

CURRICULUM VITAE

Mihai Pop

Name: Mihai Pop

Department affiliations:

Department Computer Science

Center for Bioinformatics and Computational Biology (interim director), UMIACS

Graduate Program in Applied Mathematics and Scientific Computing (affiliate)

Department of Cell Biology and Molecular Genetics (affiliate)

Graduate Program in Biological Sciences (affiliate)

Maryland Pathogen Research Institute (affiliate)

University of Maryland Cloud Computing Center (affiliate)

Rank: Associate Professor

Citizenship: USA, Romania (European Union)

Languages: Romanian (native), English (fluent), French (fluent), German (conversational)

Education

2000 - Ph.D. Computer Science, Johns Hopkins University

1998 - M.S.E. Computer Science, Johns Hopkins University

1994 - B.S. Computer Science , Politehnica University Bucharest , Romania

Employment

2011-present. Interim Director. Center for Bioinformatics and Computational Biology,
University of Maryland

2011-present. Associate Professor. University of Maryland, Department of Computer Science

2006-2011. Assistant Professor. University of Maryland, Department of Computer Science

2005-2006. Assistant Research Scientist. University of Maryland, UMIACS

2000-2005. Bioinformatics Scientist. The Institute for Genomic Research

2004-2005. Consultant. Helicos Biosciences Corporation

1995-2000. Research Assistant. Johns Hopkins University

1994-1995. Teaching Assistant. Johns Hopkins University

1993-1994. Systems and Network Administrator. Politehnica University Bucharest, Romania

Publications

Publication impact H-index: 23 (as of Nov. 2011)

Papers in Refereed Journals

The following marks apply:

* - First author worked under my supervision in this project

† - This is a genome paper, involving multiple authors. Unless otherwise noted my contribution to these papers involved performing and analyzing the assembly of the genome(s) described in the paper.

1. †Carlton, J. M., S. V. Angiuoli, et al. (44 authors). *Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii*. *Nature* 419(6906): 512-519, 2002.
2. †K.E. Nelson, C. Weinel, et al. (44 authors). *Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440*. *Environ Microbiol* 4(12): 799-808, 2002.
3. **M. Pop**, S.L. Salzberg, M. Shumway. *Genome sequence assembly: algorithms and issues*. *IEEE Computer* 35, pp. 47-54, 2002.
4. T.D. Read, S.L.Salzberg, **M. Pop**, M. Shumway, L. Umayam, L. Jiang, E. Holtzapple, J. Busch, K.L. Smith, J.M. Schupp, D. Solomon, P. Keim, C.M. Fraser. *Comparative genome sequencing as a method for discovery of novel polymorphisms in Bacillus anthracis*. *Science* 296, pp. 2028-2033, 2002
5. E.F. Kirkness, V. Bafna, A.L. Halpern, S. Levy, K. Remington, D.B. Rusch, A.L. Delcher, **M. Pop**, W. Wang, C.M. Fraser, J.C. Venter. *The dog genome: survey sequencing and comparative analysis*. *Science* 301(26), pp. 1898-1903, 2003
6. †T. D. Read, S. N. Peterson, et al. (52 authors). *The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria*. *Nature* 423(6935): 81-86, 2003.
7. **M. Pop**, A.M. Phillippy, A.L. Delcher, S.L. Salzberg. *Comparative Genome Assembly*. *Briefings in Bioinformatics* 5(3), pp. 237-248, September 2004.
8. **M. Pop**, D.S. Kosack, S.L. Salzberg. *Hierarchical scaffolding with Bambus*. *Genome Research* 14(1), pp. 149-159, 2004.
9. **M. Pop**, D. Kosack (2004). *Using the TIGR assembler in shotgun sequencing projects*. *Methods Mol. Biol.* 255, pp. 279-294, 2004.
10. B.V. Geisbrecht, S. Bouyain, **M. Pop**. *An optimized system for expression and purification of secreted bacterial proteins*. *Protein Expr. Purif.* 2005. **note: I am not senior author in this work**
11. S.L. Salzberg, J.D. Hotopp, A.L. Delcher, **M. Pop**, M.B. Eisen, W.C. Nelson. *Serendipitous discovery of Wolbachia genomes in multiple Drosophila species*. *Genome Biology* 6(3), pp. R23, 2005. **Highly accessed.**
12. †Loftus, B., I. Anderson, et al. (54 authors). *The genome of the protist parasite Entamoeba histolytica*. *Nature* 433(7028): 865-8, 2005.
13. †El-Sayed, N. M., P. J. Myler, et al. (82 authors). *The genome sequence of Trypanosoma cruzi, etiologic agent of Chagas disease*. *Science* 309(5733): 409-15, 2005.
14. S.R. Gill, **M. Pop**, R.T. DeBoy, P. Eckburg, I. Hance, B. Samuel, J. Gordon, D. Relman, C.M. Fraser, K.E. Nelson. *Metagenomic analysis of the human distal gut microbiome*. *Science* 312: 1355-1359, 2006.
15. *D.D. Sommer, A.L. Delcher, S.L. Salzberg, **M. Pop**. *Minimus: a fast, lightweight genome assembler*. *BMC Bioinformatics* 8:64, 2007. **Highly accessed.**
16. †Clark, A. G., M. B. Eisen, et al. (241 authors). *Evolution of genes and genomes on the Drosophila phylogeny*. *Nature* 450(7167), pp. 203-18, 2007.
17. †E.Ghedin, S. Wang, et al. (71 authors). *Draft Genome of the Filarial Nematode Parasite Brugia malayi*. *Science* 317:1756-1760, 2007.
18. M. Hammel, G. Sfyroera, S. Pырpassopoulos, D. Ricklin, K.X. Ramyar, **M. Pop**, Z. Jin, J.D. Lambris, and B.V. Geisbrecht. *Characterization of Ehp, a secreted complement inhibitory protein from Staphylococcus aureus*. *J Biol Chem*, 282: 30051-30061. 2007
19. *J.R. White, M. Roberts, J.A. Yorke, **M. Pop**. *Figaro: a novel statistical method for vector sequence removal*. *Bioinformatics*. 24(4):462-467. 2008.
20. **M. Pop**, S.L. Salzberg. *Bioinformatics challenges of new sequencing technology*. *Trends in Genetics*. 24, 142-149. 2008.
21. *A.M. Phillippy, M.C. Schatz, **M. Pop**. *Genome assembly forensics: finding the elusive mis-assembly*.

