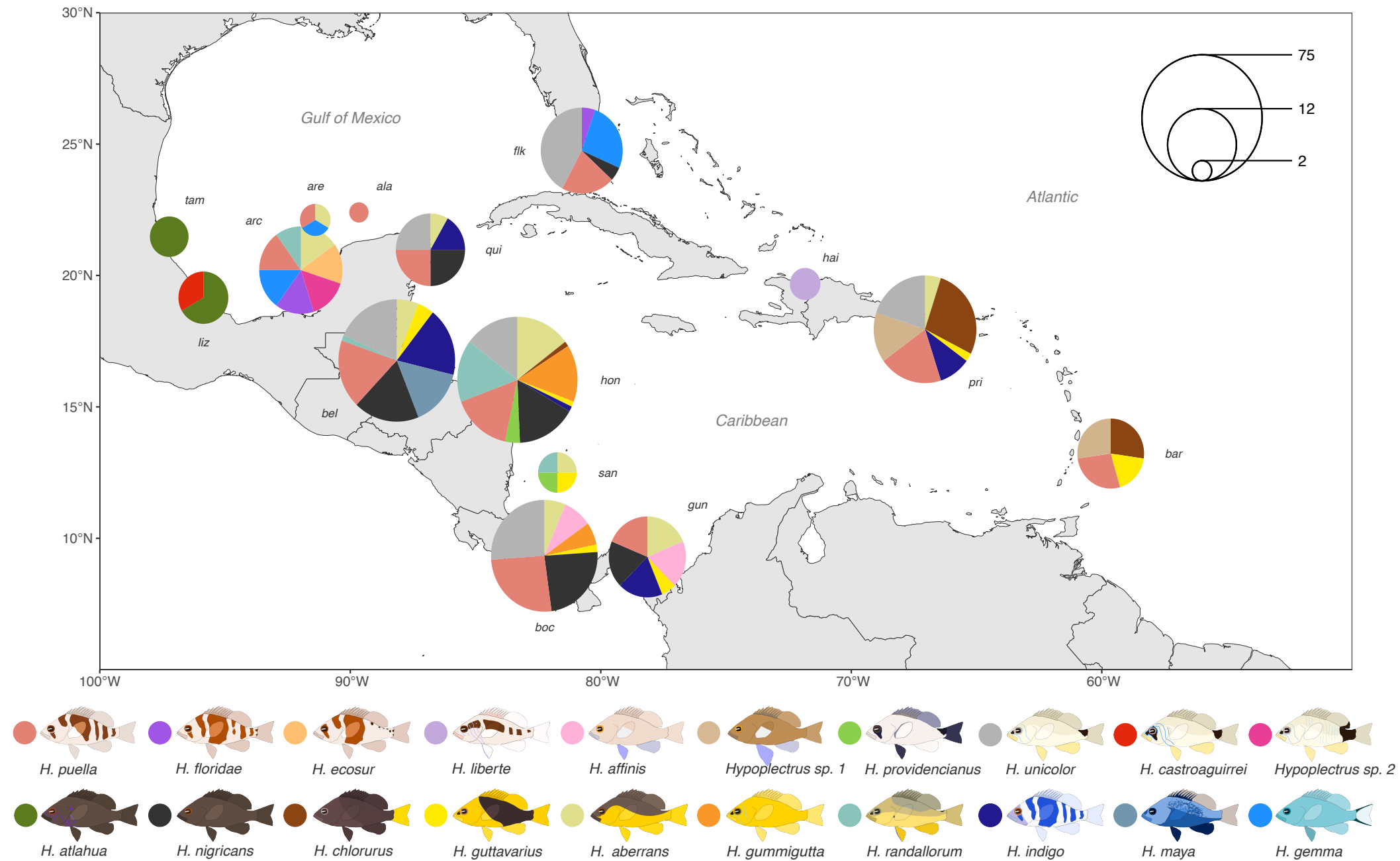
- Condense genetic variance into Principal Components
- Visualize admixture with model-based clustering
- Generate more complex plots in R with ggplot



