Neil D Lawrence

List of Publications by Year
in descending order

65 papers	3,355 citations	218677 26 h-index	206112 48 g-index
73 all docs	73 docs citations	73 times ranked	4453 citing authors

#	Article	IF	Citations
1	Solving Schrödinger Bridges via Maximum Likelihood. Entropy, 2021, 23, 1134.	2.2	11
2	Data-Driven Mode Identification and Unsupervised Fault Detection for Nonlinear Multimode Processes. IEEE Transactions on Industrial Informatics, 2020, 16, 3651-3661.	11.3	51
3	Memory and mental time travel in humans and social robots. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180025.	4.0	24
4	Gaussian Process Latent Force Models for Learning and Stochastic Control of Physical Systems. IEEE Transactions on Automatic Control, 2019, 64, 2953-2960.	5.7	29
5	The Emergence of Organizing Structure in Conceptual Representation. Cognitive Science, 2018, 42, 809-832.	1.7	8
6	Single-cell RNA-seq and computational analysis using temporal mixture modeling resolves $T_H 1/T_{FH}$ fate bifurcation in malaria. Science Immunology, 2017, 2, .	11.9	258
7	Efficient inference for sparse latent variable models of transcriptional regulation. Bioinformatics, 2017, 33, 3776-3783.	4.1	3
8	Deep recurrent Gaussian processes for outlier-robust system identification. Journal of Process Control, 2017, 60, 82-94.	3.3	17
9	A Gaussian Process Model for Inferring the Dynamic Transcription Factor Activity. , 2016, , .		1
10	An integrated probabilistic framework for robot perception, learning and memory. , 2016, , .		18
11	iCub Visual Memory Inspector: Visualising the iCub's Thoughts. Lecture Notes in Computer Science, 2016, , 48-57.	1.3	3
12	Monitoring Short Term Changes of Infectious Diseases in Uganda with Gaussian Processes. Lecture Notes in Computer Science, 2016, , 95-110.	1.3	0
13	A reverse-engineering approach to dissect post-translational modulators of transcription factor's activity from transcriptional data. BMC Bioinformatics, 2015, 16, 279.	2.6	7
14	Fast Nonparametric Clustering of Structured Time-Series. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 383-393.	13.9	39
15	Genome-wide modeling of transcription kinetics reveals patterns of RNA production delays. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13115-13120.	7.1	75
16	Warped linear mixed models for the genetic analysis of transformed phenotypes. Nature Communications, 2014, 5, 4890.	12.8	47
17	Inference of RNA Polymerase II Transcription Dynamics from Chromatin Immunoprecipitation Time Course Data. PLoS Computational Biology, 2014, 10, e1003598.	3.2	24
18	Consistent mapping of government malaria records across a changing territory delimitation. Malaria Journal, 2014, 13, .	2.3	1

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19	Gaussian Processes for Natural Language Processing. , 2014, , .		7
20	Hierarchical Bayesian modelling of gene expression time series across irregularly sampled replicates and clusters. BMC Bioinformatics, 2013, 14, 252.	2.6	77
21	Preface: Intelligent interactive data visualization. Data Mining and Knowledge Discovery, 2013, 27, 1-3.	3.7	2
22	Linear Latent Force Models Using Gaussian Processes. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2013, 35, 2693-2705.	13.9	91
23	Unravelling the enigma of selective vulnerability in neurodegeneration: motor neurons resistant to degeneration in ALS show distinct gene expression characteristics and decreased susceptibility to excitotoxicity. Acta Neuropathologica, 2013, 125, 95-109.	7.7	133
24	Mining Regulatory Network Connections by Ranking Transcription Factor Target Genes Using Time Series Expression Data. Methods in Molecular Biology, 2013, 939, 59-67.	0.9	0
25	Transcriptomic indices of fast and slow disease progression in two mouse models of amyotrophic lateral sclerosis. Brain, 2013, 136, 3305-3332.	7.6	81
26	Detecting regulatory gene–environment interactions with unmeasured environmental factors. Bioinformatics, 2013, 29, 1382-1389.	4.1	12
27	Genome-wide occupancy links Hoxa2 to Wnt–β-catenin signaling in mouse embryonic development. Nucleic Acids Research, 2012, 40, 3990-4001.	14.5	71
28	Kernels for Vector-Valued Functions: A Review. Foundations and Trends in Machine Learning, 2012, 4, 195-266.	69.0	346
29	Identifying targets of multiple co-regulating transcription factors from expression time-series by Bayesian model comparison. BMC Systems Biology, 2012, 6, 53.	3.0	20
30	Joint Modelling of Confounding Factors and Prominent Genetic Regulators Provides Increased Accuracy in Genetical Genomics Studies. PLoS Computational Biology, 2012, 8, e1002330.	3.2	94
31	Overlapping Mixtures of Gaussian Processes for the data association problem. Pattern Recognition, 2012, 45, 1386-1395.	8.1	72
32	Modeling Meiotic Chromosomes Indicates a Size Dependent Contribution of Telomere Clustering and Chromosome Rigidity to Homologue Juxtaposition. PLoS Computational Biology, 2012, 8, e1002496.	3.2	21
33	Accurate modeling of confounding variation in eQTL studies leads to a great increase in power to detect trans-regulatory effects. Nature Precedings, 2011, , .	0.1	0
34	A Simple Approach to Ranking Differentially Expressed Gene Expression Time Courses through Gaussian Process Regression. BMC Bioinformatics, 2011, 12, 180.	2.6	72
35	tigre: Transcription factor inference through gaussian process reconstruction of expression for bioconductor. Bioinformatics, 2011, 27, 1026-1027.	4.1	4
36	Elementary properties of $Ca_V1.3$ Ca^{2+} channels expressed in mouse cochlear inner hair cells. Journal of Physiology, 2010, 588, 187-199.	2.9	110

