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

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	**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 Associate 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
1999 – 2001	**Purdue University, West Lafayette, IN** Department of Computer Science	Research Assistant
1999 – 1999	**Celera Genomics, Rockville, MD** Department of Informatics Research	Intern
1999 – 2001	**Purdue University, West Lafayette, IN** Department of Computer Science	Teaching Assistant
1994 – 1995	**University of Verona, Italy** Neurosurgery Department, Gamma Knife Lab	Consultant

Awards & Honorary Memberships

2017- **Faculty of 1000**
Bioinformatics, Biomedical Informatics & Computational Biology

2017 **Teaching Award (Honorable Mention)**
Bourns College of Engineering, UC Riverside

2017 **Distinguished Scientist** *for contributions to computational biology*
Association for Computing Machinery (ACM)

2016 **Fellow** *for contributions to computational biology and data mining*
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)

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

2015 – 2018 **DOE** $1,499,999 – role: coPI (with I. Wheeldon, N. Da Silva)
Establishing the thermotolerant yeast *Kluyveromyces marxianus* as a host for biobased fuels and chemicals production

2015 – 2018 **NSF (IIS)** $499,000 – role: sole PI
III:Small:Algorithms for Genome Assembly of Ultra-deep Sequencing Data

2015 – 2018 **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 – 2016 **UCR** $70,000 – role: coPI (with K. Le Roch, F. Sladek)
An *in vivo* 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 *et al.*)
Acquisition of a Scalable Storage Cluster for Data Intensive NIH Research

2013 – 2018 **US-AID** $4,972,542 – role: coPI (with T. Close, P. Roberts)
Feed the Future Innovation Lab: Advanced Tools for Climate-Resilient Cowpeas

2013 – 2017 **NSF (IIS)** $994,370 – role: PI (with K. Le Roch)
III:Medium:Algorithms and Software Tools for Epigenetic Research

2013 – 2013 **UCOP** $34,500 – role: coPI (with F. Vahid, K. Miller, B. Linard)
Ultra-Interactive Animated Web Learning

2011 – 2012 **UCR** $60,000 – role: coPI (with E. Keogh, C. Shelton)
Bootstrapping the UCR Center for Computational Entomology

2011 – 2014 **NSF (ABI)** $428,635 – role: PI (with T. Close)
ABI Innovation: Barcoding-Free Multiplexing: Leveraging Combinatorial Pooling for High-Throughput Sequencing

Funding (continued)

2010 – 2014	**NIH (R01)** Understanding the Role of Nucleosomes Turnover in the Malaria Parasite Infection	$1,839,568 – role: coPI (with K. Le Roch)
2010 – 2011	**DARPA** ProLiFiC: Cyber-Genetic Provenance, Lineage, Forensics and Classification	$1,800,000 – role: subcontract PI (with S. Evans, J. Morrison, E. Keogh, I. Neamtiu)
2009 – 2011	**USDA (CSREES)** Advancing the Barley Genome	$1,000,000 – role: coPI (with T. Close, G. J. Muehlbauer, J. Bennetzen)
2006 – 2008	**NSF (MRI)** MRI: Acquisition of an Ultra Low-Latency Multiprocessor System with On-Board Hardware Accelerators	$330,000 – role: senior personnel (with L. Bhuyan, W. Najjar, G. Ciardo)
2006 – 2010	**USDA (CSREES)** Barley Coordinated Agricultural Project: Leveraging Genomics, Genetics, and Breeding for Gene Discovery and Barley Improvement	$5,000,000 – role: coPI (G. Muehlbauer, T. Close, *et al.*)
2005 – 2010	**NSF (DBI)** CAREER: Combinatorial Algorithms for Pattern Discovery with Applications to Data Mining and Computational Biology	$414,277 – role: PI
2003 – 2008	**NSF (DBI)** Coupling Expressed Sequences and Bacterial Artificial Chromosome Resources to Access the Barley Genome	$2,497,294 – role: coPI (with T. Close, T. Jiang)
2002 – 2005	**USDA** HarvEST: A portable EST database viewer	$335,000 – role: coPI (with T. Close)

Publications

Peer-reviewed Journal Articles

(† indicates authors that contributed equally)

[1] 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*

[2] Novo&Stitch: Accurate Reconciliation of Genome Assemblies via Optical Maps
W. Pan, S. Wanamaker, A. Ah-Fong, H. Judelson, S. Lonardi
Bioinformatics, *to appear, 2018*

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

[4] 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*

[5] 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*

[6] 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*

[7] 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*

[8] 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*

[9] 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*

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

[11] 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*

[12] 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*

[13] 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*

[14] 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*

[15] *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*

[16] 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*

[17] 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*

[18] 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*

[19] 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*

[20] 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*

[21] 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*

[22] 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*

[23] 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*

[24] 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*

[25] 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*

[26] 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*

[27] 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*

[28] 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*

[29] 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*

[30] 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*

[31] 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*

[32] 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*

[33] 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*

[34] 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*

[35] 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*

[36] 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*

[37] 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*

[38] 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*

[39] 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*

[40] A Compartmentalized Approach to the Assembly of Physical Maps
S. Bozdag, T. J. Close, S. Lonardi

BMC Bioinformatics*, vol. 10, no. 217, 2009*

[41] 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*

[42] 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*

[43] 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*

[44] 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*

[45] 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*

[46] 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*

[47] 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*

[48] 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*

[49] 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*

[50] 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*

[51] 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*

[52] 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*

[53] 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*

[54] 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*

[55] Finding Biclusters by Random Projections
S. Lonardi, W. Szpankowski, Q. Yang

