

# Carsten Marr

## List of Publications by Year in descending order

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Version: 2024-02-01

79  
papers

3,830  
citations

159585

30  
h-index

149698

56  
g-index

108  
all docs

108  
docs citations

108  
times ranked

6633  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Parameter inference with analytical propagators for stochastic models of autoregulated gene expression. <i>International Journal of Nonlinear Sciences and Numerical Simulation</i> , 2022, 23, 565-577.                                    | 1.0  | 4         |
| 2  | The value of longitudinal clinical data and paired CT scans in predicting the deterioration of COVID-19 revealed by an artificial intelligence system. <i>IScience</i> , 2022, 25, 104227.  | 4.1  | 5         |
| 3  | Computational modeling of stem and progenitor cell kinetics identifies plausible hematopoietic lineage hierarchies. <i>IScience</i> , 2021, 24, 102120.   | 4.1  | 7         |
| 4  | InstantDL: an easy-to-use deep learning pipeline for image segmentation and classification. <i>BMC Bioinformatics</i> , 2021, 22, 103.  | 2.6  | 10        |
| 5  | Fourier Transform of Percoll Gradients Boosts CNN Classification of Hereditary Hemolytic Anemias. , 2021, , .   |      | 1         |
| 6  | NG2-Glia Transiently Overcome Their Homeostatic Network and Contribute to Wound Closure After Brain Injury. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 662056.   | 3.7  | 23        |
| 7  | Tens of images can suffice to train neural networks for malignant leukocyte detection. <i>Scientific Reports</i> , 2021, 11, 7995.  | 3.3  | 15        |
| 8  | Cellular connectomes as arbiters of local circuit models in the cerebral cortex. <i>Nature Communications</i> , 2021, 12, 2785.   | 12.8 | 11        |
| 9  | T cells armed with C-X-C chemokine receptor type 6 enhance adoptive cell therapy for pancreatic tumours. <i>Nature Biomedical Engineering</i> , 2021, 5, 1246-1260.   | 22.5 | 80        |
| 10 | CHIP and hips: clonal hematopoiesis is common in patients undergoing hip arthroplasty and is associated with autoimmune disease. <i>Blood</i> , 2021, 138, 1727-1732.   | 1.4  | 58        |
| 11 | Combined tumor-directed recruitment and protection from immune suppression enable CAR T cell efficacy in solid tumors. <i>Science Advances</i> , 2021, 7, .   | 10.3 | 56        |
| 12 | Mechanistic models of blood cell fate decisions in the era of single-cell data. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100355.   | 2.6  | 2         |
| 13 | Highly accurate differentiation of bone marrow cell morphologies using deep neural networks on a large image data set. <i>Blood</i> , 2021, 138, 1917-1927.   | 1.4  | 62        |
| 14 | N6-methyladenosine (m <sup>6</sup> A) depletion regulates pluripotency exit by activating signaling pathways in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, . | 7.1  | 18        |
| 15 | Histopathology-Based Deep-Learning Predicts Atherosclerotic Lesions in Intravascular Imaging. <i>Frontiers in Cardiovascular Medicine</i> , 2021, 8, 779807.  | 2.4  | 1         |
| 16 | MitoSegNet: Easy-to-use Deep Learning Segmentation for Analyzing Mitochondrial Morphology. <i>IScience</i> , 2020, 23, 101601.  | 4.1  | 44        |
| 17 | H4K20 Methylation Is Differently Regulated by Dilution and Demethylation in Proliferating and Cell-Cycle-Arrested <i>Xenopus</i> Embryos. <i>Cell Systems</i> , 2020, 11, 653-662.e8.   | 6.2  | 6         |
| 18 | Injury triggers fascia fibroblast collective cell migration to drive scar formation through N-cadherin. <i>Nature Communications</i> , 2020, 11, 5653.  | 12.8 | 66        |

