

# Neil D Lawrence

## List of Publications by Year in descending order

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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	Kernels for Vector-Valued Functions: A Review. Foundations and Trends in Machine Learning, 2012, 4, 195-266.	69.0	346
2	Single-cell RNA-seq and computational analysis using temporal mixture modeling resolves T <sub>H</sub> 1/T <sub>H</sub> 17 fate bifurcation in malaria. Science Immunology, 2017, 2, .	11.9	258
3	Learning to learn with the informative vector machine. , 2004, , .		216
4	Local distance preservation in the GP-LVM through back constraints. , 2006, , .		136
5	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
6	Non-linear matrix factorization with Gaussian processes. , 2009, , .		111
7	Elementary properties of Ca <sub>v</sub> 1.3 Ca <sup>2+</sup> channels expressed in mouse cochlear inner hair cells. Journal of Physiology, 2010, 588, 187-199.	2.9	110
8	Hierarchical Gaussian process latent variable models. , 2007, , .		101
9	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
10	Linear Latent Force Models Using Gaussian Processes. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2013, 35, 2693-2705.	13.9	91
11	Probabilistic inference of transcription factor concentrations and gene-specific regulatory activities. Bioinformatics, 2006, 22, 2775-2781.	4.1	87
12	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
13	Topologically-constrained latent variable models. , 2008, , .		82
14	Transcriptomic indices of fast and slow disease progression in two mouse models of amyotrophic lateral sclerosis. Brain, 2013, 136, 3305-3332.	7.6	81
15	Hierarchical Bayesian modelling of gene expression time series across irregularly sampled replicates and clusters. BMC Bioinformatics, 2013, 14, 252.	2.6	77
16	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
17	A Simple Approach to Ranking Differentially Expressed Gene Expression Time Courses through Gaussian Process Regression. BMC Bioinformatics, 2011, 12, 180.	2.6	72
18	Overlapping Mixtures of Gaussian Processes for the data association problem. Pattern Recognition, 2012, 45, 1386-1395.	8.1	72

#	ARTICLE	IF	CITATIONS
19	Genome-wide occupancy links Hoxa2 to Wnt $\beta$ -catenin signaling in mouse embryonic development. Nucleic Acids Research, 2012, 40, 3990-4001.	14.5	71
20	Variational inference for Student-t models: Robust Bayesian interpolation and generalised component analysis. Neurocomputing, 2005, 69, 123-141.	5.9	69
21	Probe-level measurement error improves accuracy in detecting differential gene expression. Bioinformatics, 2006, 22, 2107-2113.	4.1	68
22	A tractable probabilistic model for Affymetrix probe-level analysis across multiple chips. Bioinformatics, 2005, 21, 3637-3644.	4.1	66
23	puma: a Bioconductor package for propagating uncertainty in microarray analysis. BMC Bioinformatics, 2009, 10, 211.	2.6	66
24	Gaussian process modelling of latent chemical species: applications to inferring transcription factor activities. Bioinformatics, 2008, 24, i70-i75.	4.1	63
25	Gaussian Process Latent Variable Models for Human Pose Estimation. , 2007, , 132-143.		58
26	Data-Driven Mode Identification and Unsupervised Fault Detection for Nonlinear Multimode Processes. IEEE Transactions on Industrial Informatics, 2020, 16, 3651-3661.	11.3	51
27	Accounting for probe-level noise in principal component analysis of microarray data. Bioinformatics, 2005, 21, 3748-3754.	4.1	49
28	Warped linear mixed models for the genetic analysis of transformed phenotypes. Nature Communications, 2014, 5, 4890.	12.8	47
29	Fast Nonparametric Clustering of Structured Time-Series. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 383-393.	13.9	39
30	A probabilistic dynamical model for quantitative inference of the regulatory mechanism of transcription. Bioinformatics, 2006, 22, 1753-1759.	4.1	34
31	Reducing the variability in cDNA microarray image processing by Bayesian inference. Bioinformatics, 2004, 20, 518-526.	4.1	29
32	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
33	Ambiguity Modeling in Latent Spaces. Lecture Notes in Computer Science, 2008, , 62-73.	1.3	26
34	A Comparison of State-of-the-Art Classification Techniques with Application to Cytogenetics. Neural Computing and Applications, 2001, 10, 39-47.	5.6	25
35	TFInfer: a tool for probabilistic inference of transcription factor activities. Bioinformatics, 2010, 26, 2635-2636.	4.1	24
36	Inference of RNA Polymerase II Transcription Dynamics from Chromatin Immunoprecipitation Time Course Data. PLoS Computational Biology, 2014, 10, e1003598.	3.2	24

