# **Genotype Pattern Mining for pairs of interacting variants underlying digenic traits**

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# **Supplementary Material**

The two programs discussed here are Multifactor Dimensionality Reduction (MDR) and Genotype Pattern Mining (GPM). *MDR* has been a mainstay in human case-control epistasis analysis [1, 2]. Below, we describe our implementation of *MDR* for permutation testing [3]. *GPM* has been newly developed and uses a general-purpose FIM algorithm, *fpgrowth* [4], as its pattern search engine. The starting point for each of the two approaches (our implementations) is a dataset in standard *plink* [5, 6] format, that is, as \*.*ped* and \*.*map* files. Small utility programs can then transform the *plink* files into a format useable by *MDR* and *GPM*. Both programs are currently available for Windows, and a Linux version is in preparation for *GPM*. Each program should be run in a command window (cmd).

## **MDR, program parameters**

The Multifactor Dimensionality Reduction (MDR) program furnishes variant patterns ordered by their Balanced Accuracy Overall (BAO) and lists as “Top Models” those with highest BAO [7]. It also judges patterns by a more complex combination of statistics and will declare a “best model”. In practice, the “best” and the “top” models are usually identical. We chose to strictly work with the BAO criterion [8] and built a standard permutation framework around *MDR* so that each variant pattern (“model”) can be assigned a significance level. *MDR* has a built-in possibility to carry out permutation testing but a *p*-value will only be issued for the best model, so we do not make use of *MDR*’s permutation feature. Calling *MDR* repeatedly from within our script, we apply the following parameter values:

-min=*n*1, -max=*n*2, -nolandscape, -top\_models\_landscape\_size=*n*3,

where the user furnishes relevant numbers as follows: *n*1 = minimum number of variants in a pattern, *n*2 = maximum number of variants in a pattern (recommended: *n*1 = *n*2 = 2), and *n*3 = number of patterns with highest BAO output by *MDR*. Also specified is the desired number *n*p of permutations. Permutations will include the observed data as a null dataset so that the smallest possible empirical significance level will be 1/*n*p. As recommended [7], *MDR* can be downloaded from <https://sourceforge.net/projects/mdr/>.

## **GPM**

This program package is available from <https://lab.rockefeller.edu/ott/programs>. It focuses on genotype (rather than variant) patterns and will output genotypes in each pattern found and the variants containing these genotypes. Missing genotypes are allowed but when *fpgrowth* furnishes patterns containing missing genotypes, these patterns will be intercepted by the *GPM* main program. Like *MDR*, *GPM* can handle patterns of length two or more although patterns containing two genotypes are the default and are recommended (see Discussion in main paper).

 Input parameters for *GPM* consist of three numbers, indicating (1) whether pattern frequencies and associated statistics should be obtained for cases or for controls, (2) minimum number of individuals carrying a pattern (support), and (3) minimum proportion of cases among individuals with the current pattern (confidence, in %). Optionally, two additional numbers can specify minimum and maximum lengths of patterns. Recommended minimum confidence is 80% (<https://borgelt.net/doc/fpgrowth/fpgrowth.html>) and minimum support should be chosen based on the sample size in the data; reasonable values are 5 or 10.

Supplementary Table S1. Parametrization of the four types of observations in *GPM* analysis.

**Hypothesis testing**. For a given pattern, *X*, we want to test its association with a phenotype, *Y*, here, of being a case (affected by disease). Table S1 shows four types of observations, α = number of cases carrying *X*, β = number of cases not carrying *X*, γ = number of controls with *X*, and δ = number of controls lacking *X*. The *fpgrowth* program will furnish association rules, *R* = “*X* → *Y*”, with associated observed support, *s* = α + γ, and observed confidence, *c* = α/(α + γ), which is an estimate for the conditional probability of being a case, P(*Y*|*X*), given an individual carries the *X* pattern. Thus, we can retrieve the 2 × 2 table above as α = *c* × *s*, β = *N*2 – α, γ = *s* – α, and δ = *N*1 – γ, and compute an appropriate test statistic in support of the alternative hypothesis of association between *X* and *Y*. We chose the likelihood ratio chi-square as our test statistic.

## **References**

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