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|----|---|------|-----------|
| 19 | Single-Cell Tracing Dissects Regulation of Maintenance and Inheritance of Transcriptional Reinduction Memory. <i>Molecular Cell</i> , 2020, 78, 915-925.e7.                                   | 9.7  | 18        |
| 20 | Gene Networks with Transcriptional Bursting Recapitulate Rare Transient Coordinated High Expression States in Cancer. <i>Cell Systems</i> , 2020, 10, 363-378.e12.                            | 6.2  | 54        |
| 21 | Automatic identification of relevant genes from low-dimensional embeddings of single-cell RNA-seq data. <i>Bioinformatics</i> , 2020, 36, 4291-4295.  | 4.1  | 7         |
| 22 | Attention Based Multiple Instance Learning for Classification of Blood Cell Disorders. <i>Lecture Notes in Computer Science</i> , 2020, , 246-256.  | 1.3  | 13        |
| 23 | Domain Model Explains Propagation Dynamics and Stability of Histone H3K27 and H3K36 Methylation Landscapes. <i>Cell Reports</i> , 2020, 30, 1223-1234.e8.                                     | 6.4  | 54        |
| 24 | A sparse deep learning approach for automatic segmentation of human vasculature in multispectral optoacoustic tomography. <i>Photoacoustics</i> , 2020, 20, 100203.                           | 7.8  | 26        |
| 25 | Reoccurring neural stem cell divisions in the adult zebrafish telencephalon are sufficient for the emergence of aggregated spatiotemporal patterns. <i>PLoS Biology</i> , 2020, 18, e3000708. | 5.6  | 3         |
| 26 | Human-level recognition of blast cells in acute myeloid leukaemia with convolutional neural networks. <i>Nature Machine Intelligence</i> , 2019, 1, 538-544.                                  | 16.0 | 122       |
| 27 | Metabolic regulation of pluripotency and germ cell fate through $\alpha$ -ketoglutarate. <i>EMBO Journal</i> , 2019, 38, .  | 7.8  | 77        |
| 28 | Multiclass Deep Active Learning for Detecting Red Blood Cell Subtypes in Brightfield Microscopy. <i>Lecture Notes in Computer Science</i> , 2019, , 685-693.                                  | 1.3  | 24        |
| 29 | Evaluation of Domain Adaptation Approaches for Robust Classification of Heterogeneous Biological Data Sets. <i>Lecture Notes in Computer Science</i> , 2019, , 673-686.                       | 1.3  | 1         |
| 30 | In-Silico Staining from Bright-Field and Fluorescent Images Using Deep Learning. <i>Lecture Notes in Computer Science</i> , 2019, , 184-186.  | 1.3  | 1         |
| 31 | Time-dependent propagators for stochastic models of gene expression: an analytical method. <i>Journal of Mathematical Biology</i> , 2018, 77, 261-312.  | 1.9  | 23        |
| 32 | Image analysis of neural stem cell division patterns in the zebrafish brain. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2018, 93, 314-322.   | 1.5  | 9         |
| 33 | MicroRNA as an Integral Part of Cell Communication: Regularized Target Prediction and Network Prediction. <i>Lecture Notes in Bioengineering</i> , 2018, , 85-100.                            | 0.4  | 0         |
| 34 | A single-cell micro-trench platform for automatic monitoring of cell division and apoptosis after chemotherapeutic drug administration. <i>Scientific Reports</i> , 2018, 8, 18042.           | 3.3  | 5         |
| 35 | Increasing Neural Stem Cell Division Asymmetry and Quiescence Are Predicted to Contribute to the Age-Related Decline in Neurogenesis. <i>Cell Reports</i> , 2018, 25, 3231-3240.e8.           | 6.4  | 35        |
| 36 | Live cell-lineage tracing and machine learning reveal patterns of organ regeneration. <i>ELife</i> , 2018, 7, .   | 6.0  | 35        |

