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

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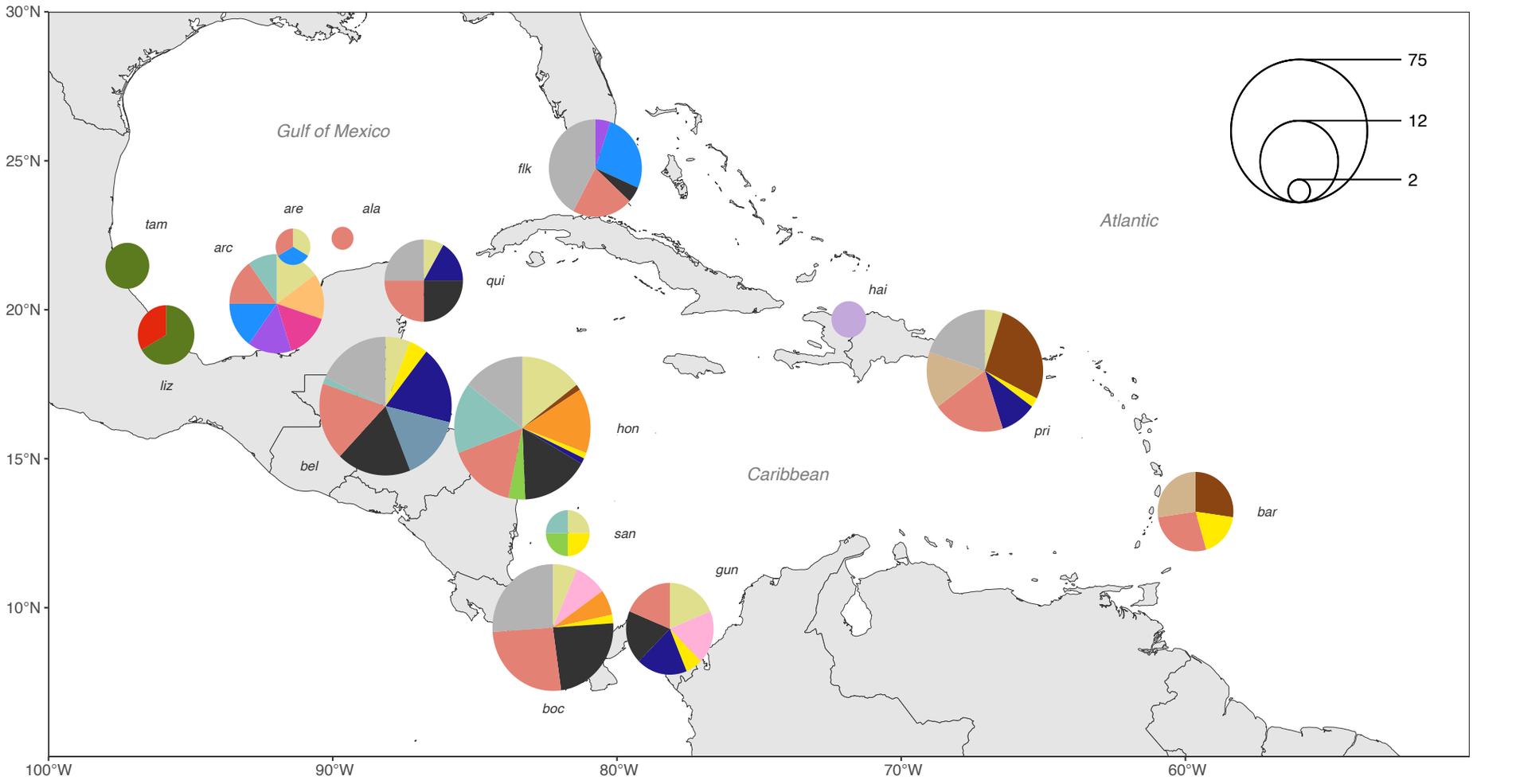
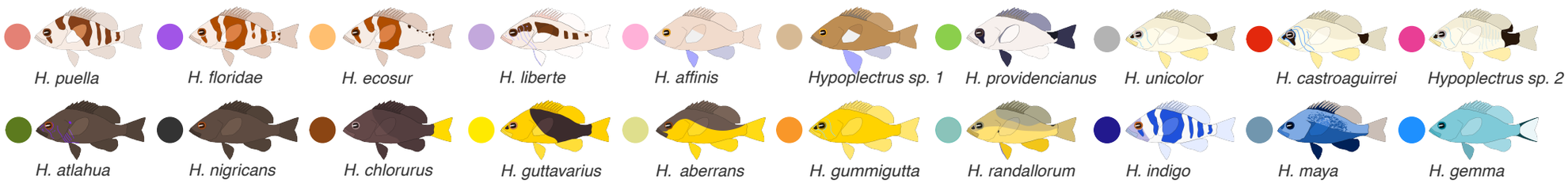
https://github.com/mhelmkampf/meg25

