

CONGEN – Population structure and evolutionary histories

The table below shows allele counts at a microsatellite locus genotyped in 12 populations of Atlantic salmon. Review the table and prepare to discuss what this data tells us about Atlantic salmon.

Table 1. Allele counts at microsatellite locus *hexSSOSL438* in Atlantic salmon. For example, 10 copies of allele “106” was found in Maine.

	96	104	106	108	110	112	114	116	120	124	126	130	132	134	136	138	140	144
Maine			10		151			1										
New Brunswick			27		99	2		4										
Nova Scotia			7		103	2												
Quebec			27	2	93			4										
Newfound			19		32		7											
Labrador			6		23	3												
Iceland					8				1	3	42	28	1	17				
Norway					4		1				65	11	3	19	5	1	5	
Finland											96	19		3				
Scotland				2	8		9				2	3	2	18	2			
Ireland	1	1			14		13				16	3	4	7				1
Spain					24		3				1	1	3	2				

F_{ST}

Purpose

is a measure of how similar or different allele frequencies are in two or more populations

Properties

when all populations being compared have the same allele frequencies
when populations are 'fixed' for alternative alleles

Example: for neutral genetic variation in humans is 0.05

Definition #1

————, where $Var(q)$ = the variance of the frequency of an allele in two or more populations, and \bar{q} = the average frequency of the allele in populations

Definition #2

F_{ST} = fractional reduction in heterozygosity in a set of sub-populations compared to expectation if they were a single randomly mating population

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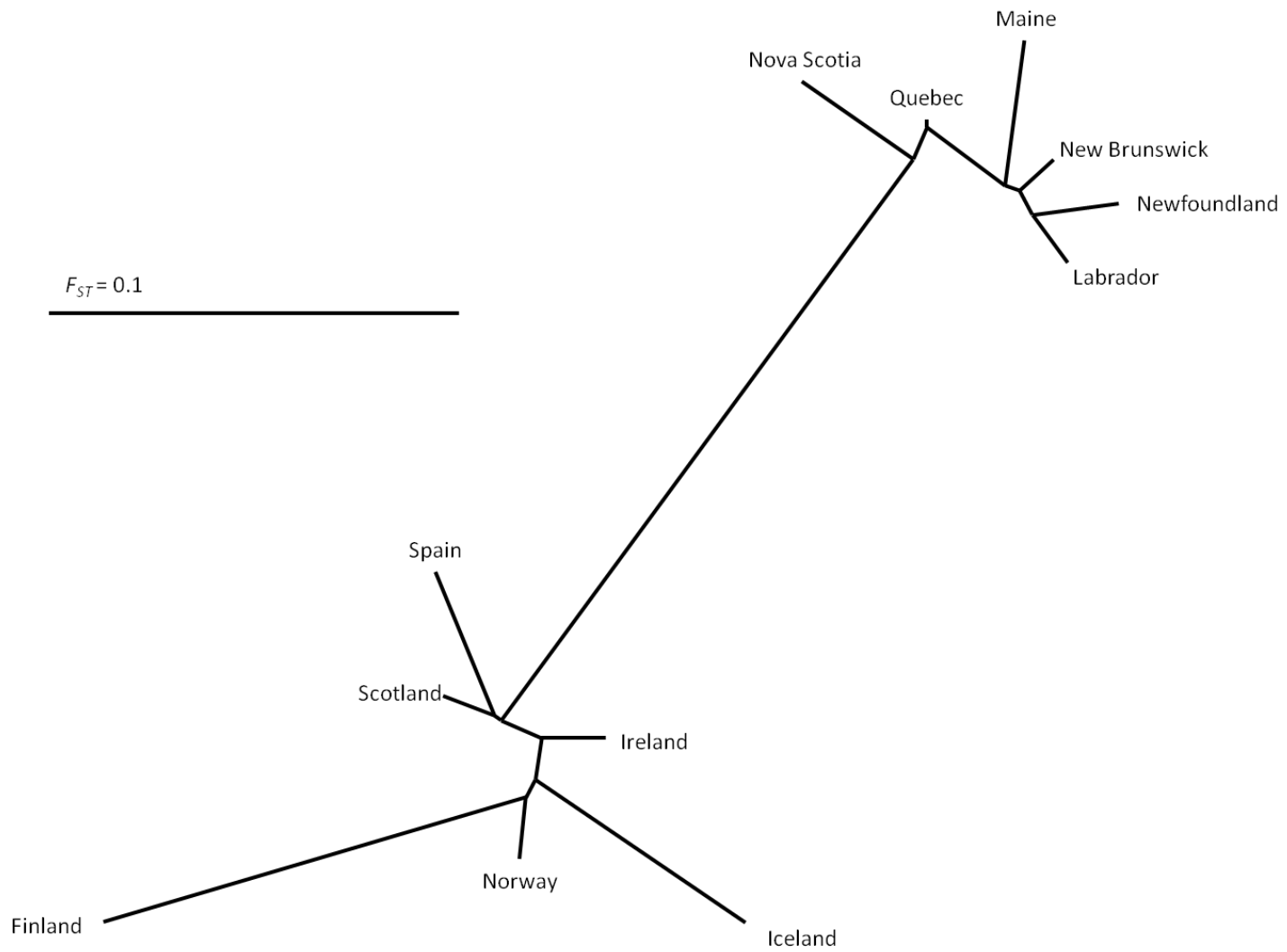
H_T = Expected heterozygosity if all subpopulations were part of a single randomly mating population. It is calculated by averaging the allele frequencies from each of the subpopulations, and calculating the expected heterozygosity from these averages.

