

Dirk Husmeier

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7982139/publications.pdf>

Version: 2024-02-01

64
papers

1,686
citations

471061

17
h-index

301761

39
g-index

68
all docs

68
docs citations

68
times ranked

1632
citing authors

#	ARTICLE	IF	CITATIONS
1	Sensitivity and specificity of inferring genetic regulatory interactions from microarray experiments with dynamic Bayesian networks. <i>Bioinformatics</i> , 2003, 19, 2271-2282.	1.8	461
2	Comparative evaluation of reverse engineering gene regulatory networks with relevance networks, graphical gaussian models and bayesian networks. <i>Bioinformatics</i> , 2006, 22, 2523-2531.	1.8	301
3	Non-homogeneous dynamic Bayesian networks with Bayesian regularization for inferring gene regulatory networks with gradually time-varying structure. <i>Machine Learning</i> , 2013, 90, 191-230.	3.4	80
4	Detecting Recombination in 4-Taxa DNA Sequence Alignments with Bayesian Hidden Markov Models and Markov Chain Monte Carlo. <i>Molecular Biology and Evolution</i> , 2003, 20, 315-337.	3.5	60
5	Modelling non-stationary gene regulatory processes with a non-homogeneous Bayesian network and the allocation sampler. <i>Bioinformatics</i> , 2008, 24, 2071-2078.	1.8	55
6	GENE REGULATORY NETWORK RECONSTRUCTION BY BAYESIAN INTEGRATION OF PRIOR KNOWLEDGE AND/OR DIFFERENT EXPERIMENTAL CONDITIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 543-572.	0.3	51
7	Non-homogeneous dynamic Bayesian networks for continuous data. <i>Machine Learning</i> , 2011, 83, 355-419.	3.4	50
8	Changes and classification in myocardial contractile function in the left ventricle following acute myocardial infarction. <i>Journal of the Royal Society Interface</i> , 2017, 14, 20170203.	1.5	50
9	Rationale and design of the Medical Research Council's Precision Medicine with Zibotentan in Microvascular Angina (PRIZE) trial. <i>American Heart Journal</i> , 2020, 229, 70-80.	1.2	40
10	Advances in computational modelling for personalised medicine after myocardial infarction. <i>Heart</i> , 2018, 104, 550-557.	1.2	39
11	Hemodynamic assessment of pulmonary hypertension in mice: a model-based analysis of the disease mechanism. <i>Biomechanics and Modeling in Mechanobiology</i> , 2019, 18, 219-243.	1.4	26
12	The Bayesian Evidence Scheme for Regularizing Probability-Density Estimating Neural Networks. <i>Neural Computation</i> , 2000, 12, 2685-2717.	1.3	24
13	BAYESIAN INTEGRATION OF BIOLOGICAL PRIOR KNOWLEDGE INTO THE RECONSTRUCTION OF GENE REGULATORY NETWORKS WITH BAYESIAN NETWORKS. , 2007, , .		22
14	Statistical inference of regulatory networks for circadian regulation. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 227-73.	0.2	22
15	Estimating prognosis in patients with acute myocardial infarction using personalized computational heart models. <i>Scientific Reports</i> , 2017, 7, 13527.	1.6	22
16	Gaussian process emulation to accelerate parameter estimation in a mechanical model of the left ventricle: a critical step towards clinical end-user relevance. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20190114.	1.5	22
17	A Non-Homogeneous Dynamic Bayesian Network with Sequentially Coupled Interaction Parameters for Applications in Systems and Synthetic Biology. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2012, 11, .	0.2	21
18	Regularization of non-homogeneous dynamic Bayesian networks with global information-coupling based on hierarchical Bayesian models. <i>Machine Learning</i> , 2013, 91, 105-154.	3.4	19

