

Stefano Lonardi

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Research Interests

Computational Molecular Biology & Bioinformatics
Genomics & Epigenetics
Data Science

Education

2001	Doctor of Philosophy (PhD) Computer Science	Purdue University, West Lafayette, IN
1999	Dottorato di Ricerca Electrical and Computer Engineering	University of Padova, Padova, Italy
1994	Laurea Computer Science	University of Pisa, Pisa, Italy

Professional Experience

2011 –	University of California, Riverside, CA Department of Computer Science and Engineering	Professor
2009 –	University of California, Riverside, CA Department of Computer Science and Engineering	Vice Chair for Undergraduate Education
2019 – 2020	Beckman Research Institute of City of Hope, Duarte, CA Division of Systems Biology	Visiting Professor
2016 – 2017	University of Southern California, Los Angeles, CA Keck School of Medicine	Visiting Professor
2013 – 2014	California Institute of Technology, Pasadena, CA Division of Biology and Biological Engineering	Visiting Professor
2007 – 2011	University of California, Riverside, CA Department of Computer Science and Engineering	Associate Professor
2001 – 2007	University of California, Riverside, CA Department of Computer Science and Engineering	Assistant Professor
1997 – 2001	Purdue University, West Lafayette, IN Department of Computer Science	Research & Teaching Assistant
1999 – 1999	Celera Genomics, Rockville, MD Department of Informatics Research	Intern

Awards & Honorary Memberships

2023	Top 10 most-cited paper in <i>The Plant Genome</i> journal Crop Science Society of America	
2021	NIH Director's Transformative Research Award National Institutes of Health	<i>National Institute of Allergy and Infectious Diseases</i>
2018	Fellow American Association for the Advancement of Science (AAAS)	<i>for contributions to computational biology, bioinformatics and data mining</i>
2017	Teaching Award (Honorable Mention) Bourns College of Engineering, UC Riverside	
2016	Distinguished Scientist Association for Computing Machinery (ACM)	<i>for contributions to computational biology</i>
2016	Fellow Institute of Electrical and Electronic Engineers (IEEE)	<i>for contributions to computational biology and data mining</i>
2016	Top-100 Most Influential Scholar in Data Mining ArnetMiner	
2005	CAREER Award National Science Foundation (NSF)	<i>Division of Information & Intelligent Systems</i>

Research funding

(blue entries indicate active awards)

2025 – 2028	NSF (IIS) III:Small:Improving <i>de novo</i> Genome Assembly using Single-copy <i>k</i> -mers	\$600,000 – role: sole PI
2024 – 2030	NSF (DBI) A BioFoundry for Extreme and Exceptional Fungi, Archaea and Bacteria (Ex-FAB)	\$22,000,000 – role: senior personnel (with M. O'Malley, I. Wheeldon, J. Stajich, J. Snyder, D. Valentine)
2022 – 2025	NSF (ABF) Data-driven engineering of the thermotolerant yeast <i>Kluyveromyces marxianus</i>	\$1,499,991 – role: coPI (with I. Wheeldon, N. Da Silva, and Argonne National Laboratory)
2021 – 2025	NIH (NIAID) NIH Director's Transformative Research Award: Rapid response for pandemics: single cell sequencing and deep learning to predict antibody sequences against an emerging antigen	\$3,071,572 – role: coPD (with A. Ray, J. Hernandez, M. H. Sazinsky)
2018 – 2022	NSF (IIS) III:Small:Improving <i>de novo</i> Genome Assembly using Optical Maps	\$499,978 – role: sole PI
2018 – 2022	DOE Establishing the Thermo-tolerant Yeast <i>Kluyveromyces marxianus</i> as a Host for Bio-based Fuels and Chemicals Production	\$1,499,999 – role: coPI (with I. Wheeldon, N. Da Silva)
2015 – 2020	NSF (IOS) BREAD ABRDC: Advancing the Cowpea Genome for Food Security	\$1,587,345 – role: coPI (with T. Close, B. L. Huynh, P. Roberts, M. Munoz-Amatriain)
2015 – 2019	NSF (IIS) III:Small:Algorithms for Genome Assembly of Ultra-deep Sequencing Data	\$499,000 – role: sole PI
2015 – 2016	UCR An <i>in vivo</i> System to Monitor the 4D Mammalian Nucleome	\$70,000 – role: coPI (with K. Le Roch, F. Sladek)
2014 – 2015	NSF (MRI) MRI: Acquisition of a Big Data Compute Cluster for Interdisciplinary Research	\$548,476 – role: coPI (with T. Girke, M. Allen, J. Stajich, J. Bailey-Serres)
2014 – 2015	UCOP Intro to Computing I and II, UCR CS 10V and 12V	\$50,000 – role: coPI (with F. Vahid, K. Miller, B. Linard)

Research funding (continued)

2014 – 2015	NIH	\$592,816 – role: senior personnel (with T. Girke <i>et al.</i>)
	Acquisition of a Scalable Storage Cluster for Data Intensive NIH Research	
2013 – 2019	US-AID	\$4,972,542 – role: coPI (with T. Close, P. Roberts)
	Feed the Future Innovation Lab: Advanced Tools for Climate-Resilient Cowpeas	
2013 – 2017	NSF (IIS)	\$994,370 – role: PI (with K. Le Roch)
	III:Medium:Algorithms and Software Tools for Epigenetic Research	
2013 – 2013	UCOP	\$34,500 – role: coPI (with F. Vahid, K. Miller, B. Linard)
	Ultra-Interactive Animated Web Learning	
2011 – 2012	UCR	\$60,000 – role: coPI (with E. Keogh, C. Shelton)
	Bootstrapping the UCR Center for Computational Entomology	
2011 – 2014	NSF (ABI)	\$428,635 – role: PI (with T. Close)
	ABI Innovation: Barcoding-Free Multiplexing: Leveraging Combinatorial Pooling for High-Throughput Sequencing	
2010 – 2014	NIH (NIAID)	\$1,839,568 – role: coPI (with K. Le Roch)
	Understanding the Role of Nucleosomes Turnover in the Malaria Parasite Infection	
2010 – 2011	DARPA	\$1,800,000 – role: subcontract PI (with S. Evans, J. Morrison, E. Keogh, I. Neamtui)
	ProLiFiC: Cyber-Genetic Provenance, Lineage, Forensics and Classification	
2009 – 2011	USDA (CSREES)	\$1,000,000 – role: coPI (with T. Close, G. J. Muehlbauer, J. Bennetzen)
	Advancing the Barley Genome	
2006 – 2008	NSF (MRI)	\$330,000 – role: senior personnel (with L. Bhuyan, W. Najjar, G. Ciardo)
	MRI: Acquisition of an Ultra Low-Latency Multiprocessor System with On-Board Hardware Accelerators	
2006 – 2010	USDA (CSREES)	\$5,000,000 – role: coPI (G. Muehlbauer, T. Close, <i>et al.</i>)
	Barley Coordinated Agricultural Project: Leveraging Genomics, Genetics, and Breeding for Gene Discovery and Barley Improvement	
2005 – 2010	NSF (DBI)	\$414,277 – role: PI
	CAREER: Combinatorial Algorithms for Pattern Discovery with Applications to Data Mining and Computational Biology	
2003 – 2008	NSF (DBI)	\$2,497,294 – role: coPI (with T. Close, T. Jiang)
	Coupling Expressed Sequences and Bacterial Artificial Chromosome Resources to Access the Barley Genome	
2002 – 2005	USDA	\$335,000 – role: coPI (with T. Close)
	HarvEST: A portable EST database viewer	

Publications

Peer-reviewed Journal Articles

(† indicates authors that contributed equally)

- [1] Predicting Antibody-Antigen Interactions with Structure-Aware LLMs: Insights from SARS-CoV-2 Variants
F. B. Ashraf, V. A. Madrigal, S. Lonardi
Journal of Chemical Information and Modeling, vol. 65, no. 16, pp. 8846–8857, 2025
- [2] RAmbler Resolves Complex Repeats in Human Chromosomes 8, 19 and X
S. Chakravarty, G. Logsdon, S. Lonardi
Genome Research, vol. 4, no. 35, pp. 863–876, 2025

