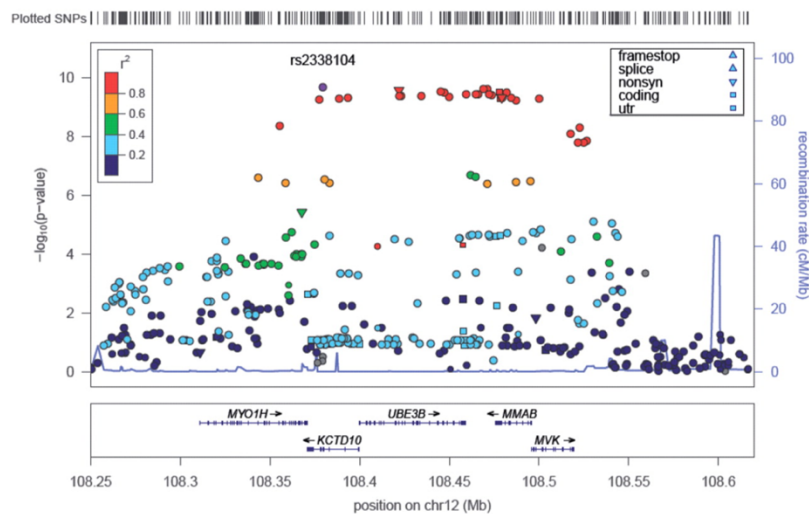


1. *LocusZoom: regional visualization of genome-wide association scan results*. Pruim 2010
Link: <https://academic.oup.com/bioinformatics/article/26/18/2336/208507>

Summary: Genome-wide association studies (GWAS) have identified hundreds of loci associated with complex human diseases and traits. This paper provides a graphical display of locus-specific association results and gives an overview of the extent of LD and the position relative to nearby genes and local recombination hotspots. An example visualization: The authors built a web application for it. Source code is available in R
Comment: I need more background knowledge to understand this paper. But I think this looks like a direction to try...

Fig. 1. An example LocusZoom plot showing the HDL cholesterol-associated region near the MMAB gene (Kathiresan et al. ...)



Bioinformatics, Volume 26, Issue 18, 15 September 2010, Pages 2336–2337, <https://doi.org/10.1093/bioinformatics/btq419>
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2. *Predictive Data Mining for Medical Diagnosis: An Overview of Heart Disease Prediction*.
Soni, et al., 2011

Summary: The paper suggested that using Decision Tree and (sometimes) Bayesian classification will result in better results compared to other methods such as KNN, Neural Networks...

Association rules: to be used on the entire data set to extract rules...

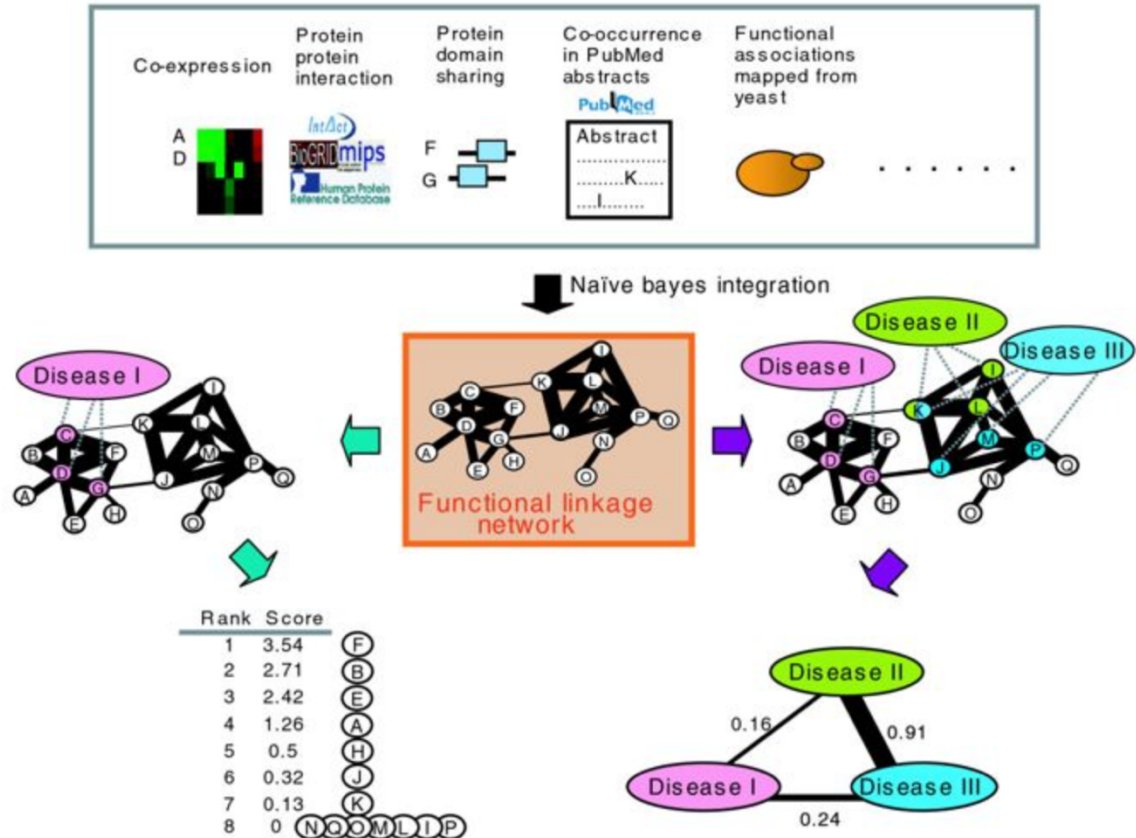
Comment: This is a normal paper trying different algorithms.

3. *Genome-wide prioritization of disease genes and identification of disease-disease associations from an integrated human functional linkage network*. Linghu, 2009.

Link: <https://genomebiology.biomedcentral.com/articles/10.1186/gb-2009-10-9-r91>

Summary: In this paper the authors investigated into the genetic basis of diseases pairs having dissimilar phenotypes, for example, hypercholesterolemia and Alzheimer's diseases.

Method: Network-based approaches. 1. Construct a gene-gene association network based on genomic/proteomic data. 2. Rank candidate genes based on network proximity to known disease associated genes. 3. Construct functional Linked Network in humans.



Comments: Patient Similarity, On the other hand, it is also disease similarity. We may go back to this paper if we want to also draw edges and nodes.

Drawbacks: This paper doesn't provide interactive graph.