HST.161 Molecular Biology and Genetics in Modern Medicine
Fall 2007

How will the number of informative meioses collected in a family study relate to the distance between the disease gene and the closest recombination breakpoint on each side of the chromosome interval which contains the disease gene?

To think about this question consider a chromosomal site G at a specific map distance m (in Morgans) from the disease gene D. The likelihood of crossing over occurring in a given meiosis between G and D is a function of m.

The value that we would like to calculate is the value of m which corresponds to a value of 0.5 for the likelihood of there being no crossover events between G and D for a given number of meioses.

Let's do this first for the case of 10 fully informative meioses.

The likelihood of there being a cross over event during a single meiosis in the interval between D and G is m.

The likelihood of there not being a cross over event during a single meiosis in the interval between D and G is 1-m.

The likelihood of there not being a cross over event during 10 meioses in the interval between D and G is $(1-m)^{10}$. To calculate the value for m for which there is an equal chance of a recombination event occurring within the D to G interval to the probability of no events occurring within the interval, we set $(1-m)^{10}=0.5$.

Solving for 1-m for this case, we get 1-m=0.933. So m=.0669 or approximately 6.7 centimorgans.

Since this value gives only one side of the interval which delineates the position of D, we must double this number to estimate the interval to which D will be bracketed by 10 meioses. This is approximately 13.3 centimorgans.

We can make the same estimate for 25 fully informative meioses, getting a value of 0.972 for 1-m, a value of 2.8 centimorgans for m, and a value of 5.6 centimorgans for the bracketing interval.

For 100 informative meioses, 1-m=0.993, m=.007 i.e. 0,7 cM and the bracketing interval is 1.4 cM.