

1. Usage:

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java -jar DAM_1.0.jar
```

2. Parameter file:

"parameters.txt" contains some parameters that DAM needs.

Please see the explanations in the example file.

3. Input file:

All the input GWAS data should be placed in the folder "data".

DAM can accept multiple input files.

There should be a header with SNP name, chromosome, location, and cases or control ID.

Each row is a SNP with the genotype information for all individuals.

Starting from the third column, each column is the genotype information for an individual.

Group (cases or control) ID should start from 0.

If there are two case groups and one control group, the group ID should be 0, 1, and 2.

Each genotype for a SNP should be encoded as 0, 1, and 2. 3 is indicating missing value.

4. Output:

The file "Associations.txt" contains the results.

The header for each line is

State	Chi-square (p-value)	Conditional Chi-square (p-value)	SNP1 (location)	SNP2 (location)	...
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5. Any questions, please contact Xuan_Guo@outlook.com.