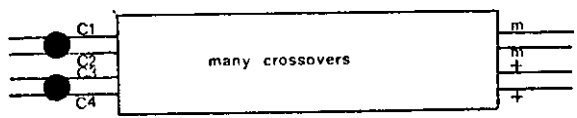
Griffiths.A. J. F. and C. 0. Person. A simple explanation for the 66.7% limiting values trad analysis.

66.7% second division and tetratype frequency limiting values are usually explained by means of functions based on the Poisson distribution. (For example, Fincham and Day 1971 Fungal genetics, 3rd Ed.) In the course of trying to teach this phenomenon to students, we hove arrived at a simple, explanation which appears to have been overlooked in educational texts.

Consider a meiosis in which a heterozygous locus m/+ is so distant from its centromere that the theoretical maximum frequency of second division segregation (66.7%) is attained. This figure con be arrived at in the following way. Assume that the sister chromatids Cl and C2 initially bear the m alleles, and C3 and C4 bear the + alleles. The distance from the centromere to m/+ is so large that a large number of independent crossovers occur throughout the region. As the number of crossovers approaches infinity, the probability of any chromatid (say Cl) ending up with an m allele will approach 1/2.

However, if Cl does eventually bear on m allele, the probability of any other chromatid (say C2) bearing an m allele is reduced to 1/3, as only one of the remaining three alleles is an m. Correspondingly, the probability of C2 bearing a + will be 2/3. The various possibilities, and the resultant segregation patterns, are shown in Table 1, which deals with Cl and C2 only, as examples.

Cl	C2	total probability	resulting segregation
p(m)=1/2	p(m)=1/3	1/6	1st division
	p(+)=2/3	2/6	2nd division
p(+)=1/2	p(+)=1/3	1/6	1st division
	p(m)=2/3	2/6	2nd division



It con be seen that a 2/3 total frequency for second division segregations is generated. Similar results are obtained if Cl and C3, and Cl and C4 are considered pairwise. The analysis can be extended to tetratype maxima.

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