#	ARTICLE	IF	CITATIONS
19	Assessing model mismatch and model selection in a Bayesian uncertainty quantification analysis of a fluid-dynamics model of pulmonary blood circulation. <i>Journal of the Royal Society Interface</i> , 2020, 17, 20200886.	1.5	17
20	Fast Parameter Inference in a Biomechanical Model of the Left Ventricle by Using Statistical Emulation. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2019, 68, 1555-1576.	0.5	16
21	Bayesian integration of biological prior knowledge into the reconstruction of gene regulatory networks with Bayesian networks. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007, 6, 85-95.	0.4	16
22	Detecting recombination with MCMC. <i>Bioinformatics</i> , 2002, 18, S345-S353.	1.8	15
23	Detecting interspecific recombination with a pruned probabilistic divergence measure. <i>Bioinformatics</i> , 2005, 21, 1797-1806.	1.8	15
24	Dynamic Bayesian networks in molecular plant science: inferring gene regulatory networks from multiple gene expression time series. <i>Euphytica</i> , 2012, 183, 361-377.	0.6	15
25	MCMC methods for inference in a mathematical model of pulmonary circulation. <i>Statistica Neerlandica</i> , 2018, 72, 306-338.	0.9	15
26	Influence of image segmentation on one-dimensional fluid dynamics predictions in the mouse pulmonary arteries. <i>Journal of the Royal Society Interface</i> , 2019, 16, 20190284.	1.5	15
27	A Bayesian approach to discriminate between alternative DNA sequence segmentations. <i>Bioinformatics</i> , 2002, 18, 226-234.	1.8	13
28	Inference of the drivers of collective movement in two cell types: <i>Dictyostelium</i> and melanoma. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20160695.	1.5	13
29	Approximate Bayesian inference in semi-mechanistic models. <i>Statistics and Computing</i> , 2017, 27, 1003-1040.	0.8	12
30	A hierarchical machine learning framework for the analysis of large scale animal movement data. <i>Movement Ecology</i> , 2021, 9, 6.	1.3	12
31	Neural network-based left ventricle geometry prediction from CMR images with application in biomechanics. <i>Artificial Intelligence in Medicine</i> , 2021, 119, 102140.	3.8	10
32	Modelling non-stationary dynamic gene regulatory processes with the BGM model. <i>Computational Statistics</i> , 2011, 26, 199-218.	0.8	9
33	Gradient Matching Methods for Computational Inference in Mechanistic Models for Systems Biology: A Review and Comparative Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 180.	2.0	9
34	Segmenting bacterial and viral DNA sequence alignments with a trans-dimensional phylogenetic factorial hidden Markov model. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2009, 58, 307-327.	0.5	8
35	A sparse hierarchical Bayesian model for detecting relevant antigenic sites in virus evolution. <i>Computational Statistics</i> , 2017, 32, 803-843.	0.8	8
36	Markov chain Monte Carlo with Gaussian processes for fast parameter estimation and uncertainty quantification in a 1D fluid-dynamics model of the pulmonary circulation. <i>International Journal for Numerical Methods in Biomedical Engineering</i> , 2021, 37, e3421.	1.0	8

