

Stefano Lonardi

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Research Interests

Computational Molecular Biology, Bioinformatics, Genomics, Epigenetics, Big Data, Data Mining, Design and Analysis of Algorithms, 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

2019 – 2020	Beckman Research Institute of City of Hope, Duarte, CA Division of Systems Biology	Visiting Professor
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	Associate Chair
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

2018	Fellow	<i>for contributions to computational biology, bioinformatics and data mining</i>
	American Association for the Advancement of Science (AAAS)	
2017	Teaching Award (Honorable Mention)	
	Bourns College of Engineering, UC Riverside	
2017	Distinguished Scientist	<i>for contributions to computational biology</i>
	Association for Computing Machinery (ACM)	
2016	Fellow	<i>for contributions to computational biology and data mining</i>
	Institute of Electrical and Electronic Engineers (IEEE)	
2016	Top-100 Most Influential Scholar in Data Mining	
	ArnetMiner	
2005	CAREER award	Division of Information & Intelligent Systems
	National Science Foundation (NSF)	

Research funding

(blue entries indicate active awards)

2018 – 2021	NSF (IIS)	\$499,978 – role: sole PI
	III:Small:Improving de novo Genome Assembly using Optical Maps	
2018 – 2021	DOE	\$1,499,999 – role: coPI (with I. Wheeldon, N. Da Silva)
	Establishing the Thermo-tolerant Yeast <i>Kluyveromyces marxianus</i> as a Host for Bio-based Fuels and Chemicals Production	
2015 – 2020	NSF (IOS)	\$1,587,345 – role: coPI (with T. Close, B. L. Huynh, P. Roberts, M. Munoz-Amatriain)
	BREAD ABRDC: Advancing the Cowpea Genome for Food Security	
2015 – 2019	NSF (IIS)	\$499,000 – role: sole PI
	III:Small:Algorithms for Genome Assembly of Ultra-deep Sequencing Data	
2015 – 2016	UCR	\$70,000 – role: coPI (with K. Le Roch, F. Sladek)
	An <i>in vivo</i> System to Monitor the 4D Mammalian Nucleome	
2014 – 2015	NSF (MRI)	\$548,476 – role: coPI (with T. Girke, M. Allen, J. Stajich, J. Bailey-Serres)
	MRI: Acquisition of a Big Data Compute Cluster for Interdisciplinary Research	
2014 – 2015	UCOP	\$50,000 – role: coPI (with F. Vahid, K. Miller, B. Linard)
	Intro to Computing I and II, UCR CS 10V and 12V	
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	

Research funding (continued)

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 (R01)	\$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, <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] 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, to appear, 2020
- [2] DeeplyEssential: A Deep Neural Network for Predicting Essential Genes in Microbes
M. A. Hasan, S. Lonardi
BMC Bioinformatics, to appear, 2020
- [3] OMGS: Optical Map-based Genome Scaffolding
W. Pan, T. Jiang, S. Lonardi
Journal of Computational Biology, vol. 27, no. 4, pp. 519–533, 2020
- [4] 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
- [5] 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

- [6] 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
- [7] Accurate Detection of Chimeric Contigs via Bionano Optical Maps
W. Pan, S. Lonardi
Bioinformatics, vol. 35, no. 10, pp. 1760–1762, 2019
- [8] 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
- [9] 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
- [10] NovoStitch: 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
- [11] A Comparative Evaluation of Genome Assembly Reconciliation Tools
H. Alhakami, H. Mirebrahim, S. Lonardi
Genome Biology, vol. 18, no. 1, p. 93, 2017
- [12] 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
- [13] 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
- [14] 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
- [15] 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

- [16] 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
- [17] 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
- [18] Higher Classification Sensitivity of Short Metagenomic Reads with CLARK-S
R. Ounit, [S. Lonardi](#)
Bioinformatics, vol. 32, no. 24, pp. 3823–3825, 2016
- [19] 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
- [20] 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
- [21] 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
- [22] 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
- [23] *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
- [24] 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
- [25] 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
- [26] 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
- [27] 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

- [28] 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
- [29] 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
- [30] 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
- [31] 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
- [32] 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
- [33] 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
- [34] 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
- [35] 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
- [36] 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
- [37] 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
- [38] 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
- [39] 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

- [40] 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
- [41] 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
- [42] 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
- [43] 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
- [44] 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
- [45] 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
- [46] 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
- [47] 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
- [48] A Compartmentalized Approach to the Assembly of Physical Maps
S. Bozdag, T. J. Close, [S. Lonardi](#)
BMC Bioinformatics, vol. 10, no. 217, 2009
- [49] 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
- [50] 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
- [51] 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
- [52] 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
- [53] 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
- [54] 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](#)
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Patents

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Technical Program Committee and Editorial Work

Editorial Board	BMC Bioinformatics (Springer, ISSN: 1471-2105) 2020–	IF 2.213
Editorial Board	Genes (MDPI, ISSN 2073-4425) 2018–	IF 3.191
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	
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	
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	
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	
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	
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	

Technical Program Committee and Editorial Work (continued)

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

UCR	CS 218: Design and Analysis of Algorithms [graduate] 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] 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	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

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
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
Reviewer	Data Analytics & Artificial Intelligence Prince Sultan University, Riyadh, Saudi Arabia	Dec 2016
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