- [3] A Drug Repurposing Approach Reveals Targetable Epigenetic Pathways in *Plasmodium vivax* Hypnozoites
S. P. Maher, M. A. Bakowski, A. Vantaux, E. L. Flannery, C. Andolina, M. Gupta, Y. Antonova-Koch, M. Argomaniz, M. Cabrera-Mora, B. Campo, A. T. Chao, A. K. Chatterjee, W. T. Cheng, C. A. Cooper, K. Cottier, M. R. Galinski, A. Harupa-Chung, H. Ji, S. B. Joseph, T. Lenz, [S. Lonardi](#), J. Matheson, S. A. Mikolajczak, V. Padin-Irizarry, K. Pan, J. Péneau, J. Prudhomme, C. Roesch, S. S. Sabnis, C. L. Saney, J. Sattabongkot, S. Sereshki, S. Suriyakan, T. Moeller, R. Ubalee, Y. Wang, P. Wasisakun, J. Yin, C. W. McNamara, C. J. Joyner, F. Nosten, B. Witkowski, K. G. L. Roch, D. E. Kyle
eLife, vol. 13, no. RP98221, 2025
- [4] MSTmap Online: Enhanced Usability, Visualization, and Accessibility
A. Mohseni, [S. Lonardi](#)
Nucleic Acids Research, gkaf332, 2025
- [5] Kingdom-Wide CRISPR Guide Design with ALLEGRO
A. Mohseni[†], R. G. Nia[†], A. Tafriahi, M. L. López, X.-Z. Liu, J. E. Stajich, [S. Lonardi](#), I. Wheeldon
Nucleic Acids Research, gkaf783, 2025
- [6] Predicting Differentially Methylated Cytosines in TET and DNMT3 Knockout Mutants via a Large Language Model
S. Sereshki, [S. Lonardi](#)
Briefings in Bioinformatics, vol. 2, no. 26, bbaf092, 2025
- [7] TRFill: Synergistic Use of HiFi and Hi-C Sequencing enables Accurate Assembly of Tandem Repeats for Population-level Analysis
H. Wen, J. Yang, X. Zhao, X. Wang, J. Lei, Y. Li, W. Du, D. Li, Y. Xu, [S. Lonardi](#), W. Pan
Genome Biology, vol. 26, p. 227, 2025
- [8] Properties and Predicted Functions of Large Genes and Proteins of Apicomplexan Parasites
T. Fang, A. Mohseni, [S. Lonardi](#), C. B. Mamoun
NAR Genomics and Bioinformatics, vol. 6, no. 2, lqae032, 2024
- [9] Identification of candidate genes controlling red seed coat color in cowpea (*Vigna unguiculata* [L.] Walp)
I. A. Herniter, M. Muñoz-Amatriáin, S. Lo, Y.-N. Guo, [S. Lonardi](#), T. J. Close
Horticulturae, vol. 10, no. 2, p. 161, 2024
- [10] A mid-density single nucleotide polymorphism panel for molecular applications in cowpea (*Vigna unguiculata* (L.) Walp)
P. Ongom, C. Fatokun, A. Togola, A. Garcia-Oliveira, E. NG, A. Kilian, [S. Lonardi](#), T. Close, O. Boukar
International Journal of Genomics, vol. 2024, no. 9912987, 2024
- [11] Insights Into the Evolution, Virulence and Speciation of *Babesia MO1* and *Babesia divergens* Through Multiomics Analyses
P. Singh, P. Vydyam, T. Fang, K. Estrada, L. M. Gonzalez, R. Grande, M. Kumar, S. Chakravarty, V. Berry, V. Ranwez, B. Carcy, D. Depoix, S. Sanchez, E. Cornillot, S. Abel, L. Ciampossin, T. Lenz, O. Harb, A. Sanchez-Flores, E. Montero, K. G. L. Roch, [S. Lonardi](#), C. B. Mamoun
Emerging Microbes and Infections, vol. 13, no. 1, 2024
- [12] Balanced Training Sets Improve Deep Learning-Based Prediction of CRISPR sgRNA Activity
V. Trivedi, A. Mohseni, [S. Lonardi](#), I. Wheeldon
ACS Synthetic Biology, vol. 13, no. 11, pp. 3774–3781, 2024
- [13] Comprehensive assessment of 11 *de novo* HiFi assemblers on complex eukaryotic genomes and metagenomes
W. Yu, H. Luo, J. Yang, S. Zhang, H. Jiang, X. Zhao, X. Hui, L. L. Da Sun, X.-q. Wei, [S. Lonardi](#), W. Pan
Genome Research, vol. 34, no. 2, pp. 326–340, 2024
- [14] A view of the pan-genome of domesticated cowpea (*Vigna unguiculata* [L.] Walp.)
Q. Liang, M. Muñoz-Amatriáin, S. Shu, S. Lo, X. Wu, J. W. Carlson, P. Davidson, D. M. Goodstein, J. Phillips, N. M. Janis, E. J. Lee, C. N. Liang, P. L. Morrell, A. D. Farmer, P. Xu, T. J. Close, [S. Lonardi](#)
The Plant Genome, no. e20319, 2023

- [15] acCRISPR: An activity-correction method for improving the accuracy of CRISPR screens
A. Ramesh, V. Trivedi, S. Lee, A. Tafirshi, C. Schwartz, A. Mohseni, M. Li, [S. Lonardi](#), I. Wheeldon
Communication Biology, vol. 6, no. 617, 2023
- [16] On the Prediction of non-CG DNA Methylation using Machine Learning
S. Sereshki, N. Lee, M. Omirou, D. Fasoula, [S. Lonardi](#)
NAR Genomics and Bioinformatics, vol. 5, no. 2, 2023
- [17] *Babesia duncani* multi-omics identifies virulence factors and drug targets
P. Singh[†], [S. Lonardi](#)[†], Q. Liang, P. Vydyam, E. Khabirova, T. Fang, S. Gihaz, J. Thekkiniath, M. Munshi, S. Abel, G. Batugedara, M. Gupta, X. M. Lu, T. Lenz, S. Chakravarty, E. Cornillot, Y. Hu, W. Ma, L. M. Gonzalez, S. Sanchez, A. Sanchez-Flores, K. Estrada, O. S. Harb, K. G. L. Roch, C. B. Mamoun
Nature Microbiology, vol. 8, pp. 845–859, 2023
- [18] Babesia BdFE1 Esterase is Required for the Anti-parasitic Activity of the ACE Inhibitor Fosinopril
P. Vydyam, J.-Y. Choi, S. Gihaz, M. Chand, M. Gewirtz, J. Thekkiniath, [S. Lonardi](#), J. C. Gennaro, C. B. Mamoun
Journal of Biological Chemistry, vol. 299, no. 11, p. 105313, 2023
- [19] Genome-wide functional screens enable the prediction of high activity CRISPR-Cas9 and -Cas12a guides in *Yarrowia lipolytica*
D. Baisya, A. Ramesh, C. Schwartz, [S. Lonardi](#), I. Wheeldon
Nature Communications, vol. 13, no. 922, 2022
- [20] Karyotype variation, spontaneous genome rearrangements affecting chemical insensitivity, and expression level polymorphisms in the phytopathogen *Phytophthora infestans* revealed using its first chromosome-scale assembly
M. E. H. Matson, Q. Liang, [S. Lonardi](#), H. S. Judelson
PLOS Pathogens, vol. 18, no. 10, e1010869, 2022
- [21] Reference-agnostic Representation and Visualization of Pan-genomes
Q. Liang, [S. Lonardi](#)
BMC Bioinformatics, vol. 22, no. 502, 2021
- [22] Mustache: Multi-scale Detection of Chromatin Loops from Hi-C and Micro-C Maps using Scale-Space Representation
A. R. Ardakany, H. T. Gezer, [S. Lonardi](#), F. Ay
Genome Biology, vol. 21, no. 256, 2020
- [23] Prediction of Histone Post-translational Modifications using Deep Learning
D. R. Baisya, [S. Lonardi](#)
Bioinformatics, vol. 36, no. 24, pp. 5610–5617, 2020
- [24] DeeplyEssential: A Deep Neural Network for Predicting Essential Genes in Microbes
M. A. Hasan, [S. Lonardi](#)
BMC Bioinformatics, vol. 21, no. 367, 2020
- [25] OMGS: Optical Map-based Genome Scaffolding
W. Pan, T. Jiang, [S. Lonardi](#)
Journal of Computational Biology, vol. 27, no. 4, pp. 519–533, 2020
- [26] Selfish: Discovery of Differential Chromatin Interactions via a Self-Similarity Measure
A. R. Ardakany, F. Ay, [S. Lonardi](#)
Bioinformatics, vol. 35, no. 14, pp. i145–i153, 2019
- [27] Seed Coat Pattern QTL and Development in Cowpea (*Vigna unguiculata* [L.] Walp.)
I. A. Herniter, R. Lo, M. Muñoz-Amatriáin, S. Lo, Y.-N. Guo, B.-L. Huynh, M. R. Lucas, Z. Jia, P. A. Roberts, [S. Lonardi](#), T. Close
Frontiers in Plant Science, vol. 10, p. 1346, 2019
- [28] The Genome of Cowpea (*Vigna unguiculata* L. Walp.)
[S. Lonardi](#)[†], M. Muñoz-Amatriáin[†], Q. Liang, S. Shu, S. Wanamaker, S. Lo, J. Tanskanen, A. Schulman, T. Zhu,

