

Haim Bar, University of Connecticut, Statistics Department

Statistical models in genomics applications:

- Model-based, empirical Bayes approach – high power, computationally efficient
- Differential variation
- Wide range of applications – gene expression, methylation, metabolomics, RNA-sequencing data, etc.

Variable selection in the large p , small n setting:

- An efficient method, based on a simple latent class model
- Accounts for correlation between variables (to eliminate multicollinearity)

Haim Bar, University of Connecticut, Statistics Department

Machine learning methods and applications:

- Detect identification regions in statistical and econometric models
- Concept mapping
- Automatic classification of sensitive information (text, sensor data, images)