Theoretical Computer Science, *vol. 368, no. 3, pp. 217–230, 2006*

[56] 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*

[57] 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*

[58] 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*

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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

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
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
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
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	**RECOMB: International Conference on Research in Computational Molecular Biology** 2013: Beijing, China | 2014: Pittsburgh, PA | 2015: Warsaw, Poland
PC member	**CPM: Symposium on Combinatorial Pattern Matching** 2004: Istanbul, Turkey | 2006: Barcelona, Spain | 2008: Pisa, Italy | 2009: Lille, France | 2011: Palermo, Italy | 2014: Moscow, Russia | 2015: Ischia, Italy
PC member	**ICCABS: IEEE Conference on Computational Advances in Bio and Medical Sciences** 2011: Orlando, FL | 2012: Las Vegas, NV | 2013: New Orleans, LA | 2014: Miami Beach, FL
PC chair	**SPIRE: String Processing and Information Retrieval** 2010: Los Cabos, Mexico
PC member	**RECOMB-CG: RECOMB Satellite Workshop on Comparative Genomics** 2014: Cold Spring Harbor, NY
PC member	**APBC: Asia Pacific Bioinformatics Conference** 2013: Vancouver BC, Canada
PC member	**ICDM: IEEE International Conference on Data Mining** 2008: Pisa, Italy | 2012: Brussels, Belgium
PC member	**KDD: ACM International Conference on Knowledge Discovery and Data Mining** 2011: San Diego, CA | 2012: Beijing, China
PC member	**SDM: SIAM International Conference on Data Mining** 2006: Bethesda, MD | 2007: Minneapolis, MN | 2008: Atlanta, GA | 2012: Anaheim, CA

Technical Program Committee and Editorial Work (continued)

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 218: Design and Analysis of Algorithms [graduate]** Spring'18, 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'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, Prof. Rachel Levy)
UCR	**CS 141: Data Structures and Algorithms** 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	**Bioinformatics and Computational Biology** Pre-reviews for Ontario Genomics (Genome Canada)	Mar 2018
Reviewer	**National Defense Science and Engineering Graduate Fellowship** Department of Defence	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
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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
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

Advisory and Review Committees (continued)

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
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

Chair	***Ad Hoc* Committee to Review the Evaluation of Faculty Teaching** Academic Senate, UC Riverside	2018–
Member	**Committee on Faculty Welfare** Academic Senate, UC Riverside	2017–
Vice Chair	**Department of Computer Science and Engineering** UC Riverside	2009–
Chair	**Strategic Planning Committee** Department of Computer Science and Engineering, UC Riverside	2017–
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
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
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

University Service (continued)

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

Dipankar Baisya	**PhD student** Department of Computer Science and Engineering, UC Riverside	2016–
Qihua Liang	**PhD candidate** Genetics, Genomics and Bioinformatics, UC Riverside	2015–
Abbas Roayaei	**PhD candidate** Department of Computer Science and Engineering, UC Riverside	2014–
Weihua Pan	**PhD candidate** Department of Computer Science and Engineering, UC Riverside	2014–
Md. Abid Hasan	**PhD candidate** Department of Computer Science and Engineering, UC Riverside	2014–
Rachid Ounit	**PhD, "Computing the Microbiome: Efficient Methods for the Analysis of Metagenomes"** Currently *CTO* at Biotia, New York, NY	2013–2017
Hind Alhakami	**PhD, "Data Structures and Algorithms for de novo Genome Assembly"** Department of Computer Science and Engineering, UC Riverside	2012–2017
Hamid Mirebrahim	**PhD, "Efficient Methods for the Analysis of Ultra-Deep Sequencing Data"** Currently *Principal Scientist* at Roche Sequencing, Pleasanton, CA	2010–2015
Anton Polishko	**PhD, "Computational Methods for Exploring Nucleosome Dynamics"** Currently *CTO* at Zulloo Inc	2009–2014
Denisa Duma	**PhD, "A Pooling Strategy for the Selective Sequencing of Very Large Genomes"** Currently *post-doc* with Icahn School of Medicine at Mount Sinai, New York, NY	2008–2013
Elena Harris	**PhD, "Computational Methods for Epigenetic Studies"** Currently *Assistant Professor* at California State University, Chico, CA	2005–2010
Vladimir Vacic	**PhD, "Computational Methods for Discovery of Cellular Regulatory Mechanisms"** Currently *Bioinformatics Scientist* at 23andme, Mountain View, CA	2003–2008
Yonghui Wu	**PhD, "On the Accurate Construction of Genetic Linkage Maps"** Currently *Principal Software* Engineer at Google Brain, Mountain View, CA	2003–2008
Serdar Bozdag	**PhD, "Combinatorial Approaches to the Physical Mapping Problem"** Currently *Assistant Professor* at Marquette University, Milwaukee, WI	2003–2008
Qiaofeng Yang	**PhD, "Graph Theoretical Approaches to the Analysis to Large-Scale Genomic Data"** Currently with Bloomberg, New York, NY	2000–2006
Jie Zheng	**PhD, "Algorithms for Identification of Repetitive Patterns in Biological Sequences"** Currently *Assistant Professor* at Nanyang Technological University, Singapore	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 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/`)

XMView	**Optical/genetic maps browser (Bionano maps)** `https://github.com/ucrbioinfo/XMView`	2017
Novo&Stitch	**Assembly Reconciliation via 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
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 (2012-)

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
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
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