- M.-C. Luo, H. Alhakami, R. Ounit, A. Hasan, J. Verdier, P. Roberts, J. Santos, A. Ndeve, J. Dolezel, J. Vrana, S. Hokin, A. Farmer, S. Cannon, T. Close
The Plant Journal, vol. 98, no. 5, pp. 767–782, 2019
- [29] Accurate Detection of Chimeric Contigs via Bionano Optical Maps
W. Pan, [S. Lonardi](#)
Bioinformatics, vol. 35, no. 10, pp. 1760–1762, 2019
- [30] Validating Genome-wide CRISPR-Cas9 Function Improves Screening in the Oleaginous Yeast *Yarrowia lipolytica*
C. Schwartz, J.-F. Cheng, R. Evans, C. A. Schwartz, J. M. Wagner, S. Anglin, A. Beitz, W. Pan, [S. Lonardi](#), M. Blenner, H. S. Alper, Y. Yoshikuni, I. Wheeldon
Metabolic Engineering, vol. 55, pp. 102–110, 2019
- [31] A Multi-parent Advanced Generation Inter-cross (MAGIC) Population for Genetic Analysis and Improvement of Cowpea (*Vigna unguiculata* L. Walp.)
B.-L. Huynh, J. Ehlers, B. E. Huang, M. Muñoz-Amatriáin, [S. Lonardi](#), J. Santos, A. Ndeve, B. Batiemo, O. Boukar, N. Cisse, I. Drabo, C. Fatokun, F. Kusi, R. Agyare, Y.-N. Guo, I. Herniter, S. Lo, S. Wanamaker, S. Xu, T. Close, P. Roberts
The Plant Journal, vol. 93, no. 6, pp. 1129–1142, 2018
- [32] Novo&Stitch: Accurate Reconciliation of Genome Assemblies via Optical Maps
W. Pan, S. Wanamaker, A. Ah-Fong, H. Judelson, [S. Lonardi](#)
Bioinformatics, vol. 34, no. 13, pp. i43–i51, 2018
- [33] A Comparative Evaluation of Genome Assembly Reconciliation Tools
H. Alhakami, H. Mirebrahim, [S. Lonardi](#)
Genome Biology, vol. 18, no. 1, p. 93, 2017
- [34] Construction of a Map-based Reference Genome Sequence for Barley, *Hordeum vulgare* L.
S. Beier, A. Himmelbach, C. Colmsee, X.-Q. Zhang, R. A. Barrero, Q. Zhang, L. Li, M. Bayer, D. Bolser, S. Taudien, M. Groth, M. Felder, A. Hastie, H. Simkova, H. Stankova, J. Vrana, S. Chan, M. Muñoz-Amatriáin, R. Ounit, S. Wanamaker, T. Schmutzer, L. Aliyeva-Schnorr, S. Grasso, J. Tanskanen, D. Sampath, D. Heavens, S. Cao, B. Chapman, F. Dai, Y. Han, H. Li, X. Li, C. Lin, J. K. McCooke, C. Tan, S. Wang, S. Yin, G. Zhou, J. A. Poland, M. I. Bellgard, A. Houben, J. Dolezel, S. Ayling, [S. Lonardi](#), P. Langridge, G. J. Muehlbauer, P. Kersey, M. D. Clark, M. Caccamo, A. H. Schulman, M. Platzer, T. J. Close, M. Hansson, G. Zhang, I. Braumann, C. Li, R. Waugh, U. Scholz, N. Stein, M. Mascher
Scientific Data (Nature), vol. 4, p. 170044, 2017
- [35] A Chromosome Conformation Capture Ordered Sequence of the Barley Genome
M. Mascher, H. Gundlach, A. Himmelbach, S. Beier, S. O. Twardziok, T. Wicker, V. Radchuk, C. Dockter, P. E. Hedley, J. Russell, M. Bayer, L. Ramsay, H. Liu, G. Haberer, X.-Q. Zhang, Q. Zhang, R. A. Barrero, L. Li, S. Taudien, M. Groth, M. Felder, A. Hastie, H. Simkova, H. Stankova, J. Vrana, S. Chan, M. Muñoz-Amatriáin, R. Ounit, S. Wanamaker, D. Bolser, C. Colmsee, T. Schmutzer, L. Aliyeva-Schnorr, S. Grasso, J. Tanskanen, A. Chailyan, D. Sampath, D. Heavens, L. Clissold, S. Cao, B. Chapman, F. Dai, Y. Han, H. Li, X. Li, C. Lin, J. K. McCooke, C. Tan, P. Wang, S. Wang, S. Yin, G. Zhou, J. A. Poland, M. I. Bellgard, L. Borisjuk, A. Houben, J. Dolezel, S. Ayling, [S. Lonardi](#), P. Kersey, P. Langridge, G. J. Muehlbauer, M. D. Clark, M. Caccamo, A. H. Schulman, K. F. Mayer, M. Platzer, T. J. Close, U. Scholz, M. Hansson, G. Zhang, I. Braumann, M. Spannagl, C. Li, R. Waugh, N. Stein
Nature, vol. 544, pp. 427–433, 2017
- [36] Comprehensive Benchmarking and Ensemble Approaches for Metagenomic Classifiers
A. McIntyre, R. Ounit, E. Afshinnekoo, R. Prill, E. Henaff, N. Alexander, S. Minot, D. Danko, J. Fook, S. Ahsanuddin, S. Tighe, N. Hasan, P. Subramanian, K. Moffat, [S. Lonardi](#), S. Levy, N. Greenfield, R. Colwell, G. Rosen, C. Mason
Genome Biology, vol. 18, no. 1, p. 182, 2017
- [37] Rasbhari: Optimizing Spaced Seeds for Database Searching, Read Mapping and Alignment-Free Sequence Comparison
L. Hahn, C.-A. Leimeister, R. Ounit, [S. Lonardi](#), B. Morgenstern
PLoS Computational Biology, vol. 12, no. 10, e1005107, 2016

