



Deep Learning based Multi-view Model for Deciphering Genetic Regulatory Keywords

Pramod Bharadwaj Chandrashekar (pbchandr@asu.edu)

Matthew Lee

Li Liu (liliu@asu.edu)

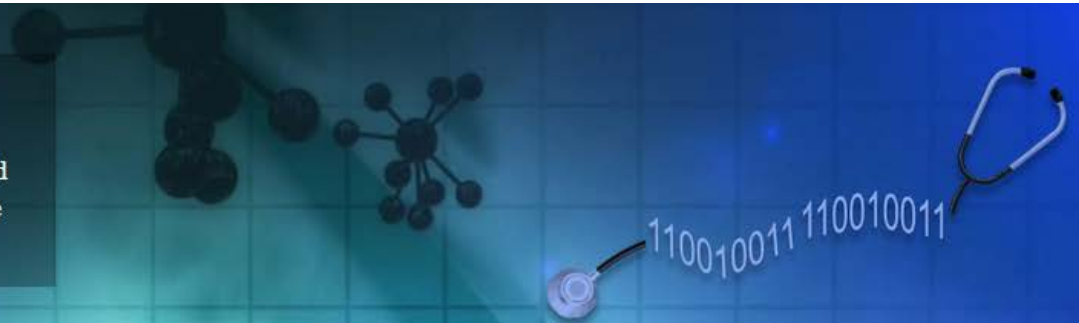
Li Liu's Lab

The laboratory of Li Liu, MD

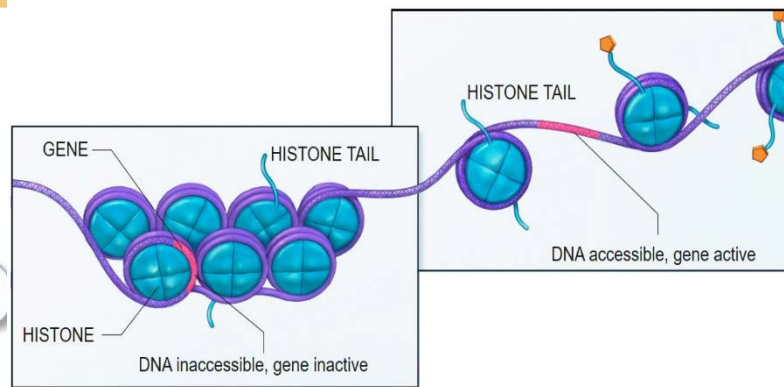
<http://liliulab.com>

Computational Medicine Lab

Address human health challenges with artificial intelligence and molecular evolution. We connect science from bench to bedside with computational innovations.



