Dirk Husmeier

List of Publications by Year
in descending order

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	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
2	Sensitivity analysis and inverse uncertainty quantification for the left ventricular passive mechanics. Biomechanics and Modeling in Mechanobiology, 2022, 21, 953-982.	1.4	5
3	Bayesian optimisation for efficient parameter inference in a cardiac mechanics model of the left ventricle. International Journal for Numerical Methods in Biomedical Engineering, 2022, 38, e3593.	1.0	5
4	Improving Cardio-Mechanic Inference by Combining in Vivo Strain Data with Ex Vivo Volumeâ€"Pressure Data. Journal of the Royal Statistical Society Series C: Applied Statistics, 2022, 71, 906-931.	0.5	2
5	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
6	Combining rapid antigen testing and syndromic surveillance improves community-based COVID-19 detection in a low-income country. Nature Communications, 2022, 13, .	5.8	7
7	Gaussian process enhanced semi-automatic approximate Bayesian computation: parameter inference in a stochastic differential equation system for chemotaxis. Journal of Computational Physics, 2021, 429, 109999.	1.9	5
8	<scp>Markov chain Monte Carlo</scp> with Gaussian processes for fast parameter estimation and uncertainty quantification in a <scp>1D</scp> fluidâ€dynamics model of the pulmonary circulation. International Journal for Numerical Methods in Biomedical Engineering, 2021, 37, e3421.	1.0	8
9	R package for statistical inference in dynamical systems using kernel based gradient matching: KGode. Computational Statistics, 2021, 36, 715-747.	0.8	0
10	A hierarchical machine learning framework for the analysis of large scale animal movement data. Movement Ecology, 2021, 9, 6.	1.3	12
11	Neural network-based left ventricle geometry prediction from CMR images with application in biomechanics. Artificial Intelligence in Medicine, 2021, 119, 102140.	3.8	10
12	Inferring microscale properties of interacting systems from macroscale observations. Physical Review Research, 2021, 3, .	1.3	0
13	3â€¦Rationale and design of the Medical Research Council Precision medicine with Zibotentan in microvascular angina (PRIZE) trial MRI sub-study. , 2021, , .		0
14	Rationale and design of the Medical Research Council's Precision Medicine with Zibotentan in Microvascular Angina (PRIZE) trial. American Heart Journal, 2020, 229, 70-80.	1.2	40
15	Analysis of Cardiac Amyloidosis Progression Using Model-Based Markers. Frontiers in Physiology, 2020, 11, 324.	1.3	3
16	Assessing model mismatch and model selection in a Bayesian uncertainty quantification analysis of a fluid-dynamics model of pulmonary blood circulation. Journal of the Royal Society Interface, 2020, 17, 20200886.	1.5	17
17	Improving the identification of antigenic sites in the H1N1 influenza virus through accounting for the experimental structure in a sparse hierarchical Bayesian model. Journal of the Royal Statistical Society Series C: Applied Statistics, 2019, 68, 859-885.	0.5	5
18	Gaussian process emulation to accelerate parameter estimation in a mechanical model of the left ventricle: a critical step towards clinical end-user relevance. Journal of the Royal Society Interface, 2019, 16, 20190114.	1.5	22

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19	Fast Parameter Inference in a Biomechanical Model of the Left Ventricle by Using Statistical Emulation. Journal of the Royal Statistical Society Series C: Applied Statistics, 2019, 68, 1555-1576.	0.5	16
20	Optimal estimation of drift and diffusion coefficients in the presence of static localization error. Physical Review E, 2019, 100, 022134.	0.8	4
21	Influence of image segmentation on one-dimensional fluid dynamics predictions in the mouse pulmonary arteries. Journal of the Royal Society Interface, 2019, 16, 20190284.	1.5	15
22	Model selection via marginal likelihood estimation by combining thermodynamic integration and gradient matching. Statistics and Computing, 2019, 29, 853-867.	0.8	1
23	Overview and Evaluation of Recent Methods for Statistical Inference of Gene Regulatory Networks from Time Series Data. Methods in Molecular Biology, 2019, 1883, 49-94.	0.4	6
24	Hemodynamic assessment of pulmonary hypertension in mice: a model-based analysis of the disease mechanism. Biomechanics and Modeling in Mechanobiology, 2019, 18, 219-243.	1.4	26
25	Statistical inference in mechanistic models: time warping for improved gradient matching. Computational Statistics, 2018, 33, 1091-1123.	0.8	1
26	ShinyKGode: an interactive application for ODE parameter inference using gradient matching. Bioinformatics, 2018, 34, 2314-2315.	1.8	3
27	Advances in computational modelling for personalised medicine after myocardial infarction. Heart, 2018, 104, 550-557.	1.2	39
28	MCMC methods for inference in a mathematical model of pulmonary circulation. Statistica Neerlandica, 2018, 72, 306-338.	0.9	15
29	Statistical modelling of cell movement. Statistica Neerlandica, 2018, 72, 265-280.	0.9	0
30	Approximate Bayesian inference in semi-mechanistic models. Statistics and Computing, 2017, 27, 1003-1040.	0.8	12
31	Inference in a Partial Differential Equations Model of Pulmonary Arterial and Venous Blood Circulation Using Statistical Emulation. Lecture Notes in Computer Science, 2017, , 184-198.	1.0	4
32	Estimating prognosis in patients with acute myocardial infarction using personalized computational heart models. Scientific Reports, 2017, 7, 13527.	1.6	22
33	Changes and classification in myocardial contractile function in the left ventricle following acute myocardial infarction. Journal of the Royal Society Interface, 2017, 14, 20170203.	1.5	50
34	Targeting Bayes factors with direct-path non-equilibrium thermodynamic integration. Computational Statistics, 2017, 32, 717-761.	0.8	2
35	A sparse hierarchical Bayesian model for detecting relevant antigenic sites in virus evolution. Computational Statistics, 2017, 32, 803-843.	0.8	8
36	Inference of the drivers of collective movement in two cell types: *Dictyostelium* and melanoma. Journal of the Royal Society Interface, 2016, 13, 20160695.	1.5	13

