Stefano**Lonardi**

Department of Computer Science and Engineering
Bourns College of Engineering
University of California
Riverside, CA 92521

Phone: ++1 (951) 827 2203
E-mail: `stelo@cs.ucr.edu`
Web: `http://www.cs.ucr.edu/~stelo`
Skype: `stefano.lonardi`

Research Interests

Computational Molecular Biology & Bioinformatics

Genomics & Epigenetics

Data Mining & Data Compression

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

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

Research funding

(blue entries indicate active awards)

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 *Kluyveromyces marxianus*	$1,499,991 – role: coPI (with I. Wheeldon, N. Da Silva, and Argonne National Laboratory)
2021 – 2026	**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 de novo Genome Assembly using Optical Maps	$499,978 – role: sole PI
2018 – 2022	**DOE** Establishing the Thermo-tolerant Yeast *Kluyveromyces marxianus* 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 *in vivo* 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)
2014 – 2015	**NIH** Acquisition of a Scalable Storage Cluster for Data Intensive NIH Research	$592,816 – role: senior personnel (with T. Girke *et al.*)
2013 – 2019	**US-AID** Feed the Future Innovation Lab: Advanced Tools for Climate-Resilient Cowpeas	$4,972,542 – role: coPI (with T. Close, P. Roberts)

Research funding (continued)

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. Neamtiu)	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, *et al.*)	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] RAmbler resolves complex repeats in human Chromosomes 8, 19 and X
S. Chakravarty, G. Logsdon, S. Lonardi
Genome Research, *to appear, 2025*

[2] Predicting Differentially Methylated Cytosines in TET and DNMT3 Knockout Mutants via a Large Language Model
S. Sereshki, S. Lonardi
Briefings in Bioinformatics, *to appear, 2025*

[3] 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*

[4] Identification of candidate genes controlling red seed coat color in cowpea (*Vigna unguiculata [L.] Walp*)

I. A. Herniter, M. Muñoz-Amatriaín, S. Lo, Y.-N. Guo, S. Lonardi, T. J. Close
Horticulturae, *vol. 10, no. 2, p. 161, 2024*

[5] 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. Padín-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, 2024*

[6] 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*

[7] 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*

[8] 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*

[9] 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*

[10] A view of the pan-genome of domesticated cowpea (*Vigna unguiculata [L.] Walp.*)
Q. Liang, M. Muñoz-Amatriaín, 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*

[11] acCRISPR: An activity-correction method for improving the accuracy of CRISPR screens
A. Ramesh, V. Trivedi, S. Lee, A. Tafrishi, C. Schwartz, A. Mohseni, M. Li, S. Lonardi, I. Wheeldon
Communication Biology, *vol. 6, no. 617, 2023*

[12] 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*

[13] *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*

[14] 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*

[15] 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*

[16] 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*

[17] Reference-agnostic Representation and Visualization of Pan-genomes
Q. Liang, S. Lonardi
BMC Bioinformatics*, vol. 22, no. 502, 2021*

[18] 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*

[19] Prediction of Histone Post-translational Modifications using Deep Learning
D. R. Baisya, S. Lonardi
Bioinformatics*, vol. 36, no. 24, pp. 5610–5617, 2020*

[20] DeeplyEssential: A Deep Neural Network for Predicting Essential Genes in Microbes
M. A. Hasan, S. Lonardi
BMC Bioinformatics*, vol. 21, no. 367, 2020*

[21] OMGS: Optical Map-based Genome Scaffolding
W. Pan, T. Jiang, S. Lonardi
Journal of Computational Biology*, vol. 27, no. 4, pp. 519–533, 2020*

[22] 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*

[23] Seed Coat Pattern QTL and Development in Cowpea (*Vigna unguiculata [L.] Walp.*)
I. A. Herniter, R. Lo, M. Muñoz-Amatriaín, 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*

[24] The Genome of Cowpea (*Vigna unguiculata L. Walp.*)
S. Lonardi†, M. Muñoz-Amatriaín†, 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*

[25] Accurate Detection of Chimeric Contigs via Bionano Optical Maps
W. Pan, S. Lonardi
Bioinformatics*, vol. 35, no. 10, pp. 1760–1762, 2019*

[26] 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*

[27] 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-Amatriaín, S. Lonardi, J. Santos, A. Ndeve, B. Batieno, 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*

[28] 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*

[29] A Comparative Evaluation of Genome Assembly Reconciliation Tools
H. Alhakami, H. Mirebrahim, S. Lonardi
Genome Biology, *vol. 18, no. 1, p. 93, 2017*

[30] 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-Amatriaín, 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*

[31] 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-Amatriaín, 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*

[32] 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. Foox, 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*

[33] 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*

[34] 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*

[35] Genome Resources for Climate-resilient Cowpea, an Essential Crop for Food Security
M. Muñoz-Amatriaín, 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*

[36] Higher Classification Sensitivity of Short Metagenomic Reads with CLARK-S
R. Ounit, S. Lonardi
Bioinformatics, *vol. 32, no. 24, pp. 3823–3825, 2016*

