F-Statistics

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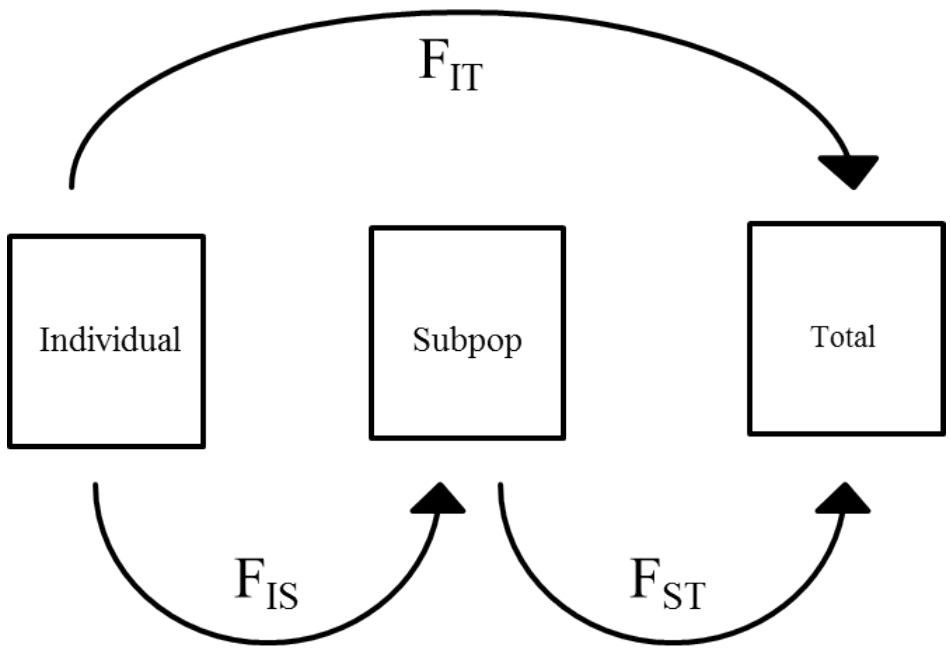
Goals for Today's Lab

- Install R packages *hierfstat* and *adegenet*
- Work through tutorial
- Work through example

Variance Components

In R, the packages *adegenet* and *hierfstat* can be used to compute F_{IS}, F_{ST}, and F_{IT} using variance components.

$$(1 - F_{IS})(1 - F_{ST}) = 1 - F_{IT}$$



Hierarchical F-Stat

Install the R packages *adegenet* and *hierfstat*!

Tutorial

Work through the Jombart (2015) tutorial parts 1, 2.1, 3, 4.1, 4.2, and 5 on your own / with partner

Practice problem

This dataset takes 7 microsatellite loci from 16 North American populations (516 individuals) of the invasive plant *Polygonum cespitosum* found in two different habitats from Matesanz et al. (2014)

Practice problem

To do:

1. Download "polygonum.stru"'
2. Compute pairwise Fst values using adegenet
3. Compute hierarchical f-stats using hierfstat

Hints

- Look at "polygonum.stru" using a text editor
- Column 1 refers to individual ID, column 2 refers to population, column 3 to habitat
- NA values are coded as -9
- 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
- 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

Next Week

Individual Assignment in Structure!

Project # 2!

Works Cited

- Matesanz, S., K. E. Theiss, K. E. Holsinger, and S. E. Sultan. 2014. Genetic Diversity and Population Structure in *Polygonum cespitosum*: Insights to an Ongoing Plant Invasion. PLoS One 9:e93217.
- Pritchard, J. K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics 155:945-959.