Martin Helmkamp

<https://github.com/mhelmkampf/meg25>

Example dataset



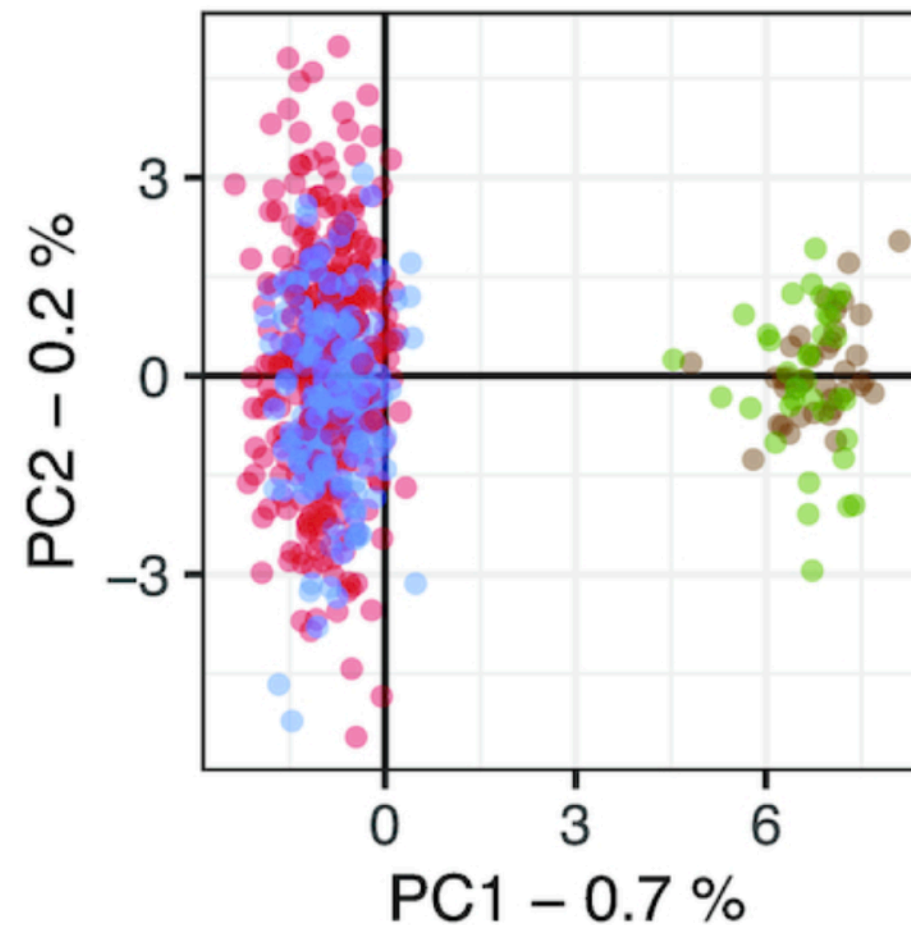
Principal Component Analysis

- **Reduces thousands of SNPs** into small number of principal components that capture the most genetic variation among individuals
 - Treats **each SNP as a variable** and encodes genotypes numerically (e.g., 0 = AA, 1 = AB, 2 = BB)
 - Calculates **covariance matrix** and extracts PCs (via eigenvalue decomposition)
 - Plots individuals based on PC scores in **2D space** (sometimes 3–6D)
- ➔ Relationship between individuals (relatedness), population structure, outliers