[37] FHAST: 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*

[38] 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*

[39] 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*

[40] Analysis of Nucleosome Positioning Landscapes Enables Gene Discovery in the Human Malaria Parasite *Plasmodium falciparum*
X. M. Lu, E. Bunnik, N. Pokhriyal, S. Nasseri, S. Lonardi, K. L. Roch
BMC Genomics, *vol. 16, no. 1005, 2015*

[41] *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*

[42] Sequencing of 15,622 Gene-bearing BACs Clarifies the Gene-dense Regions of the Barley Genome
M. Muñoz-Amatriaín†, 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*

[43] 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*

[44] 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*

[45] 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*

[46] 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*

[47] PuFFIN: A Parameter-free Method to Build Nucleosome Maps from Paired-end Reads
A. Polishko, E. M. Bunnik, K. G. Le Roch, S. Lonardi
BMC Bioinformatics, *vol. 15, no. Suppl 9, S11, 2014*

[48] Identification of Candidate Genes and Molecular Markers for Heat-induced Brown Discoloration of Seed Coats in Cowpea [*Vigna unguiculata (L.) Walp*]
M. Pottorff, P. A. Roberts, T. J. Close, S. Lonardi, S. Wanamaker, J. D. Ehlers
BMC Genomics, *vol. 15, no. 328, 2014*

[49] A Graph-Theoretical Approach to the Selection of the Minimum Tiling Path from a Physical Map
S. Bozdag, T. J. Close, S. Lonardi
IEEE/ACM Transactions on Computational Biology and Bioinformatics, *vol. 10, no. 2, pp. 352–360, 2013*

[50] Combinatorial Pooling Enables Selective Sequencing of the Barley Gene Space
S. Lonardi, D. Duma, M. Alpert, F. Cordero, M. Beccuti, P. R. Bhat, Y. Wu, G. Ciardo, B. Alsaihati, Y. Ma, S. Wanamaker, J. Resnik, S. Bozdag, M.-C. Luo, T. J. Close
PLoS Computational Biology, *vol. 9, no. 4, e1003010, 2013*

[51] Genome-wide Mapping of DNA Methylation in the Human Malaria Parasite *Plasmodium falciparum*

N. Ponts, L. Fu, E. Y. Harris, J. Zhang, D.-W. D. Chung, M. C. Cervantes, J. Prudhomme, V. Atanasova-Penichon, E. Zehraoui, E. M. Bunnik, E. M. Rodrigues, S. Lonardi, G. R. Hicks, Y. Wang, K. Le Roch
Cell Host & Microbe, *vol. 14, no. 6, pp. 696–706, 2013*

[52] Mechanisms of Small RNA Generation from cis-NATs in Response to Environmental and Developmental Cues
X. Zhang, Y. Lii, Z. Wu, A. Polishko, H. Zhang, V. Chinnusamy, S. Lonardi, J.-K. Zhu, R. Liu, H. Jin
Molecular Plant, *vol. 6, no. 3, pp. 704–715, 2013*

[53] BRAT-BW: Efficient and Accurate Mapping of Bisulfite-treated Reads
E. Y. Harris, N. Ponts, K. G. Le Roch, S. Lonardi
Bioinformatics, *vol. 28, no. 13, pp. 1795–1796, 2012*

[54] NOrMAL: Accurate Nucleosome Positioning using a Modified Gaussian Mixture Model
A. Polishko, N. Ponts, K. G. L. Roch, S. Lonardi
Bioinformatics, *vol. 28, no. 12, pp. i242–i249, 2012*

[55] MDL-based Time Series Clustering
T. Rakthanmanon, E. J. Keogh, S. Lonardi, S. Evans
Knowledge and Information Systems, *vol. 33, no. 2, pp. 371–399, 2012*

[56] A Physical, Genetic and Functional Sequence Assembly of the Barley Genome
N. Stein, A. Graner, A. Himmelbach, B. Steuernagel, D. Schulte, M. Mascher, N. Poursarebani, R. Zhou, R. Ariyadasa, T. Schmutzer, U. Scholz, H. Gundlach, K. Mayer, M. Spannagl, M. Pfeifer, M. Martis, T. Nussbaumer, A. Druka, D. Marshall, H. Liu, J. Morris, J. Russell, M. Bayer, J. Brown, P. Hedley, R. Waugh, B. Shi, P. Langridge, J. Svensson, J. Resnik, K. Madishetty, M. Moscou, P. Bhat, S. Wannamaker, T. Close, Y. Ma, D. Duma, F. Cordero, G. Ciardo, M. Beccuti, M. Alpert, S. Lonardi, H. Berges, A. Korol, Z. Frenkel, M. Groth, M. Felder, M. Platzer, S. Taudien, A. Schulman, C. Moisy, J. Tanskanen, T. Matsumoto, T. Tanaka, K. Sato, G. Fincher, D. Swarbreck, D. Sampath, M. Caccamo, M. Febrer, S. Ayling, R. Wing, G. Muehlbauer, A. Zuccolo, F. Cattonaro, M. Morgante, S. Scalabrin, S. Radovic, V. Vendramin, J. Poland, R. Wise
Nature, *vol. 491, no. 7426, pp. 711–716, 2012*

[57] Chromatin-driven *De Novo* Discovery of DNA Binding Motifs in the Human Malaria Parasite
E. Y. Harris, N. Ponts, K. G. Le Roch, S. Lonardi
BMC Genomics, *vol. 12, no. 601, 2011*

