



2. Bayesian epistasis; Interaction and causal modeling and discovery

1. Big data science: Efficient probabilistic and deep learning; New algorithms development.



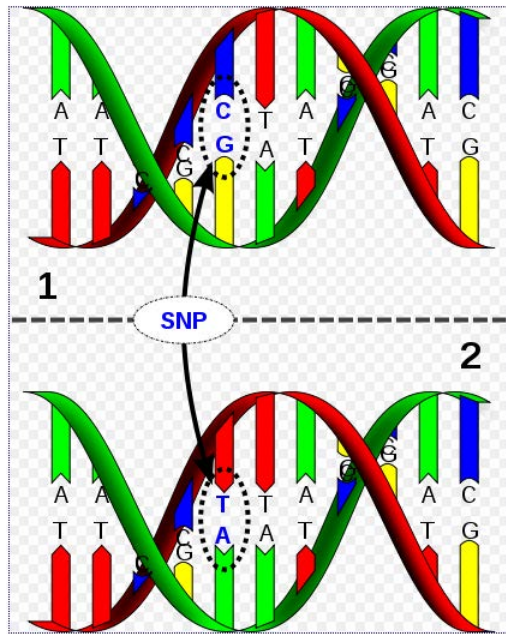
3. AI-based prediction, decision support, and precision and personalized medicine

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Detecting Genome Wide Epistasis with Efficient Bayesian Network Learning

NIH R00, PI: Jiang, Grant Number:R00LM010822



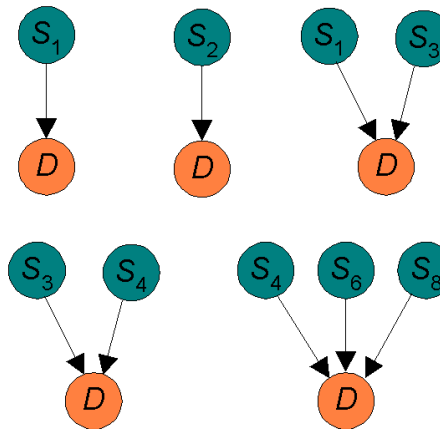
<http://en.wikipedia.org/wiki/File:Dna-SNP.svg>

Challenge: worse than exponential model search space for genetic interactions (multi-SNPs) when learning from high dimensional data

2. Novel score criteria: BNMBL and BNPP

Each of the top 50 models scored by MBS contains at least one of the significant genes associated with breast cancer

Major Contribution



1. BN-Based model representation and definition

3. Novel efficient learning algorithms: MBS, REGAL, LEAP, and IGAIN

We found that SNP rs6094514, which is mapped to the EYA2 gene on chromosome 20, often appeared along with GAB2 in Late Onset Alzheimer's patients.

Jiang et al. BMC Bioinformatics (2011) ;12: 89

Jiang et al. Genetic Epidemiology 2010 34(6) : 578-81

MBS

MBS took 4.1 Hours

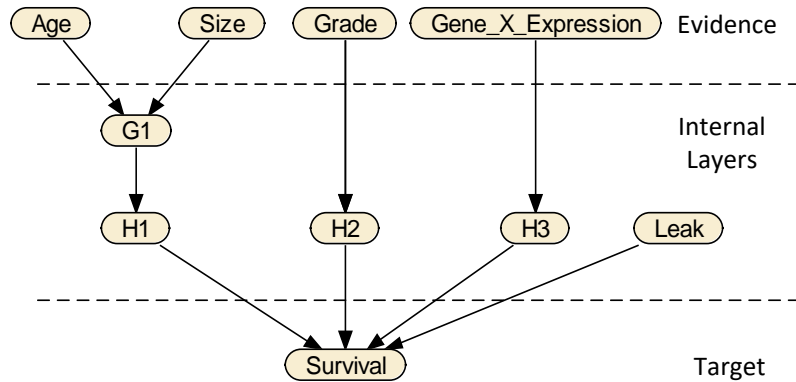
BayCom

BayCom would take 3.71 years

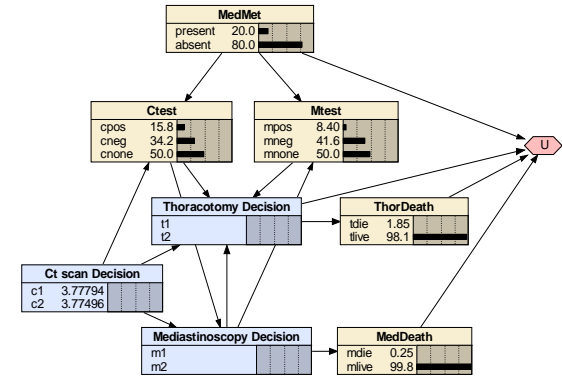
Up to 4 SNPs Combinations with 1001 SNPS

A New Generation Clinical Decision Support System

NIH/NLM R01, Submitting PI: Jiang, Grant Number:R01LM011663



Our CaMIL model for prediction



An influence diagram (developed using Netica)

W81XWH1910495

Challenge 1. Learning interactive causes from datasets is important, but it is by no means a trivial task.