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37	Memory and mental time travel in humans and social robots. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180025.	4.0	24
38	Propagating uncertainty in microarray data analysis. <i>Briefings in Bioinformatics</i> , 2006, 7, 37-47.	6.5	21
39	Modeling Meiotic Chromosomes Indicates a Size Dependent Contribution of Telomere Clustering and Chromosome Rigidity to Homologue Juxtaposition. <i>PLoS Computational Biology</i> , 2012, 8, e1002496.	3.2	21
40	Identifying targets of multiple co-regulating transcription factors from expression time-series by Bayesian model comparison. <i>BMC Systems Biology</i> , 2012, 6, 53.	3.0	20
41	Extensions of the Informative Vector Machine. <i>Lecture Notes in Computer Science</i> , 2005, , 56-87.	1.3	19
42	An integrated probabilistic framework for robot perception, learning and memory. , 2016, , .		18
43	Modeling Human Locomotion with Topologically Constrained Latent Variable Models. , 2007, , 104-118.		18
44	Deep recurrent Gaussian processes for outlier-robust system identification. <i>Journal of Process Control</i> , 2017, 60, 82-94.	3.3	17
45	Fast Variational Inference for Gaussian Process Models Through KL-Correction. <i>Lecture Notes in Computer Science</i> , 2006, , 270-281.	1.3	13
46	Detecting regulatory gene-environment interactions with unmeasured environmental factors. <i>Bioinformatics</i> , 2013, 29, 1382-1389.	4.1	12
47	Solving Schrödinger Bridges via Maximum Likelihood. <i>Entropy</i> , 2021, 23, 1134.	2.2	11
48	Missing Data in Kernel PCA. <i>Lecture Notes in Computer Science</i> , 2006, , 751-758.	1.3	10
49	Backing Off: Hierarchical Decomposition of Activity for 3D Novel Pose Recovery. , 2009, , .		10
50	Markov chain Monte Carlo algorithms for Gaussian processes. , 0, , 295-316.		9
51	The Emergence of Organizing Structure in Conceptual Representation. <i>Cognitive Science</i> , 2018, 42, 809-832.	1.7	8
52	A reverse-engineering approach to dissect post-translational modulators of transcription factor™s activity from transcriptional data. <i>BMC Bioinformatics</i> , 2015, 16, 279.	2.6	7
53	Gaussian Processes for Natural Language Processing. , 2014, , .		7
54	tigre: Transcription factor inference through gaussian process reconstruction of expression for bioconductor. <i>Bioinformatics</i> , 2011, 27, 1026-1027.	4.1	4

#	ARTICLE	IF	CITATIONS
55	Shared Gaussian Process Latent Variable Models for Handling Ambiguous Facial Expressions. , 2009, , .		3
56	Efficient inference for sparse latent variable models of transcriptional regulation. Bioinformatics, 2017, 33, 3776-3783.	4.1	3
57	iCub Visual Memory Inspector: Visualising the iCubâ€™s Thoughts. Lecture Notes in Computer Science, 2016, , 48-57.	1.3	3
58	Preface: Intelligent interactive data visualization. Data Mining and Knowledge Discovery, 2013, 27, 1-3.	3.7	2
59	Ranking of gene regulators through differential equations and Gaussian processes. , 2010, , .		1
60	Consistent mapping of government malaria records across a changing territory delimitation. Malaria Journal, 2014, 13, .	2.3	1
61	A Gaussian Process Model for Inferring the Dynamic Transcription Factor Activity. , 2016, , .		1
62	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
63	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
64	Note Relevance Determination. Perspectives in Neural Computing, 2002, , 128-133.	0.1	0
65	Monitoring Short Term Changes of Infectious Diseases in Uganda with Gaussian Processes. Lecture Notes in Computer Science, 2016, , 95-110.	1.3	0