GENE REGULATORY MECHANISM



- **Gene regulation involves controlling of gene expressions.**

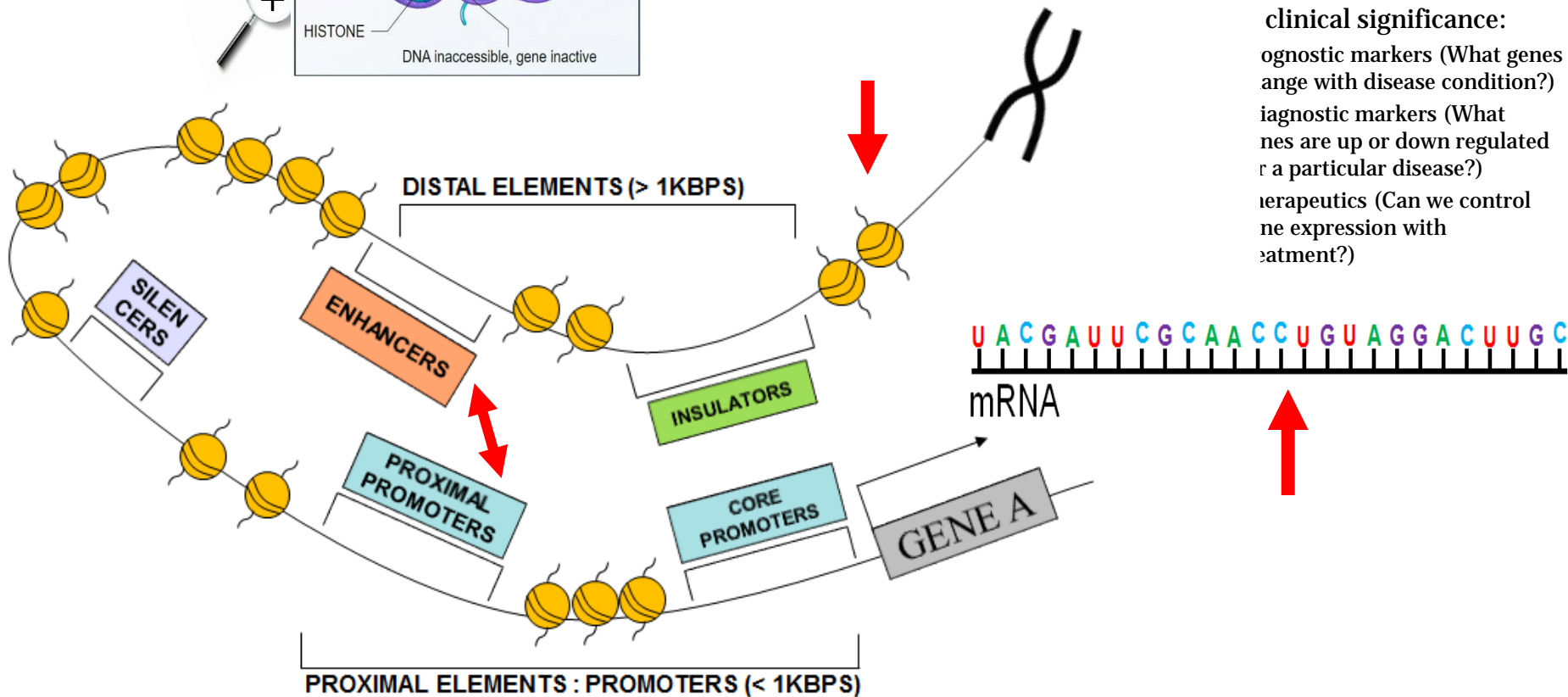
- Key for various traits and diseases

clinical significance:

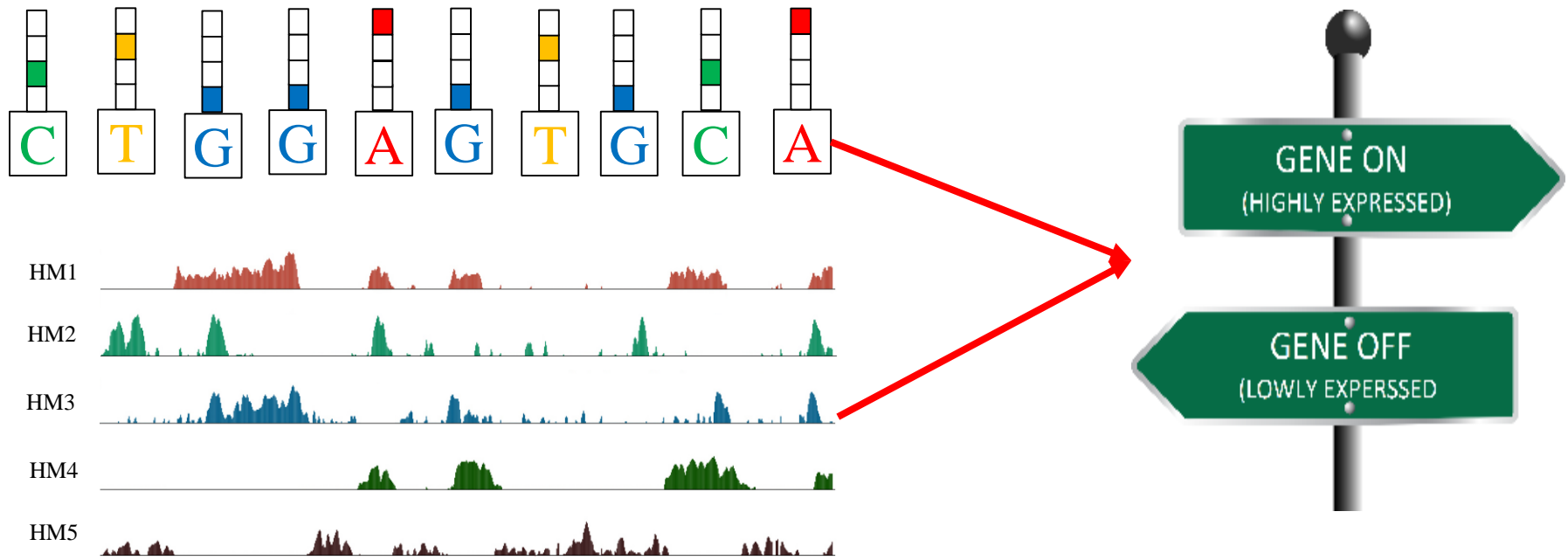
diagnostic markers (What genes are up or down regulated in a particular disease?)

therapeutic markers (What genes are up or down regulated in a particular disease?)

therapeutics (Can we control gene expression with treatment?)



