**FAM-MDR Manual**

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**Assistance**

When you need assistance on applying FAM-MDR to your data, do not hesitate to contact us:

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**Citations**

When using FAM-MDR please cite

* Cattaert T, Urrea V, Naj A, De Lobel L, De Wit V, Fu M, Mahachie John JM, Shen H, Calle ML, Ritchie MD, Edwards T and Van Steen K (2009) FAM-MDR: a flexible family-based multifactor dimensionality reduction technique to detect epistasis using related individuals. Submitted to AJHG
* [www.statgen.be/software/FAM-MDR](http://www.statgen.be/software/FAM-MDR)

When using MB-MDR please cite

* Calle ML, Urrea V, Malats N, Van Steen K (2008) MB-MDR: Model-Based Multifactor Dimensionality Reduction for detecting interactions in high-dimensional genomic data. Department of Systems Biology, Universitat de Vic
* Calle ML, Urrea V, Vellalta G, Malats N, Van Steen K (2008) Improving strategies for detecting genetic patterns of disease susceptibility in association studies. Stat Med 27:6532-6546
* <http://www.uvic.es/eps/recerca/bioinformatica/ca/inici.html>

**Data format**

*Pedigree file*

First column: Family ID

Second column: Individual ID

Third column: Father ID, 0 for founder

Fourth column: Mother ID, 0 for founder

Fifth column: Sex, 1 for male, 2 for female

Sixth column: Affection status, is not used, put all to 0

Two more columns per SNP: 1 for common allele, 2 for variant allele, 0 0 for missing genotype

*Phenotype file*

First column: Individual ID

Second column: Sex, 1 for male, 0 for female

Third column: Phenotype, NA for missing

*Map file*

First column: Chromosome

Second column: Name

Third column: Position

**Output files**

Rawoutput.txt: Raw MB-MDR output

Permchisq.txt: Test statistics in permuted datasets

Permoutput.txt: Contains SNP pair and permutations p-value of maximal test statistic

**Adaptations by the user**

Change names of pedigree, phenotype and map files

Choose number of permutations: 1000 is recommended

Choose significance level for the epistasis search: 0.05 is recommended

Choose significance level at the first MB-MDR step: 0.1 is recommended

Choosing a seed for the random number generator is highly recommended for reproducibility

Main effect and covariate adjustments can be easily included in the polygenic model statement