

CITATION REPORT

List of articles citing

Gene regulatory network inference: data integration in dynamic models-a review

DOI: 10.1016/j.biosystems.2008.12.004
BioSystems, 2009, 96, 86-103.

Source: <https://exaly.com/paper-pdf/46536764/citation-report.pdf>

Version: 2024-04-28

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
622	Genome-wide strategies for discovering genetic influences on cognition and cognitive disorders: methodological considerations. 2009 , 14, 391-418		83
621	Gene Regulatory Network Inference Using Predictive Minimum Description Length Principle and Conditional Mutual Information. 2009 ,		3
620	Integrative modeling of transcriptional regulation in response to antirheumatic therapy. 2009 , 10, 262		30
619	Identification of neutral biochemical network models from time series data. 2009 , 3, 47		35
618	Adapted Boolean network models for extracellular matrix formation. 2009 , 3, 77		14
617	Reverse engineering and verification of gene networks: principles, assumptions, and limitations of present methods and future perspectives. 2009 , 144, 190-203		55
616	Inference of gene regulatory networks using boolean-network inference methods. 2009 , 7, 1013-29		36
615	Computational approaches to the integration of gene expression, ChIP-chip and sequence data in the inference of gene regulatory networks. 2009 , 20, 863-8		9
614	Inference of Differential Equation Models by Multi Expression Programming for Gene Regulatory Networks. 2009 , 974-983		2
613	Selection of negative examples in learning gene regulatory networks. 2009 ,		4
612	Computational methods for discovering gene networks from expression data. 2009 , 10, 408-23		135
611	BACK MATTER. 2010 , 279-322		
610	Biomarkers for Environmental Exposure. 2010 , 517-547		3
609	Systems biology and modeling in neuroblastoma: practicalities and perspectives. 2010 , 10, 131-45		8
608	Challenges in Understanding Genome-Wide DNA Methylation. 2010 , 25, 26-34		4
607	A neural network based modeling and validation approach for identifying gene regulatory networks. 2010 , 73, 2419-2429		11
606	Synchronization of stochastic genetic oscillator networks with time delays and Markovian jumping parameters. 2010 , 73, 2532-2539		42

605	Learning gene regulatory networks from only positive and unlabeled data. 2010 , 11, 228		61
604	Time lagged information theoretic approaches to the reverse engineering of gene regulatory networks. 2010 , 11 Suppl 6, S19		16
603	Integrative inference of gene-regulatory networks in Escherichia coli using information theoretic concepts and sequence analysis. 2010 , 4, 116		23
602	Regulatory network modelling of iron acquisition by a fungal pathogen in contact with epithelial cells. 2010 , 4, 148		31
601	Prediction of kinetic parameters from DNA-binding site sequences for modeling global transcription dynamics in Escherichia coli. 2010 , 12, 196-211		13
600	Stochastic models for inferring genetic regulation from microarray gene expression data. <i>BioSystems</i> , 2010 , 99, 192-200	1.9	12
599	A novel gene network inference algorithm using predictive minimum description length approach. 2010 , 4 Suppl 1, S7		22
598	. 2010 ,		15
597	A top-performing algorithm for the DREAM3 gene expression prediction challenge. 2010 , 5, e8944		9
596	Using effective subnetworks to predict selected properties of gene networks. 2010 , 5, e13080		4
595	DREAM4: Combining genetic and dynamic information to identify biological networks and dynamical models. 2010 , 5, e13397		140
594	Cross-platform microarray data normalisation for regulatory network inference. 2010 , 5, e13822		17
593	TRANSWESD: inferring cellular networks with transitive reduction. 2010 , 26, 2160-8		23
592	Pattern Recognition in Bioinformatics. 2010 ,		1
591	From digital genetics to knowledge discovery: Perspectives in genetic network understanding. 2010 , 14, 173-191		4
590	Effects of cDNA microarray time-series data size on gene regulatory network inference accuracy. 2010 ,		0
589	Learning gene regulatory networks based on Dempster-Shafer evidence theory. 2010 ,		
588	Evaluating the performance of partitioning techniques for gene network inference. 2010 ,		2

587	Developing computational model-based diagnostics to analyse clinical chemistry data. 2010 , 11, 403-16	6
586	Gene Networks Validation based on Metabolic Pathways. 2011 ,	
585	Gene expression complex networks: synthesis, identification, and analysis. 2011 , 18, 1353-67	31
584	Improvement of GNs inference through biological data integration. 2011 ,	1
583	Hybrid Artificial Intelligent Systems. 2011 ,	
582	Mathematical modeling of gene expression: a guide for the perplexed biologist. 2011 , 46, 137-51	88
581	Molecular mechanisms of muscle plasticity with exercise. 2011 , 1, 1383-412	59
580	Gene network modelling using computational method by integrating with prior knowledge. 2011 ,	
579	Tackling the DREAM Challenge for Gene Regulatory Networks Reverse Engineering. 2011 , 372-382	1
578	Reverse-engineering biological interaction networks from noisy data using Regularized Least Squares and Instrumental Variables. 2011 ,	0
577	Time-seriesBased prediction of complex oscillator networks via compressive sensing. 2011 , 94, 48006	76
576	On the way toward systems biology of <i>Aspergillus fumigatus</i> infection. 2011 , 301, 453-9	10
575	The role of the transcription factor Miz-1 in lymphocyte development and lymphomagenesis-Binding Myc makes the difference. 2011 , 23, 379-87	25
574	Stages of Gene Regulatory Network Inference: the Evolutionary Algorithm Role. 2011 ,	5
573	Role of SPI-1 secreted effectors in acute bovine response to <i>Salmonella enterica</i> Serovar Typhimurium: a systems biology analysis approach. 2011 , 6, e26869	33
572	Control Engineering Approaches to Reverse Engineering Biomolecular Networks. 2011 , 83-113	
571	On Sparsity as a Criterion in Reconstructing Biochemical Networks. 2011 , 44, 11672-11678	6
570	Plant systems biology: network matters. 2011 , 34, 535-53	63

569	Where systems biology meets postharvest. 2011 , 62, 223-237		46
568	Dynamic gene network reconstruction from gene expression data in mice after influenza A (H1N1) infection. 2011 , 1, 27		11
567	Inference of complex biological networks: distinguishability issues and optimization-based solutions. 2011 , 5, 177		51
566	A computational framework for gene regulatory network inference that combines multiple methods and datasets. 2011 , 5, 52		26
565	Regulatory link mapping between organisms. 2011 , 5 Suppl 1, S4		
564	Constraint-based analysis of gene interactions using restricted boolean networks and time-series data. 2011 , 5 Suppl 2, S5		8
563	Reconstructing genome-wide regulatory network of E. coli using transcriptome data and predicted transcription factor activities. 2011 , 12, 233		40
562	Proteomics of a plant pathogen: <i>Agrobacterium tumefaciens</i> . 2011 , 11, 3134-42		4
561	Reverse engineering adverse outcome pathways. 2011 , 30, 22-38		65
560	A multiorganism based method for Bayesian gene network estimation. <i>BioSystems</i> , 2011 , 103, 425-34	1.9	1
559	Diversity of temporal correlations between genes in models of noisy and noiseless gene networks. <i>BioSystems</i> , 2011 , 104, 136-44	1.9	3
558	Robust dynamical network structure reconstruction. 2011 , 47, 1230-1235		81
557	Identification of key mechanisms controlling gene expression in <i>Leishmania</i> infected macrophages using genome-wide promoter analysis. 2011 , 11, 769-77		1
556	Inference of gene regulatory networks with the strong-inhibition Boolean model. 2011 , 13, 083002		5
555	Data Integration in Functional Analysis of MicroRNAs. 2011 , 6, 462-472		4
554	High Dimensional ODEs Coupled with Mixed-Effects Modeling Techniques for Dynamic Gene Regulatory Network Identification. 2011 , 106, 1242-1258		53
553	Network Reconstruction Based on Evolutionary-Game Data via Compressive Sensing. 2011 , 1,		74
552	Information Processing and Biological Systems. 2011 ,		2

