23 Jan 1995, revised 2 Jan 1996, 5 Jan '98, 2 Jan 03, 29Dec09

**Cross:**
AABB x aabb produces F-1. Then, F-1 is test crossed (AaBb x aabb) to produce progeny:

**Null hypothesis:** There is no linkage between A and B, thus 1:1:1:1 ratio.

**I. Cross is performed with sample size of 300 progeny.**

| phenotype | observed | expected | dev'tn | sqr of dev | sqr dev/exp |
|---|---|---|---|---|---|
| AB | 78 | 75 | 3 | 9 | 0.12 |
| Ab | 74 | 75 | -1 | 1 | 0.0133333 |
| aB | 63 | 75 | -12 | 144 | 1.92 |
| ab | 85 | 75 | 10 | 100 | 1.3333333 |

Total: 300 X sqrd: 3.3866667
d.f. = 3 P = 0.1 - 0.5

Thus, expect deviations as great as these 10% of the time.
Therefore, we conclude that the markers have not shown linkage.

**II. Cross is performed with sample size of 3000 progeny.**

| phenotype | observed | expected | dev'tn | sqr of dev | sqr dev/exp |
|---|---|---|---|---|---|
| AB | 780 | 750 | 30 | 900 | 1.2 |
| Ab | 740 | 750 | -10 | 100 | 0.1333333 |
| aB | 630 | 750 | -120 | 14400 | 19.2 |
| ab | 850 | 750 | 100 | 10000 | 13.333333 |

Total: 3000 X sqrd: 33.866667
d.f. = 3 P.= > 0.005

Thus, these deviations are expected randomly less than 0.5% of the time.
Therefore, we conclude that data would deviate this much from the expected ratios only 0.5 % of the time by random variation if they are not unlinked, and the null hypothesis is rejected.

**III. Calculate the linkage of these two markers:**

recombinant types: Ab 740
aB 630

Total recombinants: 1370
Total progeny: 3000

Recomb'nt/total progeny: 0.4566667 = 45.7 map units between A and B.