

Giulio Caravagna

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9211576/publications.pdf>

Version: 2024-02-01

54
papers

1,219
citations

566801

15
h-index

476904

29
g-index

80
all docs

80
docs citations

80
times ranked

1449
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Detecting repeated cancer evolution from multi-region tumor sequencing data. <i>Nature Methods</i> , 2018, 15, 707-714. | 9.0 | 124 |
| 2 | CAPRI: efficient inference of cancer progression models from cross-sectional data. <i>Bioinformatics</i> , 2015, 31, 3016-3026. | 1.8 | 90 |
| 3 | Algorithmic methods to infer the evolutionary trajectories in cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4025-34. | 3.3 | 80 |
| 4 | Exploiting evolutionary steering to induce collateral drug sensitivity in cancer. <i>Nature Communications</i> , 2020, 11, 1923. | 5.8 | 79 |
| 5 | Subclonal reconstruction of tumors by using machine learning and population genetics. <i>Nature Genetics</i> , 2020, 52, 898-907. | 9.4 | 77 |
| 6 | Chromatin Velocity reveals epigenetic dynamics by single-cell profiling of heterochromatin and euchromatin. <i>Nature Biotechnology</i> , 2022, 40, 235-244. | 9.4 | 72 |
| 7 | Spatially constrained tumour growth affects the patterns of clonal selection and neutral drift in cancer genomic data. <i>PLoS Computational Biology</i> , 2019, 15, e1007243. | 1.5 | 59 |
| 8 | Inferring Tree Causal Models of Cancer Progression with Probability Raising. <i>PLoS ONE</i> , 2014, 9, e108358. | 1.1 | 57 |
| 9 | Tumour suppression by immune system through stochastic oscillations. <i>Journal of Theoretical Biology</i> , 2010, 265, 336-345. | 0.8 | 56 |
| 10 | Evolutionary dynamics of residual disease in human glioblastoma. <i>Annals of Oncology</i> , 2019, 30, 456-463. | 0.6 | 47 |
| 11 | The Interplay of Intrinsic and Extrinsic Bounded Noises in Biomolecular Networks. <i>PLoS ONE</i> , 2013, 8, e51174. | 1.1 | 41 |
| 12 | TRONCO: an R package for the inference of cancer progression models from heterogeneous genomic data. <i>Bioinformatics</i> , 2016, 32, 1911-1913. | 1.8 | 39 |
| 13 | Reply to "Neutral tumor evolution". <i>Nature Genetics</i> , 2018, 50, 1633-1637. | 9.4 | 27 |
| 14 | The Calculus of Looping Sequences. , 2008, , 387-423. | | 26 |
| 15 | Learning mutational graphs of individual tumour evolution from single-cell and multi-region sequencing data. <i>BMC Bioinformatics</i> , 2019, 20, 210. | 1.2 | 25 |
| 16 | Investigating the Relation between Stochastic Differentiation, Homeostasis and Clonal Expansion in Intestinal Crypts via Multiscale Modeling. <i>PLoS ONE</i> , 2014, 9, e97272. | 1.1 | 18 |
| 17 | The MOBSTER R package for tumour subclonal deconvolution from bulk DNA whole-genome sequencing data. <i>BMC Bioinformatics</i> , 2020, 21, 531. | 1.2 | 18 |
| 18 | Bounded noises as a natural tool to model extrinsic fluctuations in biomolecular networks. <i>Natural Computing</i> , 2014, 13, 297-307. | 1.8 | 17 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | Delay Stochastic Simulation of Biological Systems: A Purely Delayed Approach. Lecture Notes in Computer Science, 2011, , 61-84. | 1.0 | 16 |
| 20 | Modeling Cumulative Biological Phenomena with Suppes-Bayes Causal Networks. Evolutionary Bioinformatics, 2018, 14, 117693431878516. | 0.6 | 15 |
| 21 | CABERNET: a Cytoscape app for augmented Boolean models of gene regulatory NETWORKS. BMC Bioinformatics, 2016, 17, 64. | 1.2 | 13 |
| 22 | Distributed delays in a hybrid model of tumor-Immune system interplay. Mathematical Biosciences and Engineering, 2013, 10, 37-57. | 1.0 | 13 |
| 23 | Fine-tuning anti-tumor immunotherapies via stochastic simulations. BMC Bioinformatics, 2012, 13, S8. | 1.2 | 12 |
| 24 | Bio-PEPAd: A non-Markovian extension of Bio-PEPA. Theoretical Computer Science, 2012, 419, 26-49. | 0.5 | 12 |
| 25 | CoGNAC: A Chaste Plugin for the Multiscale Simulation of Gene Regulatory Networks Driving the Spatial Dynamics of Tissues and Cancer. Cancer Informatics, 2015, 14s4, CIN.S19965. | 0.9 | 12 |
| 26 | Bounded noise induced first-order phase transitions in a baseline non-spatial model of gene transcription. Physica A: Statistical Mechanics and Its Applications, 2018, 492, 2056-2068. | 1.2 | 11 |