- Genome Biology. 9:R55. 2008.
22. *N. Nagarajan, T.D. Read, and **M. Pop** *Scaffolding and validation of bacterial genome assemblies using optical restriction maps*. Bioinformatics. 24(10):1229-1235. 2008. **Featured in an article from "In Sequence" - newsletter published by Genome Web.**
 23. N. Nagarajan, R. Navajas-Perez, **M. Pop**, M. Alam, R. Ming, A.H. Paterson, S.L. Salzberg. *Genome-wide analysis of repetitive elements in papaya*. Tropical Plant Biology. DOI 10.1007/s12042-008-9015-0. 2008.
 24. *B. Liu, **M. Pop**. *ARDB - antibiotic resistance genes database*. Nucleic Acids Research. 37:D443-D447, 2009.
 25. *B. Langmead, C. Trapnell, **M. Pop**, and Steven L. Salzberg. *Ultrafast and memory-efficient alignment of short DNA sequences to the human genome*. Genome Biology. 10:R25, 2009. **note: first author co-advised by me and Steven Salzberg. Highly accessed. > 100 citations. Received Genome Biology Award for best article published in 2009.**
 26. *J.R. White, **M. Pop**. *Statistical methods for detecting differentially abundant features in clinical metagenomic samples*. PLoS Computational Biology; 5(4): e1000352, 2009
 27. *N. Nagarajan, **M. Pop**. *Parametric Complexity of Sequence Assembly: Theory and Applications to Next Generation Sequencing*. Journal of Computational Biology 16(7):897-908. 2009. **7th most read article in the journal during last 12 months (as of June 2010)**
 28. **M. Pop**. *Genome assembly reborn: recent computational challenges*. Briefings in Bioinformatics 10(4):354-366. 2009.
 29. M.P. Di Bonaventura, R. DeSalle, **M. Pop**, N. Nagarajan, D. Figurski, D. H. Fine, J. Kaplan, P. Planet. *Complete genome sequence of Aggregatibacter (Haemophilus) aphrophilus NJ8700*. Journal of Bacteriology. 191:4693-4694. 2009. **Genome announcement**
 30. *B. Langmead, M.C. Schatz, J. Lin, **M. Pop**, S.L. Salzberg. *Searching for SNPs with cloud computing*. Genome Biology, 10:R134 2009 **Highly accessed. note: first and second authors co-advised with Steven Salzberg**
 31. S. Navlakha, J. White, N. Nagarajan, **M. Pop**, and Carl Kingsford. *Finding Biologically Accurate Clusterings in Hierarchical Decompositions Using the Variation of Information*. Journal of Computational Biology 16(7):897-908. 2009. **conference version in RECOMB2009 also listed below**
 32. †P.E. Chen, C. Cook, A.C. Stewart, N. Nagarajan*, D.D. Sommer*, **M. Pop**, B. Thomason, M.P. Kiley, S. Lentz, N. Nolan, S. Sozhamannan, A. Sulakvelidze, A. Mateczun, L. Du, M.E. Zwick, T.D. Read *Genomic characterization of the Yersinia genus*. Genome Biology, 11:R1, 2010 **Highly accessed.**
 33. C. Kingsford, M.C. Schatz and **M.Pop**. *Assembly complexity of prokaryotic genomes using short reads* . BMC Bioinformatics, 11:21, 2010. **Highly accessed.**
 34. *J. R. White, S. Navlakha, N. Nagarajan, M.R. Ghodsi, C. Kingsford, **M. Pop**. *Alignment and clustering of phylogenetic markers - implications for microbial diversity studies*. BMC Bioinformatics, 11:152, 2010. **Highly accessed.**
 35. *N. Nagarajan, C. Cook, M.P. diBonaventura, H. Ge, A. Richards, K.A. Bishop-Lilly, R. DeSalle, T.D. Read, **M. Pop**. *Finishing genomes with limited resources: lessons from an ensemble of microbial genomes*. BMC Genomics. 11:242, 2010. **Highly accessed.**
 36. J. V. Lopez, A. Ledger, L. Z. Santiago-Vázquez, **M. Pop**, D. D. Sommer, L. K. Ranzer, R. A. Feldman and R. G. Kerr. *Suppression subtractive hybridization PCR isolation of cDNAs from a Caribbean soft coral*. Electronic Journal of Biotechnology 14(1):2011
 37. D. A. Rasko, P. L. Worsham, T. G. Abshire, S. T. Stanley, J. D. Bannan, M. R. Wilson, R. J. Langham, R. S. Decker, L. Jiang, T. D. Read, A. M. Phillippy, S. L. Salzberg, **M. Pop**, M. N. Van Ert, L. J.