[58] An Improved Consensus Linkage Map of Barley Based on Flow-sorted Chromosomes and Single Nucleotide Polymorphism Markers
M. Muñoz-Amatriaín, M. J. Moscou, P. R. Bhat, J. T. Svensson, J. Bartoš, P. Suchánková, H. Šimková, T. R. Endo, R. D. Fenton, Y. Wu, S. Lonardi, A. M. Castillo, S. Chao, L. Cistué, A. Cuesta-Marcos, K. Forrest, M. J. Hayden, P. M. Hayes, R. D. Horsley, A. Kleinhofs, D. Moody, K. Sato, M. P. Vallés, B. B. H. Wulff, G. J. Muehlbauer, J. Doležel, T. J. Close
The Plant Genome, *vol. 4, no. 3, pp. 238–249, 2011*

[59] Nucleosome Occupancy at Transcription Start Sites in the Human Malaria Parasite: A Hard-wired Evolution of Virulence?
N. Ponts, E. Y. Harris, S. Lonardi, K. G. Le Roch
Infection, Genetics and Evolution, *vol. 11, no. 4, pp. 716–724, 2011*

[60] Accurate Construction of Consensus Genetic Maps via Integer Linear Programming
Y. Wu, T. J. Close, S. Lonardi
IEEE/ACM Transactions on Computational Biology and Bioinformatics, *vol. 8, no. 2, pp. 381–394, 2011*

[61] BRAT: Bisulfite-Treated Reads Analysis Tool
E. Y. Harris, N. Ponts, A. Levchuk, K. Le Roch, S. Lonardi
Bioinformatics, *vol. 26, no. 4, pp. 572–573, 2010*

[62] Efficient Genome-wide TagSNP Selection Across Populations via the Linkage Disequilibrium Criterion
L. Liu, Y. Wu, S. Lonardi, T. Jiang
Journal of Computational Biology, *vol. 17, no. 1, pp. 21–37, 2010*

[63] Nucleosome Landscape and Control of Transcription in the Human Malaria Parasite
N. Ponts, E. Y. Harris, J. Prudhomme, I. Wick, C. Eckhardt-Ludka, G. R. Hicks, G. Hardiman, S. Lonardi, K. G. Le Roch
Genome Research*, vol. 20, no. 2, pp. 228–238, 2010*

[64] Graphlet Kernels for Prediction of Functional Residues in Protein Structures
V. Vacic, L. M. Iakoucheva, S. Lonardi, P. Radivojac
Journal of Computational Biology*, vol. 17, no. 1, pp. 55–72, 2010*

[65] Immune Profile and Mitotic Index of Metastatic Melanoma Lesions Enhance Clinical Staging in Predicting Patient Survival
D. Bogunovic, D. W. O'Neill, I. Belitskaya-Levy, V. Vacic, Y.-L. Yu, S. Adams, F. Darvishian, R. Berman, R. Shapiro, A. C. Pavlick, S. Lonardi, J. Zavadil, I. Osmana, N. Bhardwaj
Proceedings of the National Academy of Sciences*, vol. 106, no. 48, pp. 20429–20434, 2009*

[66] A Compartmentalized Approach to the Assembly of Physical Maps
S. Bozdag, T. J. Close, S. Lonardi
BMC Bioinformatics*, vol. 10, no. 217, 2009*

[67] Development and Implementation of High-throughput SNP Genotyping in Barley
T. Close, P. Bhat, S. Lonardi, Y. Wu, N. Rostoks, L. Ramsay, A. Druka, N. Stein, J. Svensson, S. Wanamaker, S. Bozdag, M. Roose, M. Moscou, S. Chao, R. Varshney, P. Szucs, K. Sato, P. Hayes, D. Matthews, A. Kleinhofs, G. Muehlbauer, J. DeYoung, D. Marshall, K. Madishetty, R. Fenton, P. Condamine, A. Graner, R. Waugh
BMC Genomics*, vol. 10, no. 582, 2009*

[68] Small RNAs and the Regulation of Cis-natural Antisense Transcripts in *Arabidopsis*
H. Jin, V. Vacic, T. Girke, S. Lonardi, J.-K. Zhu
BMC Molecular Biology*, vol. 9, no. 6, 2008*

[69] Length-based Encoding of Binary Data in DNA
N. G. Portney, Y. Wu, L. K. Quezada, S. Lonardi, M. Ozkan
Langmuir*, vol. 24, no. 5, pp. 1613–1616, 2008*

[70] Deconvoluting BAC-gene Relationships Using a Physical Map
Y. Wu, L. Liu, T. Close, S. Lonardi
Journal of Bioinformatics and Computational Biology*, vol. 6, no. 3, pp. 603–622, 2008*

[71] A Linear-time Algorithm for Predicting Functional Annotations from Protein-Protein Interaction Networks
Y. Wu, S. Lonardi
Journal of Bioinformatics and Computational Biology*, vol. 6, no. 6, pp. 1049–1065, 2008*

[72] Efficient and Accurate Construction of Genetic Linkage Maps from the Minimum Spanning Tree of a Graph
Y. Wu, P. R. Bhat, T. J. Close, S. Lonardi
PLoS Genetics*, vol. 4, no. 10, e1000212, 2008*