- [38] BRAT-nova: Fast and Accurate Mapping of Bisulfite-treated Reads
E. Y. Harris, R. Ounit, [S. Lonardi](#)
Bioinformatics, vol. 32, no. 17, pp. 2696–2698, 2016
- [39] Genome Resources for Climate-resilient Cowpea, an Essential Crop for Food Security
M. Muñoz-Amatriáin, H. Mirebrahim, P. Xu, S. I. Wanamaker, M. Luo, H. Alhakami, M. Alpert, I. Atokple, B. J. Batieno, O. Boukar, S. Bozdag, N. Cisse, I. Drabo, J. D. Ehlers, A. Farmer, C. Fatokun, Y. Q. Gu, Y.-N. Guo, B.-L. Huynh, S. A. Jackson, F. Kusi, C. T. Lawley, M. R. Lucas, Y. Ma, M. P. Timko, J. Wu, F. You, P. A. Roberts, [S. Lonardi](#), T. J. Close
The Plant Journal, vol. 89, no. 5, pp. 1042–1054, 2016
- [40] Higher Classification Sensitivity of Short Metagenomic Reads with CLARK-S
R. Ounit, [S. Lonardi](#)
Bioinformatics, vol. 32, no. 24, pp. 3823–3825, 2016
- [41] FFAST: FPGA-based Acceleration of Bowtie in Hardware
E. B. Fernandez, J. Villarreal, [S. Lonardi](#), W. A. Najjar
IEEE/ACM Transactions on Computational Biology and Bioinformatics, vol. 12, no. 5, pp. 973–981, 2015
- [42] Using the Minimum Description Length to Discover the Intrinsic Cardinality and Dimensionality of Time Series
B. Hu, T. Rakthanmanon, Y. Hao, S. Evans, [S. Lonardi](#), E. Keogh
Data Mining and Knowledge Discovery, vol. 29, no. 2, pp. 358–399, 2015
- [43] When Less is More: ‘Slicing’ Sequencing Data Improves Read Decoding Accuracy and *De Novo* Assembly Quality
[S. Lonardi](#), H. Mirebrahim, S. Wanamaker, M. Alpert, G. Ciardo, D. Duma, T. J. Close
Bioinformatics, vol. 31, no. 18, pp. 2972–2980, 2015
- [44] Analysis of Nucleosome Positioning Landscapes Enables Gene Discovery in the Human Malaria Parasite *Plasmodium falciparum*
X. M. Lu, E. Bunnik, N. Pokhriyal, S. Nasser, [S. Lonardi](#), K. L. Roch
BMC Genomics, vol. 16, no. 1005, 2015
- [45] *De Novo* Meta-Assembly of Ultra-deep Sequencing Data
H. Mirebrahim, T. J. Close, [S. Lonardi](#)
Bioinformatics, vol. 31, no. 12, pp. i9–i16, 2015
- [46] Sequencing of 15,622 Gene-bearing BACs Clarifies the Gene-dense Regions of the Barley Genome
M. Muñoz-Amatriáin[†], [S. Lonardi](#)[†], M.-C. Luo, K. Madishetty, J. Svensson, M. Moscou, S. Wanamaker, T. Jiang, A. Kleinhofs, G. Muehlbauer, R. Wise, N. Stein, Y. Ma, E. Rodriguez, D. Kudrna, P. Bhat, S. Chao, P. Condamine, S. Heinen, J. Resnik, R. Wing, H. Witt, M. Alpert, M. Beccuti, S. Bozdag, F. Cordero, H. Mirebrahim, R. Ounit, Y. Wu, F. You, J. Zheng, H. Simkova, J. Dolezel, J. Grimwood, J. Schmutz, D. Duma, L. Altschmied, T. Blake, P. Bregitzer, L. Cooper, M. Dilbirligi, A. Falk, L. Feiz, A. Graner, P. Gustafson, P. Hayes, P. Lemaux, J. Mammadov, T. Close
The Plant Journal, vol. 84, no. 1, pp. 216–227, 2015
- [47] CLARK: Fast and Accurate Classification of Metagenomic and Genomic Sequences using Discriminative Kmers
R. Ounit, S. Wanamaker, T. J. Close, [S. Lonardi](#)
BMC Genomics, vol. 236, no. 16, 2015
- [48] DNA-encoded Nucleosome Occupancy is Associated with Transcription Levels in the Human Malaria Parasite *Plasmodium falciparum*
E. M. Bunnik, A. Polishko, J. Prudhomme, N. Ponts, S. S. Gill, [S. Lonardi](#), K. G. Le Roch
BMC Genomics, vol. 15, no. 347, 2014
- [49] Deciphering Histone Code of Transcriptional Regulation in Malaria Parasites by Large-scale Data Mining
H. Chen, [S. Lonardi](#), J. Zheng
Computational Biology and Chemistry, vol. 50, pp. 3–10, 2014

- [50] Generating and Reversing Chronic Wounds in Diabetic Mice by Manipulating Wound Redox Parameters
S. Dhall, D. C. Do, M. Garcia, J. Kim, H. Mirebrahim, J. Lyubovitsky, S. Lonardi, E. A. Nothnagel, N. L. Schiller, M. Martins-Green
Journal of Diabetes Research, vol. 2014, p. 562625, 2014
- [51] PuFFIN: A Parameter-free Method to Build Nucleosome Maps from Paired-end Reads
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Proc. of Conference on Algorithmic Aspects in Information and Management (AAIM), pp. 126–137, Hong Kong, China, 2006
- [43] Computing the Assignment of Orthologous Genes via Genome Rearrangement
 X. Chen, J. Zheng, Z. Fu, P. Nan, Y. Zhong, [S. Lonardi](#), T. Jiang
Proceedings of Asia-Pacific Bioinformatics Conference (APCB), pp. 363–378, Singapore, 2005
- [44] Time-series Bitmaps: a Practical Visualization Tool for Working with Large Time Series Databases
 N. Kumar, V. N. Lolla, E. J. Keogh, [S. Lonardi](#), C. Ratanamahatana
Proceedings of the SIAM International Conference in Data Mining (SDM), pp. 531–535, Newport Beach, CA, 2005
- [45] A Novel Bit Level Time Series Representation with Implications for Similarity Search and Clustering
 C. Ratanamahatana, E. Keogh, A. J. Bagnall, [S. Lonardi](#)
Proceedings of Pacific-Asia Conference on Knowledge Discovery and Data Mining (PAKDD), pp. 771–777, Hanoi, Vietnam, 2005
- [46] A Practical Tool for Visualizing and Data Mining Medical Time Series
 L. Wei, N. Kumar, V. Lolla, E. Keogh, [S. Lonardi](#), C. Ratanamahatana, H. Van Herle
Proceedings of IEEE International Symposium on Computer-Based Medical Systems (CBM), pp. 341–346, Dublin, Ireland, 2005
- [47] Assumption-Free Anomaly Detection in Time Series
 L. Wei, N. Kumar, V. N. Lolla, E. J. Keogh, [S. Lonardi](#), C. Ratanamahatana
Proc. of the Conference on Statistical and Scientific Database Management (SSDBM), pp. 237–240, Santa Barbara, CA, 2005
- [48] Dot Plots for Time Series Analysis
 D. Yankov, E. Keogh, [S. Lonardi](#), A. W. Fu
Proceedings of IEEE International Conference on Tools with Artificial Intelligence (ICTAI), pp. 159–168, Hong Kong, China, 2005
- [49] Discovery of Repetitive Patterns in DNA with Accurate Boundaries
 J. Zheng, [S. Lonardi](#)
Proceedings of IEEE International Conference on Bioinformatics and BioEngineering (BIBE), pp. 105–112, Minneapolis, MN, 2005
- [50] On Average Sequence Complexity
 S. Janson, [S. Lonardi](#), W. Szpankowski
Proceedings of Symposium on Combinatorial Pattern Matching (CPM), pp. 74–88, Istanbul, Turkey, 2004
- [51] Towards Parameter-Free Data Mining
 E. Keogh, [S. Lonardi](#), C. A. Ratanamahatana
Proceedings of ACM Conference on Knowledge Discovery and Data Mining (KDD), pp. 206–215, Seattle, WA, 2004
- [52] Visually Mining and Monitoring Massive Time Series
 J. Lin, E. Keogh, [S. Lonardi](#), J. P. Lankford, D. M. Nystrom
Proceedings of ACM Conference on Knowledge Discovery and Data Mining (KDD), pp. 460–469, Seattle, WA, 2004
- [53] VizTree: a Tool for Visually Mining and Monitoring Massive Time Series Databases
 J. Lin, E. Keogh, [S. Lonardi](#), J. P. Lankford, D. M. Nystrom
Proceedings of International Conference on Very Large Data Bases (VLDB), pp. 1269–1272, Toronto, Canada, 2004
- [54] Gridding and Compression of Microarray Images
[S. Lonardi](#), Y. Luo

