

INPUT FILES:

pedigree.csv - pedigree and trait data
map - genetic map
chr23.dat - marker genotypes
task.inp
par.inp

STEP 1:

COPY MQS_2point.exe, MQS_2point_max.exe, MQS_3point.exe, maxpar.inp and peeling_2006_4.pl files from BIN directory to EXAMPLE directory

STEP 2:

PREPARE ANALYSIS DATA:

FORM task.inp: specify the name of analysed trait (tra)
tra

COMMAND LINE: perl peeling_4.pl pedigree.csv

OUTPUT FILES: iway.dat, tra

STEP3:

FORM par.inp:

- a) specify the parameter values (PR)
- b) check limits of parameters (GR and GL)

nom	ICP	PR	ST	GL	GR	
1	1	0.1318	0.1	0.	1.	!!q = Pr(A)
2	1	-1.27233	0.1	-10.	10.	!!mu1 = Pr(x AA)
3	1	.7986	0.1	-10.	10.	!!mu2 = Pr(x AB)
4	1	-1.379	0.1	-10.	10.	!!mu3 = Pr(x BB)
5	0	0.001	0.0	0.	0.5	!!theta
6	1	0.553	0.1	0.	30.	!!sigma
7	1	0.471	0.1	-10.	10.	!!pga

STEP4:

FORM task.inp: specify names of analysed trait (tra),
file of marker locus (chr23.dat), output data,
output model (mod) [for MQS_2point_max] and
genetic map (map_23) [for MQS_3point].

For MQS_2point task.inp includes:

tra
chr23.dat
res_2point

For MQS_2point_max task.inp includes:

tra
chr23.dat
res_2max
mod

For MQS_3point task.inp includes:

tra
chr23.dat
res_3point

map_23

COMMAND: MQS_2point.exe

OUTPUT FILES: res_2point

COMMAND: MQS_2point_max.exe

OUTPUT FILES: res_2max, mod

COMMAND: MQS_3point.exe

OUTPUT FILES: res_3point