# Daniela Besozzi

List of Publications by Year
in descending order

| 56 papers | 1,250 citations | 471509<br>17 h-index | 414414<br>32 g-index |
|---|---|---|---|
| 60 all docs | 60 docs citations | 60 times ranked | 1305 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | USE-Net: Incorporating Squeeze-and-Excitation blocks into U-Net for prostate zonal segmentation of multi-institutional MRI datasets. Neurocomputing, 2019, 365, 31-43. | 5.9 | 185 |
| 2 | Fuzzy Self-Tuning PSO: A settings-free algorithm for global optimization. Swarm and Evolutionary Computation, 2018, 39, 70-85. | 8.1 | 171 |
| 3 | MedGA: A novel evolutionary method for image enhancement in medical imaging systems. Expert Systems With Applications, 2019, 119, 387-399. | 7.6 | 85 |
| 4 | Graphics processing units in bioinformatics, computational biology and systems biology. Briefings in Bioinformatics, 2017, 18, bbw058. | 6.5 | 84 |
| 5 | Computational Strategies for a System-Level Understanding of Metabolism. Metabolites, 2014, 4, 1034-1087. | 2.9 | 54 |
| 6 | Modeling and stochastic simulation of the Ras/cAMP/PKA pathway in the yeast Saccharomyces cerevisiae evidences a key regulatory function for intracellular guanine nucleotides pools. Journal of Biotechnology, 2008, 133, 377-385. | 3.8 | 46 |
| 7 | Biochemical parameter estimation vs. benchmark functions: A comparative study of optimization performance and representation design. Applied Soft Computing Journal, 2019, 81, 105494. | 7.2 | 45 |
| 8 | GPU-accelerated simulations of mass-action kinetics models with cupSODA. Journal of Supercomputing, 2014, 69, 17-24. | 3.6 | 44 |
| 9 | A novel framework for MR image segmentation and quantification by using MedGA. Computer Methods and Programs in Biomedicine, 2019, 176, 159-172. | 4.7 | 43 |
| 10 | Simpful: A User-Friendly Python Library for Fuzzy Logic. International Journal of Computational Intelligence Systems, 2020, 13, 1687. | 2.7 | 32 |
| 11 | Simulation of the Ras/cAMP/PKA pathway in budding yeast highlights the establishment of stable oscillatory states. Biotechnology Advances, 2012, 30, 99-107. | 11.7 | 28 |
| 12 | cuTauLeaping: A GPU-Powered Tau-Leaping Stochastic Simulator for Massive Parallel Analyses of Biological Systems. PLoS ONE, 2014, 9, e91963. | 2.5 | 28 |
| 13 | The impact of particles initialization in PSO: Parameter estimation as a case in point. , 2015, , . | | 27 |
| 14 | The role of feedback control mechanisms on the establishment of oscillatory regimes in the Ras/cAMP/PKA pathway in S. cerevisiae. Eurasip Journal on Bioinformatics and Systems Biology, 2012, 2012, 10. | 1.4 | 26 |
| 15 | GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172. | 2.6 | 26 |
| 16 | A Comparison of Genetic Algorithms and Particle Swarm Optimization for Parameter Estimation in Stochastic Biochemical Systems. Lecture Notes in Computer Science, 2009, , 116-127. | 1.3 | 24 |
| 17 | LASSIE: simulating large-scale models of biochemical systems on GPUs. BMC Bioinformatics, 2017, 18, 246. | 2.6 | 22 |
| 18 | Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. Npj Systems Biology and Applications, 2016, 2, 16011. | 3.0 | 21 |

