Modularity Based Scoring Subnetwork
(MoBaS)

Marzieh Ayati and Mehmet Koyuturk

MoBaS is a software tool for finding the disease associated subnetworks in protein-protein interaction (PPI) networks. A disease associated subnetwork is a subset of gene products that are heavily connected to each other in the protein-protein interaction network and are significantly associated with the disease when considered together.

MoBaS uses a scoring method that is parameter-free and aims to score subnetworks by assessing the disease association of pairwise interactions and incorporating the statistical significance of network connectivity and disease association.

To run MoBas, three input files are required.

1. SNP Association
2. Mapping SNP to Gene
3. Protein-protein interaction network

SNP Association

This file can be produces by PLINK.

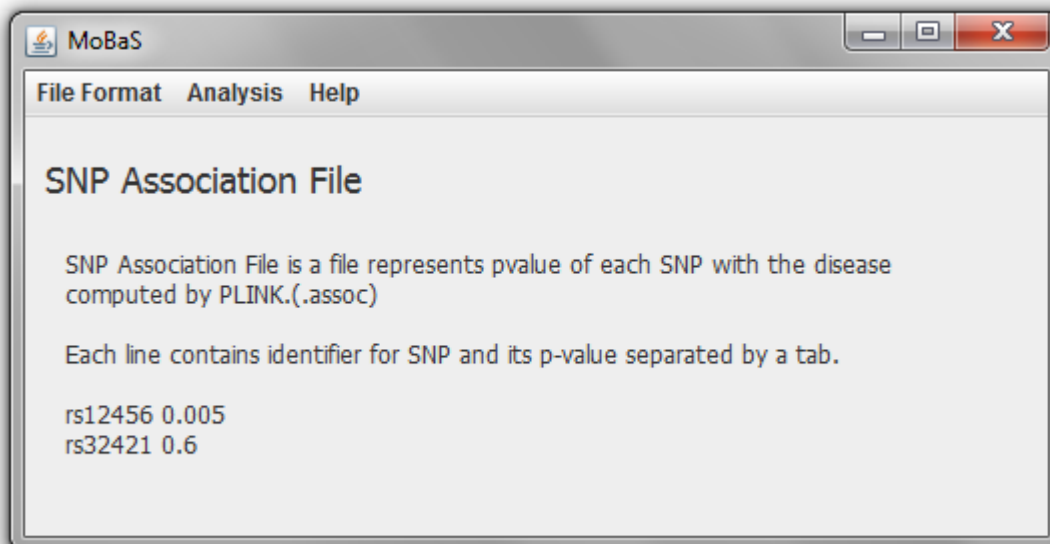SNP Association File is a file represents pvalue of each SNP with the disease computed by PLINK [1].(.assoc)

Each line contains identifier for SNP and its p-value separated by a tab

Here is a sample of .assoc file an input

rs12456 0.005

rs32421 0.06

Users can check the files is Association folder. These files has been produces for Psoriasis disease.

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Mapping SNP to Gene

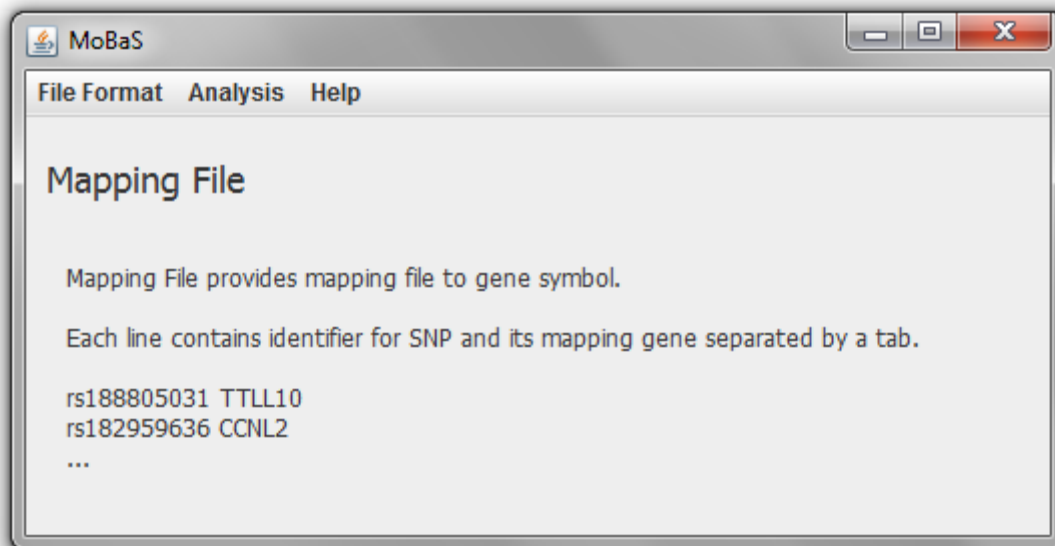Mapping File provides mapping file to gene symbol.