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|----|---|------|-----------|
| 37 | Lineage marker synchrony in hematopoietic genealogies refutes the PU.1/GATA1 toggle switch paradigm. <i>Nature Communications</i> , 2018, 9, 2697.  | 12.8 | 24        |
| 38 | cgCorrect: a method to correct for confounding cell-to-cell variation due to cell growth in single-cell transcriptomics. <i>Physical Biology</i> , 2017, 14, 036001.                          | 1.8  | 15        |
| 39 | Prospective identification of hematopoietic lineage choice by deep learning. <i>Nature Methods</i> , 2017, 14, 403-406.   | 19.0 | 160       |
| 40 | fastER: a user-friendly tool for ultrafast and robust cell segmentation in large-scale microscopy. <i>Bioinformatics</i> , 2017, 33, 2020-2028.   | 4.1  | 58        |
| 41 | A BaSiC tool for background and shading correction of optical microscopy images. <i>Nature Communications</i> , 2017, 8, 14836.   | 12.8 | 213       |
| 42 | Software tools for single-cell tracking and quantification of cellular and molecular properties. <i>Nature Biotechnology</i> , 2016, 34, 703-706.   | 17.5 | 162       |
| 43 | Analysis of Cell Lineage Trees by Exact Bayesian Inference Identifies Negative Autoregulation of Nanog in Mouse Embryonic Stem Cells. <i>Cell Systems</i> , 2016, 3, 480-490.e13.             | 6.2  | 30        |
| 44 | Early myeloid lineage choice is not initiated by random PU.1 to GATA1 protein ratios. <i>Nature</i> , 2016, 535, 299-302.   | 27.8 | 180       |
| 45 | Structure-based assessment of cancerous mitochondria using deep networks. , 2016, , .   |      | 2         |
| 46 | Single-cell gene expression profiling and cell state dynamics: collecting data, correlating data points and connecting the dots. <i>Current Opinion in Biotechnology</i> , 2016, 39, 207-214. | 6.6  | 36        |
| 47 | <i>destiny</i> : diffusion maps for large-scale single-cell data in R. <i>Bioinformatics</i> , 2016, 32, 1241-1243.   | 4.1  | 518       |
| 48 | Combinatorial Histone Acetylation Patterns Are Generated by Motif-Specific Reactions. <i>Cell Systems</i> , 2016, 2, 49-58.   | 6.2  | 19        |
| 49 | A geometric analysis of fast-slow models for stochastic gene expression. <i>Journal of Mathematical Biology</i> , 2016, 72, 87-122.   | 1.9  | 25        |
| 50 | An adaptive scheduling scheme for calculating Bayes factors with thermodynamic integration using Simpson's rule. <i>Statistics and Computing</i> , 2016, 26, 663-677.                         | 1.5  | 15        |
| 51 | Twist1 induces distinct cell states depending on TGFBR1-activation. <i>Oncotarget</i> , 2016, 7, 30396-30407.   | 1.8  | 12        |
| 52 | Inference of spatiotemporal effects on cellular state transitions from time-lapse microscopy. <i>BMC Systems Biology</i> , 2015, 9, 61.   | 3.0  | 3         |
| 53 | Opposing effects of allogrooming on disease transmission in ant societies. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20140108.               | 4.0  | 43        |
| 54 | Network plasticity of pluripotency transcription factors in embryonic stem cells. <i>Nature Cell Biology</i> , 2015, 17, 1235-1246.   | 10.3 | 130       |