- Kenefic, P. S. Keim, C. M. Fraser-Liggett and J. Ravel. *Bacillus anthracis comparative genome analysis in support of the Amerithrax investigation*. Proceedings of the National Academy of Sciences . 18(12):5027-5032. 2011
38. J. Wetzel, C. Kingsford, **M. Pop**. *Assessing the benefits of using mate-pairs to resolve repeats in de novo short-read prokaryotic assemblies*. BMC Bioinformatics. 12:95. 2011
 39. *B. Liu, **M. Pop**. *MetaPath: identifying differentially abundant metabolic pathways in metagenomic datasets*. BMC Proceedings. 5(Suppl 2):S9. 2011. **conference version in ISBRA 2010**.
 40. *M.Ghodsi, B. Liu, **M. Pop**. *DNACLUST: accurate and efficient clustering of phylogenetic marker genes*. BMC Bioinformatics. 12:271. 2011
 41. Liu*, T. Gibbons*, M. Ghodsi*, T. Treangen*, **M. Pop**. *Accurate and fast estimation of taxonomic profiles from metagenomic shotgun sequences*. BMC Genomics. 11(Suppl 2): S4. 2011. **conference version in BIBM 2010**.
 42. S. Koren*, T.J. Treangen*, **M. Pop**. *Bambus 2: Scaffolding Metagenomes*. Bioinformatics 27 (21): 2964-2971. 2011
 43. D.R. Kelley, B. Liu*, A.L. Delcher, **M. Pop**, S.L. Salzberg. *Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering*. Nucleic Acids Research. 2011.

