

# SNP6-LINK

Linkage program for calculations of mil. of 2-point Lod scores. This program package make input files for LIPED (slightly modified to LIP1234 so it can read chrom. and Bp positions of SNP's) After calculations the lod scores the program can extract data to Exel files. Windows XP/ 7 (32 bit)

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Source files (FORTRAN) for calculations of SNP6 data (Birdseed-nr.txt)

[poster 402, HGM2012, Sydney](#)

[Linkage and next generation sequencing \(NGS\) data in six large Danish families with dyslexia](#)

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Input file for LIP1234 (LIPED)

[hoved-rec.txt \(recessive inheritance\)](#)

[hoved-dom.txt \(dominant inheritance\)](#)

[hoved-xrec.txt \(X-recessive inheritance\)](#)

[hoved-xdom.txt \(X-dominante inheritance\)](#)

[split1.txt \(Family structure with 19 lines\)](#)

[split1.txt \(Family structure with 38 lines\)](#)

[for001.dat \(Family structure with 38 lines, chromosome and possision 3 910987654 from Birdseed files\)](#), txt-file - must be renamed from .txt to .dat

input file: combined Birdseed files in one file by use of EXEL: geno-types.txt

Tabulator separated (tab):

[comb-38-30-dom.txt \(renames to .for and compiles with Fortran 99\)](#)

Use split1.txt with 38 lines and extract data from 30 birdseed genotypes, chromosome and Base pair prompt g77 comb-38-30-dom.for

out a.exe (renames)

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[Download Lip1234.docx](#) (must be renamed to .for)

input file: for001.dat

output file: for002.dat

Can only work on 16-32 bit PC

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input for002.dat

output lipdata.dat

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input lipdata.dat

extract-1.exe

exe files (can be made by Fortran 99 using source the files

output SKE-snp6.txt

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input fil to all: SKE-snp6.txt output files: chromosom-#.txt

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Source files

all txt-files must be renamed from .txt to .for and comblated with a FORTRAN 99 compiler

[Download: ekstrakt-1.txt](#)

[Download: ekstrakt-2alfa.txt](#)

[Download: ekstrakt-3alfa.txt](#)

[Download: ekstrakt-4alfa.txt](#)

[Download: udskrift.txt](#)

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Sorting data to chromosome plot: Cygwin (or can be done in EXEL word)

\$ cat.exe SKE-snp6.txt |sort.exe | uniq.exe -c >resultat.txt

Sortering of SKE-snp6.txt with Cygwin.exe

SKE-snp6.txt must be located in C:\Cygwin\home\yourfolder'

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Reference:

Hans Eiberg (unpublished)

P204 HGM2012

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

Hans Eiberg and Lars Hansen