

# LOD Score

By Levi Clancy for Student Reader on Monday 17th November, 2008  
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The **LOD score** (aka  $Z$ ) gives an estimation of how closely two loci are linked (for example, a marker locus and a disease locus) *and* quantitates sample size (data reliability).

A LOD score less than 2.0 means the two loci are not linked; a LOD score between 2.0 and 3.0 is inconclusive; and a LOD score greater than 3.0 strongly indicates linkage. Lod scores are always reported in association with the *recombination frequency* ( $\theta$ , theta), measured in Morgans, which describes linkage without accounting for sample size. Please review [linkage analysis](#) if any of these concepts are unclear.

Step 1	Look at nothing more than affected/unaffected individuals and determine the mode of inheritance.
Step	Cross out individuals who cannot be identified as recombinants or

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nonrecombinants (*uninformative* individuals).

1. Persons whose parents are not shown.
2. Individuals without at least one heterozygous parent.
3. Children are uninformative when the child and both parents have the same haplotype.
4. If the allele of interest is dominant, then children with a homozygous recessive parent.

*Step*

3

Determine whether each informative individual is recombinant or nonrecombinant. Considering an informative individual's haplotype, is it consistent with their parent's haplotype and the mode of inheritance?

1. Yes, consistent with parental haplotype → Not Recombinant.
2. No, inconsistent with parental haplotype → Recombinant.
3. Remember that even unaffected individuals can be recombinant!

*Step*

4

Count how many recombinants and non-recombinants there are.

*Step*

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1. If you are provided a *recombination frequency* ( $\theta$ , aka *theta*) then go straight to the equation below.
2. If you are provided the gene-marker distance (measured in *centimorgans* or *cM*) then divide that value by 100 to calculate  $\theta$ . For example, a marker 10cM from a gene yields a  $\theta$  of  $10/100 = .10$ .
3. If you are supposed to calculate the recombination frequency

( $\theta$ ), then use the equation below with  $\theta$  values of .001, .10, .15, .20, .25, .30, .35, .40, .45 and .50. The correct  $\theta$  value will yield the highest LOD Score.

$$\text{LOD score} = Z = \log_{10} \left( \frac{\theta^{(\# \text{ OF RECOMBINANTS})} \cdot (1-\theta)^{(\# \text{ OF NONRECOMBINANTS})}}{(\frac{1}{2})^{(\# \text{ OF RECOMBINANTS})} (\frac{1}{2})^{(\# \text{ OF NONRECOMBINANTS})}} \right)$$