Prediction problem	Method	Title
Predicting TFBS	CENTIPEDE	Accurate inference of transcription factor binding from DNA sequence and chromatin accessibility data.
	DNase2TF	DNase Footprint Signatures Are Dictated by Factor Dynamics and DNA Sequence.
	PIQ	Discovery of directional and nondirectional pioneer transcription factors by modeling DNase profile magnitude and shape.
	Chromia	Genome-wide prediction of transcription factor binding sites using an integrated model.
	Ramsey et al.	Genome-wide histone acetylation data improve prediction of mammalian transcription factor binding sites.
	Cuellar-Partida et al.	Epigenetic priors for identifying active transcription factor binding sites.
	Arvey et al.	Sequence and chromatin determinants of cell-type–specific transcription factor binding.
	Iterative CENTIPEDE	Which genetics variants in DNase-seq footprints are more likely to alter binding?

	dPCA	Differential principal component analysis of ChIP-seq.
	BIRD (exon array)	Genome-wide prediction of DNase I hypersensitivity using gene expression.
	BIRD (RNA-seq)	Global prediction of chromatin accessibility using RNA-seq from small number of cells.
	Methylphet	Base-resolution methylation patterns accurately predict transcription factor bindings in vivo.
Predicting epigenome	**ChromImpute**	Large-scale imputation of epigenomic datasets for systematic annotation of diverse human tissues.
	BIRD	Genome-wide prediction of DNase I hypersensitivity using gene expression.
	Zhang et al.	Predicting genome-wide DNA methylation using methylation marks, genomic position, and DNA regulatory elements.
	Ma et al.	Predicting DNA methylation level across human tissues.
	Bock et al.	CpG island methylation in human lymphocytes is highly correlated with DNA sequence, repeats, and predicted DNA structure.
	hdfinder	Computational prediction of methylation status in human genomic sequences.

	Yuan	Targeted recruitment of histone modifications in humans predicted by genomic sequences.
	Epigram	Predicting the human epigenome from DNA motifs.
Predicting chromatin conformation	**Huang et al.**	Predicting chromatin organization using histone marks.
	Fortin and Hansen	Reconstructing A/B compartments as revealed by hi-C using long-range correlations in epigenetic data.
Predicting transcriptome	**Ouyang et al.**	ChIP-seq of transcription factors predicts absolute and differential gene expression in embryonic stem cells.
	Natarajan et al.	Predicting cell-type-specific gene expression from regions of open chromatin.
	Karlić et al.	Histone modification levels are predictive for gene expression.
	Dong et al.	Modeling gene expression using chromatin features in various cellular contexts.
	Cheng et al.	A statistical framework for modeling gene expression using chromatin features and application to modENCODE datasets.

Variables			
Predictors	**Response**	**static**	**dynamic**
genome sequence, position weight matrices of TF motifs, proximity to the nearest transcription start site (TSS) and evolutionary sequence conservation Histone modifications ChIP-seq and DNase-seq	TFBS	✓	✓
genome sequence and position weight matrices of TF motifs DNase-seq	TFBS		✓
genome sequence and position weight matrices of TF motifs DNase-seq	TFBS	✓	✓
genome sequence and position weight matrices of TF motifs Histone modifications ChIP-seq	TFBS	✓	✓
genome sequence and position weight matrices of TF motifs Histone acetylation ChIP-seq	TFBS	✓	✓
genome sequence and position weight matrices of TF motifs Histone modifications ChIP-seq and DNase-seq	TFBS	✓	✓
DNA sequence K-mers Histone modifications ChIP-seq and DNase-seq	TFBS	✓	✓
genome sequence, position weight matrices of TF motifs and SNPs DNase-seq	TFBS	✓	✓

genome sequence and position weight matrices of TF motifs Histone modifications and CTCF ChIP-seq, DNase-seq and FAIRE-seq	Differential TFBS between two biological conditions	✓	✓
genome sequence and position weight matrices of TF motifs Predicted DNase I hypersensitivity (based on Exon array)	TFBS	✓	✓
genome sequence and position weight matrices of TF motifs Predicted DNase I hypersensitivity (based on RNA-seq)	TFBS	✓	✓
genome sequence and position weight matrices of TF motifs DNA methylation (whole-genome bisulfite sequencing)	TFBS	✓	✓
Various epigenomic data	Various epigenomic data		✓
Gene expression (exon array)	DNase-Seq		✓
DNA methylation from neighboring CpG sites, genomic position, DNA sequence properties and cis-regulatory elements	Whole-genome DNA methylation	✓	✓
DNA methylation levels in surrogate tissue	DNA methylation level in target tissue		✓
DNA sequence patterns, repeat frequencies, and predicted DNA structure	CpG islands methylation status	✓	✓
Genomic sequence features	Methylation on CpG regions	✓	

Genomic sequence features	Location of histone modification marks	✓	
Genome sequence and DNA motifs	Histone modification and DNA methylation sites	✓	
Histone modifications and CTCF ChIP-seq	chromatin interaction hubs and topologically associated domain boundaries		✓
DNA methylation (from Illumina 450k microarray), DNase-seq, single-cell ATAC-seq and single-cell whole-genome bisulfite sequencing	A/B compartments		✓
Transcription factor ChIP-seq	Gene expression		✓
Genome sequence and position weight matrices of TF motifs DNase-seq	Cell-type-specific expressed genes	✓	✓
Histone modifications ChIP-seq	Gene expression values		✓
Histone modifications ChIP-seq, DNase-seq and normalized CpG score	Binary gene expression and gene expression value		✓
Histone modifications ChIP-seq	Gene exoression values		✓

Feature				Model		
intensity	shape	local	global	supervised	unsupervised	cross-locus
	✓	✓			✓	✓
	✓	✓			✓	✓
✓	✓	✓			✓	✓
✓		✓			✓	✓
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✓		✓		✓		✓
✓		✓		✓		✓

cross-sample
✓

✓
✓
✓
✓
✓

Results validated across different samples
Results validated across different samples