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37	Approximate parameter inference in systems biology using gradient matching: a comparative evaluation. BioMedical Engineering OnLine, 2016, 15, 80.	1.3	5
38	Gradient Matching Methods for Computational Inference in Mechanistic Models for Systems Biology: A Review and Comparative Analysis. Frontiers in Bioengineering and Biotechnology, 2015, 3, 180.	2.0	9
39	Inferring bi-directional interactions between circadian clock genes and metabolism with model ensembles. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 143-67.	0.2	5
40	Statistical inference of regulatory networks for circadian regulation. Statistical Applications in Genetics and Molecular Biology, 2014, 13, 227-73.	0.2	22
41	Regularization of non-homogeneous dynamic Bayesian networks with global information-coupling based on hierarchical Bayesian models. Machine Learning, 2013, 91, 105-154.	3.4	19
42	Non-homogeneous dynamic Bayesian networks with Bayesian regularization for inferring gene regulatory networks with gradually time-varying structure. Machine Learning, 2013, 90, 191-230.	3.4	80
43	Predicting ecological regime shift under climate change: New modelling techniques and potential of molecular-based approaches. Environmental Epigenetics, 2013, 59, 403-417.	0.9	5
44	A Non-Homogeneous Dynamic Bayesian Network with Sequentially Coupled Interaction Parameters for Applications in Systems and Synthetic Biology. Statistical Applications in Genetics and Molecular Biology, 2012, 11, .	0.2	21
45	Dynamic Bayesian networks in molecular plant science: inferring gene regulatory networks from multiple gene expression time series. Euphytica, 2012, 183, 361-377.	0.6	15
46	Non-homogeneous dynamic Bayesian networks forÂcontinuous data. Machine Learning, 2011, 83, 355-419.	3.4	50
47	Modelling non-stationary dynamic gene regulatory processes with the BGM model. Computational Statistics, 2011, 26, 199-218.	0.8	9
48	Segmenting bacterial and viral DNA sequence alignments with a trans-dimensional phylogenetic factorial hidden Markov model. Journal of the Royal Statistical Society Series C: Applied Statistics, 2009, 58, 307-327.	0.5	8
49	GENE REGULATORY NETWORK RECONSTRUCTION BY BAYESIAN INTEGRATION OF PRIOR KNOWLEDGE AND/OR DIFFERENT EXPERIMENTAL CONDITIONS. Journal of Bioinformatics and Computational Biology, 2008, 06, 543-572.	0.3	51
50	Addressing the Shortcomings of Three Recent Bayesian Methods for Detecting Interspecific Recombination in DNA Sequence Alignments. Statistical Applications in Genetics and Molecular Biology, 2008, 7, Article 34.	0.2	7
51	Modelling non-stationary gene regulatory processes with a non-homogeneous Bayesian network and the allocation sampler. Bioinformatics, 2008, 24, 2071-2078.	1.8	55
52	BAYESIAN INTEGRATION OF BIOLOGICAL PRIOR KNOWLEDGE INTO THE RECONSTRUCTION OF GENE REGULATORY NETWORKS WITH BAYESIAN NETWORKS. , 2007, , .		22
53	Bayesian integration of biological prior knowledge into the reconstruction of gene regulatory networks with Bayesian networks. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 85-95.	0.4	16
54	DETECTING MOSAIC STRUCTURES IN DNA SEQUENCE ALIGNMENTS. , 2006, , 1-35.		0

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55	Comparative evaluation of reverse engineering gene regulatory networks with relevance networks, graphical gaussian models and bayesian networks. Bioinformatics, 2006, 22, 2523-2531.	1.8	301
56	Detecting interspecific recombination with a pruned probabilistic divergence measure. Bioinformatics, 2005, 21, 1797-1806.	1.8	15
57	Sensitivity and specificity of inferring genetic regulatory interactions from microarray experiments with dynamic Bayesian networks. Bioinformatics, 2003, 19, 2271-2282.	1.8	461
58	Detecting Recombination in 4-Taxa DNA Sequence Alignments with Bayesian Hidden Markov Models and Markov Chain Monte Carlo. Molecular Biology and Evolution, 2003, 20, 315-337.	3.5	60
59	Detecting recombination with MCMC. Bioinformatics, 2002, 18, S345-S353.	1.8	15
60	A Bayesian approach to discriminate between alternative DNA sequence segmentations. Bioinformatics, 2002, 18, 226-234.	1.8	13
61	The Bayesian Evidence Scheme for Regularizing Probability-Density Estimating Neural Networks. Neural Computation, 2000, 12, 2685-2717.	1.3	24
62	System Relaxation and Thermodynamic Integration. Molecular Simulation, 1992, 8, 285-295.	0.9	4
63	MCMC with delayed acceptance using a surrogate model with an application to cardiovascular fluid dynamics. , 0, , .		4
64	Quantification of Myocardial Perfusion Lesions using Spatially Variant Finite Mixture Modelling of DCE-MRI. , 0, , .		2