Principal Component Analysis

Atlantic mackerel (*Scomber scombrus*) in the Northwest Atlantic, > 10,000 SNPs

● NEA – Bay of Biscay ● NEA – Greenland ● NWA – Canada ● NWA – US



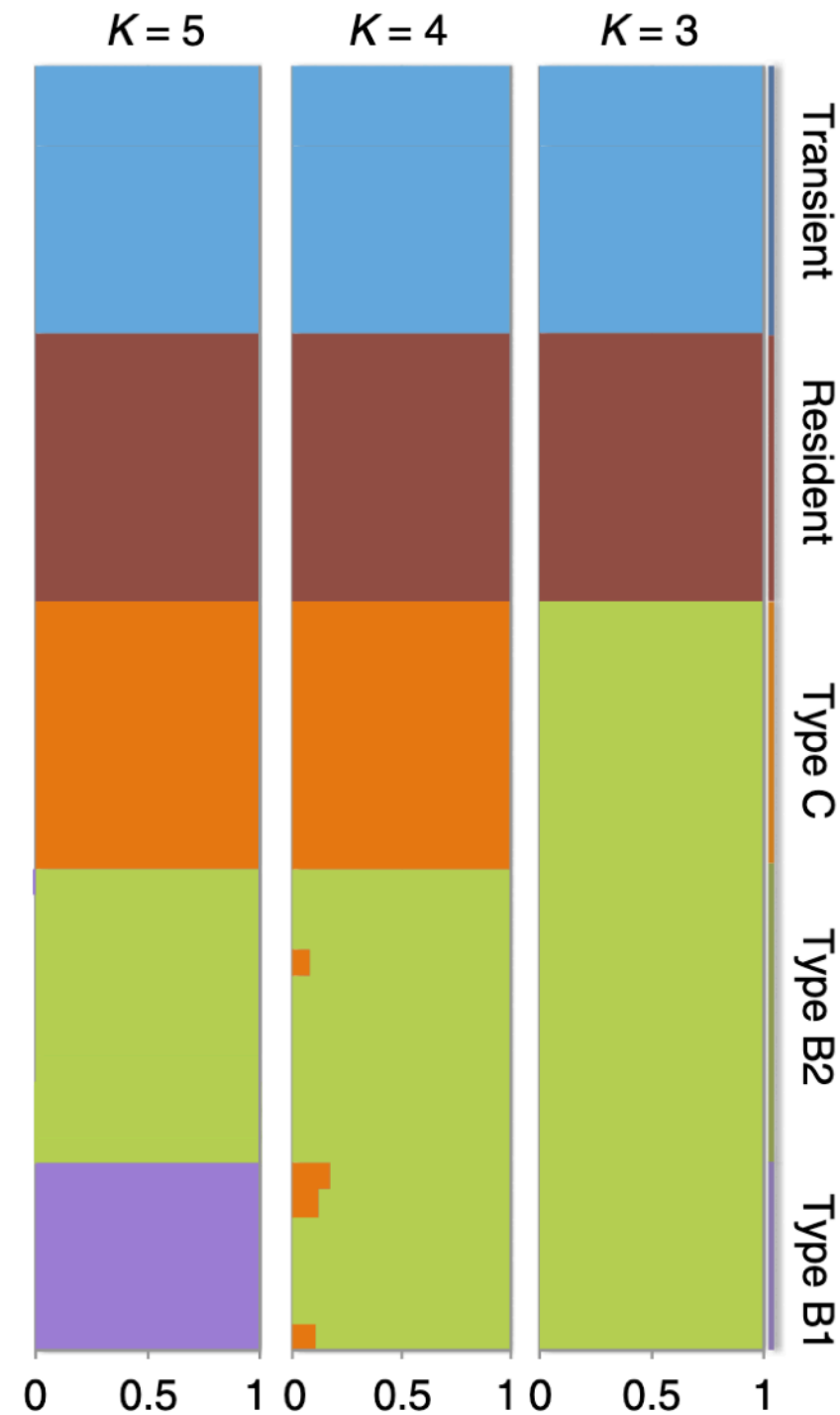
Bourret et al. 2023

Admixture analysis

- **Estimates ancestry proportions** for each individual by assuming k ancestral populations, based on genome-wide SNPs
 - Uses **model-based clustering** to estimates which SNPs likely came from which ancestral population
 - Calculates **Q-values** for each individual
(e.g., 60% ancestry from population 1, 40% from population 2)