Papers in Refereed Conferences

1. A. Aggarwal, S. R. Kosaraju, **M. Pop**. *Drawing of two-dimensional irregular meshes*; GD '98: Sixth Symposium on Graph Drawing, August 13-15,1998; Montreal, Canada. Lecture Notes in Computer Science, v. 1547, pp. 1-14. **note: authors in alphabetical order**
2. S. R. Kosaraju, **M. Pop**. *De-Amortization of Algorithms*; The Fourth Annual International Computing and Combinatorics Conference , COCOON '98, August 12-14, 1998; Taipei, Taiwan. **note: authors in alphabetical order**
3. G. Barequet, C. Duncan, M. T. Goodrich, S. Kumar, **M. Pop**. *Efficient Perspective-Accurate Silhouette Computation*; video presentation at ACM Symposium on Computational Geometry '99 . **note: authors in alphabetical order**.
4. **M. Pop**, G. Barequet, C. Duncan, M.T. Goodrich, W. Huang, S. Kumar. *Efficient Perspective-Accurate Silhouette Computation and Applications*; Proceedings of the 17th ACM Symposium on Computational Geometry, June 3-5 2001, Tufts University, Medford, MA
5. S. Navlakha, J. White, N. Nagarajan, **M. Pop**, and Carl Kingsford. *Finding Biologically Accurate Clusterings in Hierarchical Decompositions Using the Variation of Information*. RECOMB 2009. **Note: journal version also listed above**.
6. *M. Ghodsi, **M. Pop**. *Inexact local alignment search over suffix arrays*. in Proceedings of the 2009 IEEE International Conference on Bioinformatics and Biomedicine (BIBM). Washington, DC. November 1-4, pp: 83-87, 2009. **also listed as poster presentation**
7. *B. Liu, **M. Pop**. *Identifying Differentially Abundant Metabolic Pathways in Metagenomic Datasets*. in Proceedings of the 6th International Symposium on Bioinformatics Research and Applications (ISBRA). Storrs, CT. May 2010. **Note: journal version also listed above**.
8. *B. Liu, *T. Gibbons, *M. Ghodsi, and **M. Pop**. *MetaPhyler: Taxonomic profiling for metagenomic sequences*. in Proceedings of BIBM 2010. Hong Kong, December 2010. **Note: journal version also listed above**.

Book chapters

1. E. Brill, **M. Pop**. *Unsupervised Learning of Disambiguation Rules for Part-of-Speech Tagging*; in Natural

Language Processing Using Very Large Corpora; Kluwer Academic Publishers; 1999

2. **M. Pop.** *Shotgun sequence assembly.* in *Advances in Computers* vol. 60, pp. 194-159, M. Zelkowitz ed.; 2004.
3. J-H. Choi, H. Tang, S. Kim, **M. Pop.** *Computational Approaches for Genome Assembly Validation.* in *Biological data mining*, J.Y. Chen and S. Lonardi eds. Chapman & Hall/CRC Computational Science Series. pp. 163-187. 2009
4. V. Mai, **M. Pop**, M. Schell. *Metagenomic Analysis of Human Gut Microbiota.* in *Metagenomics and its Applications in Agriculture.* Nova Science Publishers, R. W. Li ed; 2010.
5. N. Nagarajan and **M. Pop.** *Sequencing and Genome Assembly Using Next-Generation Technologies.* *Methods in Molecular Biology.* 673:1-17. 2010
6. *T.J. Treangen, *D.D. Sommer, F.E. Angly, *S. Koren, **M. Pop.** *Next Generation Sequence Assembly with AMOS.* in *Current Protocols in Bioinformatics.* 2011