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|----|---|-----|-----------|
| 55 | SimiRa: A tool to identify coregulation between microRNAs and RNA-binding proteins. <i>RNA Biology</i> , 2015, 12, 998-1009.  | 3.1 | 14        |
| 56 | A case study on the use of scale separation-based analytical propagators for parameter inference in models of stochastic gene regulation. <i>Journal of Coupled Systems and Multiscale Dynamics</i> , 2015, 3, 164-173. | 0.2 | 8         |
| 57 | MCA: Multiresolution Correlation Analysis, a graphical tool for subpopulation identification in single-cell gene expression data. <i>BMC Bioinformatics</i> , 2014, 15, 240.  | 2.6 | 9         |
| 58 | Centroid Clustering of Cellular Lineage Trees. <i>Lecture Notes in Computer Science</i> , 2014, , 15-29.  | 1.3 | 3         |
| 59 | An automatic method for robust and fast cell detection in bright field images from high-throughput microscopy. <i>BMC Bioinformatics</i> , 2013, 14, 297.   | 2.6 | 117       |
| 60 | Social Transfer of Pathogenic Fungus Promotes Active Immunisation in Ant Colonies. <i>PLoS Biology</i> , 2012, 10, e1001300.  | 5.6 | 158       |
| 61 | Stability and Multiattractor Dynamics of a Toggle Switch Based on a Two-Stage Model of Stochastic Gene Expression. <i>Biophysical Journal</i> , 2012, 102, 19-29.   | 0.5 | 76        |
| 62 | Cellular Automata on Graphs: Topological Properties of ER Graphs Evolved towards Low-Entropy Dynamics. <i>Entropy</i> , 2012, 14, 993-1010.   | 2.2 | 10        |
| 63 | A Topological Characterization of Medium-Dependent Essential Metabolic Reactions. <i>Metabolites</i> , 2012, 2, 632-647.  | 2.9 | 11        |
| 64 | Multi-scale modeling of GMP differentiation based on single-cell genealogies. <i>FEBS Journal</i> , 2012, 279, 3488-3500.   | 4.7 | 19        |
| 65 | miTALOS: Analyzing the tissue-specific regulation of signaling pathways by human and mouse microRNAs. <i>Rna</i> , 2011, 17, 809-819.   | 3.5 | 52        |
| 66 | Hierarchical Differentiation of Myeloid Progenitors Is Encoded in the Transcription Factor Network. <i>PLoS ONE</i> , 2011, 6, e22649.  | 2.5 | 137       |
| 67 | Intronic microRNAs support their host genes by mediating synergistic and antagonistic regulatory effects. <i>BMC Genomics</i> , 2010, 11, 224.  | 2.8 | 126       |
| 68 | Biologically meaningful update rules increase the critical connectivity of generalized Kauffman networks. <i>Journal of Theoretical Biology</i> , 2010, 266, 436-448.   | 1.7 | 8         |
| 69 | Tissue-Specific Target Analysis of Disease-Associated MicroRNAs in Human Signaling Pathways. <i>PLoS ONE</i> , 2010, 5, e11154.   | 2.5 | 16        |
| 70 | Patterns of Subnet Usage Reveal Distinct Scales of Regulation in the Transcriptional Regulatory Network of <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2010, 6, e1000836.                             | 3.2 | 15        |
| 71 | Outer-totalistic cellular automata on graphs. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 2009, 373, 546-549.  | 2.1 | 30        |
| 72 | Zebrafish reward mutants reveal novel transcripts mediating the behavioral effects of amphetamine. <i>Genome Biology</i> , 2009, 10, R81.   | 9.6 | 71        |

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|----|---|-----|-----------|
| 73 | Dissecting the logical types of network control in gene expression profiles. BMC Systems Biology, 2008, 2, 18.  | 3.0 | 88        |
| 74 | Reply to "Comment on "Regularizing capacity of metabolic networks". Physical Review E, 2008, 77, 1  | 2.1 | 1         |
| 75 | Regularizing capacity of metabolic networks. Physical Review E, 2007, 75, 041917.   | 2.1 | 16        |
| 76 | Similar impact of topological and dynamic noise on complex patterns. Physics Letters, Section A: General, Atomic and Solid State Physics, 2006, 349, 302-305.   | 2.1 | 30        |
| 77 | Topology regulates the distribution pattern of excitations in excitable dynamics on graphs. Physical Review E, 2006, 74, 016112.                                | 2.1 | 28        |
| 78 | Topology regulates pattern formation capacity of binary cellular automata on graphs. Physica A: Statistical Mechanics and Its Applications, 2005, 354, 641-662. | 2.6 | 42        |
| 79 | Entangled-state preparation via dissipation-assisted adiabatic passages. Physical Review A, 2003, 68, .   | 2.5 | 100       |