silcLOD (**si**gnificance **l**evels and **c**ritical **LOD**s)

User documentation

silcLOD is designed to calculate nominal significance levels and critical LOD scores depending on the length of the investigated region, number of chromosomes, and the cross-over rate. The global significance level as well as the precision of the calculation have to be specified.

The program is based on the following publication:

> Lander, E., Kruglyak, L. (1995) Genetic dissection of complex traits: guidelines for interpreting and reporting linkage results. *Nature Genetics*, **11**, 241-247.

Here, Box 1 on page 242 gives the necessary formulae.

silcLOD is started by typing "silcLOD".

Within the program, you are prompted to specify the following parameters:

1. "Length of genomic region in Morgan":

   Length of the investigated region measured in Morgan. The default is given by 33 Morgan which is the length of the human genome.

2. "Number of chromosomes":

   Number of investigated chromosomes. The default is given by 23 which is the total number of human chromosomes. The entered value must be an integer.

3. "Cross over rate":

   Total crossing over rate between the genotypes. For different mapping methods, the values for humans are given in the table below according to Lander and Kruglyak, 1995, Table 1. The default is given by 2.

Mapping method	Cross over rate
Lod score analysis	1
Allele sharing in sibs and half sibs	2
Allele sharing in grandparent-grandchildren	1
Allele sharing in uncle-nephew	5/2
Allele sharing in first cousin	8/3
Allele sharing in first cousin, once removed	20/7
Allele sharing in second cousin	16/5

4. "Global significance level":

   Desired global signficance level for the investigation. The default is given by 0.05. The entered value must be less than 1.

5. "Precision":

   The precision sets the maximally allowed difference between the specified and the calculated global significance level. The default is given by 0.00000001. The entered value must be less than the value for the desired global significance level.

The results render the nominal significance level for a single marker using an infinitely dense marker map. In addition, the critical LOD scores for single markers assuming different marker maps have been used are presented. Marker maps of infinite density as well as maps assuming distances of 10cM, 5cM, 2cM, or 1cM are considered.

The output can be saved in a document entitled "silcLOD.erg" that will be saved within the current file. Alternatively, results will be displayed on screen only.

In any stage, entering "?" gives help for specifying the parameters.

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