551	Recurrent neural network for non-smooth convex optimization problems with application to the identification of genetic regulatory networks. 2011 , 22, 714-26	159
550	Inferring Gene Networks using Robust Statistical Techniques. 2011 , 10,	
549	Efficient reverse-engineering of a developmental gene regulatory network. 2012 , 8, e1002589	68
548	Genome scale inference of transcriptional regulatory networks using mutual information on complex interactions. 2012 ,	1
547	EFFECTIVE MODELS FOR GENE NETWORKS AND THEIR APPLICATIONS. 2012 , 07, 41-70	4
546	Reconstruction of large-scale gene regulatory networks using Bayesian model averaging. 2012 , 11, 259-65	15
545	Robust Approaches for Genetic Regulatory Network Modeling and Intervention: A review of recent advances. 2012 , 29, 66-76	13
544	Array-based approaches to bacterial transcriptome analysis. 2012 , 151-182	3
543	Multivariate Mutual Information Measures for Discovering Biological Networks. 2012 ,	3
542	Network analysis of transcriptional regulation in response to intramuscular interferon- β a multiple sclerosis treatment. 2012 , 12, 134-46	26
541	Reconstructing dynamic gene regulatory network for the development process of hepatocellular carcinoma. 2012 ,	1
540	Transcriptional network inference from functional similarity and expression data: a global supervised approach. 2012 , 11, Article 2	7
539	The autoimmune tautology: an in silico approach. 2012 , 2012, 792106	4
538	Learning transcriptional regulation on a genome scale: a theoretical analysis based on gene expression data. 2012 , 13, 150-61	17
537	Reconstructing dynamic gene regulatory networks from sample-based transcriptional data. 2012 , 40, 10657-67	24
536	Network Inference and Biological Dynamics. 2012 , 6, 1209-1235	44
535	Systems biology of fungal infection. 2012 , 3, 108	49
534	Development: Multiscale CSBSimulation Tools. 2012 , 87-102	1

533	Data simulation and regulatory network reconstruction from time-series microarray data using stepwise multiple linear regression. 2012 , 1, 3-17	11
532	Bioprocess systems engineering: transferring traditional process engineering principles to industrial biotechnology. 2012 , 3, e201210022	39
531	Reverse engineering of gene regulatory networks from biological data. 2012 , 2, 365-385	9
530	From genotype to phenotype: can systems biology be used to predict <i>Staphylococcus aureus</i> virulence?. 2012 , 10, 791-7	54
529	Rule-based modeling of signal transduction: a primer. 2012 , 880, 139-218	19
528	Predicting Phenotype from Genotype through Automatically Composed Petri Nets. 2012 , 87-106	5
527	Computational Modeling of Signaling Networks. 2012 ,	4
526	Omics Techniques in Crop Research: An Overview. 2012 , 289-300	0
525	Multi-scale modeling of gene regulatory networks via integration of temporal and topological biological data. 2012 , 2012, 1242-5	
524	Assessing the gain of biological data integration in gene networks inference. 2012 , 13 Suppl 6, S7	6
523	The extended TILAR approach: a novel tool for dynamic modeling of the transcription factor network regulating the adaption to in vitro cultivation of murine hepatocytes. 2012 , 6, 147	12
522	Analysis and practical guideline of constraint-based boolean method in genetic network inference. 2012 , 7, e30232	6
521	Genome-Wide Scale-Free Network Inference for <i>Candida albicans</i> . 2012 , 3, 51	23
520	An Interspecies Regulatory Network Inferred from Simultaneous RNA-seq of <i>Candida albicans</i> Invading Innate Immune Cells. 2012 , 3, 85	103
519	Haploid evolutionary constructor: new features and further challenges. 2011 , 11, 125-35	4
518	Microbial interactions: from networks to models. 2012 , 10, 538-50	1607
517	Identification of aberrant pathways and network activities from high-throughput data. 2012 , 13, 406-19	19
516	Epigenetic memories: structural marks or active circuits?. 2012 , 69, 2189-203	9

515	The Regulatory Network Computational Device. 2012 , 13, 339-375	8
514	Inferring gene regulatory networks using a hybrid GABS0 approach with numerical constraints and network decomposition. 2012 , 188, 80-99	23
513	Importance of metabolic coupling for the dynamics of gene expression following a diauxic shift in <i>Escherichia coli</i> . 2012 , 295, 100-15	11
512	Generating stochastic gene regulatory networks consistent with pathway information and steady-state behavior. 2012 , 59, 1701-10	4
511	Regulatory interactions for iron homeostasis in <i>Aspergillus fumigatus</i> inferred by a Systems Biology approach. 2012 , 6, 6	33
510	The evolution of higher-level biochemical reaction models. 2012 , 13, 3-31	2
509	Computational regulatory network construction from microRNA and transcription factor perspectives. 2013 , 3, 1-5	
508	Bioinformatics Research and Applications. 2013 ,	
507	Inference of dynamical gene-regulatory networks based on time-resolved multi-stimuli multi-experiment data applying NetGenerator V2.0. 2013 , 7, 1	96
506	Derivative-variable correlation reveals the structure of dynamical networks. 2013 , 86, 1	7
505	Systems Biology. 2013 ,	8
504	A review of spatial computational models for multi-cellular systems, with regard to intestinal crypts and colorectal cancer development. 2013 , 66, 1409-62	40
503	Network-based approaches in drug discovery and early development. 2013 , 94, 651-8	62
502	Using gene expression programming to infer gene regulatory networks from time-series data. 2013 , 47, 198-206	15
501	Reconstruction of Triple-wise Relationships in Biological Networks from Profiling Data. 2013 , 205-215	
500	Topics in Applied Statistics. 2013 ,	0
499	Gene regulatory network inference by point-based Gaussian approximation filters incorporating the prior information. 2013 , 2013, 16	1
498	Dynamic modelling of microRNA regulation during mesenchymal stem cell differentiation. 2013 , 7, 124	16

497	Dynamical models of biomarkers and clinical progression for personalized medicine: the HIV context. 2013 , 65, 954-65	11
496	Novel recurrent neural network for modelling biological networks: oscillatory p53 interaction dynamics. <i>BioSystems</i> , 2013 , 114, 191-205	1.9 22
495	Cyclic graphs with noisy-max structures and its modeling on signaling pathways. 2013 ,	
494	A framework for integrative analysis of transcriptional and post-transcriptional gene regulation. 2013 ,	
493	Incremental updating approximations in dominance-based rough sets approach under the variation of the attribute set. 2013 , 40, 17-26	79
492	Modeling and inference of genetic interactions. 2013 , 3, 453-466	
491	Systems approaches in understanding evolution and evolvability. 2013 , 113, 369-74	2
490	Microbial evolution in vivo and in silico: methods and applications. 2013 , 5, 262-77	12
489	Yeast Systems Biology. 2013 , 343-365	6
488	Gene regulatory networks inference using a multi-GPU exhaustive search algorithm. 2013 , 14 Suppl 18, S5	18
487	Learning sparse Fuzzy Cognitive Maps by Ant Colony Optimization. 2013 ,	
486	Reconstructing regulatory networks from the dynamic plasticity of gene expression by mutual information. 2013 , 41, e97	31
485	Comparative analysis of network algorithms to address modularity with gene expression temporal data. 2013 ,	
484	Reverse-engineering post-transcriptional regulation of gap genes in <i>Drosophila melanogaster</i> . 2013 , 9, e1003281	31
483	Reconstruction and analysis of nutrient-induced phosphorylation networks in <i>Arabidopsis thaliana</i> . 2013 , 4, 540	18
482	Robust data-driven incorporation of prior knowledge into the inference of dynamic regulatory networks. 2013 , 29, 1060-7	98
481	Computational Translation of Nonmammalian Species Data to Mammalian Species to Meet REACH and Next Generation Risk Assessment Needs. 2013 , 113-136	1
480	GRN2SBML: automated encoding and annotation of inferred gene regulatory networks complying with SBML. 2013 , 29, 2216-7	4

479	Reverse engineering cellular networks with information theoretic methods. 2013 , 2, 306-29	47
478	Optimal sparsity criteria for network inference. 2013 , 20, 398-408	11
477	Prior Knowledge Driven Causality Analysis in Gene Regulatory Network Discovery. 2013 ,	
476	Growing seed genes from time series data and thresholded Boolean networks with perturbation. 2013 , 10, 37-49	9
475	Integrating epigenetic prior in dynamic Bayesian network for gene regulatory network inference. 2013 ,	4
474	Genetic programming with genetic regulatory networks. 2013 ,	2
473	On the necessity of full-state measurement for state-space network reconstruction. 2013 ,	6
472	Reverse-engineering the genetic circuitry of a cancer cell with predicted intervention in chronic lymphocytic leukemia. 2013 , 110, 459-64	19
471	Model discrimination in dynamic molecular systems: application to parotid de-differentiation network. 2013 , 20, 524-39	3
470	Inferring gene correlation networks from transcription factor binding sites. 2013 , 88, 301-9	5
469	Breeding and Genetics Symposium: networks and pathways to guide genomic selection. 2013 , 91, 537-52	46
468	Global Network Alignment Method Using Node Similarity Based on Network Characteristics. 2013 , 6, 2-8	
467	Integrated analysis of transcriptomic and proteomic data. 2013 , 14, 91-110	244
466	Modeling regulatory cascades using Artificial Neural Networks: the case of transcriptional regulatory networks shaped during the yeast stress response. 2013 , 4, 110	5
465	Systems Modeling at Multiple Levels of Regulation: Linking Systems and Genetic Networks to Spatially Explicit Plant Populations. 2013 , 2, 16-49	4
464	Biochemical Systems Theory: A Review. 2013 , 2013, 1-53	85
463	Modeling signal transduction from protein phosphorylation to gene expression. 2014 , 13, 59-67	3
462	Refining ensembles of predicted gene regulatory networks based on characteristic interaction sets. 2014 , 9, e84596	