Advisory and Review Committees (continued)

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
Reviewer	Italian Scientists and Scholars in North America Foundation Award	May 2013
Reviewer	WOTRO Science for Global Development Netherlands Organization for Scientific Research	Mar 2013
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
Reviewer	Louisiana Board of Regents' Research Competitiveness Subprogram	Dec 2011
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
Reviewer	Information & Intelligent Systems (III) National Science Foundation	Mar 2010
Reviewer	Natural Sciences and Engineering Research Council of Canada	Dec 2009
Reviewer	Louisiana Board of Regents Support Fund	Dec 2008
Panelist	Information & Intelligent Systems (III) National Science Foundation (held in Arlington, VA)	Jan 2008
Reviewer	Natural Sciences and Engineering Research Council of Canada	Dec 2007
Panelist	Information Technology for Life Sciences UC Discovery Grant Program (panel held in Berkeley, CA)	Jun 2007
Reviewer	International Science and Engineering Program National Science Foundation	Feb 2006
Reviewer	Plant Genome Research Program National Science Foundation	Jan 2006
Panelist	Information Technology for Life Sciences UC Discovery Grant Program (panel held in Berkeley, CA)	Jun 2005

Advisory and Review Committees (continued)

Panelist	Information & Intelligent Systems (SEI+II) National Science Foundation (panel held in Arlington, VA)	Mar 2005
Panelist	Information Technology for Life Sciences UC Discovery Grant Program (panel held in Berkeley, CA)	Jun 2004
Reviewer	Intelligent Systems Project NASA	Mar 2004
Reviewer	INT-Western Europe Program National Science Foundation	Nov 2003
Panelist	Information Technology for Life Sciences UC Discovery Grant Program (panel held in Berkeley, CA)	Jun 2003
Panelist	ITR-Theory of Computing National Science Foundation (panel held in Arlington, VA)	Mar 2003
Reviewer	Biotechnology Program Colciencias: Fondo Colombiano de Investigaciones Cientificas	Feb 2002

University Service

Member	Grievance Consultation Panel Academic Senate, UC Riverside	2020–2023
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
Vice Chair	Department of Computer Science and Engineering UC Riverside	2009–
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
External 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
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

University Service (continued)

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

Saleh Sereshki	PhD student Department of Computer Science and Engineering, UC Riverside	2019–
Dipankar Baisya	PhD candidate Department of Computer Science and Engineering, UC Riverside	2016–
Qihua Liang	PhD candidate Genetics, Genomics and Bioinformatics, UC Riverside	2015–
Abbas Roayaei	PhD, "Efficient Algorithms for the Analysis of Hi-C Contact Maps" Department of Computer Science and Engineering, UC Riverside	2014–2019
Md. Abid Hasan	PhD, "Accurate Prediction Methods on Biomolecular Data" Department of Computer Science and Engineering, UC Riverside	2014–2019
Weihua Pan	PhD, "Optical Map-based Genome Scaffolding" Currently post-doc at Carnegie Mellon University	2014–2019
Rachid Ounit	PhD, "Computing the Microbiome: Efficient Methods for the Analysis of Metagenomes" Currently <i>CTO</i> at Biotia, New York, NY	2013–2017
Hind Alhakami	PhD, "Data Structures and Algorithms for de novo Genome Assembly" Currently <i>Bioinformatics Scientist</i> at Dovetail Genomics, Santa Cruz, CA	2012–2017
Hamid Mirebrahim	PhD, "Efficient Methods for the Analysis of Ultra-Deep Sequencing Data" Currently <i>Principal Scientist</i> at Roche Sequencing, Pleasanton, CA	2010–2015
Anton Polishko	PhD, "Computational Methods for Exploring Nucleosome Dynamics" Currently <i>CTO</i> at Zulloo Inc	2009–2014
Denisa Duma	PhD, "A Pooling Strategy for the Selective Sequencing of Very Large Genomes" Currently <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" Currently <i>Assistant Professor</i> at California State University, Chico, CA	2005–2010
Vladimir Vacic	PhD, "Computational Methods for Discovery of Cellular Regulatory Mechanisms" Currently <i>Bioinformatics Scientist</i> at 23andme, Mountain View, CA	2003–2008
Yonghui Wu	PhD, "On the Accurate Construction of Genetic Linkage Maps" Currently <i>Principal Software Engineer</i> at Google Brain, Mountain View, CA	2003–2008
Serdar Bozdag	PhD, "Combinatorial Approaches to the Physical Mapping Problem" Currently <i>Associate Professor</i> at Marquette University, Milwaukee, WI	2003–2008
Qiaofeng Yang	PhD, "Graph Theoretical Approaches to the Analysis to Large-Scale Genomic Data" Currently <i>Manager</i> at Scientific Games, Reno, NV	2000–2006
Jie Zheng	PhD, "Algorithms for Identification of Repetitive Patterns in Biological Sequences" Currently <i>Associate Professor</i> at ShanghaiTech University, Shanghai, China	2001–2006

Other students supervised

Matthew Goldberg	BS, Computer Science and Engineering, UCLA PhD student at UMD	2015-2015
Feroz 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/>)

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
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-)

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
08.2013	eXtension Webinar (http://www.eXtension.org/) Selective Sequencing Through Combinatorial Pooling	on-line
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

Invited and Conference Presentations (2010-) (continued)

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