

# Hidetoshi Shimodaira

## List of Publications by Year in descending order

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45  
papers

12,816  
citations

394421

19  
h-index

315739

38  
g-index

48  
all docs

48  
docs citations

48  
times ranked

16535  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Hypergraph Approach for Estimating Growth Mechanisms of Complex Networks. IEEE Access, 2022, 10, 35012-35025.	4.2	1
2	Non-parametric estimation of the preferential attachment function from one network snapshot. Journal of Complex Networks, 2021, 9, .	1.8	0
3	Joint estimation of non-parametric transitivity and preferential attachment functions in scientific co-authorship networks. Journal of Informetrics, 2020, 14, 101042.	2.9	5
4	Hyperlink regression via Bregman divergence. Neural Networks, 2020, 126, 362-383.	5.9	4
5	<b>PAFit</b> : An <i>R</i> Package for the Non-Parametric Estimation of Preferential Attachment and Node Fitness in Temporal Complex Networks. Journal of Statistical Software, 2020, 92, .	3.7	7
6	An Information Criterion for Auxiliary Variable Selection in Incomplete Data Analysis. Entropy, 2019, 21, 281.	2.2	2
7	Selective Inference for Testing Trees and Edges in Phylogenetics. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	11
8	Representation Learning with Weighted Inner Product for Universal Approximation of General Similarities. , 2019, , .		3
9	An information criterion for model selection with missing data via complete-data divergence. Annals of the Institute of Statistical Mathematics, 2018, 70, 421-438.	0.8	3
10	Transitivity vs Preferential Attachment: Determining the Driving Force Behind the Evolution of Scientific Co-Authorship Networks. Springer Proceedings in Complexity, 2018, , 262-271.	0.3	1
11	Spectral Graph-Based Method of Multimodal Word Embedding. , 2017, , .		1
12	Image and tag retrieval by leveraging image-group links with multi-domain graph embedding. , 2016, , .		2
13	Joint estimation of preferential attachment and node fitness in growing complex networks. Scientific Reports, 2016, 6, 32558.	3.3	43
14	Nonparametric Estimation of the Preferential Attachment Function in Complex Networks: Evidence of Deviations from Log Linearity. Springer Proceedings in Complexity, 2016, , 141-153.	0.3	2
15	Cross-validation of matching correlation analysis by resampling matching weights. Neural Networks, 2016, 75, 126-140.	5.9	5
16	Cross-Lingual Word Representations via Spectral Graph Embeddings. , 2016, , .		6
17	PAFit: A Statistical Method for Measuring Preferential Attachment in Temporal Complex Networks. PLoS ONE, 2015, 10, e0137796.	2.5	45
18	ESTIMATING SCALE-FREE NETWORKS VIA THE EXPONENTIATION OF MINIMAX CONCAVE PENALTY. Journal of the Japanese Society of Computational Statistics, 2015, 28, 139-154.	0.2	0

#	ARTICLE	IF	CITATIONS
19	Quantitative transcriptional control of ErbB receptor signaling undergoes graded to biphasic response for cell differentiation.. Journal of Biological Chemistry, 2014, 289, 20491.	3.4	1
20	Higher-order accuracy of multiscale-double bootstrap for testing regions. Journal of Multivariate Analysis, 2014, 130, 208-223.	1.0	1
21	Measuring preferential attachment in growing networks with missing-timelines using Markov chain Monte Carlo. Physica A: Statistical Mechanics and Its Applications, 2012, 391, 5031-5040.	2.6	14
22	Multiscale Bagging and Its Applications. IEICE Transactions on Information and Systems, 2011, E94-D, 1924-1932.	0.7	0
23	Frequentist and Bayesian measures of confidence via multiscale bootstrap for testing three regions. Annals of the Institute of Statistical Mathematics, 2010, 62, 189-208.	0.8	0
24	Assessing Statistical Reliability of LiNGAM via Multiscale Bootstrap. Lecture Notes in Computer Science, 2010, , 309-314.	1.3	4
25	A Scale-Free Structure Prior for Graphical Models with Applications in Functional Genomics. PLoS ONE, 2010, 5, e13580.	2.5	23
26	A preferential attachment model with Poisson growth for scale-free networks. Annals of the Institute of Statistical Mathematics, 2008, 60, 747-761.	0.8	18
27	Testing regions with nonsmooth boundaries via multiscale bootstrap. Journal of Statistical Planning and Inference, 2008, 138, 1227-1241.	0.6	55
28	Quantitative Transcriptional Control of ErbB Receptor Signaling Undergoes Graded to Biphasic Response for Cell Differentiation. Journal of Biological Chemistry, 2007, 282, 4045-4056.	3.4	157
29	Pvclust: an R package for assessing the uncertainty in hierarchical clustering. Bioinformatics, 2006, 22, 1540-1542.	4.1	2,127
30	Assessing the Uncertainty in Phylogenetic Inference. , 2005, , 463-493.		3
31	Parallelization of Phylogenetic Tree Inference Using Grid Technologies. Lecture Notes in Computer Science, 2005, , 103-116.	1.3	0
32	Mitochondrial Genome Variation in Eastern Asia and the Peopling of Japan. Genome Research, 2004, 14, 1832-1850.	5.5	446
33	Approximately unbiased tests of regions using multistep-multiscale bootstrap resampling. Annals of Statistics, 2004, 32, 2616.	2.6	256
34	Active learning algorithm using the maximum weighted log-likelihood estimator. Journal of Statistical Planning and Inference, 2003, 116, 149-162.	0.6	36
35	An Approximately Unbiased Test of Phylogenetic Tree Selection. Systematic Biology, 2002, 51, 492-508.	5.6	2,400
36	On the isotonic range statistic for testing against an ordered alternative. Journal of Statistical Planning and Inference, 2002, 105, 347-362.	0.6	14

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37	CONSEL: for assessing the confidence of phylogenetic tree selection. <i>Bioinformatics</i> , 2001, 17, 1246-1247.	4.1	1,958
38	MULTIPLE COMPARISONS OF LOG-LIKELIHOODS AND COMBINING NONNESTED MODELS WITH APPLICATIONS TO PHYLOGENETIC TREE SELECTION. <i>Communications in Statistics - Theory and Methods</i> , 2001, 30, 1751-1772.	1.0	40
39	Evaluating Hypotheses on the Origin and Evolution of the New Zealand Alpine Cicadas ( <i>Maoricicada</i> ) Using Multiple-Comparison Tests of Tree Topology. <i>Molecular Biology and Evolution</i> , 2001, 18, 223-234.	8.9	94
40	Appropriate Likelihood Ratio Tests and Marginal Distributions for Evolutionary Tree Models with Constraints on Parameters. <i>Molecular Biology and Evolution</i> , 2000, 17, 798-803.	8.9	91
41	Improving predictive inference under covariate shift by weighting the log-likelihood function. <i>Journal of Statistical Planning and Inference</i> , 2000, 90, 227-244.	0.6	942
42	Consistency of SINE Insertion Topology and Flanking Sequence Tree: Quantifying Relationships Among Cetartiodactyls. <i>Molecular Biology and Evolution</i> , 2000, 17, 1417-1424.	8.9	35
43	Multiple Comparisons of Log-Likelihoods with Applications to Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 1999, 16, 1114-1116.	8.9	3,859
44	An Application of Multiple Comparison Techniques to Model Selection. <i>Annals of the Institute of Statistical Mathematics</i> , 1998, 50, 1-13.	0.8	58
45	Assessing the Error Probability of the Model Selection Test. <i>Annals of the Institute of Statistical Mathematics</i> , 1997, 49, 395-410.	0.8	18