* Three-point testcross: more efficient mapping technique, testcross for three genes
* Constructing a Genetic Map with the Three-Point Testcross
  + Determining the Gene Order
    - Determine order on chromosome
    - Examine double-crossover progeny
      * Progeny nonrecombinant (two most numerous)
      * Double-crossover progeny (two least-numerous)
    - Determine middle gene
      * Draw original chromosomes and then double crossover and see which order works with the progeny findings
      * Non-recombinant anddouble crossover progeny should only differ in alleles of middle locus
  + Determining the Locations of Crossovers
    - Compare alleles found in single-crossover with nonrecombinants
  + Calculating the Recombination Frequencies
    - Determine map distances based on frequencies of recombination
  + Interference and the Coefficient of Coincidence
    - Should be able to calculate proportion of double-recombinant gametes with multiplication rule of probability
    - Interference: degree to which one crossover interferes with additional crossovers in same region
    - Coefficient of coincidence: ratio of observed double crossovers to expected double crossovers
* Effect of Multiple Crossovers
  + Two strand double crossover produce 0% recombination
  + Three strand double crossover produce 50% recombination
  + Four strand double crossover produce 100% recombination
  + Some multiple crossovers go undetected
  + When genes are close, crossovers are unlikely
  + Larger distance, more multiple crossovers are likely, discrepancy between genetic distances and physical distances increases
  + Mapping functions: relate recombination frequencies to actual physical distances between genes
* Mapping Human Genes
  + Unable to perform desired crosses, small number of progeny in typical family
  + Analyze pedigrees
  + Nail-patella syndrome, ABO bloodtypes
  + Lod scores: probability that genes are linked (logarithm of odds)
    - Calculate probability of obtaining observed results withassumption that genes are linked with specific degree of recombination and probability of obtaining the observed results with assumption of independent assortment
* Mapping with Molecular Markers
* Genes Can Be Located with Genomewide Association Studies