Each line contains identifier for SNP and its mapping gene separated by a tab.

Here is a sample for mapping file

rs188805031 TTLL10

rs182959636 CCNL2

Users can find a mapping file in SNP_Gene.mapping

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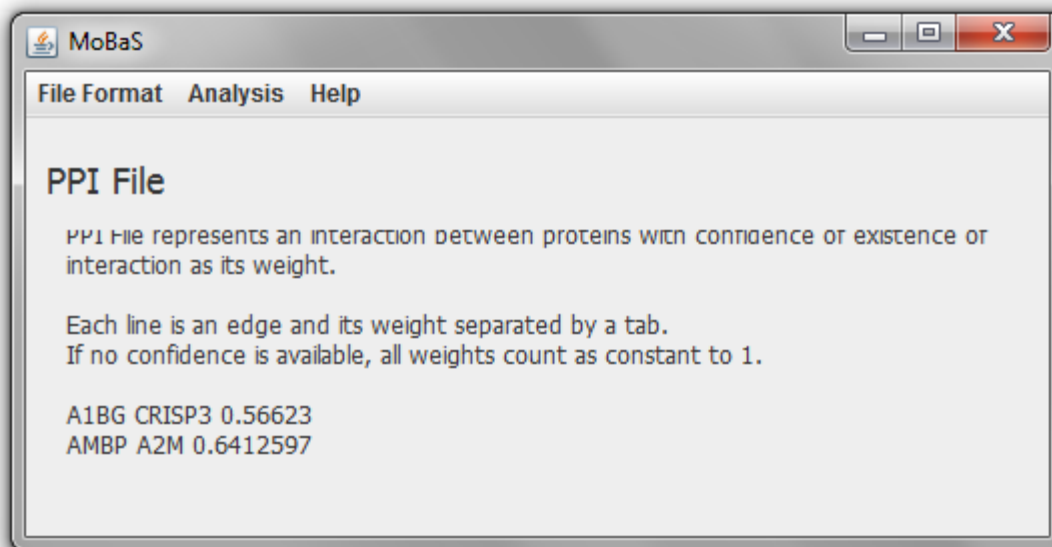### Marzieh Ayati and Mehmet Koyuturk

Protein-protein interaction network

PPI File represents an interaction between proteins with confidence of existence of interaction as its weight.

Each line is an edge and its weight separated by a tab.

If no confidence is available there, all weights count as constant to 1

A1BG   CRISP3 0.56623
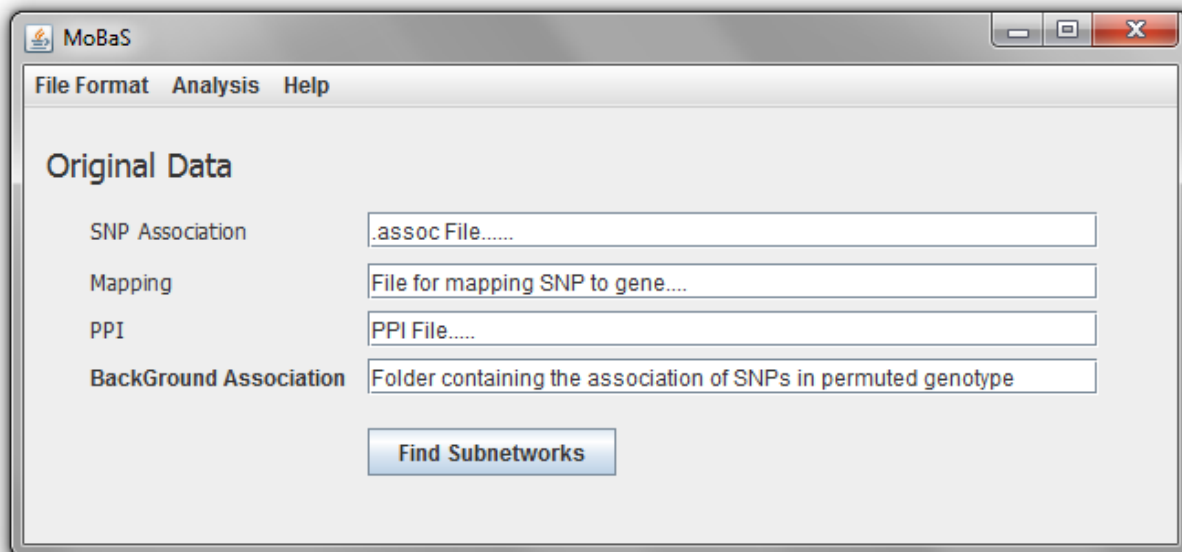
AMBP   A2M   0.6412597

ppi.txt is last HPRD PPI [2].