 - Visualizes these ancestry proportions as **stacked bar plots**, with one bar per individual
- ➔ Ancestry and admixture (i.e., mixed ancestry), population structure, assign individuals to populations

Admixture analysis

Ancestry proportions of
48 individuals of *Orcinus orca*



Foot et al. 2016, *Nature Communications*

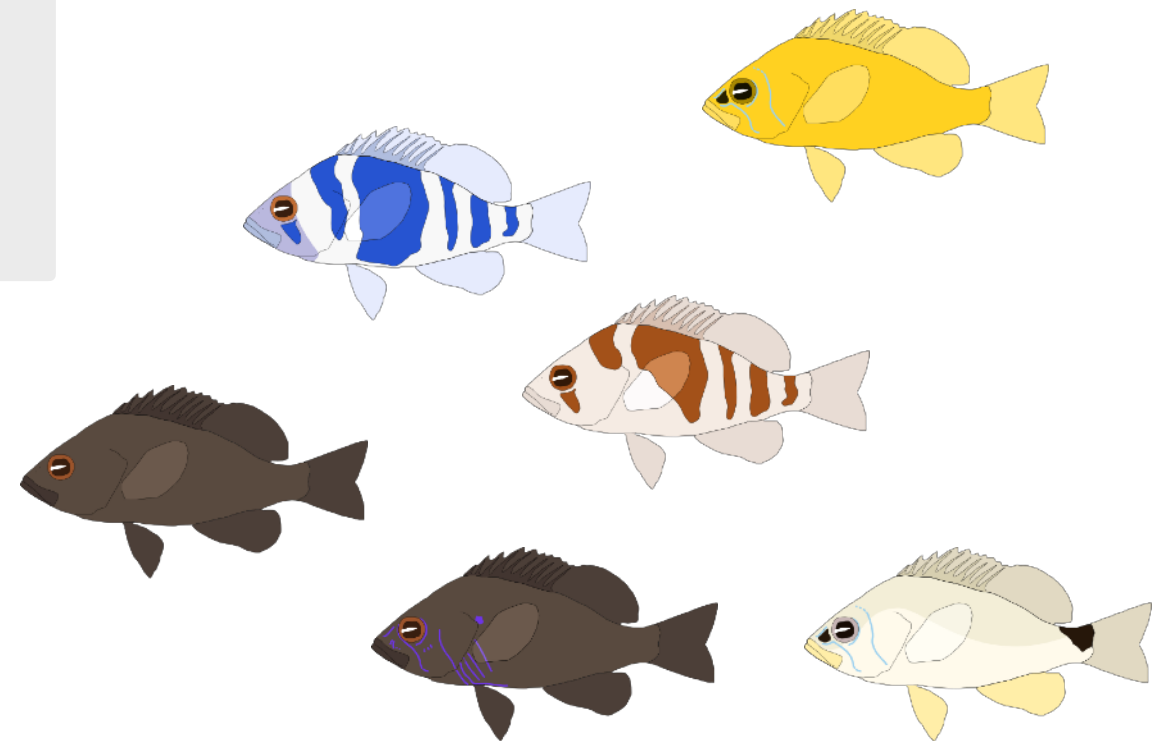
Example dataset

- 19 species of hamlet (genus *Hypoplectrus*)
- 15 sites in Caribbean and Gulf of Mexico
- 327 hamlet samples total
- Illumina short-read resequencing (mean depth 17×)
- Genotyping with GATK
- High-quality reference genome of *H. puella*