| 27 | Foundational aspects of multiscale modeling of biological systems with process algebras. Theoretical Computer Science, 2012, 431, 96-116. | 0.5 | 10 |
| 28 | Gene switching rate determines response to extrinsic perturbations in the self-activation transcriptional network motif. Scientific Reports, 2016, 6, 26980. | 1.6 | 10 |
| 29 | A Bayesian method to cluster single-cell RNA sequencing data using copy number alterations. Bioinformatics, 2022, 38, 2512-2518. | 1.8 | 10 |
| 30 | On the Interpretation of Delays in Delay Stochastic Simulation of Biological Systems. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 6, 17-29. | 0.8 | 7 |
| 31 | G<scp>e</scp>S<scp>to</scp>D<scp>ifferent</scp>: a Cytoscape plugin for the generation and the identification of gene regulatory networks describing a stochastic cell differentiation process. Bioinformatics, 2013, 29, 513-514. | 1.8 | 6 |
| 32 | Stochastic Hybrid Automata with delayed transitions to model biochemical systems with delays. Information and Computation, 2014, 236, 19-34. | 0.5 | 6 |
| 33 | Learning the structure of Bayesian Networks via the bootstrap. Neurocomputing, 2021, 448, 48-59. | 3.5 | 6 |
| 34 | Lazy Security Controllers. Lecture Notes in Computer Science, 2013, , 33-48. | 1.0 | 6 |
| 35 | PMCE: efficient inference of expressive models of cancer evolution with high prognostic power. Bioinformatics, 2022, 38, 754-762. | 1.8 | 6 |
| 36 | An Intermediate Language for the Simulation of Biological Systems. Electronic Notes in Theoretical Computer Science, 2008, 194, 19-34. | 0.9 | 5 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Modeling biological systems with delays in Bio-PEPA. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 40, 85-101. | 0.8 | 5 |
| 38 | An intermediate language for the stochastic simulation of biological systems. Theoretical Computer Science, 2009, 410, 3085-3109. | 0.5 | 3 |
| 39 | Design of the TRONCO BioConductor Package for TRanslational ONCOlogy. R Journal, 2016, 8, 39. | 0.7 | 3 |
| 40 | GPU-powered Simulation Methodologies for Biological Systems. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 130, 87-91. | 0.8 | 2 |
| 41 | Effects of delayed immune-response in tumor immune-system interplay. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 92, 106-121. | 0.8 | 2 |
| 42 | Matching Models Across Abstraction Levels with Gaussian Processes. Lecture Notes in Computer Science, 2016, , 49-66. | 1.0 | 2 |
| 43 | Measuring evolutionary cancer dynamics from genome sequencing, one patient at a time. Statistical Applications in Genetics and Molecular Biology, 2020, 19, . | 0.2 | 2 |
| 44 | Lazy Monitoring for Distributed Computing Environments. , 2012, , . | | 1 |
| 45 | Automatising the analysis of stochastic biochemical time-series. BMC Bioinformatics, 2015, 16, S8. | 1.2 | 1 |
| 46 | Ordering cancer mutational profiles of cross-sectional copy number alterations. International Journal of Data Mining and Bioinformatics, 2016, 15, 59. | 0.1 | 1 |
| 47 | Bounded Extrinsic Noises Affecting Biochemical Networks with Low Molecule Numbers. Modeling and Simulation in Science, Engineering and Technology, 2013, , 201-221. | 0.4 | 1 |
| 48 | Aspects of multiscale modelling in a process algebra for biological systems. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 40, 54-69. | 0.8 | 1 |
| 49 | P Systems with Endosomes. International Journal of Computers, Communications and Control, 2014, 4, 214. | 1.2 | 1 |
| 50 | The Influence of Nutrients Diffusion on a Metabolism-driven Model of a Multi-cellular System. Fundamenta Informaticae, 2019, 171, 279-295. | 0.3 | 0 |
| 51 | Ordering copy number alteration data to analyze colorectal cancer progression. EMBnet Journal, 2012, 18, 84. | 0.2 | 0 |
| 52 | Analysis of the spatial and dynamical properties of a multiscale model of intestinal crypts. Electronic Proceedings in Theoretical Computer Science, EPTCS, 0, 130, 79-82. | 0.8 | 0 |
| 53 | Abstract 4232: Spatially constrained tumor growth affects the patterns of clonal selection and neutral drift in cancer genomic data. , 2019, , . | | 0 |
| 54 | cyTRON and cyTRON/JS: Two Cytoscape-Based Applications for the Inference of Cancer Evolution Models. Lecture Notes in Computer Science, 2020, , 13-18. | 1.0 | 0 |