

Supplementary materials

Pedigree file example.ped:			Genotype data in the markers.snp file											
ID	sire	dam	ID	SNP markers										
1	0	0	11	2	0	1	0	1	2	1	1	2	1	
2	0	0	12	1	1	1	1	1	1	2	2	1	0	
3	0	0	13	2	2	2	2	1	1	0	1	2	1	
4	0	0	14	2	1	0	1	1	1	0	0	2	1	
5	0	0	15	0	2	0	1	1	0	2	1	1	1	
6	0	0	16	0	1	1	2	1	1	2	1	0	0	
7	0	0	17	1	1	2	2	2	1	1	1	1	1	
8	0	0	18	2	0	1	1	1	1	0	1	2	1	
9	0	0	19	1	1	0	1	0	0	0	0	2	1	
10	0	0	20	0	1	2	1	2	0	2	1	1	1	
11	0	0	21	2	1	1	1	1	1	0	1	2	0	
12	0	0												
13	0	0												
14	1	11												
15	2	12												
16	3	12												
17	3	13												
18	4	14												
19	6	14												
20	8	16												
21	5	14												

The lower triangle dense A_{22} matrix (A22L.mat) for the example data can be calculated using RelaX2 program mentioned in the input files section. The A22L.mat file has three parts. First, a row having size of the matrix. Second, a row having the ID codes. Third, values of the lower triangle A_{22} matrix. The A22L.mat file:

11	11												
11	12	13	14	15	16	17	18	19	20	21			
1.000													
0.000	1.000												
0.000	0.000	1.000											
0.500	0.000	0.000	1.000										
0.000	0.500	0.000	0.000	1.000									
0.000	0.500	0.000	0.000	0.250	1.000								
0.000	0.000	0.500	0.000	0.000	0.250	1.000							
0.250	0.000	0.000	0.500	0.000	0.000	0.000	1.000						
0.250	0.000	0.000	0.500	0.000	0.000	0.000	0.250	1.000					
0.000	0.250	0.000	0.000	0.125	0.500	0.125	0.000	0.000	1.000				
0.250	0.000	0.000	0.500	0.000	0.000	0.000	0.250	0.250	0.000	1.000			