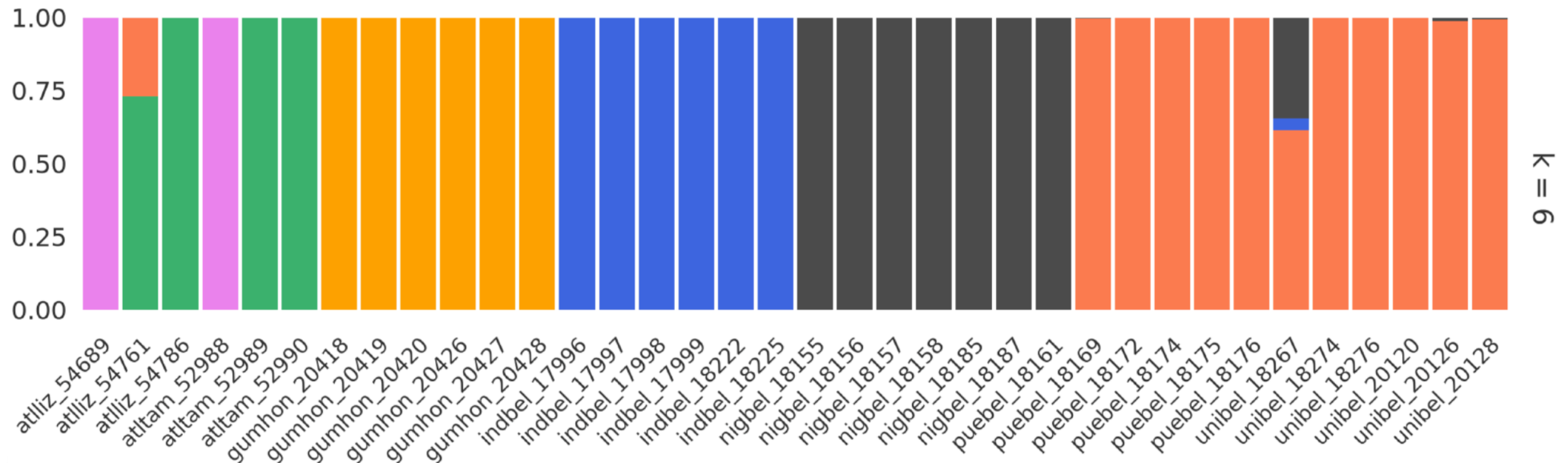
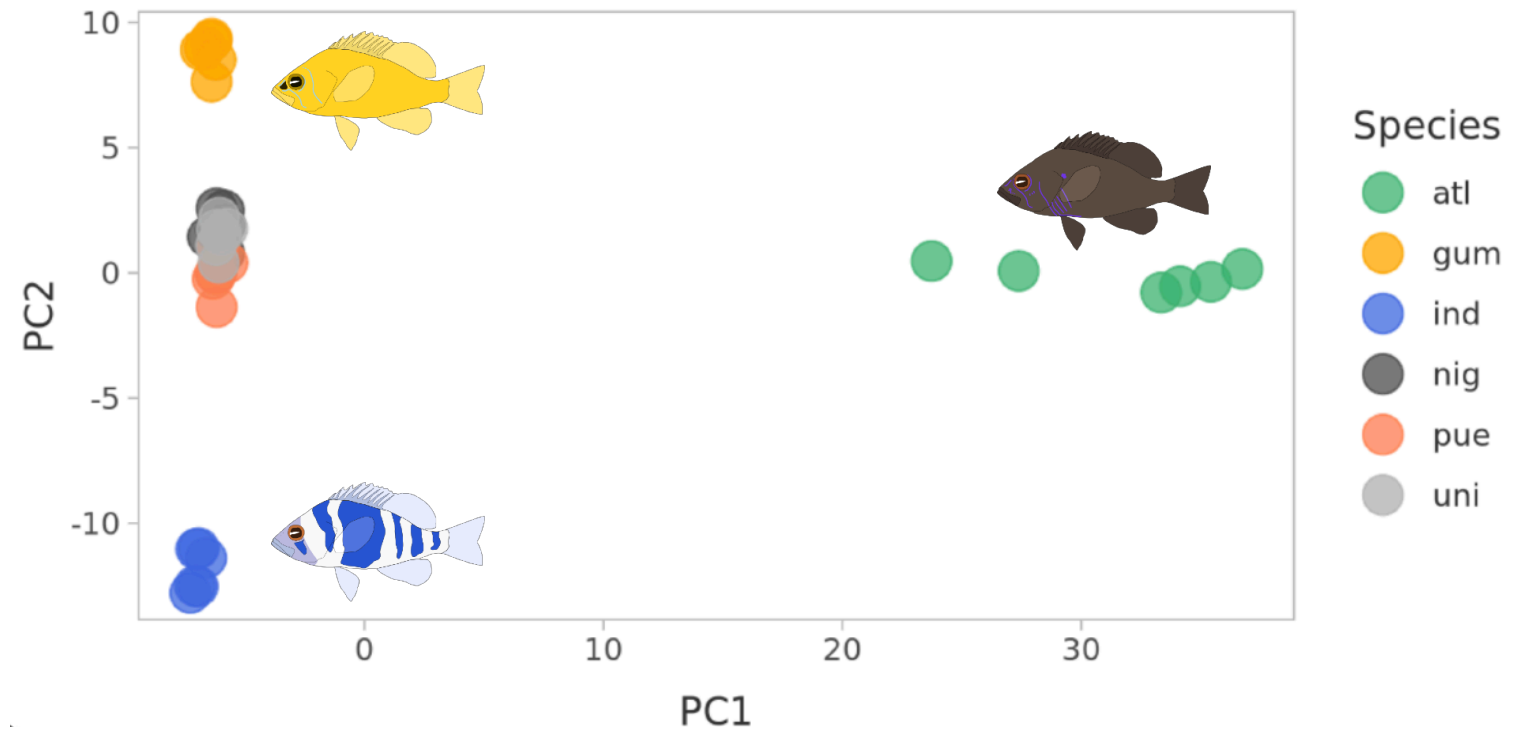
hamlets_LG12_snp.vcf.gz