Identifying modules

After preparing the input files, you can run the MoBaS. However, the user has to also permute the genotypes and provide the mean of p-values of each SNP over n permutation (n=100 in our experiment).

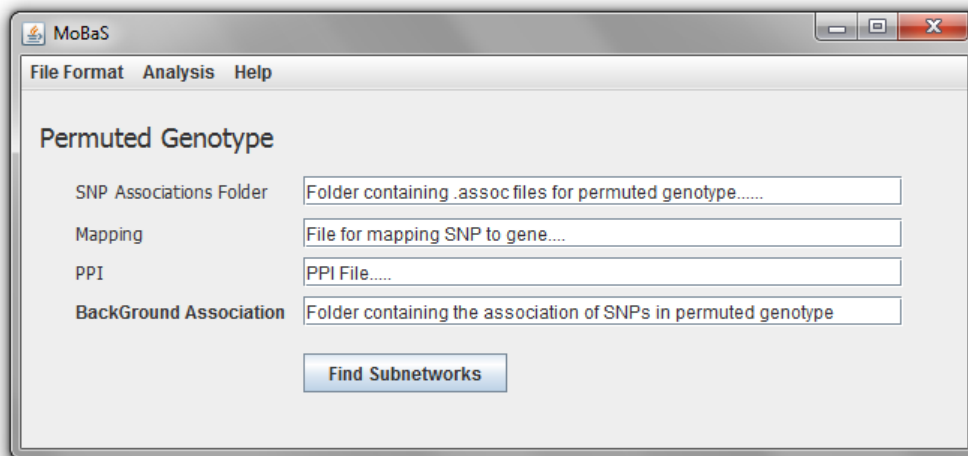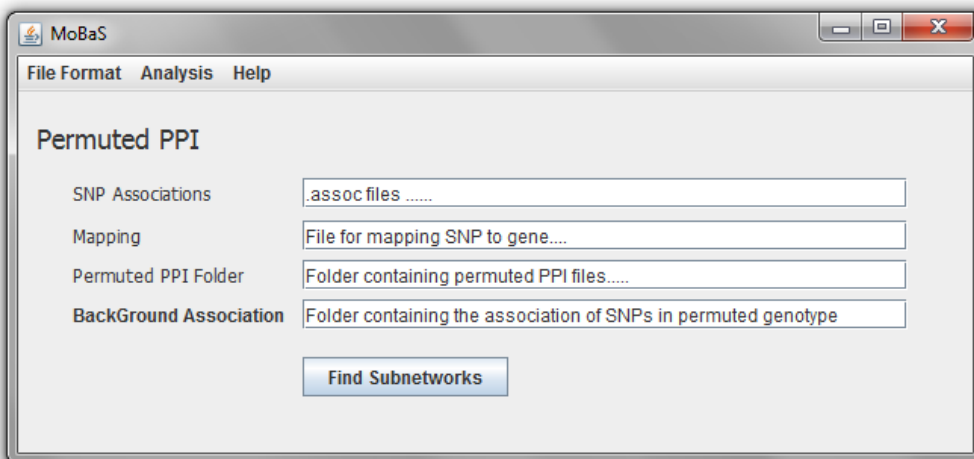MoBaS creates an output file that each line contains a score and the genes within each module.

Statistical Analysis of Modules

If the users wants to compute the statistical analysis of identified modules and its q-value, they can provide permutation of genotype or PPI as an input and MoBaS compute the q-value of each identified modules in the original dataset.

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Publications

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* M. Ayati, S. Erten, Mark R. Chance, M. Koyuturk., "MOBAS: identification of disease-associated protein subnetworks using modularity-based scoring", EURASIP Journal on Bioinformatics and Systems Biology, 2015

* M. Ayati, S. Erten, M. Koyuturk. "What Do We learn from Network-based Analysis of GWAS?", In proceeding of EvoBio'14

References

[1] Purcell, Shaun, et al. "PLINK: a tool set for whole-genome association and population-based linkage analyses." *The American Journal of Human Genetics*81.3 (2007): 559-575.

[2] Prasad, T. S. K. *et al.* (2009) Human Protein Reference Database - 2009 Update. *Nucleic Acids Research.* 37, D767-72