- Proceedings of the IEEE Computational Systems Bioinformatics Conference (CSB)**, pp. 122–130, Stanford, CA, 2004
- [55] Error Resilient LZ'77 and its Analysis
 S. Lonardi, W. Szpankowski, M. D. Ward
Proceedings of the IEEE International Symposium on Information Theory (ISIT), p. 56, Chicago, IL, 2004
- [56] Finding Biclusters by Random Projections
 S. Lonardi, W. Szpankowski, Q. Yang
Proceedings of Symposium on Combinatorial Pattern Matching (CPM), pp. 102–116, Istanbul, Turkey, 2004
- [57] Authentication of LZ-77 Compressed Data
 M. J. Atallah, S. Lonardi
Proceedings of the ACM Symposium on Applied Computing (SAC), pp. 282–287, Melbourne, FL, 2003
- [58] Probabilistic Discovery of Time Series Motifs
 B. Chiu, E. Keogh, S. Lonardi
Proceedings of the Conference on Knowledge Discovery and Data Mining (KDD), pp. 493–498, Washington, DC, 2003
- [59] A Symbolic Representation of Time Series, with Implications for Streaming Algorithms
 J. Lin, E. Keogh, S. Lonardi, B. Chiu
Proceedings of the ACM Workshop on Research Issues in Data Mining and Knowledge Discovery, pp. 2–11, San Diego, CA, 2003
- [60] Joint Source-Channel LZ'77 Coding
 S. Lonardi, W. Szpankowski
Proceedings of the IEEE Data Compression Conference (DCC), pp. 273–283, Snowbird, Utah, 2003
- [61] Efficient Selection of Unique and Popular Oligos for Large EST Databases
 J. Zheng, T. J. Close, T. Jiang, S. Lonardi
Proceedings of Symposium on Combinatorial Pattern Matching (CPM), pp. 384–401, Morelia, Mexico, 2003
- [62] Monotony of Surprise and Large-scale Quest for Unusual Words
 A. Apostolico, M. E. Bock, S. Lonardi
Proceedings of Conference on Research in Computational Molecular Biology (RECOMB), pp. 22–31, Washington, DC, 2002
- [63] Analysis of Secondary Structure Elements of Proteins Using Indexing Techniques
 C. Guerra, S. Lonardi, G. Zanotti
Proceedings of Symposium on 3D Data Processing Visualization and Transmission (3DPVT), pp. 812–823, Padova, Italy, 2002
- [64] Finding Surprising Patterns in a Time Series Database in Linear Time and Space
 E. Keogh, S. Lonardi, B. Chiu
Proceedings of the Conference on Knowledge Discovery and Data Mining (KDD), pp. 550–556, Edmonton, Alberta, Canada, 2002
- [65] Finding Motifs in Time Series
 J. Lin, E. Keogh, S. Lonardi, P. Patel
Proceedings of the Second Workshop on Temporal Data Mining (TDM), pp. 53–68, Edmonton, Alberta, Canada, 2002
- [66] Mining Motifs in Massive Time Series Databases
 P. Patel, E. Keogh, J. Lin, S. Lonardi
Proceedings of IEEE International Conference on Data Mining (ICDM), pp. 370–377, Maebashi City, Japan, 2002
- [67] Compression of Biological Sequences by Greedy Off-line Textual Substitution
 A. Apostolico, S. Lonardi
Proceedings of the IEEE Data Compression Conference (DCC), pp. 143–152, Snowbird, Utah, 2000
- [68] Linear Global Detectors of Redundant and Rare Substrings
 A. Apostolico, M. E. Bock, S. Lonardi
Proceedings of the IEEE Data Compression Conference (DCC), pp. 168–177, Snowbird, Utah, 1999
- [69] Some Theory and Practice of Greedy Off-Line Textual Substitution
 A. Apostolico, S. Lonardi
Proceedings of the IEEE Data Compression Conference (DCC), pp. 119–128, Snowbird, Utah, 1998

- [70] Encoding Pyramids by Labeling RAAM
S. Lonardi, A. Sperduti, A. Starita
Proceedings of the IEEE Workshop on Neural Networks for Signal Processing (NNSP), pp. 651–660, Ermioni, Greece, 1994

Patents

- [1] String Matching in Hardware using the FM-Index
 E. Fernandez, W. Najjar, S. Lonardi
USPTO no. 8,468,162, 2013

Technical Program Committee and Editorial Work

Guest Editor	Special issue on "3D Genomics" - BMC Bioinformatics (Springer, ISSN 1471-2105) 2024–2025	IF 3.6
Editorial Board	BMC Bioinformatics (ISSN 1471-2105) 2020–	IF 3.6
Editor in Chief	Genes - Bioinformatics Section (ISSN 2073-4425) 2020–2024	IF 4
Editorial Board	Genes (ISSN 2073-4425) 2018–2020	IF 4
PC Member	RECOMB: International Conference on Research in Computational Molecular Biology 2013: Beijing, China 2014: Pittsburgh, PA 2015: Warsaw, Poland 2020: Padova, Italy 2021: Padova, Italy 2022: San Diego, CA 2023: Istanbul, Turkey 2025: Seoul, Korea 2026: Thessaloniki, Greece	
PC member	ACM-BCB: ACM Conference on Bioinformatics, Computational Biology and Health Informatics 2014: Newport Beach, CA 2015: Atlanta, GA 2016: Seattle, WA 2017: Boston, MA (Area Chair) 2018: Washington, DC 2019: Niagara Falls, NY 2020: Atlanta, GA 2021: on-line 2022: Chicago, IL 2023: Houston, TX (Area Chair) 2024: Shenzhen, China (Area Chair) 2025: Philadelphia, PA (Area Chair)	
PC member	ISMB: Intelligent Systems for Molecular Biology 2010: Boston, MA 2012: Long Beach, CA 2013: Berlin, Germany 2014: Boston, MA 2015: Dublin, Ireland 2016: Orlando, FL (Area Chair) 2018: Chicago, IL 2019: Basel, Switzerland 2022: Madison, WI 2023: Lyon, France 2024: Montreal, Canada 2025: Liverpool, UK	
PC member	WABI: Workshop of Algorithms in Bioinformatics 2007: Philadelphia, PA 2008: Karlsruhe, Germany 2009: Philadelphia, PA 2011: Saar- bruecken, Germany 2013: Sophia Antipolis, France 2014: Wroclaw, Poland 2015: At- lanta, GA 2016: Aarhus, Denmark 2017: Boston, MA 2020: Pisa, Italy 2021: (on-line) 2022: Potsdam, Germany	
Chair/Member	Steering Committee, IEEE/ACM Transactions on Computational Biology and Bioinformatics Member (2012 – 2016), Chair (2016 – 2017)	
PC member	SPIRE: String Processing and Information Retrieval 2005: Buenos Aires, Argentina 2006: Glasgow, UK 2013: Jerusalem, Israel 2017: Palermo, Italy	
PC member	RECOMB-SEQ: RECOMB Satellite Workshop on Massively Parallel Sequencing 2014: Pittsburgh, PA 2015: Warsaw, Poland 2016: Santa Monica, CA	

Technical Program Committee and Editorial Work (continued)

PC member	BIBM: IEEE International Conference on Bioinformatics and Biomedicine 2015: Washington, DC
PC member	CPM: Symposium on Combinatorial Pattern Matching 2004: Istanbul, Turkey 2006: Barcelona, Spain 2008: Pisa, Italy 2009: Lille, France 2011: Palermo, Italy 2014: Moscow, Russia 2015: Ischia, Italy
PC member	ICCABS: IEEE Conference on Computational Advances in Bio and Medical Sciences 2011: Orlando, FL 2012: Las Vegas, NV 2013: New Orleans, LA 2014: Miami Beach, FL
PC chair	SPIRE: String Processing and Information Retrieval 2010: Los Cabos, Mexico
PC member	RECOMB-CG: RECOMB Satellite Workshop on Comparative Genomics 2014: Cold Spring Harbor, NY
PC member	APBC: Asia Pacific Bioinformatics Conference 2013: Vancouver BC, Canada
PC member	ICDM: IEEE International Conference on Data Mining 2008: Pisa, Italy 2012: Brussels, Belgium
PC member	KDD: ACM International Conference on Knowledge Discovery and Data Mining 2011: San Diego, CA 2012: Beijing, China
PC member	SDM: SIAM International Conference on Data Mining 2006: Bethesda, MD 2007: Minneapolis, MN 2008: Atlanta, GA 2012: Anaheim, CA
PC chair	BioKDD: International Workshop on Data Mining in Bioinformatics 2007: San Jose, CA 2008: Las Vegas, NV
Guest Editor	Special issue "Data Mining in Bioinformatics: Selected Papers from BIOKDD" <i>IEEE/ACM Transactions Computational Biology & Bioinformatics</i> , vol. 7, no. 2, 2010
Guest Editor	Special issue in honor of A. Apostolico's 60th birthday <i>Theoretical Computer Science</i> , vol. 395, no. 2-3, 2008
PC member	CSB: International Conference on Computational Systems Bioinformatics 2008: San Diego, CA
Guest Editor	Special Issue on "Selected Papers from BioKDD 2007" <i>Journal of Computational Biology and Bioinformatics</i>
PC member	DCC: IEEE Data Compression Conference 2007: Snowbird, UT 2008: Snowbird, UT