- Chromosome 12 only
- Subset to 36 samples from 6 populations

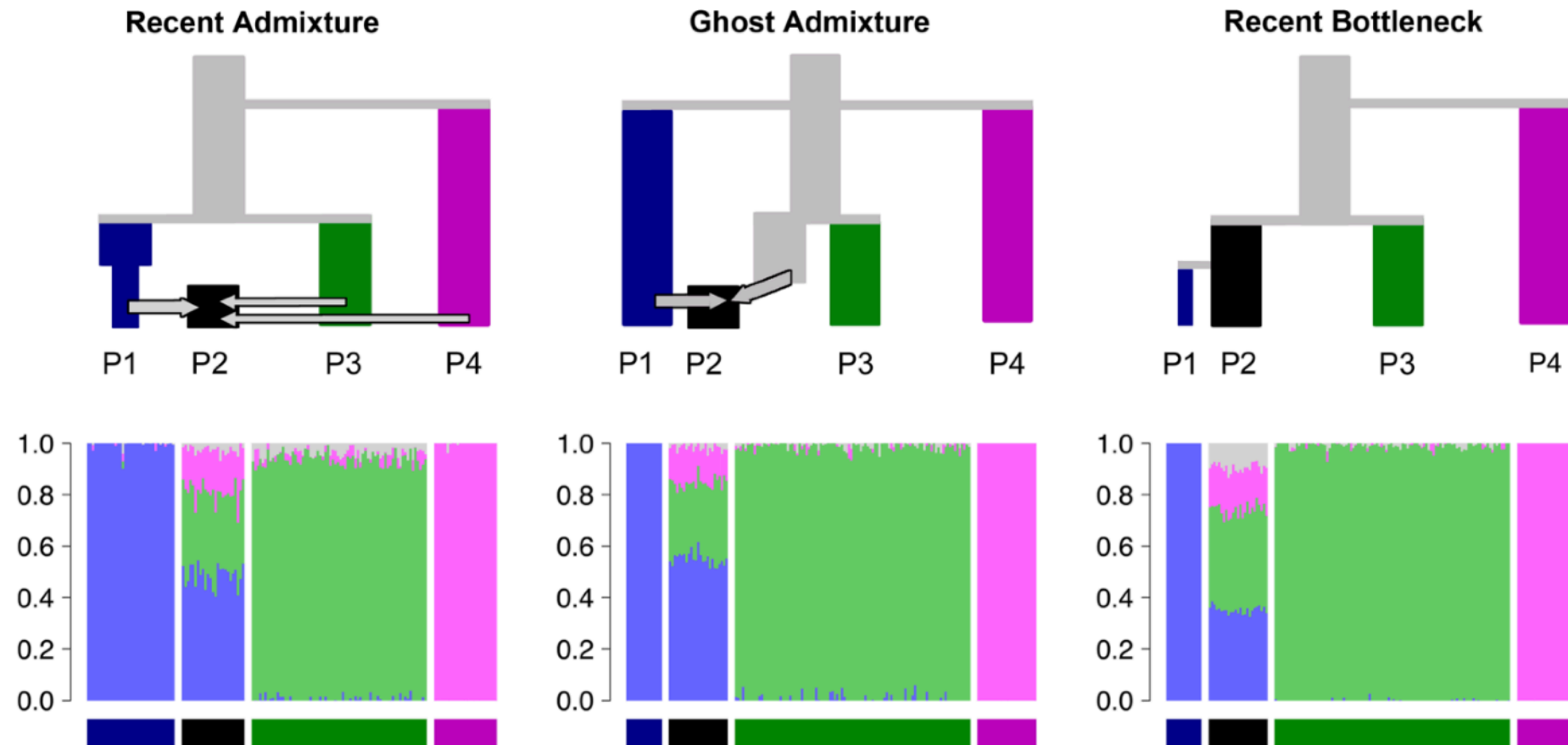


Illustrations by Kosmas Hench

