

# Paola Lecca

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5852917/publications.pdf>

Version: 2024-02-01

98  
papers

743  
citations

687220

13  
h-index

610775

24  
g-index

111  
all docs

111  
docs citations

111  
times ranked

1066  
citing authors

#	ARTICLE	IF	CITATIONS
1	Session details: Theme: Artificial intelligence and agents: BIO - Bioinformatics track. , 2021, , .		0
2	Biexponential fitting for noisy data with error propagation. Mathematical Methods in the Applied Sciences, 2021, 44, 10154-10171.	1.2	3
3	Identification of Potential Leukocyte Biomarkers Related to Drug Recovery of CFTR: Clinical Applications in Cystic Fibrosis. International Journal of Molecular Sciences, 2021, 22, 3928.	1.8	10
4	Editorial: Network-Oriented Approaches to Anticancer Drug Response. Frontiers in Bioengineering and Biotechnology, 2021, 9, 692369.	2.0	0
5	Machine Learning for Causal Inference in Biological Networks: Perspectives of This Challenge. Frontiers in Bioinformatics, 2021, 1, .	1.0	21
6	The theory of active agents for simulating dynamical networks and its $\mathcal{L}$ -calculus specification. , 2021, , .		0
7	On the asymptotic stability of advection-diffusion equations of mass transport in a bubble column bioreactor. Journal of Physics: Conference Series, 2021, 2090, 012035.	0.3	0
8	The effects of gravitational potential on chemical reaction rates. Journal of Physics: Conference Series, 2021, 2090, 012034.	0.3	6
9	Analysis of SARS-CoV-2 protein interactome map. , 2021, , .		1
10	Composite nanocellulose-based hydrogels with spatially oriented degradation and retarded release of macromolecules. Journal of Biomedical Materials Research - Part A, 2020, 108, 1509-1519.	2.1	12
11	Control Theory and Cancer Chemotherapy: How They Interact. Frontiers in Bioengineering and Biotechnology, 2020, 8, 621269.	2.0	6
12	On TD-WGcluster: Theoretical Foundations and Guidelines for the User. Methods in Molecular Biology, 2020, 2074, 233-262.	0.4	2
13	Complex Systems, Data and Inference. SpringerBriefs in Statistics, 2020, , 1-18.	0.3	0
14	Stiffness estimate of information propagation in biological systems modelled as spring networks. , 2020, , .		1
15	Observability of Bacterial Growth Models in Bubble Column Bioreactors. Lecture Notes in Computer Science, 2020, , 309-322.	1.0	0
16	Model Identifiability. SpringerBriefs in Statistics, 2020, , 37-48.	0.3	0
17	Dynamic Models. SpringerBriefs in Statistics, 2020, , 19-35.	0.3	0
18	Session details: Theme: AI and agents: BIO - Bioinformatics track. , 2020, , .		0

#	ARTICLE	IF	CITATIONS
19	Computing organoidsâ€™ volume in medical images: the case study of cystic fibrosis. , 2020, , .		0
20	Determining structural parameter identifiability in biological dynamical models by analysing the statistical properties of the likelihood behaviour. , 2019, , .		0
21	Identifying necessary and sufficient conditions for the observability of models of biochemical processes. Biophysical Chemistry, 2019, 254, 106257.	1.5	9
22	A reaction-based model of the state space of chemical reaction systems enables efficient simulations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	1
23	Quantum Mechanics in Biology. , 2019, , 1-23.		0
24	Statistical Physics in Biology. , 2019, , 25-50.		0
25	Graph Theory and Physics Meet Network Biology. , 2019, , 51-78.		0
26	Applied Descriptors for Complexity and Centrality to Network Biology. , 2019, , 79-104.		0
27	How Monte Carlo heuristics aid to identify the physical processes of drug release kinetics. MethodsX, 2018, 5, 204-216.	0.7	1
28	Hybrid deterministic/stochastic simulation of complex biochemical systems. Molecular BioSystems, 2017, 13, 2672-2686.	2.9	11
29	Network-Oriented Approaches to Anticancer Drug Response. Methods in Molecular Biology, 2017, 1513, 101-117.	0.4	4
30	A hierarchical model to predict the probability of germination of bacterial spores. , 2017, , .		0
31	Deterministic Differential Equations. , 2016, , 67-98.		0
32	Time Series Analysis of the Bacillus subtilis Sporulation Network Reveals Low Dimensional Chaotic Dynamics. Frontiers in Microbiology, 2016, 7, 1760.	1.5	6
33	Network-Based Conceptualization of Observational Data. , 2016, , 47-65.		0
34	From Network Inference to the Study of Human DiseasesaaThe work is partially supported by the National Research Foundation of Luxembourg (AFR 9139104).. , 2016, , 119-140.		0
35	Accurate prediction of the age incidence of chronic myeloid leukemia with an improved two-mutation mathematical model. Integrative Biology (United Kingdom), 2016, 8, 1261-1275.	0.6	7
36	Module Detection in Dynamic Networks by Temporal Edge Weight Clustering. Lecture Notes in Computer Science, 2016, , 54-70.	1.0	1

