Supplementary Materials for

Computational methods for the prediction of chromatin interaction and organization using sequence and epigenomic profiles

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Table S1 Code availability of computational methods for the prediction of chromatin interaction and organization

Tool Name	URLs	Implementation
Computational methods for the prediction of chromatin interaction		
Unsupervised Methods		
PreSTIGE	http://prestige.case.edu	Web software
ABC	https://github.com/broadinstitute/ABC-Enhancer-Gene-Prediction	Python
Ernst et al.	/	/
Thurman et al.	/	/
ELMER	https://github.com/lijingya/ELMER http://bioconductor.org/packages/ELMER	R
Naville et al.	https://github.com/DyogenIBENS/Regulus	Python
CISMAPPER	/	/
Cicero	https://github.com/cole-trapnell-lab/cicero-release	R
C3D	https://github.com/LupienLab/C3D	BASH and R
EpiTensor	/	MACS2
CITD	https://cb.utdallas.edu/CITD/index.htm	/
SWIPE-NMF	https://github.com/kaiyuanmifen/SWIPE-NMF	R
Supervised Methods		
JEME	https://github.com/yiplabcuhk/JEME/	R, Weka
FOCS	https://github.com/Shamir-Lab/FOCS	R
IM-PET	www.healthcare.uiowa.edu/labs/tan/IM-PET_Package.tgz	/
RIPPLE	http://pages.discovery.wisc.edu/~sroy/ripple/download.html	C++, Matlab
PETModule	http://hulab.ucf.edu/research/projects/PETModule/	Python
TargetFinder	https://github.com/shwhalen/targetfinder	Python
McEnhancer	https://ohlerlab.mdc-berlin.de/software/McEnhancer_134/	Python
CISD	https://github.com/huizhangucas/CISD	BASH, R
EP_Bayes	https://github.com/ManchesterBioinference/EP_Bayes	Python, R

3DEpiLoop	https://bitbucket.org/4dnucleome/3depiloop	R
Multi-levels 3D	/	/
CRUP	https://github.com/VerenaHeinrich/CRUP https://zenodo.org/record/3469676#.XzOQyDMpWmQ	R
EAGLE	https://github.com/EvansGao/EAGLE	Perl, Matlab
DeepTACT	/	/
EPIP	http://www.cs.ucf.edu/~xiaoman/EPIP/	Python
3DPredictor	https://github.com/labdevgen/3Dpredictor	Python, R, Java
PEP	http://acgt.cs.tau.ac.il/focs	Python
EPIANN	https://github.com/wgmao/EPIANN	Python, R
EP2vec	https://github.com/wanwenzeng/ep2vec	Python
SPEID	https://github.com/macompbio/	Python
EnContact	https://github.com/liwenran/EnContact	Python
Computational methods for the prediction of chromatin organization		
Loops		
CISD-loop	https://github.com/huizhangucas/CISD	BASH and R
CTCF-MP	https://github.com/ma-compbio/CTCF-MP	Python
Lollipop	https://github.com/ykai16/Lollipop	Python
DeepMILO	https://github.com/khuranalab/DeepMILO	Python
TADs		
CITD	https://cb.utdallas.edu/CITD/index.htm	/
PGSA	/	/
TAD–Lactuca	https://github.com/LoopGan/TAD-Lactuca	Python
nTDP	http://www.cs.cmu.edu/~ckingsf/research/ntdp	Python
BART	https://github.com/huangjialiangcn/HubPredictor	R
Contact map		
Rambutan	/	/

Farré et al.	Keras package (https://github.com/keras-team/ keras) TensorFlow (https://www.tensorflow.org/).	Python
Akita	https://github.com/calico/basenji/tree/master/manuscripts/akita	Python
DeepC	https://github.com/rschwess/deepC	Python, tensorflow, R and Perl
3D structures		
MiChroM	/	/
HiP-HoP	https://www.sciencedirect.com/science/article/pii/S1097276518307871?via%3Dihub#sec4.1c	LAMMPS, Bowtie2, SAMtools, BEDtools, MACS2. etc.
Chromatin states-based model	https://github.com/ZhangGroup-MITChemistry/DRAGON	LAMMPS
Bkhetan et al.	/	/