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

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

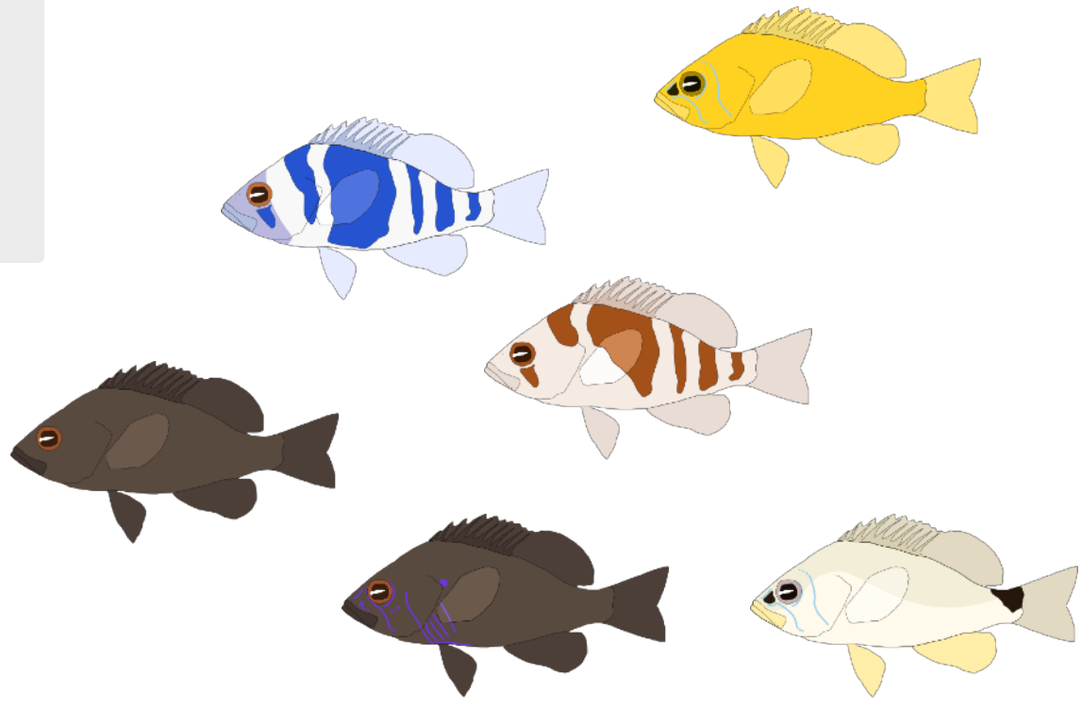
Example dataset

- 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*

