How many genes?
Mapping mouse traits, cont.

Lecture 2B, Statistics 246

January 22, 2004

Let's estimate the recombination fraction *r* between D12Mit51 and D12Mit132

132 51	A	H	B	Total
A	26	10	0	36
H	10	46	9	65
B	0	5	23	28
Total	36	61	32	129

2-locus genotypes at D12Mit51 and D12Mit132.
129 offspring from H×H, where A×B→H.

Estimation of *r*

First note that we can't simply count recombinants. Why? Because recombination can occur in the paternal or the maternal meiosis, or both, and all we see are the genotypes of the offspring. In most cases, the parental origin of the recombination can be inferred, but not in every case.

Denoting the two markers by 1 and 2, the NOD alleles by *a*, and B6 alleles by *b*, then the *parental* haplotypes are a_1a_2 on one chromosome, and b_1b_2 on the other. Each parent passes on a_1a_2 with probability *(1-r)/2,* and similarly for b_1b_2 , while they pass on each of the *recombinant* haplotypes a_1b_2 and b_1a_2 with probability *r/2.*

In practice, recombinations have slightly different frequencies in male and female meioses, but we ignore this refinement.