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|---|---------|-----|-----------|
| 19 | Computational Intelligence for Parameter Estimation of Biochemical Systems. , 2018, , . | | 21 |
| 20 | Estimating reaction constants in stochastic biological systems with a multi-swarm PSO running on GPUs. , 2012, , . | | 19 |
| 21 | Proactive Particles in Swarm Optimization: A self-tuning algorithm based on Fuzzy Logic. , 2015, , . | | 18 |
| 22 | GPU-powered model analysis with PySB/cupSODA. Bioinformatics, 2017, 33, 3492-3494. | 4.1 | 17 |
| 23 | Analysis of single-cell RNA sequencing data based on autoencoders. BMC Bioinformatics, 2021, 22, 309. | 2.6 | 15 |
| 24 | Surfing on Fitness Landscapes: A Boost on Optimization by Fourier Surrogate Modeling. Entropy, 2020, 22, 285. | 2.2 | 14 |
| 25 | cupSODA: A CUDA-Powered Simulator of Mass-Action Kinetics. Lecture Notes in Computer Science, 2013, , 344-357. | 1.3 | 13 |
| 26 | Coupling Mechanistic Approaches and Fuzzy Logic to Model and Simulate Complex Systems. IEEE Transactions on Fuzzy Systems, 2020, 28, 1748-1759. | 9.8 | 13 |
| 27 | Massive Exploration of Perturbed Conditions of the Blood Coagulation Cascade through GPU Parallelization. BioMed Research International, 2014, 2014, 1-20. | 1.9 | 10 |
| 28 | Fuzzy modeling and global optimization to predict novel therapeutic targets in cancer cells. Bioinformatics, 2020, 36, 2181-2188. | 4.1 | 10 |
| 29 | ACDC: Automated Cell Detection and Counting for Time-Lapse Fluorescence Microscopy. Applied Sciences (Switzerland), 2020, 10, 6187. | 2.5 | 9 |
| 30 | Modeling cell proliferation in human acute myeloid leukemia xenografts. Bioinformatics, 2019, 35, 3378-3386. | 4.1 | 8 |
| 31 | BioSimWare: A Software for the Modeling, Simulation and Analysis of Biological Systems. Lecture Notes in Computer Science, 2010, , 119-143. | 1.3 | 7 |
| 32 | In vivo and in silico analysis of PCNA ubiquitylation in the activation of the Post Replication Repair pathway in S. cerevisiae. BMC Systems Biology, 2013, 7, 24. | 3.0 | 7 |
| 33 | The Multi-Level Mechanism of Action of a Pan-Ras Inhibitor Explains its Antiproliferative Activity on Cetuximab-Resistant Cancer Cells. Frontiers in Molecular Biosciences, 2021, 8, 625979. | 3.5 | 7 |
| 34 | Cycles and communicating classes in membrane systems and molecular dynamics. Theoretical Computer Science, 2007, 372, 242-266. | 0.9 | 6 |
| 35 | Reaction-Based Models of Biochemical Networks. Lecture Notes in Computer Science, 2016, , 24-34. | 1.3 | 6 |
| 36 | SMGen: A Generator of Synthetic Models of Biochemical Reaction Networks. Symmetry, 2022, 14, 119. | 2.2 | 6 |

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|---|---------|----|-----------|
| 37 | ginSODA: massive parallel integration of stiff ODE systems on GPUs. Journal of Supercomputing, 2019, 75, 7844-7856. | 3.6 | 5 |
| 38 | Computational Intelligence for Life Sciences. Fundamenta Informaticae, 2019, 171, 57-80. | 0.4 | 5 |
| 39 | Screening for Combination Cancer Therapies With Dynamic Fuzzy Modeling and Multi-Objective Optimization. Frontiers in Genetics, 2021, 12, 617935. | 2.3 | 5 |
| 40 | The Impact of Representation on the Optimization of Marker Panels for Single-cell RNA Data. , 2021, , . |  | 5 |
| 41 | If You Can't Beat It, Squash It: Simplify Global Optimization by Evolving Dilation Functions. , 2021, , . |  | 5 |
| 42 | GPU-powered and settings-free parameter estimation of biochemical systems. , 2016, , . |  | 4 |
| 43 | Gillespie's Stochastic Simulation Algorithm on MIC coprocessors. Journal of Supercomputing, 2017, 73, 676-686. | 3.6 | 4 |
| 44 | ProCell: Investigating cell proliferation with Swarm Intelligence. , 2019, , . |  | 3 |
| 45 | Which random is the best random? A study on sampling methods in Fourier surrogate modeling. , 2020, , . |  | 3 |
| 46 | Efficient and Settings-Free Calibration of Detailed Kinetic Metabolic Models with Enzyme Isoforms Characterization. Lecture Notes in Computer Science, 2020, , 187-202. | 1.3 | 3 |
| 47 | cuProCell: GPU-Accelerated Analysis of Cell Proliferation With Flow Cytometry Data. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 3173-3181. | 6.3 | 2 |
| 48 | On the automatic calibration of fully analogical spiking neuromorphic chips. , 2020, , . |  | 2 |
| 49 | Selected papers from the 15th and 16th international conference on Computational Intelligence Methods for Bioinformatics and Biostatistics. BMC Bioinformatics, 2021, 22, 90. | 2.6 | 1 |
| 50 | FiCoS: A fine-grained and coarse-grained GPU-powered deterministic simulator for biochemical networks. PLoS Computational Biology, 2021, 17, e1009410. | 3.2 | 1 |
| 51 | An Experimental and Computational Protocol to Study Cell Proliferation in Human Acute Myeloid Leukemia Xenografts. Methods in Molecular Biology, 2021, 2185, 241-258. | 0.9 | 1 |
| 52 | Modeling Calcium Signaling in S. cerevisiae Highlights the Role and Regulation of the Calmodulin-Calcineurin Pathway in Response to Hypotonic Shock. Frontiers in Molecular Biosciences, 0, 9, . | 3.5 | 1 |
| 53 | HyperBeta: characterizing the structural dynamics of proteins and self-assembling peptides. Scientific Reports, 2021, 11, 7783. | 3.3 | 0 |
| 54 | Editorial: Network-Oriented Approaches to Anticancer Drug Response. Frontiers in Bioengineering and Biotechnology, 2021, 9, 692369. | 4.1 | 0 |

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|---|---------|----|-----------| 
| 55 | A comparison of multi-objective optimization algorithms to identify drug target combinations. , 2021, , . | | 0 |
| 56 | Fourier Surrogate Models of Dilated Fitness Landscapes in Systems Biology : or how we learned to torture optimization problems until they confess. , 2020, , . | | 0 |