Table S2 Required input data of computational methods for the prediction of chromatin interaction and organization

	DNA sequence	DNA methylation	Distance	CTCF	Cohesin	p300	RNAP II	TF binding	Chromatin Accessibility				Histone Marks				TAD	HiC	Gene Expression
									DHS	ATAC-seq	MNase-seq	FAIRE-seq	H3K4me1	H3K4me3	H3K27ac	Other			
Computational methods for the prediction of chromatin interaction																			
PreSTIGE			√	√									√						√
ABC			√	√					√	/√					√			/	/
Ernst et al.			√	√			√	√					√	√	√	√			√
Thurman et al.		√	√					√	√					√					√
ELMER		√																	√
Naville et al.			√			√		√	√				√	√	√				
CISMAPPER			/					√						/	√	/			√
Cicero			√							√									
C3D									√										
EpiTensor									√				√	√	√	√	√		√
CITD				√				√					√	√	√	√			√
SWIPE-NMF				√				√	√				√	√	√	√	√	√	√
JEME		√	√						√				√	√	√				√
FOCS		√	√						√										√
IM-PET	√		√			√		√	/				√	√	√				√
RIPPLE								√	√				√	√	√	√			√
PETModule			√			√		√	√										
TargetFinder		√		√	√	√		√	√			√	√	√	√	√			√

McEnhancer	√								√										
CISD											√							√	
EP_Bayes	√						√							√		√			√
3DEpiLoop			√	√	√		√	√					√			√	√	√	
Multi-levels 3D			√										√	√	√	√	√	√	
CRUP													√	√	√	√		/	√
EAGLE			√			√		√	√	/√		√	√		√				√
DeepTACT	√								√										
3DPredictor			√	√															√
EPIP			√						√				√	√	√				
PEP	√																		
EPIANN	√																		
EP2vec	√																		
SPEID	√																		
EnContact	√																		
Computational methods for the predictioin of chromatin organization																			
CISD-loop											√							√	
CTCF-MP	√		√	√					√										
Lollipop				√	√				√				√	√	√	√			√
DeepMILO	√			√															
CITD				√				√					√	√	√	√			√
PGSA				√				√	√							√			

TAD–Lactuca	√			√									√	√	√	√			
nTDP									/				√	√	/	√			
BART	/			√									√	√	√	√			
Rambutan	√								√										
Farré et al.	√			√			√	√					√	√	√	√			
Akita	√																		
DeepC	√																		
MiChroM													√	√	√	√			
HiP-HoP				√	/					√					√				
Chromatin states-Based model				√	/				√				√	√	√	√			
Bkhetan et al.	√			√	√		/	√					√	√		√			

(/ presents optional, /√ presents or)

Table S3 Databases of available predictions supplied by computational methods

Number	Tool Name	Brief Description	URLs
1	PreSTIGE	Predicted enhancer-gene pairs for 13 cell lines	https://genetics.cwru.edu/prestige/
2	JEME	Enhancer-promoter network in 935 samples of human primary cells, tissues and cell lines	http://yiplab.cse.cuhk.edu.hk/jeme/
3	FOCS	Extensive enhancer–promotor maps of 2630 samples taken from ENCODE, Roadmap Epigenomics, FANTOM5, and a new compendium of GRO-seq	http://acgt.cs.tau.ac.il/focs/
4	EnContact	1,545,180 positive EEI predicted in seven cell lines	https://github.com/liwenran/EnContact
5	EAGLE	7,680,203 enhancer-gene interactions involving 31,375 genes and 138,547 enhancers across 89 tissue/cell types in mouse; 7,437,255 enhancer-gene interactions involving 43,724 genes and 177,062 enhancers across 110 tissue/cell types in human	https://enhanceratlas.org/
6	CITD	Chromatin interaction, topological domains and their states on 100 cell types from ENCODE and Roadmap with different resolutions	https://cb.utdallas.edu/CITD/index.htm
7	PETModule	Predicted ETGs in 8 human cells and 2 mouse cells	http://hulab.ucf.edu/research/projects/PETModule/
8	SWIPE-NMF	Enhancer-promoter network in 127 human cell lines	https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/DNBBB2