[73] Compression-based Data Mining of Sequential Data
E. Keogh, S. Lonardi, C. Ratanamahatana, L. Wei, S.-H. Lee, J. Handley
Data Mining and Knowledge Discovery*, vol. 14, no. 1, pp. 99–129, 2007*

[74] Experiencing SAX: a Novel Symbolic Representation of Time Series
J. Lin, E. Keogh, L. Wei, S. Lonardi
Data Mining and Knowledge Discovery*, vol. 15, no. 2, pp. 107–144, 2007*

[75] Error Resilient LZ'77 Data Compression: Algorithms, Analysis, and Experiments
S. Lonardi, W. Szpankowski, M. D. Ward
IEEE Transactions on Information Theory*, vol. 53, no. 5, pp. 1799–1813, 2007*

[76] Composition Profiler: A Tool for Discovery and Visualization of Amino Acid Composition Differences
V. Vacic, V. N. Uversky, A. K. Dunker, S. Lonardi
BMC Bioinformatics*, vol. 8, no. 211, 2007*

[77] A Parallel Edge Betweenness Clustering Tool for Protein-Protein Interaction Networks
Q. Yang, S. Lonardi
International Journal of Data Mining and Bioinformatics, *vol. 1, no. 3, pp. 241–247, 2007*

[78] A Bit Level Representation for Time Series Data Mining with Shape Based Similarity
A. Bagnall, C. Ratanamahatana, E. Keogh, S. Lonardi, G. Janacek
Data Mining and Knowledge Discovery, *vol. 13, no. 1, pp. 11–40, 2006*

[79] Efficient Information Compression in Sensor Networks
S. Lin, V. Kalogeraki, D. Gunopulos, S. Lonardi
International Journal of Sensor Networks, *vol. 1, no. 3, pp. 229–240, 2006*

[80] Efficient Discovery of Unusual Patterns in Time Series
S. Lonardi, J. Lin, E. Keogh, B. Chiu
New Generation Computing, *vol. 25, no. 1, pp. 61–93, 2006*

[81] Finding Biclusters by Random Projections
S. Lonardi, W. Szpankowski, Q. Yang
Theoretical Computer Science, *vol. 368, no. 3, pp. 217–230, 2006*

[82] Oligospawn: A Web-based Tool for the Design of Overgo Probes from Large Unigene Databases
J. Zheng, J. T. Svensson, K. Madishetty, T. J. Close, T. Jiang, S. Lonardi
BMC Bioinformatics, *vol. 7, no. 7, 2006*

[83] Assignment of Orthologous Genes via Genome Rearrangement
X. Chen, J. Zheng, Z. Fu, P. Nan, Y. Zhong, S. Lonardi, T. Jiang
IEEE/ACM Transactions on Computational Biology and Bioinformatics, *vol. 2, no. 4, pp. 302–315, 2005*

[84] Visualizing and Discovering Non-Trivial Patterns In Large Time Series Databases
J. Lin, E. Keogh, S. Lonardi
Information Visualization, *vol. 4, no. 2, pp. 61–82, 2005*

[85] Storage and Transmission of Microarray Images
Y. Luo, S. Lonardi
Drug Discovery Today, *vol. 10, no. 23, pp. 1689–1695, 2005*

[86] Integrating Lite-Weight but Ubiquitous Data Mining into GUI Operating Systems
L. Wei, E. J. Keogh, X. Xi, S. Lonardi
Journal of Universal Computer Science, *vol. 11, no. 11, pp. 1820–1834, 2005*

[87] Augmenting LZ-77 with Authentication and Integrity Assurance Capabilities
M. J. Atallah, S. Lonardi
Concurrency and Computation: Practice and Experience, *vol. 16, no. 11, pp. 1063–1076, 2004*

[88] On Average Sequence Complexity
S. Janson, S. Lonardi, W. Szpankowski
Theoretical Computer Science, *vol. 326, no. 1-3, pp. 213–227, 2004*

[89] Efficient Selection of Unique and Popular Oligos for Large EST Databases
J. Zheng, T. J. Close, T. Jiang, S. Lonardi
Bioinformatics, *vol. 20, no. 13, pp. 2101–2112, 2004*

[90] Monotony of Surprise and Large-scale Quest for Unusual Words
A. Apostolico, M. E. Bock, S. Lonardi
Journal of Computational Biology, *vol. 10, no. 2/3, pp. 283–311, 2003*

[91] Verbumculus and the Discovery of Unusual Words
A. Apostolico, F.-C. Gong, S. Lonardi
Journal of Computer Science and Technology, *vol. 19, no. 1, pp. 22–41, 2003*

[92] A Speed-up for the Commute between Subword Trees and DAWGs
A. Apostolico, S. Lonardi

Information Processing Letters*, vol. 83, no. 3, pp. 159–161, 2002*

[93] Efficient Detection of Unusual Words
A. Apostolico, M. E. Bock, S. Lonardi, X. Xu
Journal of Computational Biology*, vol. 7, no. 1/2, pp. 71–94, 2000*

[94] Off-Line Compression by Greedy Textual Substitution
A. Apostolico, S. Lonardi
Proceedings of the IEEE*, vol. 88, no. 11, pp. 1733–1744, 2000*

