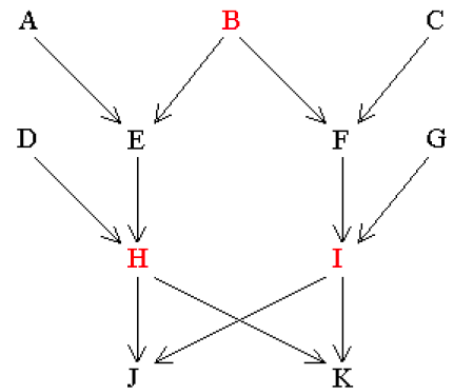


**Read, Complete and bring a hard copy to class.**  
**We will discuss this in class so it is OK if you are a bit confused, but try.**

**A common ancestor** is any preceding individual in the pedigree who passes genes directly to two or more persons **through different independent routes or paths.**

Here B is the common ancestor of H and I.

H, I and B are common ancestors to J and K.



While A, C, D, E, F and G all pass genes to both J and K, they do not do so by different independent routes. For example the path from A to K is A>E>H>K which is the same path as A>E>H>J. A has a direct relationship with J. B has a direct relationship with both H and I as well as with J and K. Individuals that share a common ancestor are said to have a collateral relationship. E, F, H, I, J and K all have collateral relationships with each other.

the coefficient of relatedness (R), is used to calculate the proportion of alleles that two individuals have in common as a result of their genetic relationship. It is not an absolute measurement but it is a description of the probability that any two individuals will share an allele at a given locus. It is also an estimate of the proportion of the genome that would be shared. The absolute amount of genetic material that is shared between two individuals will vary because recombination during cell division to make gametes is random, but on average the coefficient of relatedness is accurate.

One can calculate the coefficient of relatedness with the following equation where  $R_{xy}$  is the relatedness between individuals X and Y. The symbol  $\Sigma$  means “the sum of” indicating that you must add together the values from all paths when there is more than one.  $\frac{1}{2}$  is the value because each gamete carries  $\frac{1}{2}$  of the parent’s genome, and n is the number of steps between individuals on a path.

$$(R_{XY}) = \Sigma (1/2)^n$$

To calculate the **direct relationship**, for example A and J in the above figure, the number of direct steps between the individuals is counted and used in the above formula for this single path. Paths must always follow the same direction. For A and J the path is A>E>H>J and there are three links.

When individuals are not directly related but share a common ancestor, such as H and I in the figure above, the path will first go up the pedigree and then down the pedigree. H>E>B>F>I which is 4 steps. Therefore,  $R_{HI} = (\frac{1}{2})^4$  . or  $\frac{1}{16}$  There is only one path.

Things get complicated with inbreeding. For example, there are multiple path to connect J and K (the offspring of cousin mating)

J>H>E>B>F>I>K 6 steps  $(\frac{1}{2})^6$   
and also

J>I>F>B>E>H>K 6 steps  $(\frac{1}{2})^6$

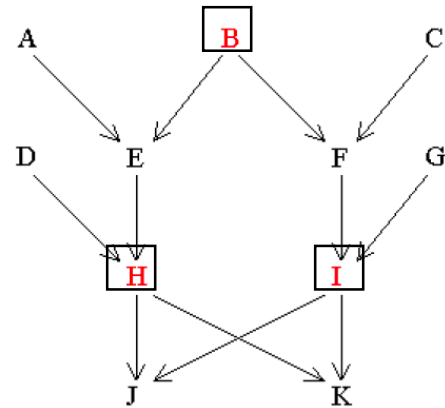
In addition to being siblings

J>H>K 2 steps  $(\frac{1}{2})^2$

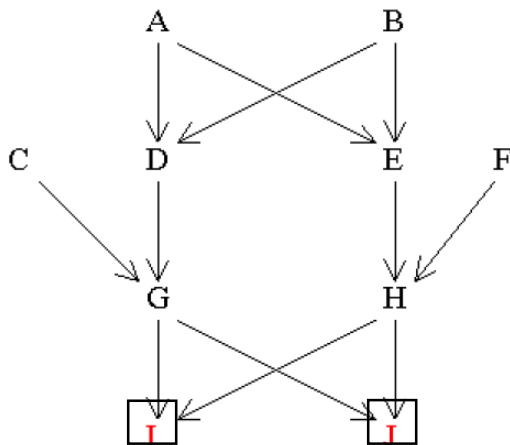
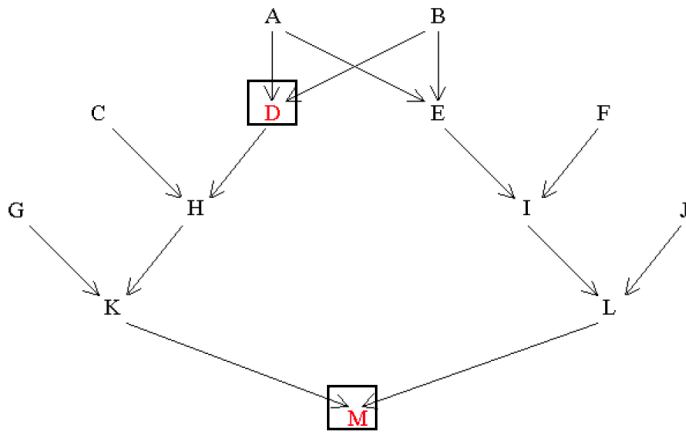
And

J>I>K 2 steps  $(\frac{1}{2})^2$

$$\begin{aligned} R_{JK} &= (\frac{1}{2})^6 + (\frac{1}{2})^6 + (\frac{1}{2})^2 + (\frac{1}{2})^2 \\ &= \frac{1}{64} + \frac{1}{64} + \frac{1}{4} + \frac{1}{4} \\ &= \frac{2}{64} + \frac{1}{2} \\ &= \frac{1}{32} + \frac{1}{2} \\ &= \frac{17}{32} \end{aligned}$$



Practice with some more complicated relationships



- First identify all common ancestors for red (boxed) individuals.
- Then identify all different paths through each ancestor
- Then add the results of each path to calculate relatedness of the individuals.