↓

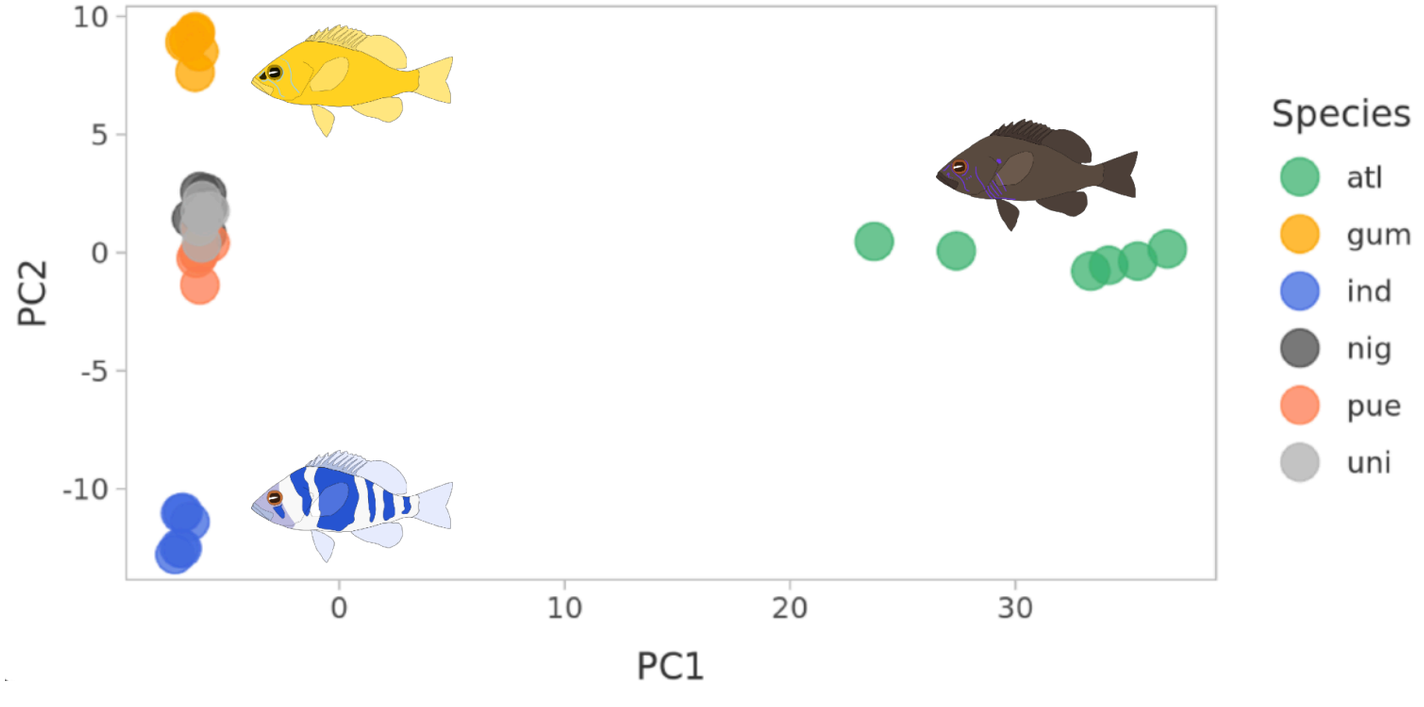
hamlets_LG12_snp.vcf.gz

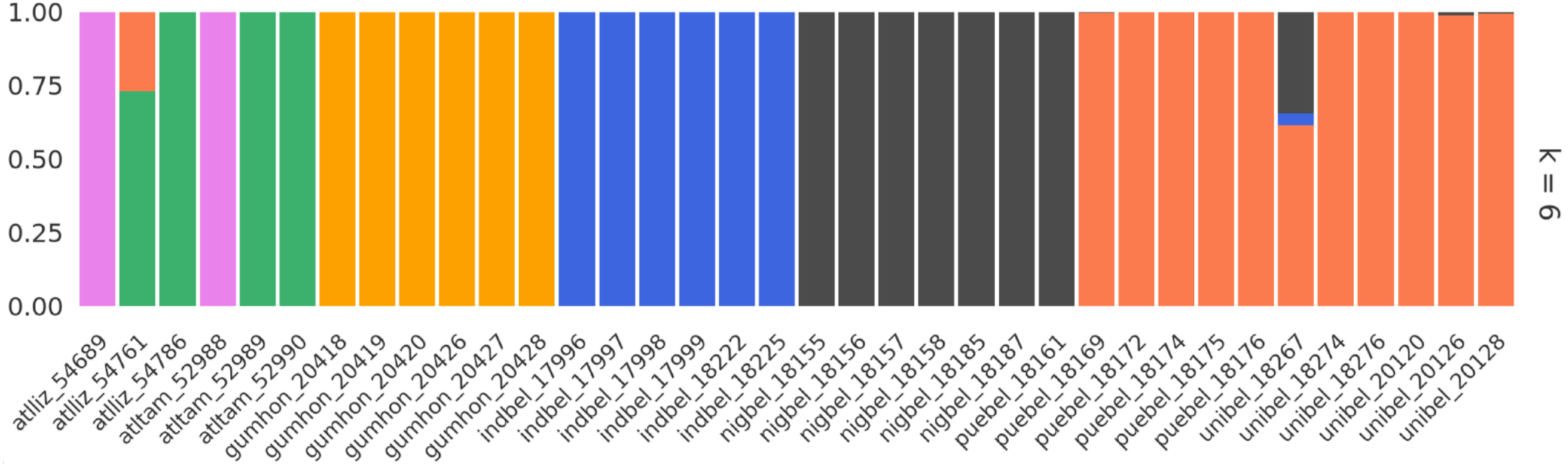
- Chromosome 12 only
- Subset to 36 samples from 6 populations