461	Regulatory networks controlling nitrogen sensing and uptake in <i>Candida albicans</i> . 2014 , 9, e92734	39
460	Discovery of possible gene relationships through the application of self-organizing maps to DNA microarray databases. 2014 , 9, e93233	15
459	Network reconstruction using nonparametric additive ODE models. 2014 , 9, e94003	17
458	Modeling genome-wide dynamic regulatory network in mouse lungs with influenza infection using high-dimensional ordinary differential equations. 2014 , 9, e95276	11
457	Inferring cell-scale signalling networks via compressive sensing. 2014 , 9, e95326	1
456	MIDER: network inference with mutual information distance and entropy reduction. 2014 , 9, e96732	82
455	Gene network biological validity based on gene-gene interaction relevance. 2014 , 2014, 540679	5
454	Exact and heuristic methods for network completion for time-varying genetic networks. 2014 , 2014, 684014	2
453	Gene regulatory networks and their applications: understanding biological and medical problems in terms of networks. 2014 , 2, 38	86
452	The gene regulatory network for breast cancer: integrated regulatory landscape of cancer hallmarks. 2014 , 5, 15	42
451	Interactive exploration of integrated biological datasets using context-sensitive workflows. 2014 , 5, 21	4
450	Foundations for modeling the dynamics of gene regulatory networks: a multilevel-perspective review. 2014 , 12, 1330003	10
449	Systems Biology of Infectious Diseases and Vaccines. 2014 , 331-358	2
448	Gene Networks Inference through Linear Grouping of Variables. 2014 ,	3
447	Revealing networks from dynamics: an introduction. 2014 , 47, 343001	116
446	Data identification for improving gene network inference using computational algebra. 2014 , 76, 2923-40	3
445	Sexually-dimorphic targeting of functionally-related genes in COPD. 2014 , 8, 118	38
444	Large-Scale Networks in Engineering and Life Sciences. 2014 ,	10

443	Untangling statistical and biological models to understand network inference: the need for a genomics network ontology. 2014 , 5, 299	11
442	Augmenting microarray data with literature-based knowledge to enhance gene regulatory network inference. 2014 , 10, e1003666	23
441	Untangling complex dynamical systems via derivative-variable correlations. 2014 , 4, 5030	24
440	Molecular mechanisms of system responses to novel stimuli are predictable from public data. 2014 , 42, 1442-60	23
439	Functional association networks as priors for gene regulatory network inference. 2014 , 30, i130-8	30
438	Integrative omics analysis. A study based on Plasmodium falciparum mRNA and protein data. 2014 , 8 Suppl 2, S4	12
437	Identifying disease candidate genes via large-scale gene network analysis. 2014 , 10, 175-88	18
436	A consensus approach to predict regulatory interactions. 2014 ,	
435	Pheno2GRN. 2014 ,	
434	Reconstruction of gene regulatory networks from short time series high throughput data: Review and new findings. 2014 ,	1
433	Supervised method for construction of microRNA-mRNA networks: application in cardiac tissue aging dataset. 2014 , 2014, 318-21	3
432	Dynamic transcription factor activity and networks during ErbB2 breast oncogenesis and targeted therapy. 2014 , 6, 1170-82	10
431	Integration of prior biological knowledge and epigenetic information enhances the prediction accuracy of the Bayesian Wnt pathway. 2014 , 6, 1034-48	6
430	Sparse Additive Ordinary Differential Equations for Dynamic Gene Regulatory Network Modeling. 2014 , 109, 700-716	53
429	Cascade: a R package to study, predict and simulate the diffusion of a signal through a temporal gene network. 2014 , 30, 571-3	5
428	A systems approach to integrative biology: an overview of statistical methods to elucidate association and architecture. 2014 , 54, 296-306	9
427	Gene Networks Inference through One Genetic Algorithm Per Gene. 2014 ,	3
426	Integrative biological analysis for neuropsychopharmacology. 2014 , 39, 5-23	16

425	Fungal Genomics. 2014,	0
424	Reconstructing biological gene regulatory networks: where optimization meets big data. 2014, 7, 29-47	34
423	A quantitative atlas of Even-skipped and Hunchback expression in <i>Clogmia albipunctata</i> (Diptera: Psychodidae) blastoderm embryos. 2014, 5, 1	30
422	A feature selection technique for inference of graphs from their known topological properties: Revealing scale-free gene regulatory networks. 2014, 272, 1-15	37
421	Gene regulatory networks in the immune system. 2014, 35, 211-8	46
420	Tamoxifen integromics and personalized medicine: dynamic modular transformations underpinning response to tamoxifen in breast cancer treatment. 2014, 18, 15-33	18
419	Bayesian network prior: network analysis of biological data using external knowledge. 2014, 30, 860-7	29
418	Computational Intelligence Methods for Bioinformatics and Biostatistics. 2014,	
417	Network-based approach reveals Y chromosome influences prostate cancer susceptibility. 2014, 54, 24-31	17
416	Novel application of multi-stimuli network inference to synovial fibroblasts of rheumatoid arthritis patients. 2014, 7, 40	6
415	Reverse Engineering Methodology for Bioinformatics Based on Genetic Programming, Differential Expression Analysis and Other Statistical Methods. 2014, 161-177	
414	Bioattractors: dynamical systems theory and the evolution of regulatory processes. 2014, 592, 2267-81	69
413	Entropic Biological Score: a cell cycle investigation for GRNs inference. 2014, 541, 129-37	13
412	Approaches to in vitro tissue regeneration with application for human disease modeling and drug development. 2014, 19, 754-62	33
411	A Clustering based Method Accelerating Gene Regulatory Network Reconstruction. 2014, 29, 1993-2002	10
410	Chapter 5: Theory and Method of Completion for a Boolean Regulatory Network Using Observed Data. 2014, 123-145	1
409	Linear grouping of predictor instances to infer gene networks. 2015, 4, 1	
408	Methods for biological data integration: perspectives and challenges. 2015, 12,	127

407	Parameter Estimation for Gene Regulatory Networks from Microarray Data: Cold Shock Response in <i>Saccharomyces cerevisiae</i> . 2015 , 77, 1457-92	4
406	Inferring genetic architecture from systems genetics studies. 139-160	
405	Prediction of tissue-specific effects of gene knockout on apoptosis in different anatomical structures of human brain. 2015 , 16 Suppl 13, S3	6
404	Reconstructing Large-scale Cellular Networks Using a Sparse Approximation Approach. 2015 , 48, 251-256	
403	BRANE Cut: biologically-related a priori network enhancement with graph cuts for gene regulatory network inference. 2015 , 16, 368	8
402	An Extended Constrained Total Least-Squares Method for the Identification of Genetic Networks from Noisy Measurements. 2015 , 54, 10583-10592	
401	SBMLsqueezer 2: context-sensitive creation of kinetic equations in biochemical networks. 2015 , 9, 68	19
400	CyNetworkBMA: a Cytoscape app for inferring gene regulatory networks. 2015 , 10, 11	3
399	TGF- β -induced epithelial-mesenchymal transition modeling. 2015 , 637, 012035	
398	Nontrivial Characteristics Embedded in Microarray Coexpression Profiles. 2015 , 604, 012022	
397	Time-Delayed Models of Gene Regulatory Networks. 2015 , 2015, 347273	22
396	Reconstruction of the temporal signaling network in <i>Salmonella</i> -infected human cells. 2015 , 6, 730	14
395	Inferring regulatory networks from experimental morphological phenotypes: a computational method reverse-engineers planarian regeneration. 2015 , 11, e1004295	56
394	A Sparse Reconstruction Approach for Identifying Gene Regulatory Networks Using Steady-State Experiment Data. 2015 , 10, e0130979	1
393	Multi-Target Analysis and Design of Mitochondrial Metabolism. 2015 , 10, e0133825	7
392	Network Modeling Reveals Cross Talk of MAP Kinases during Adaptation to Caspofungin Stress in <i>Aspergillus fumigatus</i> . 2015 , 10, e0136932	48
391	Semi-Supervised Multi-View Learning for Gene Network Reconstruction. 2015 , 10, e0144031	29
390	Reverse Engineering of Genome-wide Gene Regulatory Networks from Gene Expression Data. 2015 , 16, 3-22	52