PCA and admixture plot



Admixture caveats

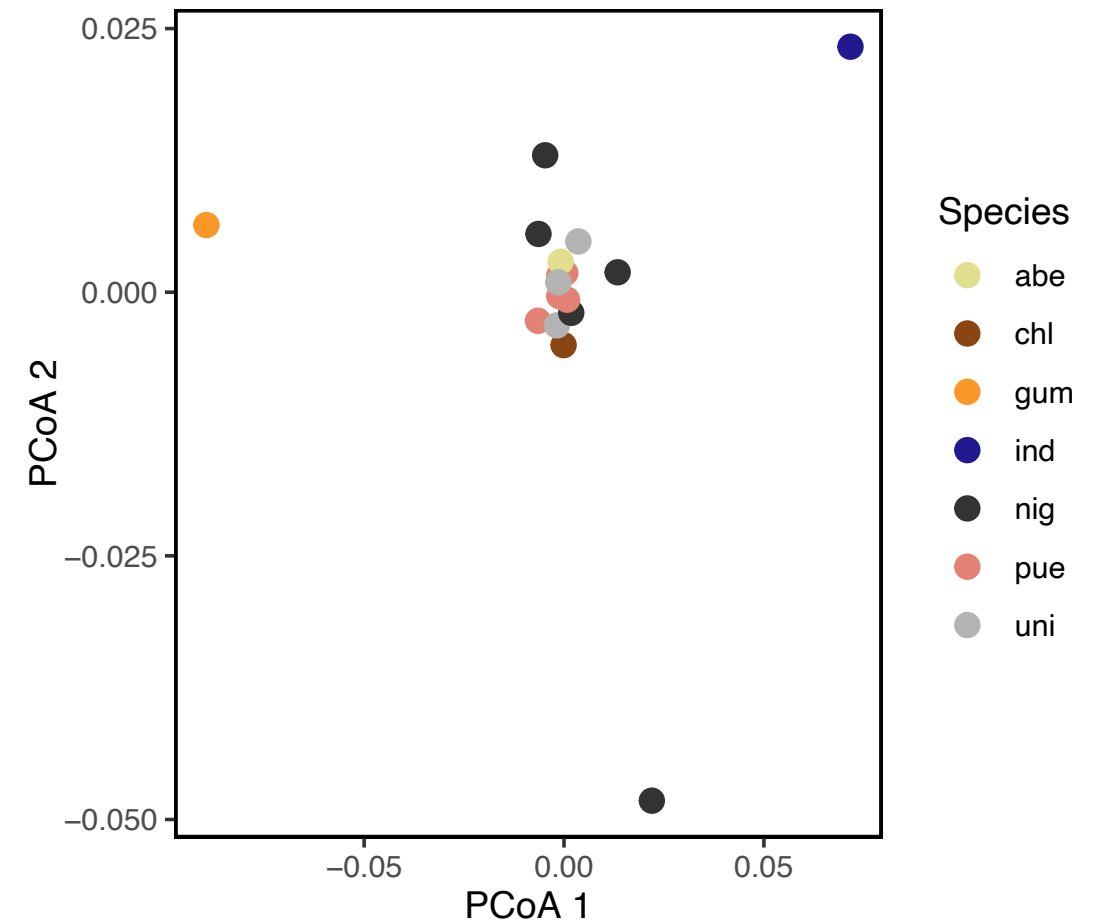
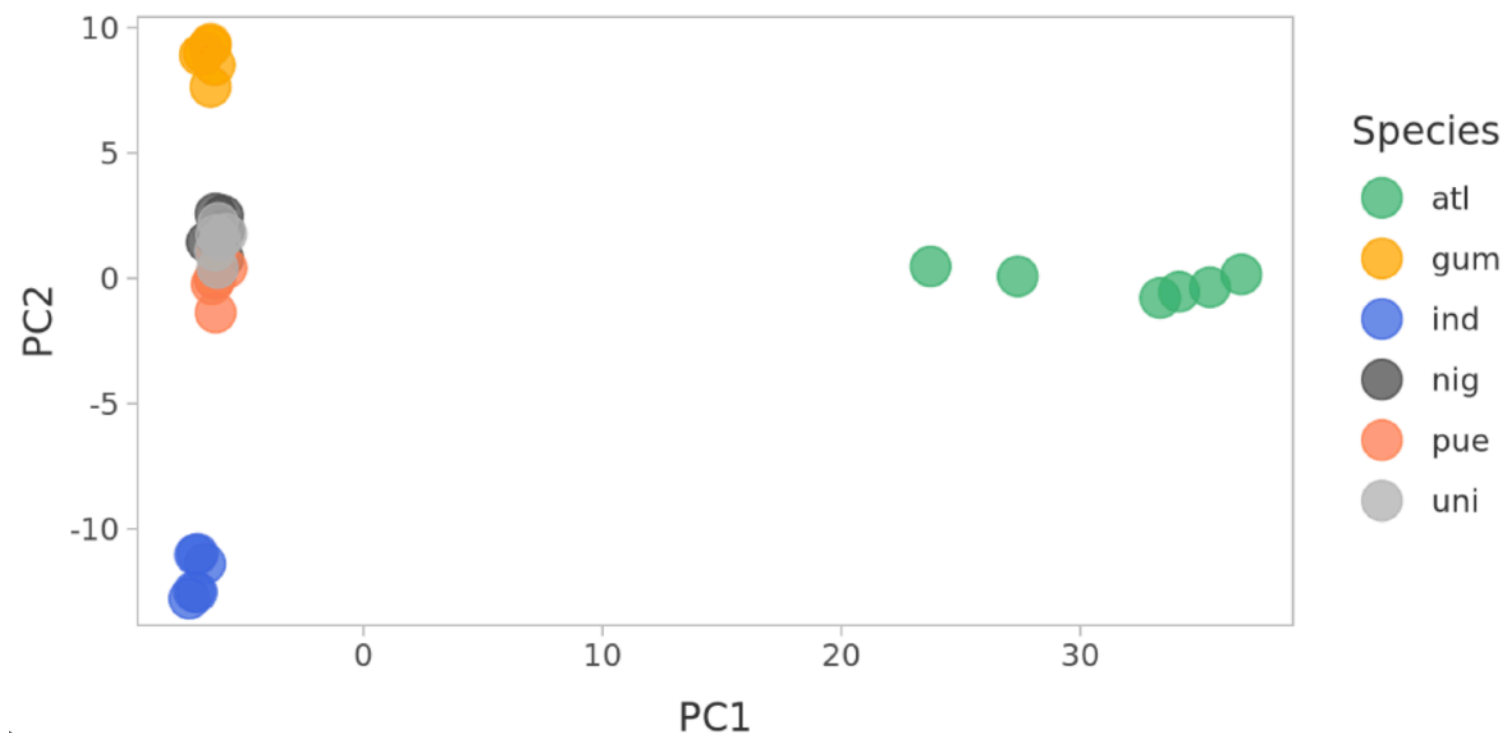