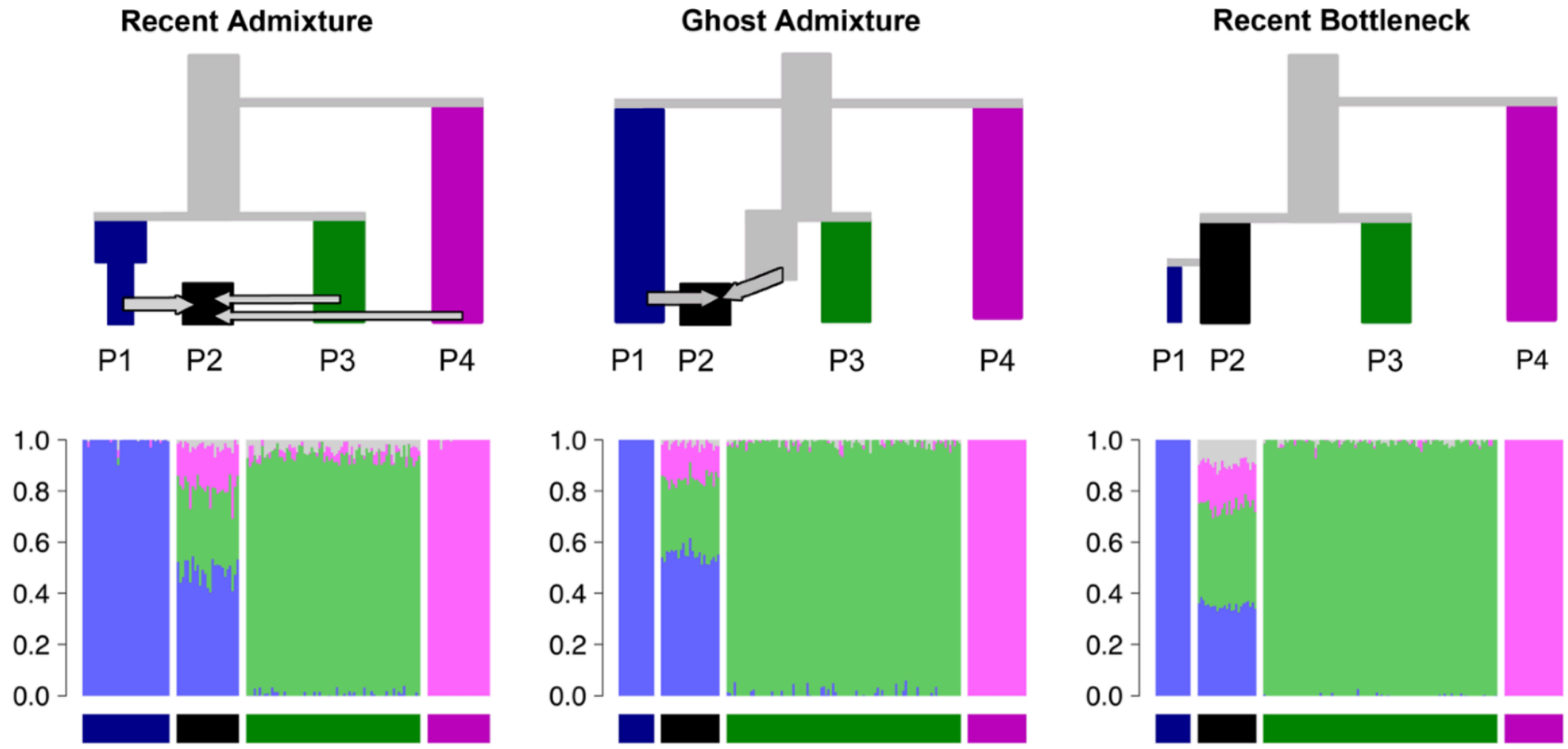
Illustrations by Kosmas Hench

PCA and admixture plot