#	ARTICLE	IF	CITATIONS
37	Network Inference From Time-Course Data. , 2016, , 21-45.		0
38	Overview of Biological Network Inference and Modeling of Dynamics. , 2016, , 1-11.		0
39	Network Inference From Steady-State Data. , 2016, , 13-19.		0
40	Session details: Volume I: Artificial intelligence and agents, distributed systems, and information systems: Computational biology and bioinformatics track. , 2016, , .		0
41	MP66-01 SPOP MUTATION LEADS TO GENOMIC INSTABILITY IN PROSTATE CANCER. Journal of Urology, 2015, 193, .	0.2	0
42	Detecting modules in biological networks by edge weight clustering and entropy significance. Frontiers in Genetics, 2015, 6, 265.	1.1	22
43	Defining order and timing of mutations during cancer progression: the TO-DAG probabilistic graphical model. Frontiers in Genetics, 2015, 6, 309.	1.1	9
44	SPOP mutation leads to genomic instability in prostate cancer. ELife, 2015, 4, .	2.8	148
45	Session details: Volume I: Artificial intelligence and agents, distributed systems, and information systems: Computational biology and bioinformatics track. , 2015, , .		0
46	Abstract 1108: SPOP mutation leads to genomic instability in prostate cancer. , 2015, , .		1
47	Abstract NG01: SPOP mutation is associated with genomic instability in prostate cancer. , 2015, , .		1
48	Methods of biological network inference for reverse engineering cancer chemoresistance mechanisms. Drug Discovery Today, 2014, 19, 151-163.	3.2	14
49	Session details: Volume I: Artificial intelligence & agents, distributed systems, and information systems: BioHealth informatics track. , 2014, , .		0
50	Stochastic chemical kinetics. Biophysical Reviews, 2013, 5, 323-345.	1.5	38
51	Biological network inference for drug discovery. Drug Discovery Today, 2013, 18, 256-264.	3.2	31
52	Parameter sensitivity analysis of stochastic models: Application to catalytic reaction networks. Computational Biology and Chemistry, 2013, 42, 5-17.	1.1	13
53	A Model Predicting Rolling Cells Percentage in Inflamed Brain Venules. Lecture Notes in Computational Vision and Biomechanics, 2013, , 65-80.	0.5	0
54	Mechanistic Models of Astrocytic Glucose Metabolism Calibrated on PET Images. Lecture Notes in Computational Vision and Biomechanics, 2013, , 131-155.	0.5	0

#	ARTICLE	IF	CITATIONS
55	An integrative network inference approach to predict mechanisms of cancer chemoresistance. Integrative Biology (United Kingdom), 2013, 5, 458.	0.6	5
56	Deterministic chemical kinetics. , 2013, , 1-34.		1
57	The stochastic approach to biochemical kinetics. , 2013, , 35-82.		0
58	Reaction-diffusion systems. , 2013, , 208-278.		1
59	KInfer: a tool for model calibration. , 2013, , 280-321.		0
60	Modelling living systems with BlenX. , 2013, , 322-346.		0
61	Simulation of ecodynamics: key nodes in food webs. , 2013, , 348-372.		0
62	The exact stochastic simulation algorithms. , 2013, , 83-115.		0
63	The structure of biochemical models. , 2013, , 182-206.		0
64	Modelling in systems biology. , 2013, , 117-180.		1
65	Deterministic versus stochastic modelling in biochemistry and systems biology. , 2013, , .		13
66	Inferring biochemical reaction pathways: the case of the gemcitabine pharmacokinetics. BMC Systems Biology, 2012, 6, 51.	3.0	8
67	Modelling non-homogeneous stochastic reaction-diffusion systems: the case study of gemcitabine-treated non-small cell lung cancer growth. BMC Bioinformatics, 2012, 13, S14.	1.2	4
68	A Process-Algebra Model of the Cell Mechanics of Autoreactive Lymphocytes Recruitment. Lecture Notes in Computational Vision and Biomechanics, 2012, , 311-333.	0.5	1
69	Algorithmic Modeling Quantifies the Complementary Contribution of Metabolic Inhibitions to Gemcitabine Efficacy. PLoS ONE, 2012, 7, e50176.	1.1	17
70	Model Identification Using Correlation-Based Inference and Transfer Entropy Estimation. , 2011, , .		2
71	Poster: Modelling the tumor shrinkage pharmacodynamics with BlenX. , 2011, , .		1
72	Network Inference from Time-Dependent Omics Data. Methods in Molecular Biology, 2011, 719, 435-455.	0.4	6

