

Lab 3 Example

1 Download and look at data

- Download “polygonum.stru”
- Look at “polygonum.stru” using a text editor
 - Column 1 refers to individual ID (516 total individuals)
 - Column 2 refers to population (16 total populations)
 - Column 3 refers to habitat (2 different habitats)
 - Remaining columns refer to alleles for 7 different loci
 - NA values are coded as -9

2 Pairwise Fst

- Read data into R using *read.structure()* and save it to object called “markers”
 - Use *str()* to look at “markers” object
- Compute pairwise Fst values
- Interpret with a partner: Do populations seem to be equally genetically distinct?

3 Compute hierarchical F-stats

- Convert to genind object called “for.hier”
 - Add habitat column back to “for.hier”
- Use *varcomp.glob()* to compute hierarchical f-stats
- Levels should correspond to habitat and population
- Interpret results with a partner: At what hierarchical level does it appear that most variation within populations is found? Among individuals within populations, among populations within habitats, or among habitats?