Challenge 2. Big data driven machine learning is not yet fully utilized in medicine.

Leveraging Deep Learning and Bayesian Networks to Identify Risk Factors and Support Personalized Prediction for Metastatic Breast Cancer

DoD BCRP Level II, PI: Jiang, Grant Number:W81XWH1910495

Modeling and Discovery of Biomedical Knowledge (CCMD) from Big Data (BD2K) NIH/NLM BD2K, Role: co-investigator.

Cure grant awarded by the Pennsylvania Department of Health (PA DOH 4100070287). Role: co-investigator.

Long Term Goals for Jiang's AI Lab

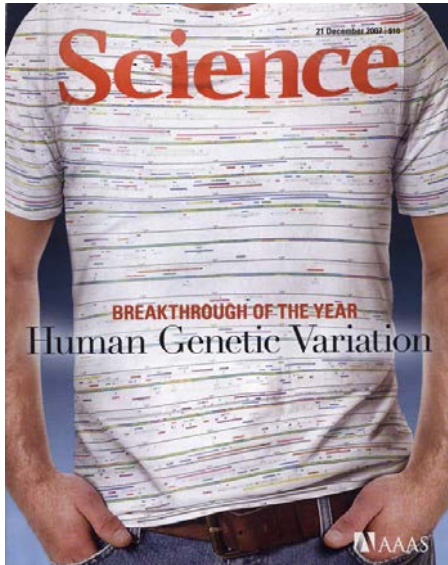


Image source: 21 DECEMBER 2007
VOL 318 SCIENCE

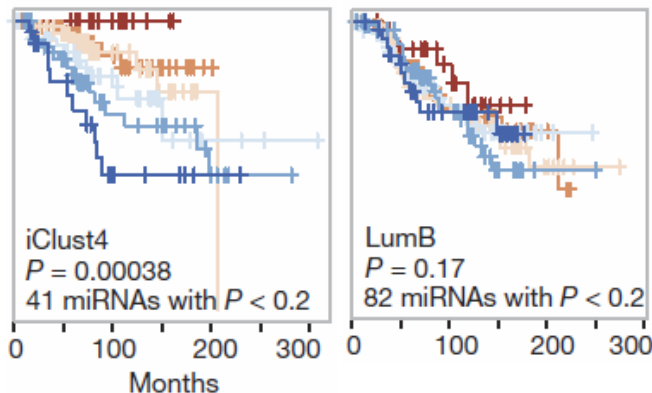
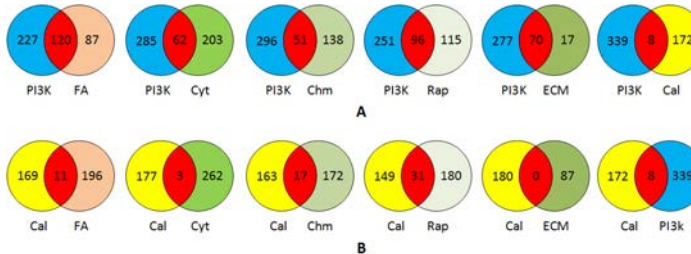
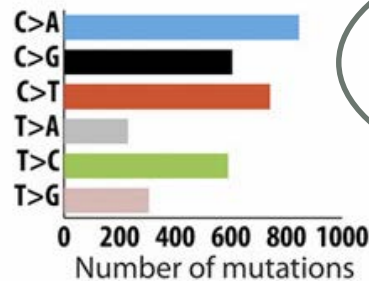


Image source: Dvinge et al. Nature
497.7449 (2013): 378-382



1. Continue to develop new methods to help further out understanding of disease mechanisms.

2. Continue to develop methods to help promote precision health.



Mutational catalogue of a cancer genome

Image source: Alexandrov et al. Cell Reports 3.1 (2013): 246-259

AI and machine learning approach to precision medicine!

3. Continue to tackle challenges of learning from big data.

miRNAs have an increased prognostic value in the genomically stable iClust4