[95] A Whole-Genome Assembly of Drosophila
E. W. Myers, G. G. Sutton, A. L. Delcher, I. M. Dew, D. P. Fasulo, M. J. Flanigan, S. A. Kravitz, C. M. Mobarry, K. H. J. Reiner, K. A. Remington, E. L. Anson, R. A. Bolanos, H. H. Chou, C. M. Jordan, A. L. Halpern, S. Lonardi, E. M. Beasley, R. C. Brandon, L. Chen, P. J. Dunn, Z. Lai, Y. Liang, D. R. Nusskern, M. Zhan, Q. Zhang, X. Zheng, G. M. Rubin, M. D. Adams, J. C. Venter
Science*, vol. 287, no. 5461, pp. 2196–2204, 2000*

[96] Fractal Image Approximation and Orthogonal Bases
S. Lonardi, P. Sommaruga
Signal Processing: Image Communication*, vol. 14, no. 5, pp. 413–423, 1999*

[97] Shape Recovery and Volume Calculation from Biplane Angiography in the Stereotactic Radiosurgery Treatment of Arteriovenous Malformation
R. Foroni, J. Hoch, G. Giri, A. Pasoli, M. Gerosa, A.Pasqualin, A. Nicolato, E. Piovan, P. Zampieri, E. Bortolazzi, S. Lonardi
International Journal of Radiation Oncology, Biology and Physics*, vol. 35, no. 3, pp. 565–577, 1996*

Edited Books

[1] Proceedings of 17th Intl Symposium on String Processing and Information Retrieval (SPIRE 2010)
E. Chavez, S. Lonardi, (eds.)
Lecture Notes in Computer Science 6393, Springer, 2010

[2] Biological Data Mining
J. Y. Chen, S. Lonardi, (eds.)
CRC Press, 2009

[3] Proceedings of 8th Intl Workshop on Data Mining in Bioinformatics (BIOKDD 2008)
S. Lonardi, J. Y. Chen, M. Zaki, (eds.)
ACM Press, 2008

[4] Proceedings of 7th Intl Workshop on Data Mining in Bioinformatics (BIOKDD 2007)
S. Lonardi, J. Y. Chen, M. Zaki, (eds.)
ACM Press, 2007

Book Chapters

[1] Computational Biology
P. Ferragina, S. Kurtz, S. Lonardi, G. Manzini
Handbook on Data Structures and Applications (2nd edition)*, pp. 917–933, 2018*

[2] Bisulfite-Conversion-Based Methods for DNA Methylation Sequencing Data Analysis
E. Y. Harris, S. Lonardi
Computational Methods for Next Generation Sequencing Data Analysis*, pp. 227–244, 2016*

[3] Computational Biology
S. Kurtz, S. Lonardi
Handbook on Data Structures and Applications*, pp. 58.1–58.17, 2004*

Peer-reviewed Conference Proceedings

[1] AbAffinity: A Large Language Model for Predicting Antibody Binding Affinity against SARS-CoV-2
F. B. Ashraf, A. Ray, S. Lonardi
AAAI Workshop on Foundation Models for Biological Discoveries (FMs4Bio25), *to appear, Philadelphia, PA, 2025*

[2] Identification of Antigen Specific B-cell receptors from single-cell V(D)J sequences using a Large Language Model, ASPred
K. Paco, Z. Zhang, M. Paco, P. Olatoyinbo, S. Zebardast, D. Patel, I. Condori, J. Lay, K. L. Roch, T. Yang, J. Felix, J. Hernandez, M. Sazinsky, I. Tolstorukov, S. Lonardi, A. Ray
Proceedings of Latinx in AI Workshop at NeurIPS-24, *p. 13, Vancouver, Canada, 2024*

[3] RAmbler: *de novo* genome assembly of complex repetitive regions
S. Chakravarty, G. Logsdon, S. Lonardi
Proceedings of ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM BCB), *p. 13, Houston, TX, 2023*

[4] Selfish: Discovery of Differential Chromatin Interactions via a Self-Similarity Measure
A. R. Ardakany, F. Ay, S. Lonardi
Proceedings of Conference on Intelligent Systems for Molecular Biology (ISMB), *pp. i145–i153, Basel, Switzerland, 2019*

[5] OMGS: Optical Map-based Genome Scaffolding
W. Pan, T. Jiang, S. Lonardi
Proceedings of Conference on Research in Computational Molecular Biology (RECOMB), *pp. 190–207, Washington, DC, 2019*

[6] mClass: Cancer Type Classification with Somatic Point Mutation Data
M. A. Hasan, S. Lonardi
Proceedings of 16th RECOMB Comparative Genomics Satellite Workshop (RECOMB-CG), *pp. 131–145, Magog-Orford, Canada, 2018*

[7] Novo&Stitch: Accurate Reconciliation of Genome Assemblies via Optical Maps
W. Pan, S. Wanamaker, A. Ah-Fong, H. Judelson, S. Lonardi
Proceedings of Conference on Intelligent Systems for Molecular Biology (ISMB), *pp. i43–i51, Chicago, IL, 2018*