PROBLEM FORMULATION



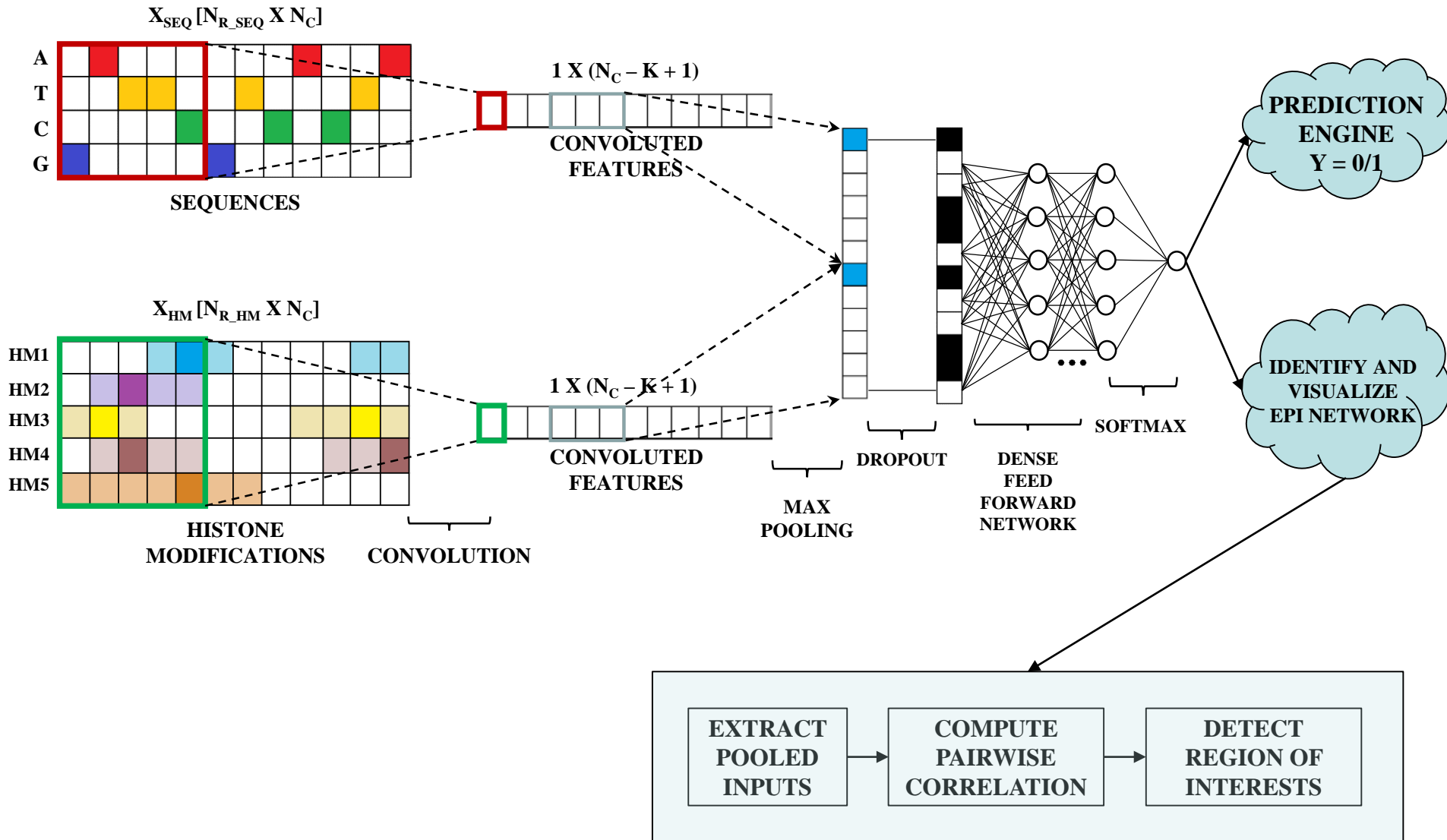
INPUT

- Gene Sequence
 - ± 5000 base pairs around transcription start site
- **Histone Modification ChIP-seq maps**
 - Five Histones: H3K4me1, H3K9me3, H3K27me3, H3K36me3, H3K27ac
 - Read Counts of the histone activity used

OUTPUT

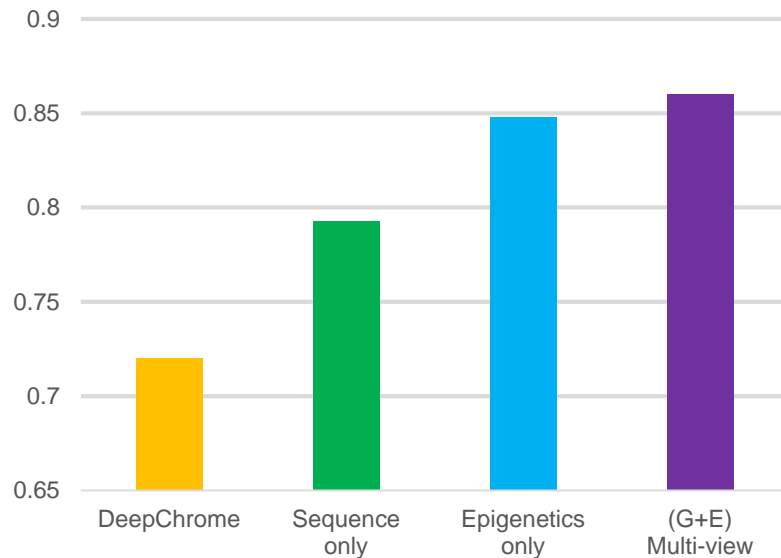
- Discretized RNA-seq signals
 - Gives expression level of genes
 - Median cutoff to discretize into high and low expression