389	Inferring Broad Regulatory Biology from Time Course Data: Have We Reached an Upper Bound under Constraints Typical of In Vivo Studies?. 2015 , 10, e0127364	3
388	CoGNAC: A Chaste Plugin for the Multiscale Simulation of Gene Regulatory Networks Driving the Spatial Dynamics of Tissues and Cancer. 2015 , 14, 53-65	8
387	A network model for angiogenesis in ovarian cancer. 2015 , 16, 115	47
386	A review on computational systems biology of pathogen-host interactions. 2015 , 6, 235	61
385	Improvement of reliabilities of regulations using a hierarchical structure in a genetic network. 2015 ,	
384	Inference of gene regulatory networks via multiple data sources and a recommendation method. 2015 ,	2
383	A discretized differential evolution algorithm for the inference of Gene Regulatory Networks. 2015	
382	A tree-like Bayesian structure learning algorithm for small-sample datasets from complex biological model systems. 2015 , 9, 49	5
381	Physical and Mathematical Modeling in Experimental Papers. 2015 , 163, 1577-83	19
380	Controlling networks of nonlinearly-coupled nodes using response surfaces. 2014 , 4, 7574	1
379	Vision from next generation sequencing: multi-dimensional genome-wide analysis for producing gene regulatory networks underlying retinal development, aging and disease. 2015 , 46, 1-30	43
378	Overview of Computational Approaches for Inference of MicroRNA-Mediated and Gene Regulatory Networks. 2015 , 97, 111-145	2
377	Robust reconstruction of complex networks from sparse data. 2015 , 114, 028701	102
376	Analysis of Deterministic Cyclic Gene Regulatory Network Models with Delays. 2015 ,	6
375	Computational Systems Biology <i>Zeitschrift für Naturwissenschaften</i> . 2015 , 21, 46-48	
374	One genetic algorithm per gene to infer gene networks from expression data. 2015 , 4, 1	2
373	Computational approaches to identify regulators of plant stress response using high-throughput gene expression data. 2015 , 3-4, 20-29	13
372	Inference of quantitative models of bacterial promoters from time-series reporter gene data. 2015 , 11, e1004028	16

371	A knowledge driven supervised learning approach to identify gene network of differentially up-regulated genes during neuronal senescence in <i>Rattus norvegicus</i> . <i>BioSystems</i> , 2015 , 135, 9-14	1.9	1
370	ARMADA: Using motif activity dynamics to infer gene regulatory networks from gene expression data. 2015 , 85, 62-74		1
369	Regulatory network inferred using expression data of small sample size: application and validation in erythroid system. 2015 , 31, 2537-44		7
368	Computational prediction of molecular pathogen-host interactions based on dual transcriptome data. 2015 , 6, 65		43
367	Structural determinants of criticality in biological networks. 2015 , 6, 127		22
366	Big Data Analytics and Its Prospects in Computational Proteomics. 2015 , 591-598		9
365	Gene network coherence based on prior knowledge using direct and indirect relationships. 2015 , 56, 142-51		11
364	Uncovering transportation networks from traffic flux by compressed sensing. 2015 , 88, 1		3
363	The identification of cis-regulatory elements: A review from a machine learning perspective. <i>BioSystems</i> , 2015 , 138, 6-17	1.9	30
362	A multi-view genomic data simulator. 2015 , 16, 151		7
361	Integrating Microarray Data and GRNs. 2016 , 1375, 137-53		4
360	A New Approach to Link Prediction in Gene Regulatory Networks. 2015 , 404-415		6
359	Prior knowledge driven Granger causality analysis on gene regulatory network discovery. 2015 , 16, 273		7
358	Mining Gene Regulatory Networks by Neural Modeling of Expression Time-Series. 2015 , 12, 1365-73		7
357	A Multi-GPU Hitting Set Algorithm for GRNs Inference. 2015 ,		3
356	SMARTS: reconstructing disease response networks from multiple individuals using time series gene expression data. 2015 , 31, 1250-7		12
355	Single-cell transcriptional analysis to uncover regulatory circuits driving cell fate decisions in early mouse development. 2015 , 31, 1060-6		35
354	Constructing gene network based on biclusters of expression data. 2016 , 15,		

353	How to Predict Molecular Interactions between Species?. 2016 , 7, 442	22
352	Data-based Reconstruction of Gene Regulatory Networks of Fungal Pathogens. 2016 , 7, 570	5
351	Differential Biphasic Transcriptional Host Response Associated with Coevolution of Hemagglutinin Quasispecies of Influenza A Virus. 2016 , 7, 1167	8
350	Stable Gene Regulatory Network Modeling From Steady-State Data. 2016 , 3,	8
349	Genetic Network Inference Using Hierarchical Structure. 2016 , 7, 57	3
348	Computational challenges in modeling gene regulatory events. 2016 , 7, 188-195	6
347	Reconstructing gene regulatory network based on candidate auto selection method. 2016 ,	
346	Adaptive input data transformation for improved network reconstruction with information theoretic algorithms. 2016 , 15, 507-520	
345	Simultaneous execution method of gene clustering and network inference. 2016 ,	
344	Reconstruction of opinion dynamics network with bounded confidence via compressive sensing. 2016 ,	0
343	A review of simulation and modeling approaches in microbiology. 2016 , 6, 845-853	2
342	Inference of Gene Regulatory Networks Using Coefficient of Determination, Tsallis Entropy and Biological Prior Knowledge. 2016 ,	2
341	Inferring phage-bacteria infection networks from time-series data. 2016 , 3, 160654	8
340	Microbial phenomics information extractor (MicroPIE): a natural language processing tool for the automated acquisition of prokaryotic phenotypic characters from text sources. 2016 , 17, 528	11
339	Reverse engineering gene regulatory networks from measurement with missing values. 2016 , 2017, 2	13
338	The Local Edge Machine: inference of dynamic models of gene regulation. 2016 , 17, 214	14
337	Multiple Kernel Learning Algorithms and Their Use in Biomedical Informatics. 2016 , 559-564	
336	TSDDMI: Inference of time-delayed gene regulatory network using S-system model with delayed mutual information. 2016 , 72, 218-25	8

335	Fast integration-based prediction bands for ordinary differential equation models. 2016 , 32, 1204-10	14
334	Use of systems biology to decipher host-pathogen interaction networks and predict biomarkers. 2016 , 22, 600-6	26
333	Boolean modeling techniques for protein co-expression networks in systems medicine. 2016 , 13, 555-69	1
332	A supervised weighted similarity measure for gene expressions using biological knowledge. 2016 , 595, 150-160	5
331	An integrated approach to infer dynamic protein-gene interactions - A case study of the human P53 protein. 2016 , 110, 3-13	7
330	Mathematical Models and Computational Methods for Inference of Genetic Networks. 2016 , 30-48	
329	Modeling dynamic gene expression in STREPTOMYCES COELICOLOR: Comparing single and multi-objective setups. 2016 , 151-184	
328	Crosstalk pathway inference using topological information and biclustering of gene expression data. <i>BioSystems</i> , 2016 , 150, 1-12	1.9 6
327	Diet-induced weight loss leads to a switch in gene regulatory network control in the rectal mucosa. 2016 , 108, 126-133	11
326	Correlation-based iterative clustering methods for time course data: The identification of temporal gene response modules for influenza infection in humans. 2016 , 1, 28-39	10
325	A Method to Identify and Analyze Biological Programs through Automated Reasoning. 2016 , 2,	30
324	Biological Networks for Cancer Candidate Biomarkers Discovery. 2016 , 15, 1-7	6
323	Integrative approach for inference of gene regulatory networks using lasso-based random featuring and application to psychiatric disorders. 2016 , 9 Suppl 2, 50	4
322	Inferring sparse networks for noisy transient processes. 2016 , 6, 21963	4
321	Data based identification and prediction of nonlinear and complex dynamical systems. 2016 , 644, 1-76	177
320	Reconstruction of gene regulatory modules from RNA silencing of IFN- β modulators: experimental set-up and inference method. 2016 , 17, 228	3
319	Next generation sequencing technology and genomewide data analysis: Perspectives for retinal research. 2016 , 55, 1-31	39
318	Social choice in distributed classification tasks: Dealing with vertically partitioned data. 2016 , 332, 56-71	8

