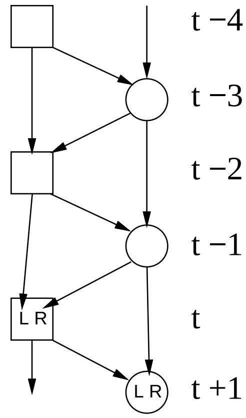
Genome 562 Spring, 2007
Population Genetics J. Felsenstein

Key to problem 2, Homework no. 6



This is an attempt to show how I would do the problem, both the easier way that I suggested in my hint posted to the class mailing list, and the harder way similar to what a lot of you tried.

Easier way. Let's just refer to the individuals by their generation number. In generation $t+1$ there is a probability of non-IBD within the individual called h_{t+1} and a probability of non-IBD between individual $t+1$ and individual t called k_{t+1}. Now just take individual $t+1$ and ask where its two copies of the gene came from. One (the Left one) came from individual t, the other (the Right one) came from $t-1$. So $h_{t+1} = k_t$. Now choose one copy from $t+1$ and one from t, and where the one from $t+1$ came from. Half of the time it is copy L and came from t. If it did, half of the time it came from the copy you chose in t and then could not be IBD. The other half of the time it came from the copy you didn't choose in t and the probability of non-IBD is then h_t. The rest of the time it is the R copy and came from $t-1$, so given that the probability of non-IBD with a copy in t is k_t.

That gives the other equation as $k_{t+1} = \frac{1}{4}h_t + \frac{1}{2}k_t$. The two equations are then identical to the two equations you get for repeated full-sib mating. Whether the inbreeding goes at the same rate as repeated full sibs depends on whether the equivalent amount of time in the two systems is the time for a parent to produce an offspring and have it reach mating age (in which case the two systems inbreed at the same rate, or the time until both individuals are replaced, in which case the half-sibs mating system inbreeds twice as fast as repeated full sibs.

The hard way. OK, that's the easy way. If instead we tried to go back to the origin of the L and R genes in both individuals, we have to be more careful but it can work (it took me many tries). For the h_{t+1} formula the steps are the same and so is the result. For the k_{t+1} formula, in each individual we can choose either the L or the R copy, so there are four cases, each with probability $\frac{1}{4}$:

LL The copy from individual $t+1$ comes from individual t, and there is a $\frac{1}{2}$ chance that it comes from copy R in that individual, in which case it can be non-IBD with probability h_t. So the contribution for this case is $\frac{1}{2}h_t$.

LR The copies come respectively from $t-2$ and $t-1$ so the contribution to the non-IBD from this case is k_{t-1}.

RL The copy from individual $t+1$ comes from individual t, and as in case LL there is a $\frac{1}{2}$ probability that it comes from copy L in that individual in which case it is non-IBD with probability h_t. So the contribution is $\frac{1}{2}h_t$.

RR Both copies from from individual $t-1$ independently, so the probability that they are non-IBD is also $\frac{1}{2}h_{t-1}$

Putting all these together the two equations are:

$$h_{t+1} = k_t \tag{1}$$

$$k_{t+1} = \frac{1}{8}h_t + \frac{1}{4}k_{t-1} + \frac{1}{8}h_t + \frac{1}{8}h_{t-1} \tag{2}$$

Substituting the first equation into the second, eliminating all the h's, we get

$$k_{t+1} = \frac{1}{2}k_{t-1} + \frac{1}{8}k_{t-2}$$

This gives the cubic equation

$$\lambda^3 - \frac{1}{2}\lambda - \frac{1}{8} = 0$$

If you solve this numerically this gives as the largest root $\lambda = (1+\sqrt{5})/4$, the same as full-sib mating. Or you can factor it into

$$\left(\lambda^2 - \frac{1}{2}\lambda - \frac{1}{4}\right)\left(\lambda + \frac{1}{2}\right)$$

where the first factor is the same expression we had for full-sib mating.

As a check I used the method of coefficients of kinship, working generation by generation using a simple program I have, and got these probabilities of non-IBD:

generation	h	k
1	1	1
2	1	0.75
3	0.75	0.625
4	0.625	0.5
5	0.5	0.40625
6	0.40625	0.328125
7	0.328125	0.256625
8	0.256625	0.21484375
9	0.21484375	0.173828125

and from generation 4 on these fit the equations.