Admixture caveats

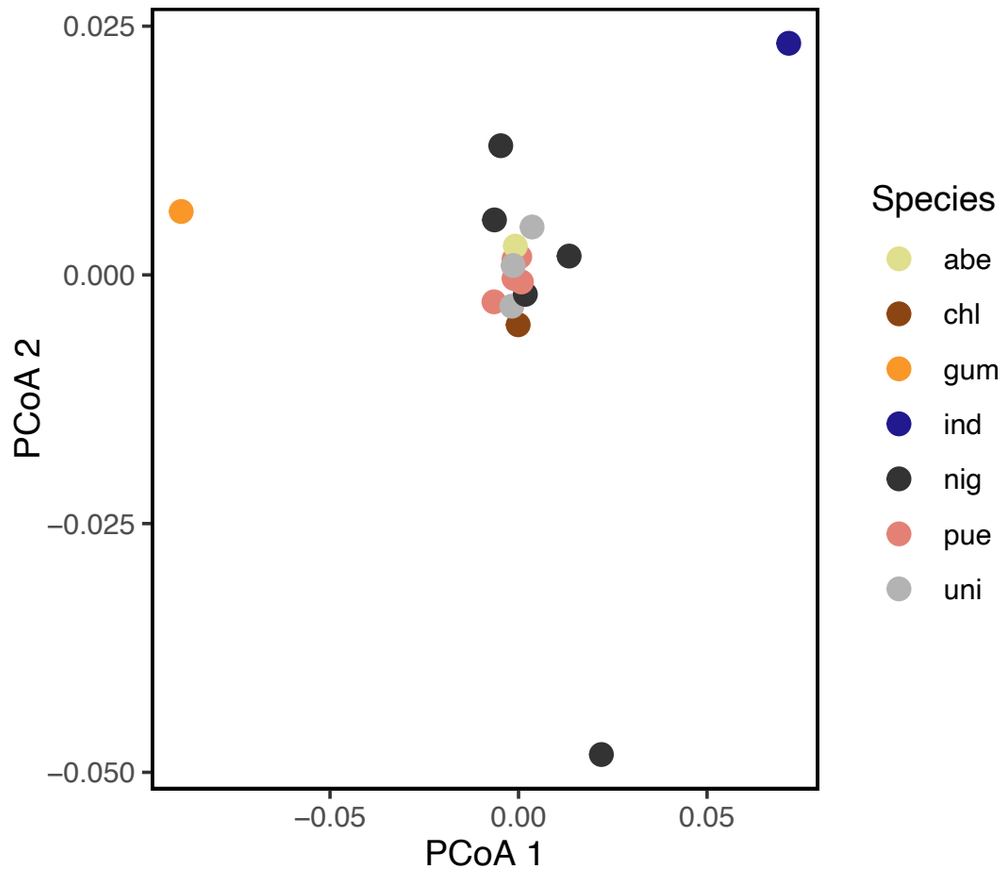


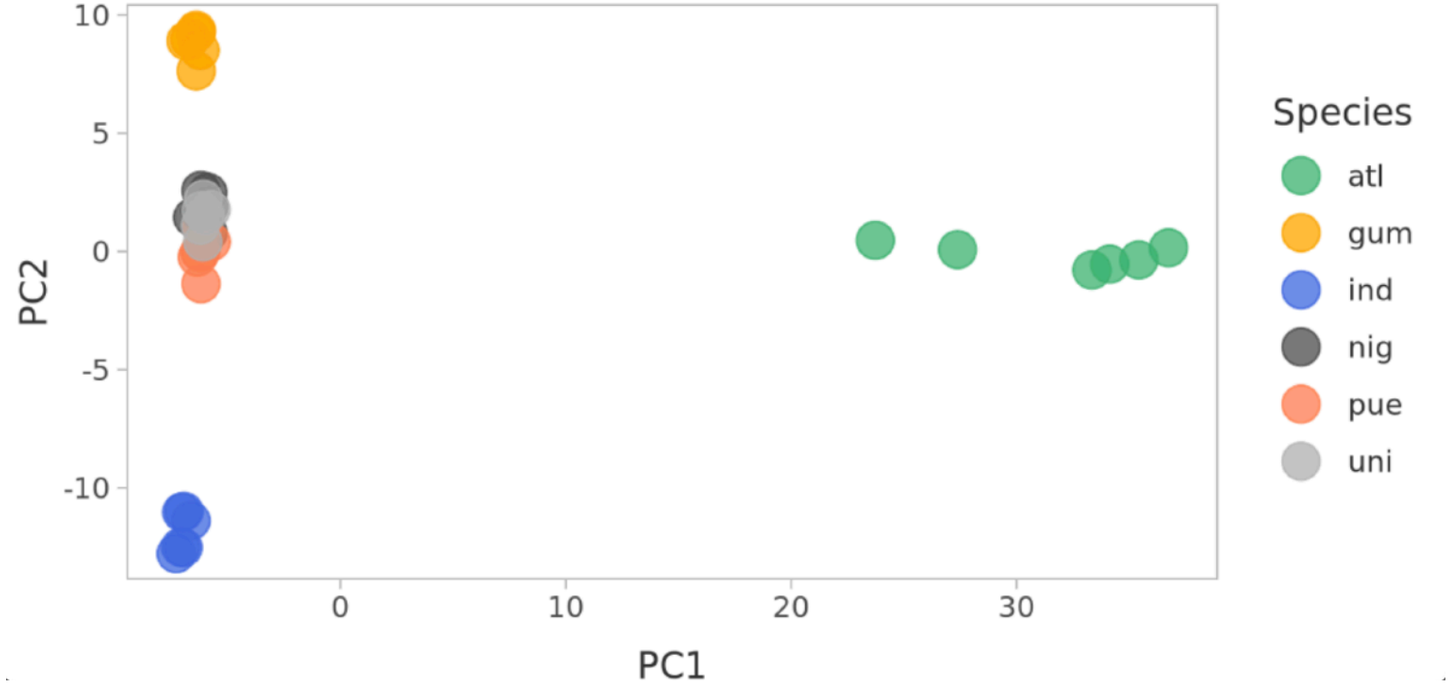
- Demographic histories other than recent admixture can lead to the same results
- Populations are assumed to be in HWE