[8] Efficient and Accurate Detection of Topologically Associating Domains from Contact Maps
A. R. Ardakany, S. Lonardi
Proceedings of the Workshop on Algorithms in Bioinformatics (WABI), *22:1–22:11, Boston, MA, 2017*

[9] ThIEF: Finding Genome-wide Trajectories of Epigenetics Marks
A. Polishko, M. A. Hasan, W. Pan, E. Bunnik, K. L. Roch, S. Lonardi
Proceedings of the Workshop on Algorithms in Bioinformatics (WABI), *19:1–19:16, Boston, MA, 2017*

[10] Scrible: Ultra-Accurate Error-Correction of Pooled Sequenced Reads
D. Duma, F. Cordero, M. Beccuti, G. Ciardo, T. J. Close, S. Lonardi
Proceedings of the Workshop on Algorithms in Bioinformatics (WABI), *pp. 162–174, Atlanta, GA, 2015*

[11] De Novo Meta-Assembly of Ultra-deep Sequencing Data
H. Mirebrahim, T. J. Close, S. Lonardi
Proceedings of Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB), *pp. i9–i16, Dublin, Ireland, 2015*

[12] Higher Classification Accuracy of Short Metagenomic Reads by Discriminative Spaced k-mers
R. Ounit, S. Lonardi
Proceedings of the Workshop on Algorithms in Bioinformatics (WABI), *pp. 286–295, Atlanta, GA, 2015*

[13] Deciphering Histone Code of Transcriptional Regulation in Malaria Parasites by Large-scale Data Mining
H. Chen, S. Lonardi, J. Zheng
Proceedings of Asia Pacific Bioinformatics Conference (APBC), *Shanghai, China, 2014*

[14] PuFFIN: A Parameter-free Method to Build Nucleosome Maps from Paired-end Reads
A. Polishko, E. M. Bunnik, K. G. Le Roch, S. Lonardi
Proceedings of RECOMB Workshop on Massively Parallel Sequencing (RECOMB-SEQ), *Pittsburgh, PA, 2014*

[15] Accurate Decoding of Pooled Sequenced Data Using Compressed Sensing
D. Duma, M. Wootters, A. C. Gilbert, H. Q. Ngo, A. Rudra, M. Alpert, T. J. Close, G. Ciardo, S. Lonardi
Proceedings of the Workshop on Algorithms in Bioinformatics (WABI), *pp. 70–84, Sophia Antipolis, France, 2013*

[16] Multithreaded FPGA Acceleration of DNA Sequence Mapping
E. B. Fernandez, W. A. Najjar, S. Lonardi, J. Villarreal
Proceedings of IEEE High Performance Extreme Computing (HPEC), *pp. 1–6, Waltham, MA, 2012*

[17] NOrMAL: Accurate Nucleosome Positioning using a Modified Gaussian Mixture Model
A. Polishko, N. Ponts, K. G. Le Roch, S. Lonardi
Proceedings of Conference on Intelligent Systems for Molecular Biology (ISMB), *pp. 242–249, Long Beach, CA, 2012*

[18] String Matching in Hardware using the FM-Index
E. Fernandez, W. Najjar, S. Lonardi
Proceedings of IEEE Symposium on Field-Programmable Custom Computing Machines (FCCM), *pp. 218–225, Salt Lake City, Utah, 2011*

[19] Discovering the Intrinsic Cardinality and Dimensionality of Time Series using MDL
B. Hu, T. Rakthanmanon, Y. Hao, S. Evans, S. Lonardi, E. Keogh
Proceedings of IEEE International Conference on Data Mining (ICDM), *pp. 1086–1091, Vancouver, Canada, 2011*

[20] Towards Discovering the Intrinsic cardinality and Dimensionality of Time Series using MDL
B. Hu, T. Rakthanmanon, Y. Hao, S. Evans, S. Lonardi, E. Keogh
Proceedings of Solomonoff 85th Memorial Conference, *pp. 184–197, Melbourne, Australia, 2011*

[21] Time Series Epenthesis: Clustering Time Series Streams Requires Ignoring Some Data
T. Rakthanmanon, E. J. Keogh, S. Lonardi, S. Evans
Proceedings of IEEE International Conference on Data Mining (ICDM), *pp. 547–556, Vancouver, Canada, 2011*

[22] Exploration of Short Reads Mapping in Hardware
E. Fernandez, W. Najjar, E. Harris, S. Lonardi
Proceedings of International Conference on Field Programmable Logic and Applications, *pp. 360–363, Milano, Italy, 2010*

[23] Novel Gene Discovery in the Human Malaria Parasite using Nucleosome Positioning Data
N. Pokhriyal, N. Ponts, E. Harris, K. Le Roch, S. Lonardi
Proceedings of LSS Computational Systems Bioinformatics Conference (CSB), *pp. 124–135, Stanford, CA, 2010*

[24] CPM's 20th Anniversary: A Statistical Retrospective
E. Y. Harris, T. Lecroq, G. Kucherov, S. Lonardi
Proceedings of Combinatorial Pattern Matching (CPM), *pp. 1–11, Lille, France, 2009*

[25] Computing the Minimal Tiling Path from a Physical Map by Integer Linear Programming
S. Bozdag, T. Close, S. Lonardi
Proceedings of the Workshop on Algorithms in Bioinformatics (WABI), *pp. 148–161, Universitat Karlsruhe, Germany, 2008*