= Average expected heterozygosity within subpopulations. This is obtained by calculating the expected heterozygosity within each population and taking the average of these heterozygosities.

Table 2. Pairwise F_{ST} values for the Atlantic salmon populations listed in Table 1.

	Maine	New Brun	Nova Scotia	Quebec	Newfou ndland	Labrador	Iceland	Norway	Finland	Scotland	Ireland	Spain
Maine	0.00	0.05	0.08	0.05	0.06	0.06	0.30	0.27	0.35	0.24	0.25	0.26
New Brun	0.05	0.00	0.07	0.02	0.04	0.03	0.30	0.25	0.34	0.23	0.25	0.25
Nova Scotia	0.08	0.07	0.00	0.05	0.08	0.08	0.29	0.24	0.34	0.21	0.23	0.24
Quebec	0.05	0.02	0.05	0.00	0.05	0.04	0.25	0.21	0.29	0.18	0.20	0.21
Newfoundland	0.06	0.04	0.08	0.05	0.00	0.04	0.32	0.27	0.35	0.25	0.26	0.27
Labrador	0.06	0.03	0.08	0.04	0.04	0.00	0.30	0.25	0.34	0.23	0.24	0.24
Iceland	0.30	0.30	0.29	0.25	0.32	0.30	0.00	0.09	0.17	0.10	0.08	0.14
Norway	0.27	0.25	0.24	0.21	0.27	0.25	0.09	0.00	0.12	0.06	0.05	0.07
Finland	0.35	0.34	0.34	0.29	0.35	0.34	0.17	0.12	0.00	0.18	0.16	0.19
Scotland	0.24	0.23	0.21	0.18	0.25	0.23	0.10	0.06	0.18	0.00	0.03	0.05
Ireland	0.25	0.25	0.23	0.20	0.26	0.24	0.08	0.05	0.16	0.03	0.00	0.06
Spain	0.26	0.25	0.24	0.21	0.27	0.24	0.14	0.07	0.19	0.05	0.06	0.00

Figure 1. An unrooted tree summarizing FST matrix of Table 2.



