Fast linkage calculation of Affymetrix SNP 6.0 genotype data using a new program SNP6-LINK

RC-LINK

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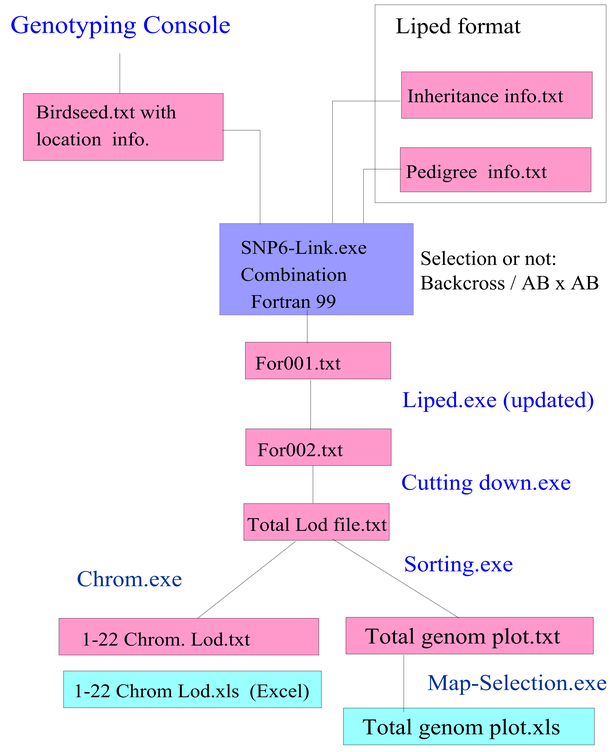
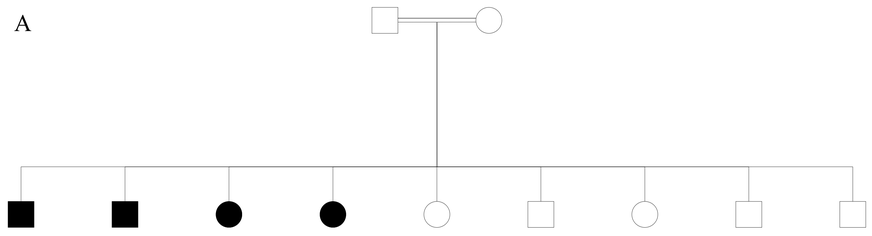
Ott 1976 (Am J Hum Genet 28, 528-529) introduced the program LIPED for linkage calculation of markers in large family pedigrees with or without loops and the program is ideal for two-point linkage analyses calculations. We have previously constructed a helper program, LIPED.COM, that automatically make an input data file to LIPED, allowing LOD score calculations for more than 800 markers to be calculated and the results to be present in a usable form. This program has been tested by mapping more than 800 marker systems using families from the Copenhagen Family Bank (Eiberg et al. Clin Genet 1989; 36:415-418).

The development of the SNP microarray chip technology (Affymetrix chip) for testing >10^6 SNP alleles has made new demands for the linkage analysis, and we have therefore modified our linkage helper programs to analyze genotype output files for >10^6 loci. The materials can be analyzed fast and the results shown graphically. This program, SNP6-LINK, demands a simple FORTRAN programming for each new project and several families can be analyzed in one process. The program can also use Illumina genotype output files for calculations.

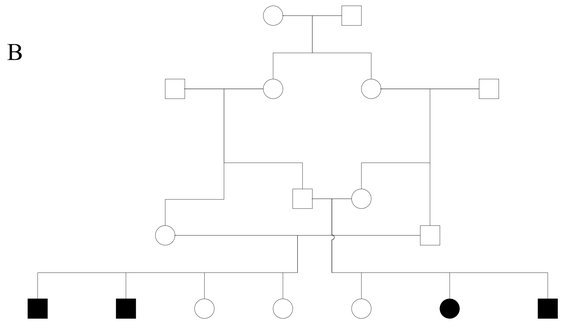
Several parameters can be adjusted before calculations as heterozygote mating for recessive traits, which reduce the output graphical presentation to fewer but informative positive or negative LOD scores. Also Bed-files for uploading of LOD scores to UCSC Genome Browser can be produced. The LOD score calculations for more than a million SNP's in nuclear families takes less than half an hour, and can be run using low RAM PC with Windows Excell and a FORTRAN 99 compiler.



A

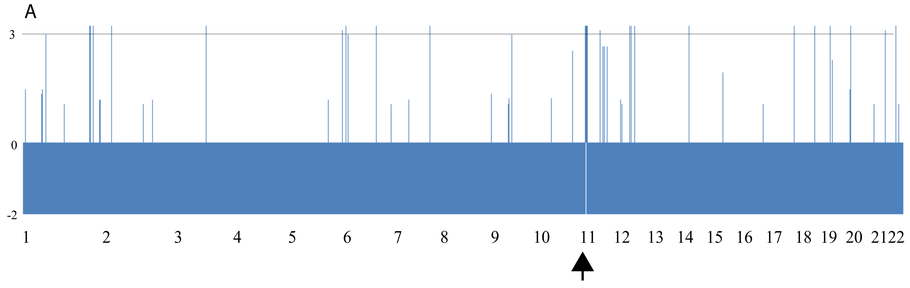


B



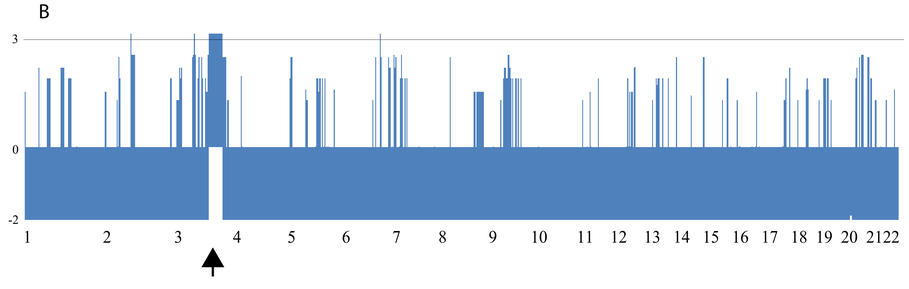
Lod score at different chromosomes. Z=3.2 on chromosome 11.
Exclusion (Z=-2) at all other chromosomes

A



Lod score at different chromosomes. Z=3.2 on chromosome 3.
Exclusion (Z= -2) at all other chromosomes.

B



LIPED input file: pedigree-info.txt Family B

						Info about	Birdseed data
19	2			1			
11		M	-	2			
12		F	-	3			
21		M	-	4			
22	11	12	F	-	5		
23		M	-	6			
24	11	12	F	-	7		
33	21	22	M	-	8	698-4	s4
34	21	22	F	-	9	698-1	s2
340		F	-	10			s2
35	23	24	M	-	11	698-2	s10
36	23	24	F	-	12	698-5	s5
360		F	-	13		698-5	s5
41	33	360	M	+	14	515-04	s1
43	33	360	M	+	15	698-8	s8
44	33	360	F	-	16	698-6	s6
45	33	360	F	-	17	698-7	s7
46	35	340	F	-	18		
48	35	340	F	+	19	698-3	s3
49	35	340	M	+	20	698-9	s9
360	36				21		
340	34				22		
7000					23		

References:
Family A:
Rehman S, et al. 2011. Autozygosity mapping of a large consanguineous Pakistani family reveals a novel non-syndromic autosomal recessive mental retardation locus on 11p15-tel. Neurogenetics 2011 Neurogenetics. 2011 Aug;12(3):247-51.

Fam. B:
(S. Dad et al. in prep)