

Table S1. Recent approaches for integrative inference of context-specific gene regulatory networks

Fields	Description	Notes
Category	Paper selection criteria	
Author	First author et al, year	
Method name	Name of the method, if available	
Algorithm/Methodology	Algorithms	
	gene expression	mRNA expression or perturbation
	ChIP	Use of TF ChIP-seq
	Motif	Use of TF motifs
Data types	Histone mark	Use of histone mark ChIP-seq
	Accessibility	Use of DNase-seq, ATAC-seq, DNA methylation
	3C	Use of chromatin conformation capture (3C) techniques
	Prior	Use of structure or parameter prior
Output	Short description of the output result	

Category	Author	Method name (if designated)	Algorithm/Methodology	Data types							Output
				gene expression	ChIP	Motif	Histone mark	Accessibility	3C	Prior	
Integrating data to infer genome-scale context-specific transcriptional regulatory networks	Ament et al., 2018		LASSO regression	microarray RNA-seq		Y		DNase-seq			GRN for HD in mouse
	Chasman et al., 2019	MERLIN-P	dependency network	RNA-seq		Y		DNase-seq		Y	GRN in human neuronal stem cell lineage
	Miraldi et al., 2019	mLASSO-StARS	dependency network	RNA-seq		Y		ATAC-seq		Y	GRN in human Th 17 cells
	Mallm et al., 2019		Mutual Information (ARACNe-AP)	RNA-seq	Y	Y	Y	DNA methylation, ATAC-seq			GRN in human B-cells
	Pearl et al., 2019		Pearson, LASSO regression	microarray		Y		DNase-seq			Human brain GRN
	Wang et al., 2018	NetRex	linear model	RNA-seq						Y	Drosophila GRN
	Deng et al., 2018	JRmGRN	Gaussian Graphical Model	RNA-seq							GRN in Arabidopsis in multiple conditions
	Tu et al., 2020	NETI2	Gaussian Graphical Model	RNA-seq							A non-cancer network and multiple cancer networks
	Zhou et al., 2020	FSSEM	Structural Equation Model	RNA-seq							GRN under two conditions
	Castro et al., 2019	Inferelator-AMuSR	regularized linear regression, multi-task learning	microarray		Y		ATAC-seq		Y	GRN in Yeast and Bacteria
	Osmanbeyoglu et al., 2019	PSIONIC	multi-task learning	RNA-seq		Y		ATAC-seq			Tumor-specific GRN
Data integration for predicting cis-regulatory elements controlling expression of target genes	Hait et al., 2018	FOCS	elastic net regression	RNA-seq				DNase-seq			enhancer-promoter interactions
	Vijayabaskar et al., 2019		LASSO regression	RNA-seq	Y		Y	DNase-seq			cis-regulatory network
	Tong et al., 2018	MICMIC	Mutual Information	RNA-seq				DNA methylation			cancer driver methylated region-target genes network
	Fulco et al., 2019	ABC model	Activity-by-contact	RNA-seq			Y	Dnase-seq	Hi-C		enhancer-promoter interactions
	Singh et al., 2019	SPEID	deep neural net		Y		Y	DNase-seq	Hi-C		enhancer-promoter interactions
	Li et al., 2019	DeepTACT	deep neural net					DNase-seq	PChI-C		enhancer-promoter interactions
	Talukder et al., 2019	EPIP	AdaBoost		Y		Y	DNase-seq	Hi-C		enhancer-promoter interactions
	Zhang et al., 2019	HiC-Reg	random forest regression		Y	Y	Y	DNase-seq	Hi-C		Hi-C contact counts
Methods to learn regulatory networks from single cell omic data types	Belokopytova et al., 2020	3DPredictor	Gradient boosting	RNA-seq	Y	Y			Hi-C		Hi-C contact counts
	González-Bias et al., 2020	ScoMAP	dependency network, LDA, random forest regression	scRNA-seq		Y		scATAC-seq			enhancer-gene networks, scATAC-seq, scRNA-seq cell clusters, GRN
	Jansen et al., 2019	SOMatic	Self-organizing maps	scRNA-seq	Y	Y		scATAC-seq			scATAC-seq, scRNA-seq cell clusters, GRN
	Zeng et al., 2019	DC3	Matrix factorization	scRNA-seq		Y		scATAC-seq	HiChIP		single cell population-specific network