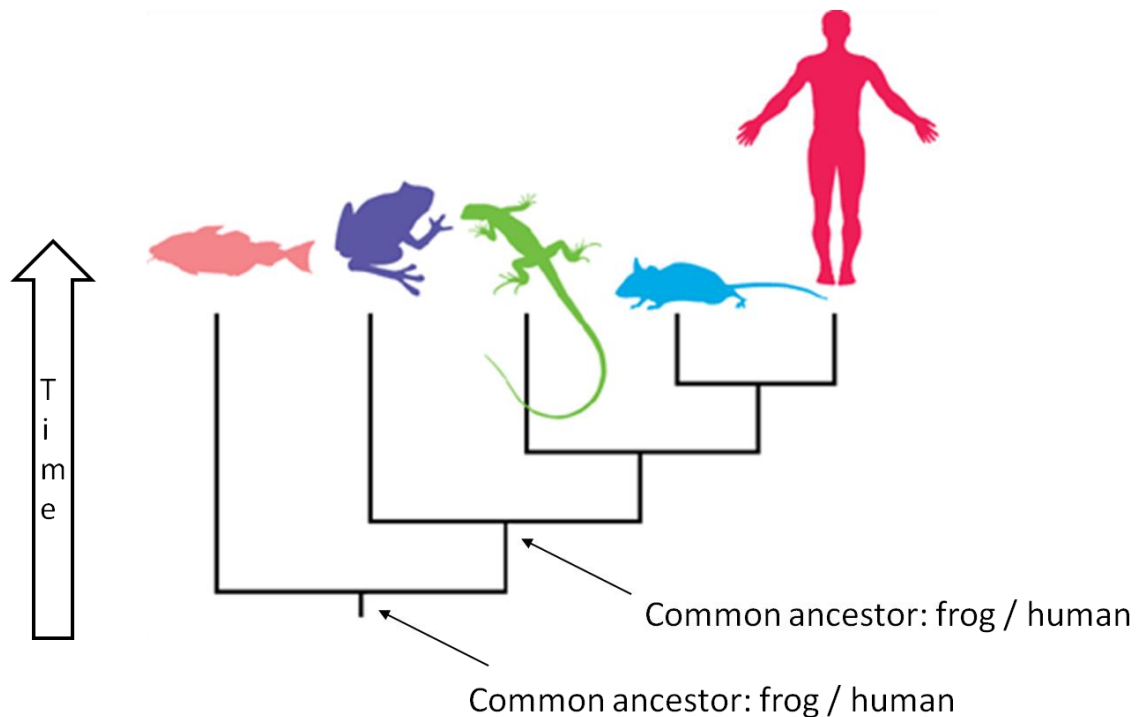
READING EVOLUTIONARY TREES

Unrooted trees

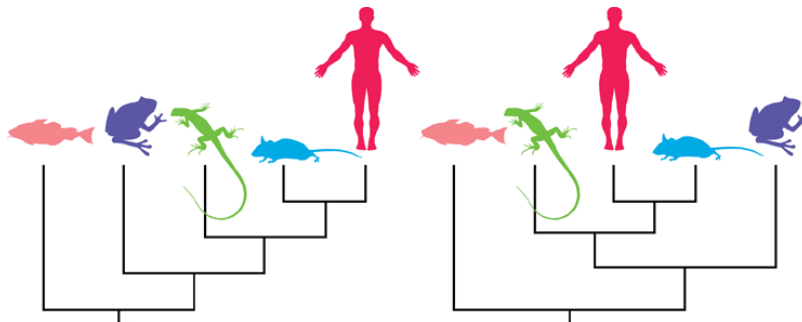
Unrooted trees show similarity. The length of the branches on the tree indicates how different the taxa are. (See example above).

Rooted trees

Rooted trees show evolutionary histories. They show how species are related to each other. They have an axis depicting time. Rooted trees are interpreted by examining how far back in time species share a common ancestor. See example below.