#	ARTICLE	IF	CITATIONS
37	Addressing the Shortcomings of Three Recent Bayesian Methods for Detecting Interspecific Recombination in DNA Sequence Alignments. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2008, 7, Article 34.	0.2	7
38	Combining rapid antigen testing and syndromic surveillance improves community-based COVID-19 detection in a low-income country. <i>Nature Communications</i> , 2022, 13, .	5.8	7
39	Overview and Evaluation of Recent Methods for Statistical Inference of Gene Regulatory Networks from Time Series Data. <i>Methods in Molecular Biology</i> , 2019, 1883, 49-94.	0.4	6
40	Predicting ecological regime shift under climate change: New modelling techniques and potential of molecular-based approaches. <i>Environmental Epigenetics</i> , 2013, 59, 403-417.	0.9	5
41	Inferring bi-directional interactions between circadian clock genes and metabolism with model ensembles. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 143-67.	0.2	5
42	Approximate parameter inference in systems biology using gradient matching: a comparative evaluation. <i>BioMedical Engineering OnLine</i> , 2016, 15, 80.	1.3	5
43	Improving the identification of antigenic sites in the H1N1 influenza virus through accounting for the experimental structure in a sparse hierarchical Bayesian model. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2019, 68, 859-885.	0.5	5
44	Gaussian process enhanced semi-automatic approximate Bayesian computation: parameter inference in a stochastic differential equation system for chemotaxis. <i>Journal of Computational Physics</i> , 2021, 429, 109999.	1.9	5
45	Sensitivity analysis and inverse uncertainty quantification for the left ventricular passive mechanics. <i>Biomechanics and Modeling in Mechanobiology</i> , 2022, 21, 953-982.	1.4	5
46	Bayesian optimisation for efficient parameter inference in a cardiac mechanics model of the left ventricle. <i>International Journal for Numerical Methods in Biomedical Engineering</i> , 2022, 38, e3593.	1.0	5
47	System Relaxation and Thermodynamic Integration. <i>Molecular Simulation</i> , 1992, 8, 285-295.	0.9	4
48	Inference in a Partial Differential Equations Model of Pulmonary Arterial and Venous Blood Circulation Using Statistical Emulation. <i>Lecture Notes in Computer Science</i> , 2017, , 184-198.	1.0	4
49	Optimal estimation of drift and diffusion coefficients in the presence of static localization error. <i>Physical Review E</i> , 2019, 100, 022134.	0.8	4
50	MCMC with delayed acceptance using a surrogate model with an application to cardiovascular fluid dynamics. , 0, , .		4
51	ShinyKCode: an interactive application for ODE parameter inference using gradient matching. <i>Bioinformatics</i> , 2018, 34, 2314-2315.	1.8	3
52	Analysis of Cardiac Amyloidosis Progression Using Model-Based Markers. <i>Frontiers in Physiology</i> , 2020, 11, 324.	1.3	3
53	Targeting Bayes factors with direct-path non-equilibrium thermodynamic integration. <i>Computational Statistics</i> , 2017, 32, 717-761.	0.8	2
54	Quantification of Myocardial Perfusion Lesions using Spatially Variant Finite Mixture Modelling of DCE-MRI. , 0, , .		2

#	ARTICLE	IF	CITATIONS
55	Improving Cardio-Mechanic Inference by Combining in Vivo Strain Data with Ex Vivo Volume-Pressure Data. Journal of the Royal Statistical Society Series C: Applied Statistics, 2022, 71, 906-931.	0.5	2
56	Statistical inference in mechanistic models: time warping for improved gradient matching. Computational Statistics, 2018, 33, 1091-1123.	0.8	1
57	Model selection via marginal likelihood estimation by combining thermodynamic integration and gradient matching. Statistics and Computing, 2019, 29, 853-867.	0.8	1
58	Classification of Myocardial Blood Flow based on Dynamic Contrast-Enhanced Magnetic Resonance Imaging using Hierarchical Bayesian Models. Journal of the Royal Statistical Society Series C: Applied Statistics, 2022, 71, 1085-1115.	0.5	1
59	DETECTING MOSAIC STRUCTURES IN DNA SEQUENCE ALIGNMENTS. , 2006, , 1-35.		0
60	Statistical modelling of cell movement. Statistica Neerlandica, 2018, 72, 265-280.	0.9	0
61	R package for statistical inference in dynamical systems using kernel based gradient matching: KCode. Computational Statistics, 2021, 36, 715-747.	0.8	0
62	Inferring microscale properties of interacting systems from macroscale observations. Physical Review Research, 2021, 3, .	1.3	0
63	Rationale and design of the Medical Research Council Precision medicine with Zibotentan in microvascular angina (PRIZE) trial MRI sub-study. , 2021, , .		0
64	Emulation-accelerated Hamiltonian Monte Carlo algorithms for parameter estimation and uncertainty quantification in differential equation models. Statistics and Computing, 2022, 32, 1.	0.8	0