Courses Taught

- UCR **CS 144: Algorithms for Bioinformatics**
Spring'25, Winter'24, Spring'23, Spring'22, Spring'20
- UCR **CS 218: Design and Analysis of Algorithms [graduate]**
Fall'21, Winter'20, Fall'18, Spring'18, Spring'17, Fall'16, Fall'15, Winter'14, Fall'12, Fall'07,
Winter'07, Winter'06, Winter'05
- UCR **CS 234: Computational Methods for the Analysis of Biomolecular Data [graduate]**
Fall'25, Spring'24, Fall'22, Winter'21, Winter'19, Winter'17, Winter'16, Winter'15, Winter'13,
Winter'11, Winter'10, Winter'09, Winter'08, Fall'06, Fall'05, Fall'03
- Harvey Mudd C. **MATH/COMP/BIO 118: Introduction to Mathematical and Computational Biology**
Spring'13 (with Prof. Steve Adolph and Prof. Rachel Levy)
- UCR **CS 141: Data Structures and Algorithms**
Spring'19, Fall'17, Fall'14, Spring'14, Spring'13, Fall'11, Fall'10, Fall'09, Spring'07, Fall'04,
Winter'04, Winter'03, Spring'02
- UCR **CS 260: Advanced Topics in Computational Biology [graduate seminar]**
Winter'18, Spring'15, Spring'12, Winter'11
- UCR **CS 179G: Design Project in Computer Science**
Spring'04
- UCR **GEN 240B: Advances in Bioinformatics and Genomics [graduate]**
Two guest lectures: Spring'06, Spring'05, Spring'03, Spring'02
- UCR **CS 260, Pattern Discovery in Biosequences [graduate seminar]**
Winter'03, Fall'01
- UCR **CS 150, The Theory of Automata and Formal Languages**
Spring'06, Fall'02

Advisory and Review Committees (2011-)

Reviewer	UCR RAISE Seed Grant Applications UC Riverside	Oct 2025
Reviewer	Path Towards Precision Medicine Qatar Research, Development, and Innovation Council	Mar 2025
Panelist	CAREER Information & Intelligent Systems (III) National Science Foundation (on-line panel)	Nov 2024
Reviewer	Cross-Border Threat Screening and Supply Chain Defense Insect and Pathogen Detection Department of Homeland Security	May 2024
Ad hoc Reviewer	Plant Genome Research Program National Science Foundation	Apr 2024
Panelist	Information & Intelligent Systems (III) National Science Foundation (on-line panel)	Mar 2023
Reviewer	Italian Science Fund (FIS) Italian Ministry of University and Research	Oct 2022
Ad hoc Reviewer	EPSCoR NSF CAREER pre-evaluations University of Nebraska-Lincoln	Sep 2022
Panelist	Division of Biological Infrastructure (Innovation: Bioinformatics) National Science Foundation (on-line panel)	Nov 2021
Reviewer	Swiss National Research Swiss National Science Foundation (SNSF)	Aug 2021
Reviewer	Institute for Genomics and Bioinformatics (ORU Sunset Review) University of California, Irvine	Feb 2021
Reviewer	Post-doc Fellowships Program University of Verona	Nov 2020
Reviewer	Agora Programme Swiss National Science Foundation (SNSF)	Nov 2020
Reviewer	DoD Research and Education Program for HBCU/MI Department of Defense	June 2020
Reviewer	Post-doc Fellowships Program University of Verona	Mar 2020
Reviewer	DoD Basic Research Program for HBCU/MI Department of Defense	May 2019
Panelist	Information & Intelligent Systems (III) National Science Foundation (on-line panel)	May 2019
Reviewer	CSR Anonymization Peer Review Study National Institutes of Health	Feb 2019
Reviewer	CSR Anonymization Peer Review Study National Institutes of Health	June 2018
Panelist	Space Biology and Computational Biology NASA (on-line panel)	May 2018
Reviewer	Bioinformatics and Computational Biology Pre-reviews for Ontario Genomics (Genome Canada)	Mar 2018
Reviewer	National Defense Science and Engineering Graduate Fellowship Department of Defense	Feb 2018

Advisory and Review Committees (2011-) (continued)

Reviewer	Center of Excellence for Cross-Border Threat Screening and Supply Chain Defense Department of Homeland Security	Dec 2017
Panelist	Information & Intelligent Systems (III) National Science Foundation (on-line panel)	Dec 2017
Panelist	Biomedical Research Shared Instrumentation (S10) National Institutes of Health (on-line panel)	Oct 2017
Reviewer	IEEE Computer Society IEEE Fellow Evaluating Committee	May 2017
Panelist	Biomedical Research Shared Instrumentation (S10) National Institutes of Health (on-line panel)	Nov 2016
Reviewer	Ateneo Projects University of Padova, Italy	Oct 2016
Chair	GeneLab Innovation for Translational Systems Biology and Informatics Research NASA (panel held in Arlington, VA)	Sep 2016
Reviewer	Swiss National Research Programme "Big Data" Swiss National Science Foundation (SNSF)	Aug 2016
Reviewer	IEEE Computer Society IEEE Fellow Evaluating Committee	Mar 2016
Panelist	Biodata Management and Analysis (BDMA) Study Section National Institutes of Health (panel held in Long Beach, CA)	Feb 2016
Reviewer	National Priorities Research Program Qatar National Research Fund (QNRF)	Jan 2016
Reviewer	National Priorities Research Program Qatar National Research Fund (QNRF)	Feb 2015
Panelist	Biodata Management and Analysis (BDMA) Study Section National Institutes of Health (panel held in Los Angeles, CA)	Feb 2015
Reviewer	Department of Public Health and Innovation Italian Ministry of Health	Dec 2014
Panelist	Computational Analyses Exploiting Reference Epigenomic Maps Study Section National Institutes of Health (on-line panel)	May 2014
Panelist	Biodata Management and Analysis (BDMA) Study Section National Institutes of Health (panel held in San Francisco, CA)	Feb 2014
Panelist	Biodata Management and Analysis (BDMA) Study Section National Institutes of Health (panel held in Los Angeles, CA)	Feb 2013
Reviewer	Department of Public Health and Innovation Italian Ministry of Health	Apr 2012
Panelist	Information & Intelligent Systems (III) National Science Foundation (panel held in Arlington, VA)	Oct 2011
Panelist	Communications, Computer Science, and Digital Media UC Discovery Grant Program (panel held in Oakland, CA)	Jun 2011
Panelist	Information & Intelligent Systems (III) National Science Foundation (panel held in Arlington, VA)	Mar 2011

University Service

Member	Committee on Academic Personnel Academic Senate, UC Riverside	2025-2028
Member	Computing and Data Science Instruction (CDI) building committee Department of Computer Science and Engineering, UC Riverside	2024-2025
Vice Chair	Department of Computer Science and Engineering Vice Chair of Undergraduate Education, Dept. of CSE, UC Riverside	2009–
Member	Lecturer Search Committee Department of Computer Science and Engineering, UC Riverside	2024
Member	Faculty Search Committee Department of Computer Science and Engineering, UC Riverside	2021-2022
Member	Grievance Consultation Panel Academic Senate, UC Riverside	2020–2023
Participant	VPAP Academic Leadership Series UC Riverside	2021
Member	Faculty Search Committee Department of Computer Science and Engineering, UC Riverside	2019-2020
Member	Peer Review Committee UC Riverside	2017-2020
Chair	Ad Hoc Committee to Review the Evaluation of Teaching (iEval) Academic Senate, UC Riverside	2018–2019
Member	Committee on Faculty Welfare Academic Senate, UC Riverside	2017–2020
Member	Provost Faculty Leadership Program UC Riverside	2017–2018
Chair	Strategic Planning Committee Department of Computer Science and Engineering, UC Riverside	2017–2019
Member	Faculty Search Committee (Cyber-security Cluster) Department of Computer Science and Engineering, UC Riverside	2016–2017
Member	Title IX Director Search Committee UC Riverside	2016
Chair	Lecturer Search Committee Department of Computer Science and Engineering, UC Riverside	2015–2016
Chair	Committee on Privilege and Tenure Academic Senate, UC Riverside	2014–2016
<i>Ex-officio</i>	Committee on Academic Freedom Academic Senate, UC Riverside	2014–2016
Member	Faculty Search Committee (Data Science Cluster) UC Riverside	2015-2016
Member	Faculty Search Committee (Assistant Project Scientist of Plant Crop Genetics) College of Natural and Agricultural Sciences, UC Riverside	2015-2016
Chair	Lecturer Search Committee Department of Computer Science and Engineering, UC Riverside	2014–2015

