

COMPUTATIONAL ACTIVITY 2

September 19, 2019

CODE FROM ACTIVITY #1

- `name_of_dataset <- read.table("Dataset", header = TRUE, sep = "\t")`
- `library(adegenet)`
- `genind <- df2genind(name_of_dataset, ploidy = 2, sep = "/",
pop=population, NA.char="0")`

POPULATION GENETICS

Objectives:

1. Analyze F-statistics
2. Cluster individuals based on allele frequencies
 1. DAPC
 2. STRUCTURE

PREPARATION

- `git pull` while in your GEN_462_2019 folder using git (Windows) or your terminal (Mac)
- Open R Studio
- Open the in-class exercise, Basic_Population_Genetics.Rmd in the Computational2 folder, in R Studio
- Set working directory to InClass folder in Computational2


| \$overall | | | | | | | | | |
|-----------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Ho | Hs | Ht | Dst | Htp | Dstp | Fst | Fstp | Fis | Dest |
| 0.6299 | 0.7083 | 0.7717 | 0.0634 | 0.7757 | 0.0674 | 0.0821 | 0.0869 | 0.1108 | 0.2310 |



Observed
Heterozygosity

\$overall

| Ho | Hs | Ht | Dst | Htp | Dstp | Fst | Fstp | Fis | Dest |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 0.6299 | 0.7083 | 0.7717 | 0.0634 | 0.7757 | 0.0674 | 0.0821 | 0.0869 | 0.1108 | 0.2310 |

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- FST measures the proportional reduction in heterozygosity of the total population due to differentiation among subpopulations
 - FST (**fixation index**) often used as a measure of population differentiation
 - 0 – 0.05: Little genetic differentiation
 - 0.05 – 0.15: Moderate genetic differentiation
 - 0.15 – 0.25: Great genetic differentiation
 - > 0.25: Very great genetic differentiation

\$overall

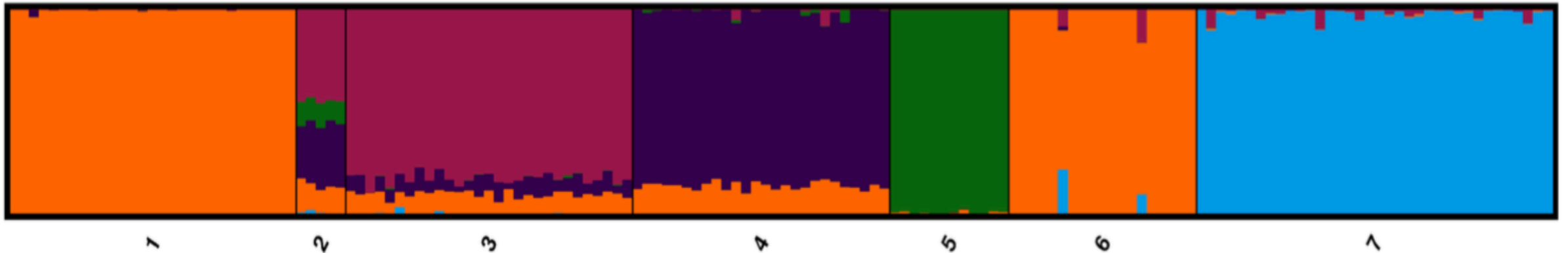
| Ho | Hs | Ht | Dst | Htp | Dstp | Fst | Fstp | Fis | Dest |
|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| 0.6299 | 0.7083 | 0.7717 | 0.0634 | 0.7757 | 0.0674 | 0.0821 | 0.0869 | 0.1108 | 0.2310 |



FIS measures the average proportional reduction in heterozygosity within subpopulations due to inbreeding

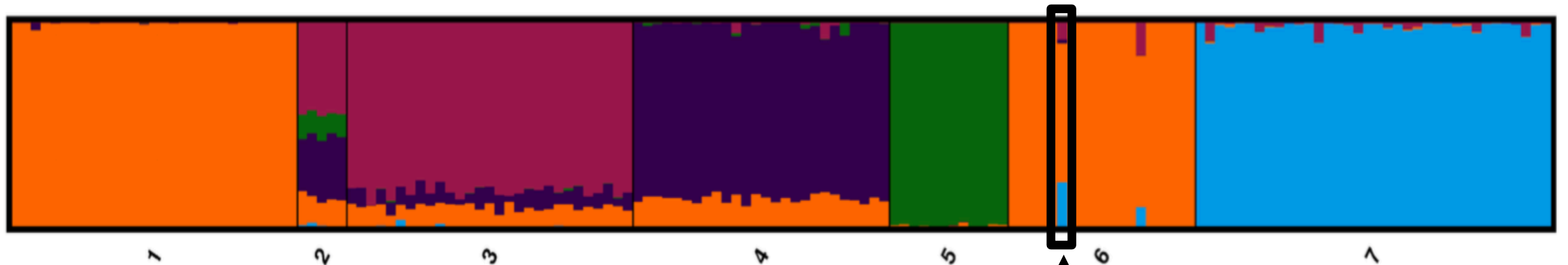
STRUCTURE

- “Bayesian iterative algorithm by placing samples into groups whose members share similar patterns of variation. *STRUCTURE* both identifies populations from the data and assigns individuals to that population representing the best fit for the variation patterns found.”



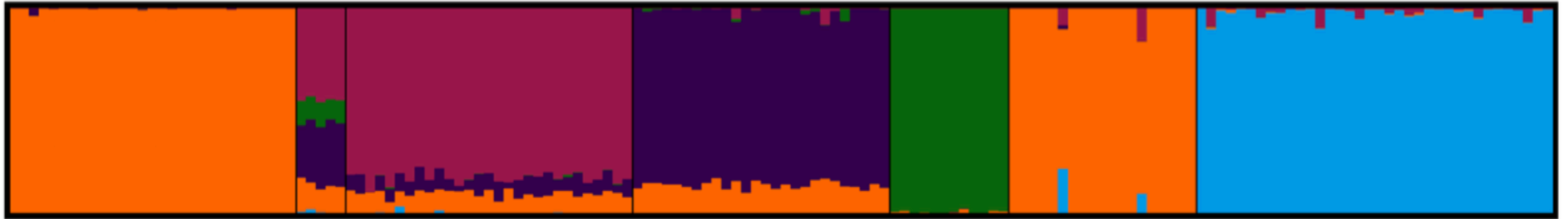
Sampling location
(assumed population)

STRUCTURE



Individual

STRUCTURE



Grouped