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37	TFInfer: a tool for probabilistic inference of transcription factor activities. Bioinformatics, 2010, 26, 2635-2636.	4.1	24
38	Ranking of gene regulators through differential equations and Gaussian processes. , 2010, , .		1
39	Model-based method for transcription factor target identification with limited data. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7793-7798.	7.1	87
40	Shared Gaussian Process Latent Variable Models for Handling Ambiguous Facial Expressions. , 2009, , .		3
41	Non-linear matrix factorization with Gaussian processes. , 2009, , .		111
42	puma: a Bioconductor package for propagating uncertainty in microarray analysis. BMC Bioinformatics, 2009, 10, 211.	2.6	66
43	Backing Off: Hierarchical Decomposition of Activity for 3D Novel Pose Recovery. , 2009, , .		10
44	Gaussian process modelling of latent chemical species: applications to inferring transcription factor activities. Bioinformatics, 2008, 24, i70-i75.	4.1	63
45	Topologically-constrained latent variable models. , 2008, , .		82
46	Ambiguity Modeling in Latent Spaces. Lecture Notes in Computer Science, 2008, , 62-73.	1.3	26
47	Hierarchical Gaussian process latent variable models. , 2007, , .		101
48	Modeling Human Locomotion with Topologically Constrained Latent Variable Models. , 2007, , 104-118.		18
49	Gaussian Process Latent Variable Models for Human Pose Estimation. , 2007, , 132-143.		58
50	Probabilistic inference of transcription factor concentrations and gene-specific regulatory activities. Bioinformatics, 2006, 22, 2775-2781.	4.1	87
51	A probabilistic dynamical model for quantitative inference of the regulatory mechanism of transcription. Bioinformatics, 2006, 22, 1753-1759.	4.1	34
52	Local distance preservation in the GP-LVM through back constraints. , 2006, , .		136
53	Probe-level measurement error improves accuracy in detecting differential gene expression. Bioinformatics, 2006, 22, 2107-2113.	4.1	68
54	Propagating uncertainty in microarray data analysis. Briefings in Bioinformatics, 2006, 7, 37-47.	6.5	21

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55	Fast Variational Inference for Gaussian Process Models Through KL-Correction. Lecture Notes in Computer Science, 2006, , 270-281.	1.3	13
56	Missing Data in Kernel PCA. Lecture Notes in Computer Science, 2006, , 751-758.	1.3	10
57	Variational inference for Student-t models: Robust Bayesian interpolation and generalised component analysis. Neurocomputing, 2005, 69, 123-141.	5.9	69
58	A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips. Bioinformatics, 2005, 21, 3637-3644.	4.1	66
59	Accounting for probe-level noise in principal component analysis of microarray data. Bioinformatics, 2005, 21, 3748-3754.	4.1	49
60	Extensions of the Informative Vector Machine. Lecture Notes in Computer Science, 2005, , 56-87.	1.3	19
61	Reducing the variability in cDNA microarray image processing by Bayesian inference. Bioinformatics, 2004, 20, 518-526.	4.1	29
62	Learning to learn with the informative vector machine. , 2004, , .		216
63	Note Relevance Determination. Perspectives in Neural Computing, 2002, , 128-133.	0.1	0
64	A Comparison of State-of-the-Art Classification Techniques with Application to Cytogenetics. Neural Computing and Applications, 2001, 10, 39-47.	5.6	25
65	Markov chain Monte Carlo algorithms for Gaussian processes. , 0, , 295-316.		9