317	Microarray Data Analysis. 2016,		1
316	Inferring causal molecular networks: empirical assessment through a community-based effort. 2016, 13, 310-8		158
315	Incorporating biological knowledge for construction of fuzzy networks of gene associations. 2016, 42, 144-155		9
314	Relative stability of network states in Boolean network models of gene regulation in development. <i>BioSystems</i> , 2016, 142-143, 15-24	1.9	29
313	Making sense of genomes of parasitic worms: Tackling bioinformatic challenges. 2016, 34, 663-686		27
312	MoCha: Molecular Characterization of Unknown Pathways. 2016, 23, 291-7		8
311	New Method for Joint Network Analysis Reveals Common and Different Coexpression Patterns among Genes and Proteins in Breast Cancer. 2016, 15, 743-54		15
310	Design of Probabilistic Boolean Networks Based on Network Structure and Steady-State Probabilities. 2017, 28, 1966-1971		27
309	Gene co-expression analysis for functional classification and gene-disease predictions. 2018, 19, 575-592		377
308	Applying attractor dynamics to infer gene regulatory interactions involved in cellular differentiation. <i>BioSystems</i> , 2017, 155, 29-41	1.9	2
307	A system of recurrent neural networks for modularising, parameterising and dynamic analysis of cell signalling networks. <i>BioSystems</i> , 2017, 153-154, 6-25	1.9	1
306	Bioinformatics from a Big Data Perspective: Meeting the Challenge. 2017, 349-359		
305	A STATISTICAL FRAMEWORK FOR DATA INTEGRATION THROUGH GRAPHICAL MODELS WITH APPLICATION TO CANCER GENOMICS. 2017, 11, 161-184		13
304	GeneSPIDER - gene regulatory network inference benchmarking with controlled network and data properties. 2017, 13, 1304-1312		9
303	GeNICE: A Novel Framework for Gene Network Inference by Clustering, Exhaustive Search, and Multivariate Analysis. 2017, 24, 809-830		1
302	From Genes to Networks: Characterizing Gene-Regulatory Interactions in Plants. 2017, 1629, 1-11		0
301	Evaluation of artificial time series microarray data for dynamic gene regulatory network inference. 2017, 426, 1-16		2
300	A hybrid framework for reverse engineering of robust Gene Regulatory Networks. 2017, 79, 15-27		4

299	The feasibility of genome-scale biological network inference using Graphics Processing Units. 2017 , 12, 8	4
298	Backward-stochastic-differential-equation approach to modeling of gene expression. 2017 , 95, 032418	3
297	GFD-Net: A novel semantic similarity methodology for the analysis of gene networks. 2017 , 68, 71-82	6
296	Developmental switching in <i>Physarum polycephalum</i> : Petri net analysis of single cell trajectories of gene expression indicates responsiveness and genetic plasticity of the Waddington quasipotential landscape. 2017 , 50, 464003	7
295	Fast and Highly Scalable Bayesian MDP on a GPU Platform. 2017 ,	1
294	Gene co-opening network deciphers gene functional relationships. 2017 , 13, 2428-2439	11
293	Genetics and Evolution of Social Behavior in Insects. 2017 , 51, 219-239	26
292	Changes in Gene Expression in Space and Time Orchestrate Environmentally Mediated Shaping of Root Architecture. 2017 , 29, 2393-2412	27
291	Reverse engineering highlights potential principles of large gene regulatory network design and learning. 2017 , 3, 17	7
290	A time series driven decomposed evolutionary optimization approach for reconstructing large-scale gene regulatory networks based on fuzzy cognitive maps. 2017 , 18, 241	17
289	Estimating genome-wide regulatory activity from multi-omics data sets using mathematical optimization. 2017 , 11, 41	8
288	Computational dynamic approaches for temporal omics data with applications to systems medicine. 2017 , 10, 20	18
287	Computing a Worm: Reverse-Engineering Planarian Regeneration. 2017 , 637-654	7
286	More than meets the eye: Emergent properties of transcription factors networks in <i>Arabidopsis</i> . 2017 , 1860, 64-74	5
285	Computational inference of gene regulatory networks: Approaches, limitations and opportunities. 2017 , 1860, 41-52	48
284	Bioinformatics. 2017 ,	0
283	Inferring transcriptional logic from multiple dynamic experiments. 2017 , 33, 3437-3444	1
282	The Ability of Different Imputation Methods to Preserve the Significant Genes and Pathways in Cancer. 2017 , 15, 396-404	5

281	Improving GRN re-construction by mining hidden regulatory signals. 2017 , 11, 174-181	2
280	Inference of genetic networks from time-series of gene expression levels using random forests. 2017 ,	3
279	Double impact: natural molluscicide for schistosomiasis vector control also impedes development of <i>Schistosoma mansoni</i> cercariae into adult parasites. 2017 , 11, e0005789	14
278	Bioinformatics Tools for Data Analysis. 2017 , 339-351	
277	SiGNet: A signaling network data simulator to enable signaling network inference. 2017 , 12, e0177701	5
276	Cell cycle time series gene expression data encoded as cyclic attractors in Hopfield systems. 2017 , 13, e1005849	8
275	Inferring gene regulatory networks from single-cell data: a mechanistic approach. 2017 , 11, 105	32
274	An improved Bayesian network method for reconstructing gene regulatory network based on candidate auto selection. 2017 , 18, 844	17
273	Gene Regulatory Network Inference from Perturbed Time-Series Expression Data via Ordered Dynamical Expansion of Non-Steady State Actors. 2018 , 15, 1093-1106	1
272	Machine learning for bioinformatics and neuroimaging. 2018 , 8, e1248	14
271	Using evolutionary genomics, transcriptomics, and systems biology to reveal gene networks underlying fungal development. 2018 , 32, 249-264	7
270	Independence screening for high dimensional nonlinear additive ODE models with applications to dynamic gene regulatory networks. 2018 , 37, 2630-2644	0
269	Network Structure Inference, A Survey. 2018 , 51, 1-39	53
268	Large scale modeling of genetic networks using gene knockout data. 2018 ,	
267	Sparse dynamical Boltzmann machine for reconstructing complex networks with binary dynamics. 2018 , 97, 032317	12
266	Dynamic modeling and network approaches for omics time course data: overview of computational approaches and applications. 2018 , 19, 1051-1068	15
265	Identifying a Probabilistic Boolean Threshold Network From Samples. 2018 , 29, 869-881	14
264	Reconstructing Genetic Regulatory Networks Using Two-Step Algorithms with the Differential Equation Models of Neural Networks. 2018 , 10, 823-835	3

263	Latent Variable Time-varying Network Inference. 2018 ,		3
262	Gene networks modeling of microarray time series using Fuzzy Granger causality. 2018 ,		
261	On dynamic network modeling of stationary multivariate processes. 2018 , 51, 850-855		1
260	The SQUAD Method for the Qualitative Modeling of Regulatory Networks. 2018 , 1819, 197-214		1
259	Ambiguity in logic-based models of gene regulatory networks: An integrative multi-perturbation analysis. 2018 , 13, e0206976		2
258	[Regular Paper] Inference of Genetic Networks Using Random Forests: Use of Different Weights for Time-Series and Static Gene Expression Data. 2018 ,		1
257	Extensive evaluation of the generalized relevance network approach to inferring gene regulatory networks. 2018 , 7,		6
256	Detection of network motifs using three-way ANOVA. 2018 , 13, e0201382		3
255	Initial state perturbations as a validation method for data-driven fuzzy models of cellular networks. 2018 , 19, 333		1
254	Large-Scale Functional Analysis of CRP-Mediated Feed-Forward Loops. 2018 , 19,		3
253	Analysis of Gene Expression Time Series Data of Ebola Vaccine response using the NeuCube and Temporal Feature Selection. 2018 ,		1
252	A guide to gene regulatory network inference for obtaining predictive solutions: Underlying assumptions and fundamental biological and data constraints. <i>BioSystems</i> , 2018 , 174, 37-48	1.9	17
251	Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations. 2018 , 11, 135		0
250	Characterization of Peroxisomal Regulation Networks. 2018 , 89, 367-382		3
249	Finite-time parametric identification for the model representing the metabolic and genetic regulatory effects of sequential aerobic respiration and anaerobic fermentation processes in <i>Escherichia coli</i> . 2018 , 35, 299-317		
248	Towards precise reconstruction of gene regulatory networks by data integration. 2018 , 6, 113-128		3
247	A big data pipeline: Identifying dynamic gene regulatory networks from time-course Gene Expression Omnibus data with applications to influenza infection. 2018 , 27, 1930-1955		6
246	Inference of gene networks from gene expression time series using recurrent neural networks and sparse MAP estimation. 2018 , 16, 1850009		1

