

Input file of the software ‘GEEARP’ :

Row	Input	Options	Description
1	Pedigree file		The pedigree file with six columns (or more), the first six columns should be: Family ID FatherID MotherID Sex Affection Whether there are genotypes following the six columns does not matter.
2	IBD file		This is the posterior IBD file, and it should be with the same format as the output from Merlin. That is, (in Merlin, ‘--grid’ is suggested when getting IBD) FAMILY ID1 ID2 MARKER P0 P1 P2
3	One/Two-locus Model	1 2 B	1: One-locus model; 2: Two-locus model; B: Both
4	Subset/All Analysis	S A B	S: Subset analysis; A: All data together; B: Both subset and all analyses
5	Un/Constrained model	U C B	U: Unconstrained model; C: Constrained model; B: Both If the selection in the previous row is ‘S’, it doesn’t matter what’s your selection here, but you need to give it a word – ‘U’, ‘C’, or ‘B’. You cannot just skip this row.
6	Bootstrap or not ?	Y N	Y: Bootstrap; N: No bootstrap
7	No. of Bootstrap Samples		Give it a number that how many bootstrap samples would you like. If the selection in the previous row is ‘N’, please also give a number here. Don’t skip it.
8	No. of Initial values tests		Give it a number that how many initial sets would you want to test, and the initial values for gene locations are randomly selected.
9	Full sibs or not ?	1 0	See if you want to analyze FS in this analysis. 1: Yes; 0: No
10	Half sibs or not ?	1 0	See if you want to analyze HS in this analysis. 1: Yes; 0: No
11	First cousins or not ?	1 0	See if you want to analyze FC in this analysis. 1: Yes; 0: No
12	Grandparent-grandchild or not ?	1 0	See if you want to analyze GP in this analysis. 1: Yes; 0: No
13	Avuncular pairs or not ?	1 0	See if you want to analyze AP in this analysis. 1: Yes; 0: No

Principle: Don’t skip any of the 13 rows. See the ‘example’ folder to find examples for one-locus model and two-locus model. The input files are named in name ‘in’, and it should always have the above 13 rows.