- Demographic histories other than recent admixture can lead to the same results
- Populations are assumed to be in HWE

Lawson et al. 2018, *Nature Communications*

Pairwise F_{ST} PCoA compared to PCA

- Based on few microsatellite markers, not genome-wide
- Per-population, no per-individual estimates / substructure



```
admixture input.bed k          # Run admixture analysis (Linux command line)
read.vcfR(path_to_vcf_file)    # Read VCF file into R (vcfR package)
glPca(genlight_object)         # Calculate principal components (adeigenet package)
```

- Principal Component Analysis of SNP data reveals genetic clusters, population structure and outliers at a glance by reducing complex variation to key axes
- Admixture analysis excels at detecting recent admixture and ancestry proportions, but requires choosing the right k and careful interpretation
- Both methods are complementary and can be used to assign individuals to populations without prior labels or grouping assumptions (unsupervised clustering)

Nucleotide diversity π

Addendum

Average number of nucleotide differences per site between all possible pairs of sequences

$$\hat{\pi} = \frac{n}{n-1} \sum_{ij} x_i x_j \pi_{ij} :$$

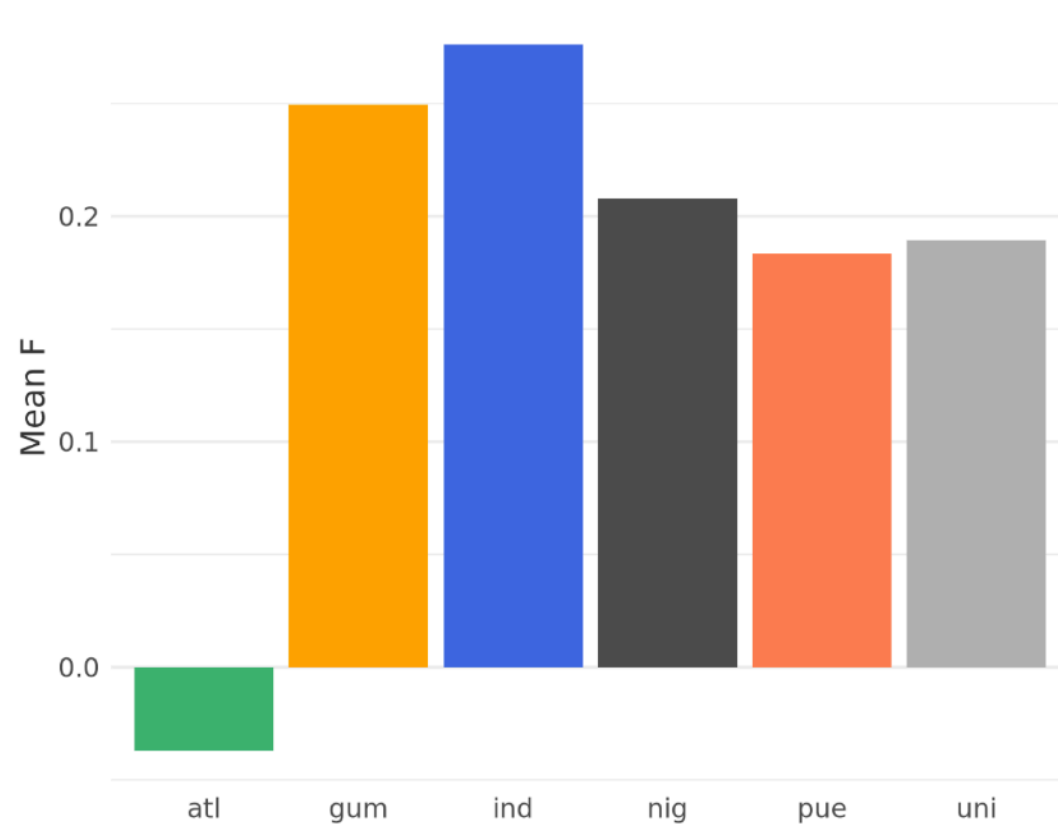
- 2 chromosomes per individual
- 15 pairwise comparisons
- π per site: no. diff / comparisons

Average $\pi = 0.29$ ←

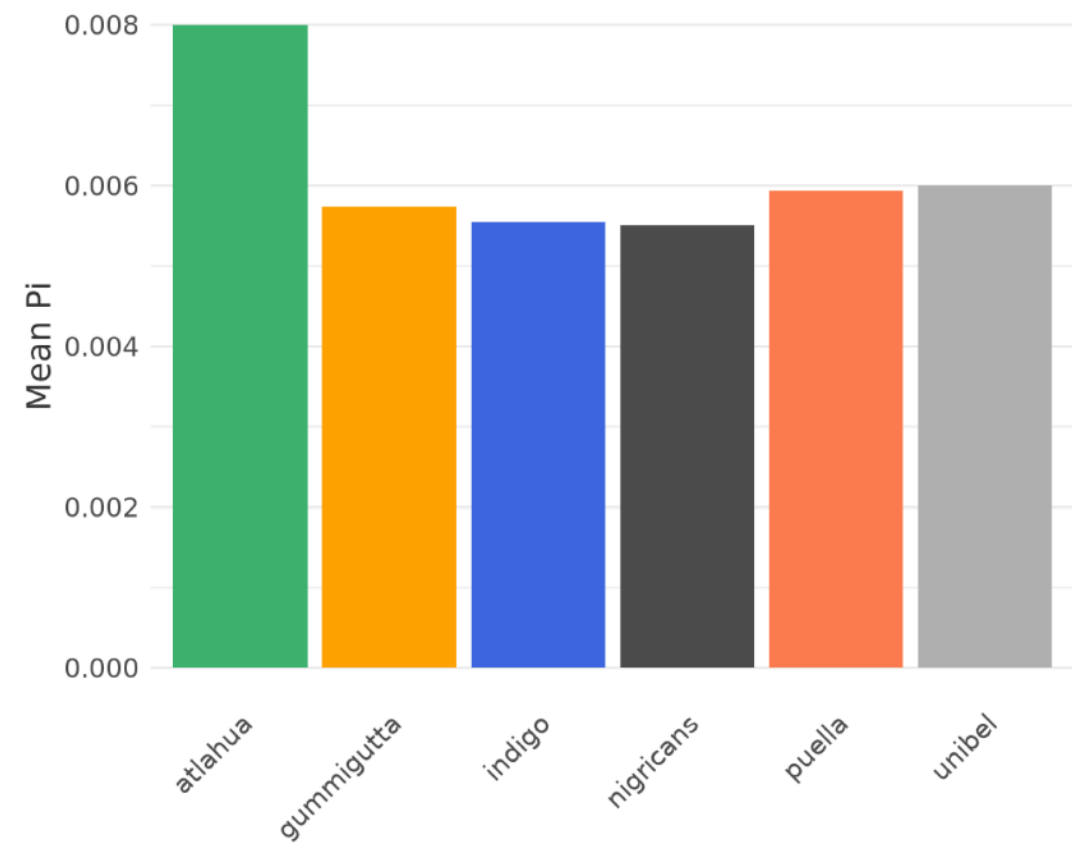
Site:	1	2	3	4	5
Sample A:	A	G	C	T	T
	A	G	C	T	T
Sample B:	A	G	T	T	T
	A	G	T	T	T
Sample C:	G	G	T	C	T
	G	G	C	T	T
No. diff:	8	0	9	5	0
π per site:	0.53	0	0.60	0.33	0

Genetic diversity

Addendum



Inbreeding coefficient F_{IS}



Nucleotide diversity π