PROPOSED MULTI-VIEW MODEL



RESULTS

AUC scores of various models



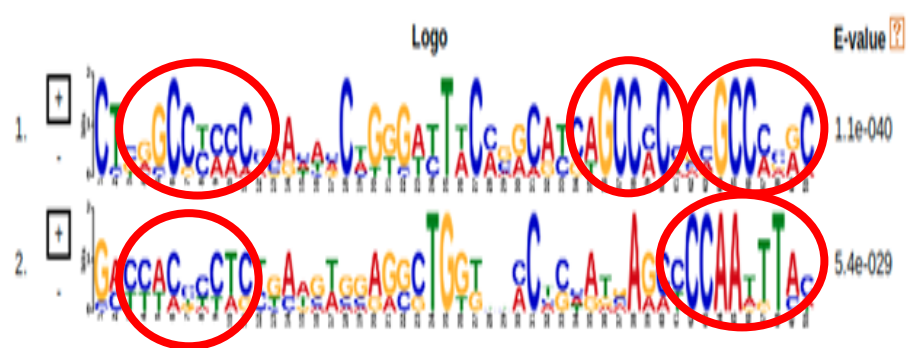
	G + E	DeepChrome
Accuracy	0.7862	0.813
Balanced Accuracy	0.7862	0.518
F1-score	0.7862	0.116
AUC	0.86	0.72

Comparison of various performance metrics between our model and state-of-the-art DeepChrome model

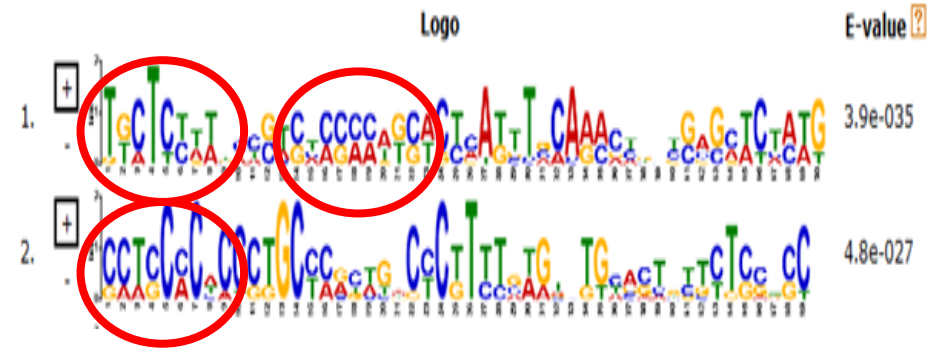
Histone modifications	Low Expression Genes		High Expression Genes	
	Enhancers	Promoters	Enhancers	Promoters
H3K9me3	38	39	0	0
H3K27ac	2	1	88	90
H3K36me3	40	41	10	10
H3K4me1	9	8	2	0
H3K27me3	11	9	0	0

Multi-view model can identify regions with high HM activity

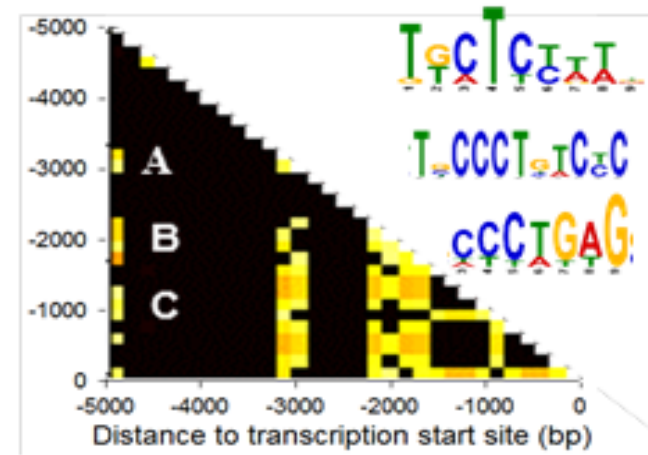
RESULTS



MOTIFS in enhancer regions of randomly selected high expression genes



MOTIFs in promoter regions of randomly selected high expression genes



Enhancer promoter pair for a randomly
select gene (FTL gene)