245	Gene Discovery of Characteristic Metabolic Pathways in the Tea Plant () Using OmicsRBased Network Approaches: A Future Perspective. 2018 , 9, 480	24
244	Griffin: A Tool for Symbolic Inference of Synchronous Boolean Molecular Networks. 2018 , 9, 39	2
243	Advances in Integrating Genomics and Bioinformatics in the Plant Breeding Pipeline. 2018 , 8, 75	43
242	In Silico Prediction of Large-Scale Microbial Production Performance: Constraints for Getting Proper Data-Driven Models. 2018 , 16, 246-256	10
241	Structure Optimization for Large Gene Networks Based on Greedy Strategy. 2018 , 2018, 9674108	6
240	The Spring of Systems Biology-Driven Breeding. 2018 , 23, 706-720	27
239	Quantitative assessment of protein activity in orphan tissues and single cells using the metaVIPER algorithm. 2018 , 9, 1471	41
238	Gene Expression for Simulation of Biological Tissue. 2018 ,	
237	Unravelling miRNA regulation in yield of rice (<i>Oryza sativa</i>) based on differential network model. 2018 , 8, 8498	17
236	Network community-based model reduction for vortical flows. 2018 , 97, 063103	14
235	Biological Pathways. 2019 , 1047-1062	
234	Network Inference and Reconstruction in Bioinformatics. 2019 , 805-813	22
233	Discovery of stroke-related blood biomarkers from gene expression network models. 2019 , 12, 118	7
232	ATEN: And/Or tree ensemble for inferring accurate Boolean network topology and dynamics. 2020 , 36, 578-585	1
231	Controlling large Boolean networks with single-step perturbations. 2019 , 35, i558-i567	10
230	Network using Michaelis-Menten kinetics: constructing an algorithm to find target genes from expression data. 2019 ,	
229	Genome structure predicts modular transcriptome responses to genetic and environmental conditions. 2019 , 28, 3681-3697	4
228	Combining Mathematical Models With Experimentation to Drive Novel Mechanistic Insights Into Macrophage Function. 2019 , 10, 1283	6

227	On Penalty Parameter Selection for Estimating Network Models. 2021 , 56, 288-302	7
226	Inferring Functional Connectivity From Time-Series of Events in Large Scale Network Deployments. 2019 , 16, 857-870	4
225	Predicting gene regulatory interactions based on spatial gene expression data and deep learning. 2019 , 15, e1007324	18
224	Identifying the most influential roads based on traffic correlation networks. 2019 , 8,	8
223	Integrative approaches to reconstruct regulatory networks from multi-omics data: A review of state-of-the-art methods. 2019 , 83, 107120	19
222	Leveraging chromatin accessibility for transcriptional regulatory network inference in T Helper 17 Cells. 2019 , 29, 449-463	37
221	Multi-study inference of regulatory networks for more accurate models of gene regulation. 2019 , 15, e1006591	35
220	Effective induction of gene regulatory networks using a novel recommendation method. 2019 , 22, 91	1
219	A survey of evolutionary algorithms using metameric representations. 2019 , 20, 441-478	19
218	Dynamical resilience of networks against targeted attack. 2019 , 528, 121329	6
217	WASABI: a dynamic iterative framework for gene regulatory network inference. 2019 , 20, 220	19
216	High-Performance Modelling and Simulation for Big Data Applications. 2019 ,	2
215	A novel method of gene regulatory network structure inference from gene knock-out expression data. 2019 , 24, 446-455	9
214	Ecological Metabolomics: Challenges and Perspectives. 2019 , 293-378	
213	Prostate Cancer Gene Regulatory Network Inferred from RNA-Seq Data. 2019 , 20, 38-48	5
212	Genomic Prediction Including SNP-Specific Variance Predictors. 2019 , 9, 3333-3343	3
211	Differential co-expression-based detection of conditional relationships in transcriptional data: comparative analysis and application to breast cancer. 2019 , 20, 236	21
210	Reconfigurable Probabilistic AI Architecture for Personalized Cancer Treatment. 2019 ,	1

209	Computational Inference of Gene Co-Expression Networks for the identification of Lung Carcinoma Biomarkers: An Ensemble Approach. 2019 , 10,	3
208	Bayesian topology identification of linear dynamic networks. 2019 ,	10
207	Ensemble and Greedy Approach for the Reconstruction of Large Gene Co-Expression Networks. 2019 , 21, 1139	1
206	Detecting direct associations in a network by information theoretic approaches. 2019 , 62, 823-838	8
205	Evolutionary acquisition of complex traits in artificial epigenetic networks. <i>BioSystems</i> , 2019 , 176, 17-26 ^{1.9}	
204	Stability in GRN Inference. 2019 , 1883, 323-346	1
203	Computational methods for Gene Regulatory Networks reconstruction and analysis: A review. 2019 , 95, 133-145	57
202	Optimized time-lag differential method for constructing gene regulatory network. 2019 , 478, 222-238	2
201	Learning of Tree-Structured Gaussian Graphical Models on Distributed Data Under Communication Constraints. 2019 , 67, 17-28	1
200	Computational prediction of gene regulatory networks in plant growth and development. 2019 , 47, 96-105	30
199	Fuzzy logic based approaches for gene regulatory network inference. 2019 , 97, 189-203	14
198	Modeling Long ncRNA-Mediated Regulation in the Mammalian Cell Cycle. 2019 , 1912, 427-445	1
197	Gene Regulatory Networks. 2019 ,	22
196	BayesPiles. 2019 , 10, 1-23	4
195	Learning Fuzzy Cognitive Maps with modified asexual reproduction optimisation algorithm. 2019 , 163, 723-735	49
194	Construction of Transcriptional Regulatory Network of Alzheimer's Disease Based on PANDA Algorithm. 2019 , 11, 226-236	9
193	A Multi-Laplacian Prior and Augmented Lagrangian Approach to the Exploratory Analysis of Time-Varying Gene and Transcriptional Regulatory Networks for Gene Microarray Data. 2019 , 16, 1816-1829	5
192	Inferring Large-Scale Gene Regulatory Networks Using a Randomized Algorithm Based on Singular Value Decomposition. 2019 , 16, 1997-2008	2

191	Bayesian Data Fusion of Gene Expression and Histone Modification Profiles for Inference of Gene Regulatory Network. 2020 , 17, 516-525	3
190	Identification of Minimum Set of Master Regulatory Genes in Gene Regulatory Networks. 2020 , 17, 999-1009	2
189	Gene regulatory network inference resources: A practical overview. 2020 , 1863, 194430	28
188	Gene networks in cancer are biased by aneuploidies and sample impurities. 2020 , 1863, 194444	2
187	Computational approaches in cancer multidrug resistance research: Identification of potential biomarkers, drug targets and drug-target interactions. 2020 , 48, 100662	22
186	Applications of disease pathways in biology and medicine. 2020 , 629-668	2
185	Can dynamic network modelling be used to identify adaptive microbiomes?. 2020 , 34, 2065-2074	3
184	Exploiting causality in gene network reconstruction based on graph embedding. 2020 , 109, 1231-1279	19
183	Analysis of time-series regulatory networks. 2020 , 21, 16-24	5
182	Learning Asynchronous Boolean Networks From Single-Cell Data Using Multiobjective Cooperative Genetic Programming. 2020 , PP,	1
181	A survey of gene regulatory networks modelling methods: from differential equations, to Boolean and qualitative bioinspired models. 2020 , 2, 207-226	10
180	Computational Analysis of the Global Effects of in the Immune Response to Coronavirus Infection Using Gene Networks. 2020 , 11,	2
179	Multi-task learning for the simultaneous reconstruction of the human and mouse gene regulatory networks. 2020 , 10, 22295	6
178	Underpinning miRNA-miRNA co-functional interaction patterns in the metabolism of <i>Oryza sativa</i> by genome-scale network analysis. 2020 , 6, e05496	1
177	Reconstructing irreducible links in temporal networks: which tool to choose depends on the network size. 2020 , 1, 015001	3
176	A Bayesian data fusion based approach for learning genome-wide transcriptional regulatory networks. 2020 , 21, 219	1
175	Introduction. 2020 , 3-32	1
174	Can We Assume the Gene Expression Profile as a Proxy for Signaling Network Activity?. 2020 , 10,	5

173	Meta Gene Regulatory Networks in Maize Highlight Functionally Relevant Regulatory Interactions. 2020 , 32, 1377-1396	20
172	The Phenotype Paradox: Lessons From Natural Transcriptome Evolution on How to Engineer Plants. 2020 , 11, 75	3
171	Supervised learning of gene-regulatory networks based on graph distance profiles of transcriptomics data. 2020 , 6, 21	9
170	In silico disease model: from simple networks to complex diseases. 2020 , 441-460	0
169	Systems biology, drug development, and clinical outcomes. 2020 , 109-123	
168	Reverse engineering directed gene regulatory networks from transcriptomics and proteomics data of biomining bacterial communities with approximate Bayesian computation and steady-state signalling simulations. 2020 , 21, 23	6
167	Structure Learning of Sparse GGMs Over Multiple Access Networks. 2020 , 68, 987-997	1
166	Gene regulatory network and its constituent transcription factors that control nitrogen-deficiency responses in rice. 2020 , 227, 1434-1452	20
165	A transcriptional regulatory network of Rsv3-mediated extreme resistance against Soybean mosaic virus. 2020 , 15, e0231658	5
164	Molecular networks in Network Medicine: Development and applications. 2020 , 12, e1489	63
163	Mayer-Type Optimal Control of Probabilistic Boolean Control Network With Uncertain Selection Probabilities. 2021 , 51, 3079-3092	10
162	A mathematical model exhibiting the effect of DNA methylation on the stability boundary in cell-fate networks. 2021 , 16, 436-457	6
161	Gene Regulatory Network Inference. 2021 , 86-95	1
160	A control theoretic three timescale model for analyzing energy management in mammalian cancer cells. 2021 , 19, 477-508	1
159	MKL-GRNI: A parallel multiple kernel learning approach for supervised inference of large-scale gene regulatory networks. 2021 , 7, e363	3
158	Unique superdiffusion induced by directionality in multiplex networks. 2021 , 23, 013016	4
157	Data-driven Boolean Network Inference Using a Genetic Algorithm with Marker-based Encoding. 2021 , PP,	1
156	Differential Expression Analysis of RNA-Seq Data and Co-expression Networks. 2021 , 29-76	

