

ROUGH ESTIMATE OF EXPECTED NUMBER OF COINCIDENT BOUNDARIES

Our 12-relative sample generated 1962 matches, from 66 comparisons run on GEDmatch at 3cM with P=3.

We found about 30 matches per pair of testers. The coincidences run across 2 SNPs – noting that reported end-of-segment generally goes to nearest SNP within the segment (since SNPs are used to define segment end). About 1,000,000 SNPs are tested. A coincidence can occur at either end of a match.

Thus our rough estimate of expected coincidences is:

$$66*30*30*2/(1,000,000/2) = 0.24$$