[26] A Probabilistic Method for Small RNA Flowgram Matching
V. Vacic, H. Jin, J.-K. Zhu, S. Lonardi
Proceedings of Pacific Symposium on Biocomputing (PSB), *pp. 75–86, Big Island of Hawaii, 2008*

[27] On the Accurate Construction of Consensus Genetic Maps
Y. Wu, T. J. Close, S. Lonardi
Proceedings of LSS Computational Systems Bioinformatics Conference (CSB), *pp. 285–296, Stanford, CA, 2008*

[28] A Compartmentalized Approach to the Assembly of Physical Maps
S. Bozdag, T. Close, S. Lonardi
Proceedings of IEEE International Symposium on Bioinformatics & Bioengineering (BIBE), *pp. 218–225, Boston, MA, 2007*

[29] Efficient Algorithms for Genome-Wide TagSNP Selection across Populations via the Linkage Disequilibrium Criterion
L. Liu, Y. Wu, S. Lonardi, T. Jiang
Proceedings of LSS Computational Systems Bioinformatics Conference (CSB), *pp. 67–78, San Diego, CA, 2007*

[30] Soft-core Processor Customization using the Design of Experiments Paradigm

D. Sheldon, F. Vahid, S. Lonardi
Proceedings of IEEE Conference on Design, Automation and Test in Europe (DATE), *pp. 821–826, Nice, France, 2007*

[31] Two Level Microprocessor-Accelerator Partitioning
S. Sirowy, Y. Wu, S. Lonardi, F. Vahid
Proceedings of IEEE Conference on Design, Automation and Test in Europe (DATE), *pp. 313–318, Nice, France, 2007*

[32] Clock-Frequency Partitioning for Multiple Clock Domains Systems-on-a-Chip
S. Sirowy, Y. Wu, F. Vahid, S. Lonardi
Proceedings of IEEE Conference on Design, Automation and Test in Europe (DATE), *pp. 397–402, Nice, France, 2007*

[33] Deconvoluting BAC-gene Relationships using a Physical Map
Y. Wu, L. Liu, T. Close, S. Lonardi
Proceedings of LSS Computational Systems Bioinformatics Conference (CSB), *pp. 203–214, San Diego, CA, 2007*

[34] Efficient and Accurate Construction of Genetic Linkage Maps from Noisy and Missing Genotyping Data
Y. Wu, P. Bhat, T. J. Close, S. Lonardi
Proceedings of the Workshop on Algorithms in Bioinformatics (WABI), *pp. 395–406, Philadelphia, PA, 2007*

[35] A Linear-time Algorithm for Predicting Functional Annotations from Protein-Protein Interaction Networks
Y. Wu, S. Lonardi
Proceedings of the Workshop on Data Mining in Bioinformatics (BIOKDD), *pp. 35–41, San Jose, CA, 2007*

[36] A Graph Decomposition Approach to the Identification of Network Building Modules
Q. Yang, S. Lonardi
Proceedings of the Workshop on Data Mining in Bioinformatics (BIOKDD), *pp. 50–59, San Jose, CA, 2007*

[37] Intelligent Icons: Integrating Lite-weight Data Mining and Visualization into GUI Operating Systems
E. Keogh, L. Wei, X. Xi, S. Lonardi, J. Shieh, S. Sirowy
Proceedings of the IEEE International Conference on Data Mining (ICDM), *pp. 912–916, Hong Kong, China, 2006*

[38] Online Information Compression in Sensor Networks
S. Lin, V. Kalogeraki, D. Gunopulos, S. Lonardi
Proceedings of the IEEE International Conference on Communications (ICC), *pp. 3371–3376, Istanbul, Turkey, 2006*

[39] Error-Resilient LZW Data Compression
Y. Wu, S. Lonardi, W. Szpankowski
Proceedings of the IEEE Data Compression Conference (DCC), *pp. 193–202, Snowbird, Utah, 2006*

[40] Evolution versus Intelligent Design: Comparing the Topology of Protein-Protein Interaction Networks to the Internet
Q. Yang, G. Siganos, M. Faloutsos, S. Lonardi
Proceedings of LSS Computational Systems Bioinformatics Conference (CSB), *pp. 299–310, Stanford, CA, 2006*

[41] A Compression-boosting Transform for Two-dimensional Data
Q. Yang, S. Lonardi, A. Melkman
Proc. of Conference on Algorithmic Aspects in Information and Management (AAIM), *pp. 126–137, Hong Kong, China, 2006*

[42] 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*

[43] 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*

[44] 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*

[45] 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*

[46] 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*

[47] 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*

[48] 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*

[49] On Average Sequence Complexity
S. Janson, S. Lonardi, W. Szpankowski
Proceedings of Symposium on Combinatorial Pattern Matching (CPM), *pp. 74–88, Istanbul, Turkey, 2004*

[50] 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*

[51] 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*

[52] 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*

[53] 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*

[54] 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*

[55] 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*

[56] 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*

[57] 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*

[58] 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*

[59] Joint Source-Channel LZ'77 Coding
S. Lonardi, W. Szpankowski
Proceedings of the IEEE Data Compression Conference (DCC), *pp. 273–283, Snowbird, Utah, 2003*