155	Measuring topological descriptors of complex networks under uncertainty. 2021 , 103, 022311	4
154	Emergence of co-expression in gene regulatory networks. 2021 , 16, e0247671	6
153	Finding gene network topologies for given biological function with recurrent neural network. 2021 , 12, 3125	2
152	Mechanistic Gene Networks Inferred from Single-Cell Data are Better Predictors than Neural Networks.	
151	The finding and researching algorithm for potentially oscillating enzymatic systems.. 2021 , 25, 318-330	0
150	Network modeling and inference of peroxisome proliferator-activated receptor pathway in high fat diet-linked obesity. 2021 , 519, 110647	1
149	Mechanism-Centric Approaches for Biomarker Detection and Precision Therapeutics in Cancer. 2021 , 12, 687813	1
148	Network Inference of Transcriptional Regulation in Germinating Low Phytic Acid Soybean Seeds. 2021 , 12, 708286	0
147	Decoding gene regulation in the fly brain.	0
146	Topological analysis of interaction patterns in cancer-specific gene regulatory network: persistent homology approach. 2021 , 11, 16414	2
145	Omics Technologies and Molecular Farming: Applications and Challenges. 2021 , 47-67	
144	LifeR attractors : understanding developmental systems through reverse engineering and in silico evolution. 2012 , 751, 93-119	28
143	High-Dimensional Ordinary Differential Equation Models for Reconstructing Genome-Wide Dynamic Regulatory Networks. 2013 , 173-190	2
142	Inference of Gene Regulatory Network Through Adaptive Dynamic Bayesian Network Modeling. 2019 , 91-113	1
141	Towards Human Cell Simulation. 2019 , 221-249	3
140	A Petri-Net-Based Framework for Biomodel Engineering. 2014 , 317-366	5
139	Computational Scientific Discovery. 2017 , 719-734	7
138	Reverse Engineering of Gene Regulatory Networks Combining Dynamic Bayesian Networks and Prior Biological Knowledge. 2018 , 323-336	6

137	SFFS-MR: A Floating Search Strategy for GRNs Inference. 2010 , 407-418	6
136	Integration of Epigenetic Data in Bayesian Network Modeling of Gene Regulatory Network. 2011 , 87-96	6
135	Pattern Recognition in Biological Time Series. 2011 , 164-172	4
134	Revisiting the Training of Logic Models of Protein Signaling Networks with ASP. 2012 , 342-361	10
133	Inferring Time-Delayed Gene Regulatory Networks Using Cross-Correlation and Sparse Regression. 2013 , 64-75	8
132	A Survey of Current Integrative Network Algorithms for Systems Biology. 2013 , 479-495	3
131	Reverse-engineering biological networks from large data sets.	4
130	Developmental switching in <i>Physarum polycephalum</i> : Petri net analysis of single cell trajectories of gene expression indicates responsiveness and genetic plasticity of the Waddington quasipotential landscape.	1
129	Multi-study inference of regulatory networks for more accurate models of gene regulation.	3
128	Leveraging chromatin accessibility for transcriptional regulatory network inference in T Helper 17 Cells.	2
127	Genome structure predicts modular transcriptome responses to genetic and environmental conditions.	2
126	OpenAnnotate: a web server to annotate the chromatin accessibility of genomic regions.	7
125	Reconstruction of Large-Scale Gene Regulatory Networks Using Bayesian Model Averaging. 2011 ,	5
124	BENIN. 2019 ,	1
123	Development and use of the Cytoscape app GFD-Net for measuring semantic dissimilarity of gene networks. 2014 , 3, 142	10
122	FlyOde - a platform for community curation and interactive visualization of dynamic gene regulatory networks in <i>Drosophila</i> eye development. 2015 , 4, 1484	2
121	Gene expression prediction by soft integration and the elastic net-best performance of the DREAM3 gene expression challenge. 2010 , 5, e9134	25
120	Petri Nets with Fuzzy Logic (PNFL): reverse engineering and parametrization. 2010 , 5, e12807	25

119	Using regulatory and epistatic networks to extend the findings of a genome scan: identifying the gene drivers of pigmentation in merino sheep. 2011 , 6, e21158	27
118	Regulatory Snapshots: integrative mining of regulatory modules from expression time series and regulatory networks. 2012 , 7, e35977	7
117	Reverse engineering Boolean networks: from Bernoulli mixture models to rule based systems. 2012 , 7, e51006	2
116	Passing messages between biological networks to refine predicted interactions. 2013 , 8, e64832	108
115	An Evaluation of Methods for Inferring Boolean Networks from Time-Series Data. 2013 , 8, e66031	33
114	Modeling the Drosophila gene cluster regulation network for muscle development. 2014 , 9, e90285	1
113	Ensemble inference and inferability of gene regulatory networks. 2014 , 9, e103812	21
112	Clustering and Differential Alignment Algorithm: Identification of Early Stage Regulators in the Arabidopsis thaliana Iron Deficiency Response. 2015 , 10, e0136591	11
111	Transcriptome Dynamics and Potential Roles of Sox6 in the Postnatal Heart. 2016 , 11, e0166574	6
110	Exploring candidate biological functions by Boolean Function Networks for Saccharomyces cerevisiae. 2017 , 12, e0185475	4
109	Using single-index ODEs to study dynamic gene regulatory network. 2018 , 13, e0192833	5
108	Data- and knowledge-based modeling of gene regulatory networks: an update. 2015 , 14, 346-78	24
107	Parallel Algorithms for Inferring Gene Regulatory Networks: A Review. 2018 , 19, 603-614	2
106	Inference of Genetic Networks From Time-Series and Static Gene Expression Data: Combining a Random-Forest-Based Inference Method With Feature Selection Methods. 2020 , 11, 595912	2
105	A Novel Scale-free Network Construction Method and Its Application in Gene Expression Profiles Simulation*. 2012 , 39, 581-590	3
104	A posterior probability approach for gene regulatory network inference in genetic perturbation data. 2016 , 13, 1241-1251	10
103	Overview of methods of reverse engineering of gene regulatory networks: Boolean and Bayesian networks. 2012 , 28, 163-170	2
102	Emergent correlations in gene expression dynamics as footprints of resource competition. 2021 , 44, 131	

- 101 Mechanistic gene networks inferred from single-cell data with an outlier-insensitive method. **2021**, 342, 108722
- 100 Placental Gene Co-expression Network for Maternal Plasma Lipids Revealed Enrichment of Inflammatory Response Pathways. **2021**, 12, 681095
- 99 Mathematical Modelling of Leukemia Treatment. **2021**, 20, 274-281 3
- 98 Analysis of Gene Interactions Using Restricted Boolean Networks and Time-Series Data. **2010**, 61-76 0
- 97 Predictive minimum description length principle approach to inferring gene regulatory networks. **2011**, 696, 37-43 1
- 96 Information Propagation in the Long-Term Behavior of Gene Regulatory Networks. **2011**, 195-217
- 95 A Knowledge Based Decision Support System for Bioinformatics and System Biology. **2011**, 215-228 1
- 94 Gene Regulatory Networks Validation Framework Based in KEGG. **2011**, 279-286 0
- 93 Finding the Minimal Gene Regulatory Function in the Presence of Undefined Transitional States Using a Genetic Algorithm. **2012**, 238-249
- 92 Handling Unlabeled Data in Gene Regulatory Network. **2013**, 113-120 1
- 91 Extending Partially Known Networks. **2013**, 87-105
- 90 Computational Tools and Resources for Integrative Modeling in Systems Biology. **2013**, 399-428
- 89 13 Functional Genomics to Characterize Opportunistic Pathogens. **2014**, 321-347
- 88 Developments on the Regulatory Network Computational Device. **2014**, 4, 55-91
- 87 Gene Regulatory Networks Under Positive Feedback. **2015**, 73-85
- 86 Introduction. **2015**, 1-11
- 85 Overview of Cellular Computing-Basic Principles and Applications. **2016**, 637-662
- 84 Inferring phage-bacteria infection networks from time series data.