University Service (continued)

Ext. Member	Bioinformatics Faculty Search Committee College of Natural and Agricultural Sciences, UC Riverside	2014–2015
Member	Vice Provost for International Affairs Search Committee UC Riverside	2013–2014
Member	Committee on Privilege and Tenure Academic Senate, UC Riverside	2013–2014
Member	Faculty Search Committee Department of Computer Science and Engineering, UC Riverside	2011–2014
Ext. Member	Academic Coordinator for Bioinformatics Search College of Natural and Agricultural Sciences, UC Riverside	2011–2014
Member	CEPCEB Award Committee College of Natural and Agricultural Sciences, UC Riverside	2012–2014
Chair	Distinguished Lecture Series, Dept. of Computer Science & Eng., UC Riverside Barbara Liskov, Moshe Vardi, Prabhakar Raghavan, Deborah Estrin, Eugene Myers	2009–2010
Chair	Distinguished Lecture Series, Dept. of Computer Science & Eng., UC Riverside Demetri Terzopoulos, Frans Kaashoek, Michael Waterman, Leslie Lamport, Michael Jordan	2007–2008
Chair	Faculty Search Committee, Dept. of Computer Science & Eng., UC Riverside Hired: Harsha Madhyastha, Philip Brisk, Iulian Neamtiu, Rajiv Gupta	2006–2010
Chair	Weekly Colloquium, Department of Computer Science and Engineering UC Riverside	2006–2010
Ext. member	Bioinformatics Faculty Search Committee College of Natural and Agricultural Sciences, UC Riverside	2006–2008
Member	Academic Integrity Committee Bourns College of Engineering, UC Riverside	2006–2008
Member	Faculty Search Committee Plant Cell Biology, UC Riverside	2005–2006
Member	Graduate Admissions Committee Genetics, Genomics and Bioinformatics PhD Program, UC Riverside	2005–2006
Member	Executive Committee Bourns College of Engineering, UC Riverside	2005–2008
Member	Steering committee of the ChemGen IGERT program College of Natural and Agricultural Sciences, UC Riverside	2005–2008
Member	Graduate Committee Department of Computer Science and Engineering, UC Riverside	2003–2005
Member	Faculty Search Committee Department of Computer Science and Engineering, UC Riverside	2001–2002

PhD students supervised

Iftikhar Kalanther	PhD student Computer Science and Engineering, UC Riverside	2024–
Fatima Nawmi	PhD student Computer Science and Engineering, UC Riverside	2024–
S. Papadopoulos	PhD student Computer Science and Engineering, UC Riverside	2023–
Faisal Bin Ashraf	PhD student Computer Science and Engineering, UC Riverside	2022–
Amir Mohseni	PhD candidate Computer Science and Engineering, UC Riverside	2020–
S. Chakravarty	PhD candidate Computer Science and Engineering, UC Riverside	2020–
Saleh Sereshki	PhD candidate <i>Post-doc</i> with the Icahn School of Medicine at Mount Sinai, New York, NY	2019–2024
Dipankar Baisya	PhD, "Deep Learning Algorithms for Single Guide RNA CRISPR Efficiency" <i>Applied Scientist</i> at Amazon Science, Seattle, WA	2016–2021
Qihua Liang	PhD, "Methods for Comparative Genome Analysis with Applications to Pan-genomics" <i>Bioinformatics Scientist</i> at Zymergen, Emeryville, CA	2015–2020
Abbas Roayaei	PhD, "Efficient Algorithms for the Analysis of Hi-C Contact Maps" <i>Post-doc</i> at La Jolla Institute for Immunology, San Diego, CA	2014–2019
Md. Abid Hasan	PhD, "Accurate Prediction Methods on Biomolecular Data" <i>Principal Scientist</i> at Roche Sequencing, Pleasanton, CA	2014–2019
Weihua Pan	PhD, "Optical Map-based Genome Scaffolding" <i>Research Professor</i> at Shenzhen Agricultural Genome Research Institute, China	2014–2019
Rachid Ounit	PhD, "Computing the Microbiome: Efficient Methods for the Analysis of Metagenomes" <i>EAS Lead</i> at Karius, Redwood City, CA	2013–2017
Hind Alhakami	PhD, "Data Structures and Algorithms for de novo Genome Assembly" <i>Bioinformatics Scientist</i> at Dovetail Genomics, Santa Cruz, CA	2012–2017
H. Mirebrahim	PhD, "Efficient Methods for the Analysis of Ultra-Deep Sequencing Data" <i>Principal Scientist</i> at Roche Sequencing, Pleasanton, CA	2010–2015
Anton Polishko	PhD, "Computational Methods for Exploring Nucleosome Dynamics" <i>CTO</i> at Zulloo Inc	2009–2014
Denisa Duma	PhD, "A Pooling Strategy for the Selective Sequencing of Very Large Genomes" <i>Post-doc</i> with Icahn School of Medicine at Mount Sinai, New York, NY	2008–2013
Elena Harris	PhD, "Computational Methods for Epigenetic Studies" <i>Associate Professor</i> at California State University, Chico, CA	2005–2010
Vladimir Vacic	PhD, "Computational Methods for Discovery of Cellular Regulatory Mechanisms" <i>Bioinformatics Scientist</i> at 23andme, Mountain View, CA	2003–2008
Yonghui Wu	PhD, "On the Accurate Construction of Genetic Linkage Maps" <i>Distinguished Engineer</i> at Google Brain, Mountain View, CA	2003–2008
Serdar Bozdog	PhD, "Combinatorial Approaches to the Physical Mapping Problem" <i>Associate Professor</i> at University of North Texas, Denton, TX	2003–2008

PhD students supervised (continued)

Qiaofeng Yang	PhD, "Graph Theoretical Approaches to the Analysis to Large-Scale Genomic Data" <i>Manager</i> at Scientific Games, Reno, NV	2000–2006
Jie Zheng	PhD, "Algorithms for Identification of Repetitive Patterns in Biological Sequences" <i>Associate Professor</i> at ShanghaiTech University, Shanghai, China	2001–2006

Other students supervised

Hao Feng	MS, Computer Science and Engineering, UC Riverside	2023-2024
Richard Ky	BS, Computer Science, San Jose State University Cal-Bridge Mentee - joined UC Irvine	2022-2024
Justin Wang	MS, Computer Science and Engineering, UC Riverside Patent agent at Sterne Kessler, Washington DC	2022-2022
M. Goldberg	BS, Computer Science and Engineering, UCLA PhD student at UMD	2015-2015
F. Abdul-Kadar	MS, Computer Science and Engineering, UC Riverside Currently with ESRI	2014-2016
Alan Venegas	BS, Computer Science and Engineering, UC Riverside	2013-2015
Alberto Castellini	Research associate, MPI Molecular Plant Physiology, Potsdam, Germany Visiting scholar at UC Riverside	2015
Sara Nasser	MS, Computer Science and Engineering, UC Riverside Currently with Western Digital	2013-2014
Matthew Alpert	BS, Computer Science, UC Riverside, 2012 Undergrad Researcher; 2011 UC Riverside CEPCEB Undergraduate Research Award	2010-2012
Mo Cao	MS, Computer Science and Engineering, UC Riverside Currently with Xangati	2011-2012
Burair Alsaihati	MS, Computer Science and Engineering, UC Riverside Currently with Joint Center for Genomics Research, KACST	2010-2011
Davide Verzotto	PhD, University of Padova, 2012 Visiting scholar at UC Riverside	2009-2011
Neeti Pokhriyal	MS, Computer Science and Engineering, UC Riverside MS thesis "Nucleosome Landscape Analysis for Novel Gene Discovery Via Machine Learning"	2008-2009
George Hsu	MS, Computer Science and Engineering, UC Riverside MS thesis "Transcription Factor Binding Site Identification Using Support Vector Machines"	2004-2005
San Nguyen	MS, Computer Science and Engineering, UC Riverside Currently with Raytheon	2005-2006
Vi Pham	MS, Computer Science and Engineering, UC Riverside	2005-2006
Hongwei Ji	MS, Computer Science and Engineering, UC Riverside Currently with EBSCO publishing	2003-2004
Kun Yan	MS, Computer Science and Engineering, UC Riverside	2003-2004
Yu Luo	MS, Computer Science and Engineering, UC Riverside Currently with Glidewell Dental	2003-2004