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





Genetic clustering

Summary

```
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 (adegenet 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

Add-on

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

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

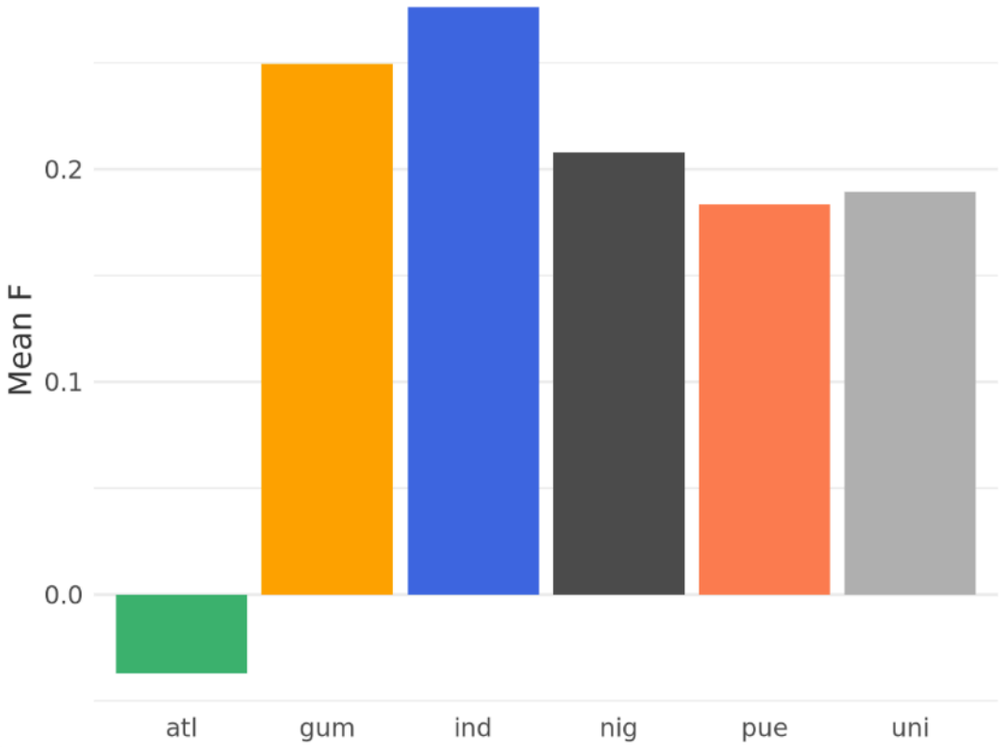
- 2 chromosomes per individual
- 15 pairwise comparisons
- π per site: no. diff / comparisons

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

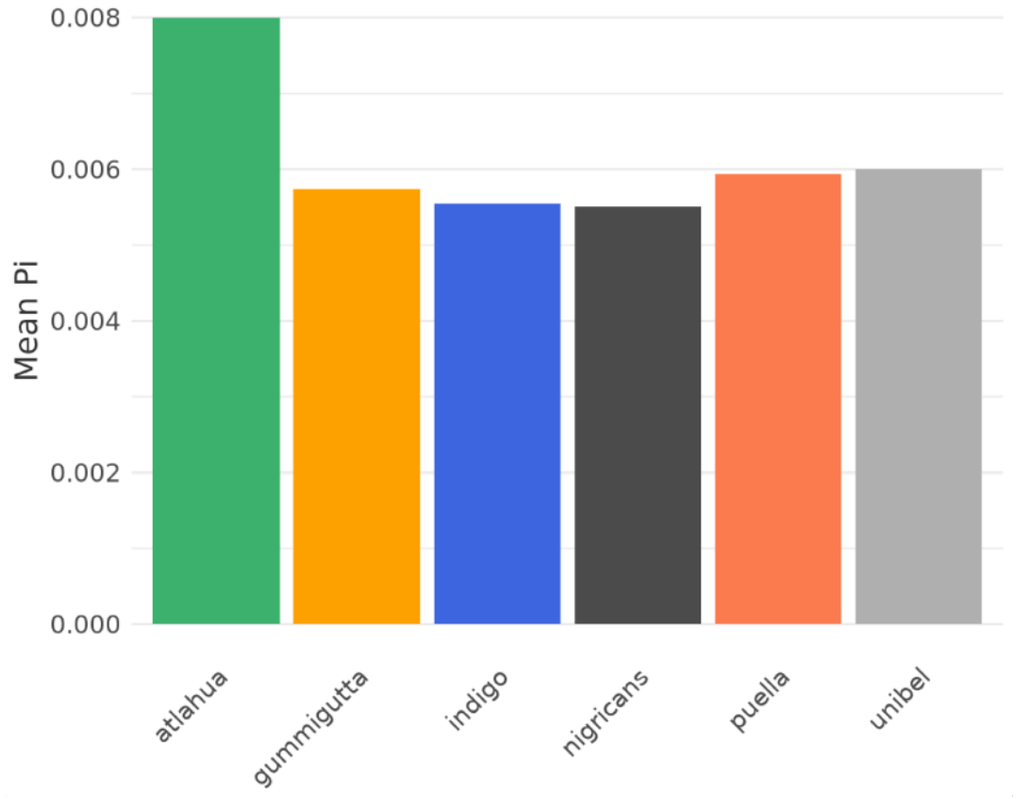
Average π = 0.29 ←

Genetic diversity

Add-on



Inbreeding coefficient F_{IS}



Nucleotide diversity π