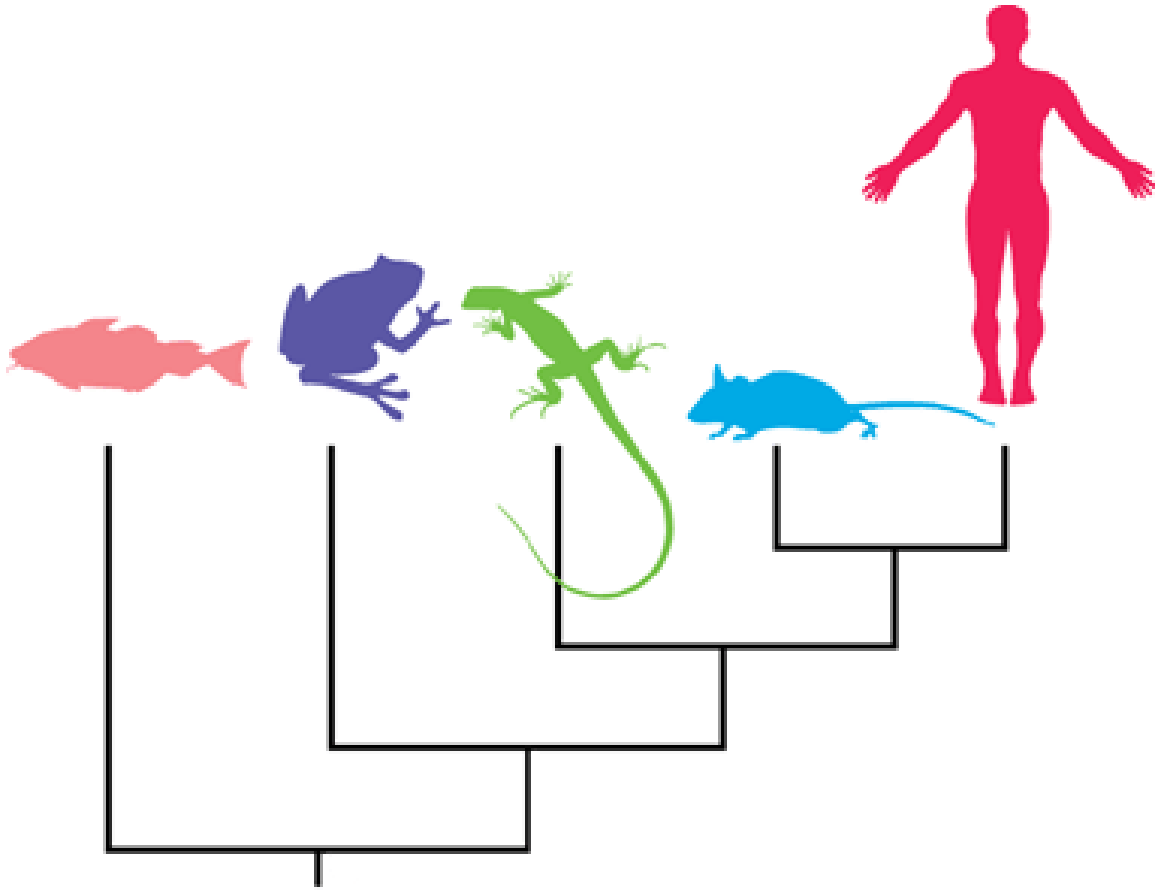


Note: The branches on trees can be rotated without changing their meaning. The two trees below are identical.



PRACTICE READING TREES

In the tree below, is the frog more closely related to the fish or the person?



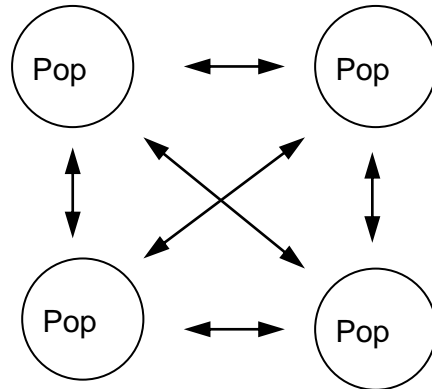
PRACTICE MAKING TREES

Draw a rooted evolutionary tree for the following species:

Fruit fly
Human
E. coli
Whale
Oak tree
Sponge
Lamprey
Turtle
Platypus
Frog
Euglena
Rainbow trout

F_{ST} FOR TWO SIMPLE MODELS OF EVOLUTION

“Island Model” of Migration



Assumptions:

1. Infinite number of populations
2. All populations have the same N_e .
3. The migration rate, m , into a population is the proportion of individuals in a population that were born elsewhere.
3. Migration rates are equal and symmetric between populations (see figure above for an example).

Given this model, $F_{ST} = \frac{1}{4Nm + 1}$.

“Isolation Model” of Population Fragmentation

Assumptions:

1. A population is instantaneously split into two other populations, each having the same effective size as the original population.
2. The two new populations are completely isolated from each other from each other and from all other populations for t generations.
3. The effective size of each population remains constant.

Given this model, $F_{ST} \approx \frac{t}{2N_e}$

F_{ST} exercise

Which scenarios will have the highest values of F_{ST} for the “island model” of gene flow?

$$F_{ST} = \frac{1}{4Nm + 1}$$

Low m

High m

Small N_e

High N_e

F_{ST} Exercise

Genetic data show the historic value of F_{ST} for bighorn sheep populations is 0.2. Let us interpret this as meaning:

How many sheep must move between populations to prevent “abnormal” amounts of inbreeding (i.e., keep F_{ST} 0.2)? Fill in the table below

Ne	Number of migrants per generation
= 10	_____
= 100	_____
= 1000	_____

This is called the _____ rule.