Software

(available at <https://github.com/ucrbioinfo/>)

Allegro	Design Cas9 sgRNA library for thousands of species https://github.com/ucrbioinfo/allegro	2024
RAmbler	Repeat Assembler using HiFi reads https://github.com/ucrbioinfo/rambler	2024
L-Map	Prediction and analysis of differentially methylated cytosines https://github.com/ucrbioinfo/dmc_prediction	2024
AMPS	Context-specific DNA methylation prediction https://github.com/ucrbioinfo/AMPS	2023
DeepGuide	Prediction of high activity CRISPR-Cas9 and -Cas12a guides in <i>Yarrowia lipolytica</i> https://github.com/AmirUCR/deepguide_reborn	2023
AMPS	Context-specific DNA methylation prediction using a deep neural network https://github.com/ucrbioinfo/AMPS	2022
PGV	Reference-agnostic Representation and Visualization of Pan-genomes https://github.com/ucrbioinfo/PGV	2020
DeeplyEssential	Identification of Essential Genes in Bacteria https://github.com/ucrbioinfo/DeeplyEssential	2019
Epi2En	Prediction of Enhancer Regions from Epigenetic data https://github.com/ucrbioinfo/Epi2En	2019
Selfish	Discovery of Differential Chromatin Interactions via a Self-Similarity Measure https://github.com/ucrbioinfo/SELFISH	2019
DeepHistone	Prediction of Histone PTMs from Transcription Factor Binding data https://github.com/ucrbioinfo/DeepHistone	2018
OMGS	Genome Scaffolding tool via Bionano Optical Maps https://github.com/ucrbioinfo/OMGS	2018
Chimericognizer	Chimeric Contig Detection via Bionano Optical Maps https://github.com/ucrbioinfo/Chimericognizer	2017
XMView	Optical/genetic Maps Browser (Bionano maps) https://github.com/ucrbioinfo/XMView	2017
Novo&Stitch	Assembly Reconciliation via Bionano Optical Maps https://github.com/ucrbioinfo/Novo_Stitch	2017
EAST	Detection of Topologically Associating Domains from Contact Maps https://github.com/ucrbioinfo/EAST	2016
ThIEF	Finding Genome-wide Trajectories of Epigenetics Marks https://github.com/ucrbioinfo/ThIEF	2016
BRAT-NOVA	Bisulfite-treated Reads Analysis Tool http://compbio.cs.ucr.edu/brat/	2016
CLARK/CLARK-S	Classification of Genomics and Metagenomic Sequences http://clark.cs.ucr.edu/	2015
Slicemblem	Meta-Assembler for Ultra-deep Sequencing Data http://slicemblem.cs.ucr.edu/	2015
PuFFIN	Genome-wide Nucleosome Maps from Paired-end Sequencing Data https://github.com/ucrbioinfo/PuFFIN	2014

Software (continued)

(available at <https://github.com/ucrbioinfo/>)

NOrMAL	Nucleosome Positioning using a Modified Gaussian Mixture Model https://github.com/ucrbioinfo/NOrMAL	2013
BRAT-BW	Bisulfite-treated Reads Analysis Tool http://compbio.cs.ucr.edu/brat/	2012
MergeMap	Construction of Consensus Genetic Maps via Integer Linear Programming http://mstmap.org/	2011
MSTMap	Construction of Genetic Linkage Maps from the Minimum Spanning Tree of a Graph http://mstmap.org/	2008
Comp. Profiler	Discovery and Visualization of Amino Acid Composition Differences http://www.cprofiler.org/	2007
OligoSpawn	Selecting Unique and Popular Oligos from Unigene Databases http://mstmap.org/	2007

Invited and Conference Presentations (2010-)

09.2024	Israel Stringology Conference RAmbler resolves complex repeats in human chromosomes 8, 19 and X	Neve Ilan, Israel
07.2024	Computational Genomics Summer Institute, UCLA How to “squeeze” the best genome assembly out of your HiFi reads	Los Angeles, CA
07.2023	Computational Genomics Summer Institute, UCLA How to “squeeze” the best genome assembly out of your HiFi reads	Los Angeles, CA
04.2023	Fourth International Babesiosis Meeting The nuclear genome of <i>Babesia duncani</i>	New Haven, CT
04.2021	Third International Babesiosis Meeting A preview of the <i>Babesia duncani</i> genome assembly	New Haven, CT
04.2020	MRB Seminar Series, University of California Exploring the 3D genome structure in Hi-C contact maps	Riverside, CA
04.2020	Computer Science and Engineering Colloquium, University of California Exploring the 3D genome structure in Hi-C contact maps	Riverside, CA
01.2020	Bionano User Group Meeting Improving the Contiguity and Correctness of Genome Assembly via Optical Maps	San Diego, CA
11.2019	CEPCEB Plant3D Retreat Exploring Hi-C Contact maps	Lake Arrowhead, CA
09.2019	Beckman Research Institute, City of Hope Exploring Differential Chromatin Interactions and Loops in Hi-C Contact Maps	Duarte, CA
03.2019	University of Georgia Improving the Contiguity and Correctness of Genome Assembly via Optical Maps	Athens, GA
02.2019	SoCal SysBio Conference, UC Irvine Improving the Contiguity and Correctness of Genome Assembly via Optical Maps	Irvine, CA
03.2018	Mathematics, Statics and Computer Science Department, Marquette University Improving the Contiguity and Correctness of Genome Assembly via Optical Maps	Milwaukee, WI
03.2018	Computer Science Department, Purdue University Improving the Contiguity and Correctness of Genome Assembly via Optical Maps	West Lafayette, IN
01.2018	Data Science Seminar Series Improving the Contiguity and Correctness of Genome Assembly via Optical Maps	Riverside, CA
07.2016	Workshop on Advanced Algorithms on Strings Decoding and Correcting Short Reads from Combinatorial Pooling Experiments	Venice, Italy
07.2015	ISMB/ECCB'15 <i>De Novo</i> Meta-Assembly of Ultra-deep Sequencing Data	Dublin, Ireland
04.2015	Department of Computer Science, Harvey Mudd College Combinatorial Pooling for Sequencing and Assembly of Barley and Cowpea Genomes	Claremont, CA
12.2013	CEPCEB Annual Symposium, University of California Computational Epigenetics	Riverside, CA
12.2013	Department of Computer Science, University of Verona Computational Epigenetics and the Human Malaria Parasite	Verona, Italy
11.2013	Division of Biology and Biological Engineering, California Institute of Technology Computational Epigenetics and the Human Malaria Parasite	Pasadena, CA

Invited and Conference Presentations (2010-) (continued)

04.2013	Department of Computer Science, Georgia State University Computational Epigenetics and the Human Malaria Parasite	Atlanta, GA
03.2013	Indiana University School of Informatics, IUPUI Computational Epigenetics and the Human Malaria Parasite	Indianapolis, IN
01.2013	Third Southern California Systems Biology Conference, University of California Nucleosome Positioning in the Human Malaria Parasite	Irvine, CA
01.2013	UCLA Bioinformatics Seminar Series, University of California Nucleosome Positioning in the Human Malaria Parasite	Los Angeles, CA
11.2012	Distinguished Lecture, Computational Biology and Bioinformatics, IUPUI Computational Epigenetics	Indianapolis, IN
06.2012	Keynote, "High-Throughput Sequencing: from Technology to Discovery", UC Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space	Irvine, CA
04.2012	Genetics/Genomics/Bioinformatics PI Brainstorming Seminars, University of California Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space	Riverside, CA
04.2012	Department of Computer Science and Engineering, University of California Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space	Riverside, CA
02.2012	Department of Computer Science, University of Minnesota Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space	Minneapolis, MN
02.2012	"Group Testing: Designs, Algorithms, and Appl. to Biology", Univ. of Minnesota Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space	Minneapolis, MN
10.2010	IGERT Colloquium on Video Bioinformatics, University of California Computational Challenges in Barley Genomics	Riverside, CA
06.2010	Genetics/Genomics/Bioinformatics Seminar Series, University of California Computational challenges in Barley Genomics	Riverside, CA
04.2010	Dept. of Computational Biology and Bioinformatics, Univ. of Southern California Computational challenges in Barley Genomics	Los Angeles, CA