[60] 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*

[61] 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*

[62] 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*

[63] 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*

[64] 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*

[65] 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*

[66] 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*

[67] 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*

[68] 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*

[69] 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	IF 4.096
Editor in Chief	**Genes - Bioinformatics Section (MDPI, ISSN 2073-4425)** 2020–2024	IF 4.096
Editorial Board	**BMC Bioinformatics (Springer, ISSN 1471-2105)** 2020–	IF 3.242
Editorial Board	**Genes (MDPI, ISSN 2073-4425)** 2018–2020	IF 4.096
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	
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)	
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 | Liverpool, UK	
PC member	**WABI: Workshop of Algorithms in Bioinformatics** 2007: Philadelphia, PA | 2008: Karlsruhe, Germany | 2009: Philadelphia, PA | 2011: Saarbruecken, Germany | 2013: Sophia Antipolis, France | 2014: Wroclaw, Poland | 2015: Atlanta, 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: Pittsburg, PA | 2015: Warsaw, Poland | 2016: Santa Monica, CA	
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	

Technical Program Committee and Editorial Work (continued)

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"** *IEEE/ACM Transactions Computational Biology & Bioinformatics*, vol. 7, no. 2, 2010
Guest Editor	**Special issue in honor of A. Apostolico's 60th birthday** *Theoretical Computer Science*, 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"** *Journal of Computational Biology and Bioinformatics*
PC member	**DCC: IEEE Data Compression Conference** 2007: Snowbird, UT | 2008: Snowbird, UT

Courses

UCR	**CS 144: Algorithms for Bioinformatics** 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]** 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 (2010-)

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
Ext. 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
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

Advisory and Review Committees (2010-) (continued)

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	**Computing and Data Science Instruction (CDI) building committee** Department of Computer Science and Engineering, UC Riverside	2024-25
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
Ex-officio	**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
External Member	**Bioinformatics Faculty Search Committee** College of Natural and Agricultural Sciences, UC Riverside	2014–2015

University Service (continued)

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
External 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
External 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** Computer Science and Engineering, UC Riverside	2019–
Dipankar Baisya	**PhD, "Deep Learning Algorithms for Single Guide RNA CRISPR Efficiency"** *Applied Scientist* at Amazon Science, Seattle, WA	2016–2021
Qihua Liang	**PhD, "Methods for Comparative Genome Analysis with Applications to Pan-genomics"** *Bioinformatics Scientist* at Zymergen, Emeryville, CA	2015–2020
Abbas Roayaei	**PhD, "Efficient Algorithms for the Analysis of Hi-C Contact Maps"** *Post-doc* at La Jolla Institute for Immunology, San Diego, CA	2014–2019
Md. Abid Hasan	**PhD, "Accurate Prediction Methods on Biomolecular Data"** *Principal Scientist* at Roche Sequencing, Pleasanton, CA	2014–2019
Weihua Pan	**PhD, "Optical Map-based Genome Scaffolding"** *Research Professor* at Shenzhen Agricultural Genome Research Institute, China	2014–2019
Rachid Ounit	**PhD, "Computing the Microbiome: Efficient Methods for the Analysis of Metagenomes"** *EAS Lead* at Karius, Redwood City, CA	2013–2017
Hind Alhakami	**PhD, "Data Structures and Algorithms for de novo Genome Assembly"** *Bioinformatics Scientist* at Dovetail Genomics, Santa Cruz, CA	2012–2017
H. Mirebrahim	**PhD, "Efficient Methods for the Analysis of Ultra-Deep Sequencing Data"** *Principal Scientist* at Roche Sequencing, Pleasanton, CA	2010–2015
Anton Polishko	**PhD, "Computational Methods for Exploring Nucleosome Dynamics"** *CTO* at Zulloo Inc	2009–2014
Denisa Duma	**PhD, "A Pooling Strategy for the Selective Sequencing of Very Large Genomes"** *Post-doc* with Icahn School of Medicine at Mount Sinai, New York, NY	2008–2013
Elena Harris	**PhD, "Computational Methods for Epigenetic Studies"** *Associate Professor* at California State University, Chico, CA	2005–2010
Vladimir Vacic	**PhD, "Computational Methods for Discovery of Cellular Regulatory Mechanisms"** *Bioinformatics Scientist* at 23andme, Mountain View, CA	2003–2008
Yonghui Wu	**PhD, "On the Accurate Construction of Genetic Linkage Maps"** *Distinguished Engineer* at Google Brain, Mountain View, CA	2003–2008
Serdar Bozdag	**PhD, "Combinatorial Approaches to the Physical Mapping Problem"** *Associate Professor* 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"** *Manager* at Scientific Games, Reno, NV	2000–2006
Jie Zheng	**PhD, "Algorithms for Identification of Repetitive Patterns in Biological Sequences"** *Associate Professor* 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	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 Nasseri	**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 *Yarrowia lipolytica*** `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
Slicembler	**Meta-Assembler for Ultra-deep Sequencing Data** `http://slicembler.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 *Babesia duncani*	New Haven, CT
04.2021	**Third International Babesiosis Meeting** A preview of the *Babesia duncani* 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** *De Novo* 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