

COMPUTATIONAL ACTIVITY 2

September 13, 2018

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_2018 folder using git (Windows) or your terminal (Mac)
- Open R Studio
- Open the in-class exercise, Basic_Population_Genetics.Rmd in the Computational_2 folder, in R Studio
- Set working directory to Example_Data in Computational_2

\$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



- 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

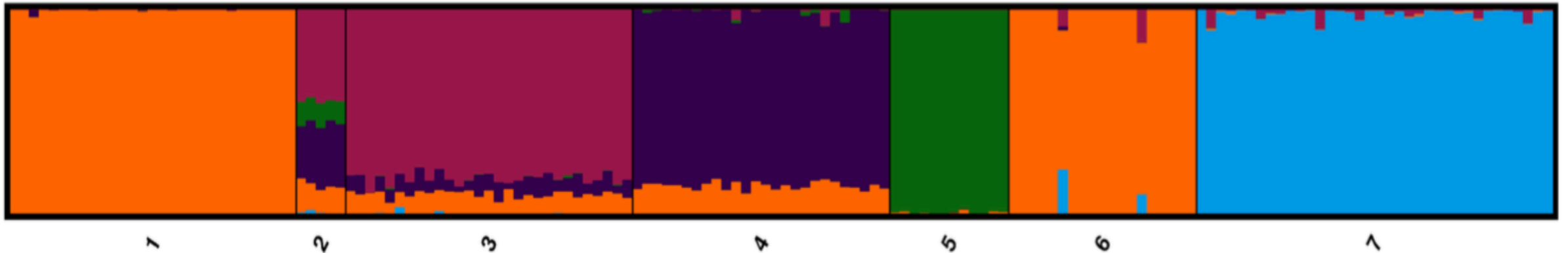
Ho	Hs	Ht	Dst	Htp	Dstp	Fst	Fstp	Fis	Dest
0.6299	0.7083	0.7717	0.0634	0.7757	0.0674	0.0821	0.0869	0.1108	0.2310



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

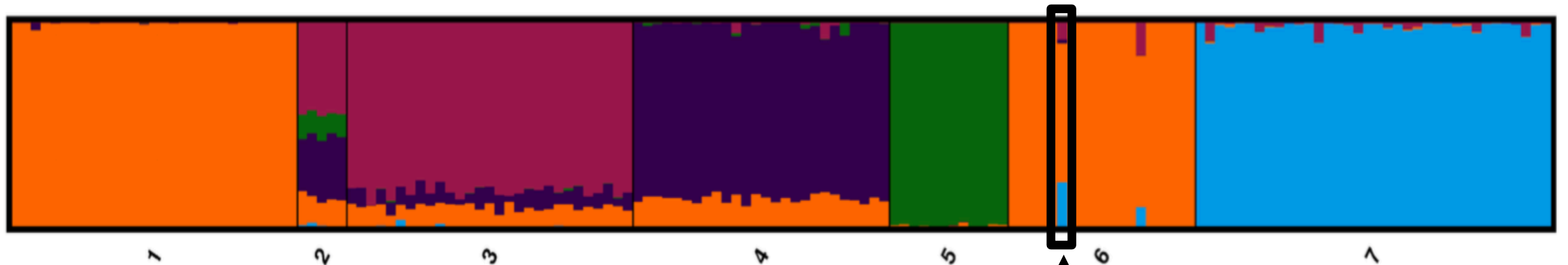
STRUCTURE

- “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