- 83 Construction of Gene Network System Associated with Economic Traits in Cattle. **2016**, 26, 904-910
- 82 Network Identification Methods.
- 81 Inferring Genome-Wide Interaction Networks. **2017**, 1526, 99-117 2
- 80 Integrating Multi-view Data: A Hypergraph Based Approach. **2017**, 347-357
- 79 Using A Prior Knowledge after Genetic Network Inference: Integrating Multiple Kinds of Knowledge. **2017**, 17, 53-71
- 78 Dual RNA sequencing (dRNA-Seq) of bacteria and their host cells.
- 77 Post-inference Methods of Prior Knowledge Incorporation in Gene Regulatory Network Inference.
- 76 Cell cycle time series gene expression data encoded as cyclic attractors in Hopfield systems.
- 75 Quantitative Assessment of Protein Activity in Orphan Tissues and Single Cells Using the metaVIPER Algorithm.
- 74 References. **2018**, 117-122
- 73 Identifying the dynamic gene regulatory network during latent HIV-1 reactivation using high-dimensional ordinary differential equations. **2018**, 11, 135-153
- 72 Deciphering gene regulation from gene expression dynamics using deep neural network. 1
- 71 Systems and Synthetic Biology Approach to Understand the Importance of Host-Pathogen Interaction. **2019**, 433-446
- 70 Inference of Gene Regulatory Networks by Topological Prior Information and Data Integration. **2019**, 265-304 0
- 69 Genes and Cell Type Specification in Cerebellar Development. **2019**, 1-19 1
- 68 Genomic prediction including SNP-specific variance predictors.
- 67 Can we assume the gene expression profile as a proxy for signaling network activity?. 8
- 66 Identification of new therapeutic targets in CRLF2-overexpressing B-ALL through discovery of TF-gene regulatory interactions.

- 65 Modeling cross-regulatory influences on monogenic transcripts and proteins under single and combinatorial gene knockdowns in *Populus trichocarpa*.
- 64 The Method of Construction and Analysis of Gene Regulatory Network. **2020**, 1761-1765
- 63 Gene networks in cancer are biased by aneuploidies and sample impurities. 1
- 62 A mathematical model exhibiting the effect of DNA methylation on the stability boundary in cell-fate networks.
- 61 Issues and Strategies for Modeling Gene Regulatory Networks. **2020**,
- 60 Overview of Cellular Computing-Basic Principles and Applications. **2020**, 1895-1920
- 59 Inference of Gene Regulatory Networks by Topological Prior Information and Data Integration. 1-51
- 58 Correlation imputation in single cell RNA-seq using auxiliary information and ensemble learning.
- 57 Modeling gene regulatory networks: Classical models, optimal perturbation for identification of network. **2020**, 17, 112-101
- 56 Network Modeling and Inference of Peroxisome Proliferator-Activated Receptor Pathway in High fat diet-linked Obesity.
- 55 Correlation Imputation in Single cell RNA-seq using Auxiliary Information and Ensemble Learning. **2020**, 2020, 0
- 54 Optimal Function Prediction of Key Aberrant Genes in Early-onset Preeclampsia Using a Modified Network-based Guilt by Association Method. **2018**, 47, 1688-1693
- 53 Challenges and opportunities in network-based solutions for biological questions. **2021**, 0
- 52 Emerging Machine Learning Techniques for Modelling Cellular Complex Systems in Alzheimer's Disease.. **2021**, 1338, 199-208 0
- 51 Fuzzy and Rough Set Theory Based Computational Framework for Mining Genetic Interaction Triplets from Gene Expression Profiles for Lung Adenocarcinoma. **2021**, PP, 2
- 50 Disentangling direct from indirect relationships in association networks.. **2022**, 119, 0
- 49 Network biology and artificial intelligence drive the understanding of the multidrug resistance phenotype in cancer.. **2022**, 60, 100811 3
- 48 Bayesian networks as a novel tool to enhance interpretability and predictive power of ecological models. **2022**, 68, 101539 1

- 47 Identifying large-scale interaction atlases using probabilistic graphs and external knowledge.. **2022**, 6, e27
- 46 Inference of genetic regulatory networks with regulatory hubs using vector autoregressions and automatic relevance determination with model selections.. **2021**, 20, 121-143 1
- 45 Stabilization of Boolean control networks with state-triggered impulses. **2022**, 65, 1
- 44 Faster MCMC for Gaussian latent position network models. 1-26
- 43 Degree of Freedom of Gene Expression in *Saccharomyces cerevisiae*.. **2022**, e0083821
- 42 Correlation Imputation for Single-Cell RNA-seq.. **2022**,
- 41 Dynamical Modeling for non-Gaussian Data with High-dimensional Sparse Ordinary Differential Equations. **2022**, 107483 0
- 40 Genes and Cell Type Specification in Cerebellar Development. **2022**, 333-351
- 39 Inferring network structures via signal Lasso. **2021**, 3, 0
- 38 Network-based analysis of fluid flows: Progress and outlook. **2022**, 131, 100823 1
- 37 Presentation1.pdf. **2018**,
- 36 Presentation2.zip. **2018**,
- 35 Data_Sheet_1.PDF. **2020**,
- 34 Data_Sheet_2.ZIP. **2020**,
- 33 Table_1.XLSX. **2020**,
- 32 Data_Sheet_1.PDF. **2019**,
- 31 Network Biology for Biomarker Discovery and Therapy in Cancer. **2022**, 163-183
- 30 Coordinated control of neuronal differentiation and wiring by a sustained code of transcription factors. 0

29	Crosstalk between PI3K/AKT/mTOR and WNT/ β Catenin signaling in GBM - Could combination therapy checkmate the collusion?. 2022 , 110350		0
28	A Novel Strategy for Dynamic Modelling of Genome-Scale Interaction Networks.		
27	American Society of Maxillofacial Surgeons: The Last 25 Years and the Next 25 Years. 2022 , 3, 255-262		
26	The Application of Databases and Bioinformatics for the Genome Editing of Crops. 2022 , 173-195		
25	CELLoGeNe - an Energy Landscape Framework for Logical Networks Controlling Cell Decisions. 2022 , 104743		
24	Combining kinetic orders for efficient S-System modelling of gene regulatory network. <i>BioSystems</i> , 2022 , 104736	1.9	0
23	Inference of Genetic Networks using Random Forests: A Quantitative Weighting Method for Gene Expression Data. 2022 ,		1
22	Using genome-wide expression compendia to study microorganisms. 2022 , 20, 4315-4324		0
21	Probabilistic Matrix Factorization for Gene Regulatory Network Inference.		0
20	Computational systems biology in disease modeling and control, review and perspectives. 2022 , 8,		1
19	Temporary and permanent control of partially specified Boolean networks. 2022 , 104795		0
18	Molecular Mechanisms Regulating the Oil Biosynthesis in Olive (<i>Olea europaea</i> L.) Fruits Revealed by Transcriptomic Analysis. 2022 , 12, 2718		0
17	Measurement and meaning in gene expression evolution. 2023 , 111-129		0
16	ViLoN β multi-layer network approach to data integration demonstrated for patient stratification.		0
15	The applications of network analysis in fruit ripening. 2023 , 311, 111785		0
14	Network-based approaches for modeling disease regulation and progression. 2022 ,		0
13	A Novel Reverse Engineering Approach for Gene Regulatory Networks. 2023 , 310-321		1
12	Improving gene regulatory network inference and assessment: The importance of using network structure.		0

11	Inference of genetic networks using random forests:Performance improvement using a new variable importance measure. 2022 , 22, 88-109	0
10	Rangeland species potential mapping using machine learning algorithms. 2023 , 189, 106900	0
9	GENECI: A novel evolutionary machine learning consensus-based approach for the inference of gene regulatory networks. 2023 , 155, 106653	0
8	Mini-review: Gene regulatory network benefits from three-dimensional chromatin conformation and structural biology. 2023 , 21, 1728-1737	0
7	Optimizing Multi-variable Time Series Forecasting Using Metaheuristics. 2023 , 103-117	0
6	A novel strategy for dynamic modeling of genome-scale interaction networks. 2023 , 39,	0
5	Improving gene regulatory network inference and assessment: The importance of using network structure. 14,	0
4	Inferring gene regulatory networks using transcriptional profiles as dynamical attractors.	0
3	A translome-transcriptome multi-omics gene regulatory network reveals the complicated functional landscape of maize. 2023 , 24,	0
2	Iterative transcription factor screening enables rapid generation of microglia-like cells from human iPSC.	1
1	Explainable fault prediction using learning fuzzy cognitive maps.	0