#	ARTICLE	IF	CITATIONS
73	Identifying key species in ecosystems with stochastic sensitivity analysis. Ecological Modelling, 2011, 222, 2542-2551.	1.2	33
74	BLENX MODELS OF Î±-SYNUCLEIN AND PARKIN KINETICS IN NEUROPATHOLOGY OF PARKINSON'S DISEASE. Journal of Biological Systems, 2011, 19, 149-181.	0.5	5
75	Stochastic simulation of the spatio-temporal dynamics of reaction-diffusion systems: the case for the bicoid gradient. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	7
76	Calibration of dynamic models of biological systems with Kinfer. European Biophysics Journal, 2010, 39, 1019-1039.	1.2	20
77	Redi: A Simulator of Stochastic Biochemical Reaction-Diffusion Systems. , 2010, , .		2
78	Correlation-Based Network Inference and Modelling in Systems Biology: The NF-kappa B Signalling Network Case Study. , 2010, , .		3
79	Stochastic simulation of the spatio-temporal dynamics of reaction-diffusion systems: the case for the bicoid gradient. Journal of Integrative Bioinformatics, 2010, 7, 150.	1.0	4
80	A new probabilistic generative model of parameter inference in biochemical networks. , 2009, , .		23
81	On the Performances in Simulation of Parallel Databases: An Overview on the Most Recent Techniques for Query Optimization. , 2009, , .		1
82	Estimating the Parameters of Cyclin-Triggered Gene Expression in Cell Cycle Control Network. , 2009, , .		0
83	Deducing Chemical Reaction Rate Constants and Their Regions of Confidence from Noisy Measurements of Time Series of Concentration. , 2009, , .		7
84	On the Parameter Inference in Chaotic Chemical Systems. , 2009, , .		0
85	Simulating the cellular passive transport of glucose using a time-dependent extension of Gillespie algorithm for stochastic Îµ-calculus. International Journal of Data Mining and Bioinformatics, 2007, 1, 315.	0.1	13
86	Cell Cycle Control in Eukaryotes: A BioSpi model. Electronic Notes in Theoretical Computer Science, 2007, 180, 51-63.	0.9	28
87	A time-dependent extension of gillespie algorithm for biochemical stochastic Îµ-calculus. , 2006, , .		11
88	Translating SBML Models into the Stochastic Îµ-Calculus for Stochastic Simulation. Lecture Notes in Computer Science, 2006, , 73-88.	1.0	0
89	Predicting cell adhesion probability via the biochemical stochastic Îµ-calculus. , 2004, , .		1
90	A Stochastic Process Algebra Approach to Simulation of Autoreactive Lymphocyte Recruitment. Simulation, 2004, 80, 273-288.	1.1	30

#	ARTICLE	IF	CITATIONS
91	Concurrency in leukocyte vascular recognition: developing the tools for a predictive computer model. Trends in Immunology, 2004, 25, 411-416.	2.9	21
92	The DIAMINE Landmine Detection System. AIP Conference Proceedings, 2003, , .	0.3	3
93	A BIOSPI MODEL OF LYMPHOCYTE-ENDOTHELIAL INTERACTIONS IN INFLAMED BRAIN VENULES. , 2003, , 521-32.		2
94	EXPLODET PROJECT: METHODS OF AUTOMATIC DATA PROCESSING AND ANALYSIS FOR THE DETECTION OF HIDDEN EXPLOSIVE. , 2003, , .		0
95	Electromagnetic fields in Schwarzschild and Reissner-Nordström geometry: Quantum corrections to the black hole entropy. Physical Review D, 1998, 57, 1108-1111.	1.6	79
96	Developing An Hierarchical Simulator for Beta-binders. , 0, , .		2
97	The Present and the Future Perspectives of Biological Network Inference. Advances in Bioinformatics and Biomedical Engineering Book Series, 0, , 118-140.	0.2	1
98	Structural and Dynamical Heterogeneity in Ecological Networks. Advances in Bioinformatics and Biomedical Engineering Book Series, 0, , 141-162.	0.2	0