Contracts and Grants

Current

1. Sep 1, 2008 - Aug 31, 2012 (\$445,358, PI). National Science Foundation. IIS-0812111 *III-CXT-Small: Graphs to Diversity: extracting genomic variation from sequence graphs.*
2. Sep 24, 2008 - Jul 31, 2012 (\$780,000, PI). NIH. R01-HG004885: *Assembly and analysis software for exploring the human microbiome.*
3. Apr 1, 2009 - Mar 31, 2012 (\$380,000, PI). National Science Foundation. IIS-0844494 *Algorithms for the analysis of data from massively-parallel genome sequencing*
4. May 1, 2009 - April 30, 2012. (\$183,175, PI on subcontract to U. Wisc.) NIH R01-HG-000225. *New physical methodologies for genomic analysis.*
5. Sep 23, 2009 - Jul 31, 2014. (\$380,604, PI on subcontract to U. Pittsburgh). NIH U01-HL-098962. *Pathogenesis of obstruction/emphysema and the microbiome (POEM) in HIV.*
6. Jan 1, 2011 - Dec 31, 2013. (\$307,814, PI on subcontract to UM. School of Medicine). Bill and Melinda Gates Foundation. *Metagenomics-Based Discovery of New Viral Pathogens Causing Diarrheal Disease.*
7. Aug 1, 2011 - Jul 31, 2012. (\$2,150,999, PI). Office of Naval Research N000141110905. *Personalized Medicine Initiative (Congressional earmark to establish a personalized medicine infrastructure at the University of Maryland).*
8. Sep 1, 2011 - Aug 31, 2014 (\$492,809, PI). National Science Foundation IIS-1117247 *III: Small: Genome Assembly Using Sparse Sequence Information.*

Completed

1. Sep 24, 2009 - Jul 31, 2010 (\$110,000, PI). NIH. administrative supplement to R01-HG-004885: *Assembly and analysis software for exploring the human microbiome.*
2. Aug 27, 2009 - Aug 26, 2010. (\$3,000, PI on subcontract to JHU). NASA. *Community structure of the microbiome of a Mars-like environment, the Atacama Desert, Chile*
3. Jan 1, 2007- Sep 31, 2010 (\$980,123, PI). Henry Jackson Foundation. *Assembly and gene finding algorithms for genome sequences generated by pyrosequencing.*
4. Sep 1, 2007- Mar 31, 2011(\$201,256, PI on subcontract to UM School of Medicine). Bill and Melinda Gates Foundation. SR00000277: *New Technologies in Diagnosis of Enteric Diseases.*
5. Aug 1, 2009 - Jul 31, 2011. (\$43,570, PI on subcontract to JHU). NSF DEB-0918907. *MSB: Community*

Structure, Genomic Heterogeneity, and Metabolic Diversity of the Microbiome of the oldest and driest desert on Earth, the Atacama desert in Northern Chile.

Poster presentations (last 3 years)

1. N. Nagarajan, M. Pop. *Parametric Complexity of Sequence Assembly: Theory and Applications to Next Generation Sequencing*. RECOMB, Tucson, AZ. May 2009. **One of 3 posters selected for oral presentation.**
2. J. Wetzel, M.C. Schatz, C. Kingsford, **M. Pop**. *Upper bounds on the ability to reconstruct prokaryotic genomes with next-generation sequencing technologies*. Workshop on Algorithms in Bioinformatics, Philadelphia, PA, September, 2009. **One of 2 posters selected for oral presentation.**
3. M.C. Schatz, **M. Pop**. *Commodity computing in genomics research*. CLuE PI meeting. Mountain View, CA. October 2009.
4. M. Ghodsi, **M. Pop**. *Inexact local alignment search over suffix arrays*. IEEE Conference on Bioinformatics and Biomedicine (BIBM). Washington, DC. November 1-4, 2009. **also listed as paper above**
5. J.R. White, **M. Pop**. *Microbial dynamics of human obesity*. IEEE Conference on Bioinformatics and Biomedicine (BIBM), November 1-4. 2009
6. **M. Pop**. *Assembly and clustering of metagenomic data*. Human Microbiome Project Research Network Meeting, Houston, TX. January 19-21. 2010
7. B. Liu, **M. Pop**. *Comparative Analysis of Metabolic Pathways In Metagenomics*. International Symposium on Bioinformatics Research and Applications (ISBRA), Storrs, CT. May 23-26. 2010. **Best poster award.**
8. J. Lopez, J. White, J. Patel, A. Ottesen, **M. Pop**, P. Blackwelder, C. Arce, M. Allard. *Dynamics of Microbial Symbiont Communities in the Florida Reef Sponge, Axinella corrugata, Measured by Deep DNA Sequencing*. International Human Microbiome Congress, Vancouver, BC, Canada. March 9-11, 2011.
9. B. Liu, T. Treangen, **M. Pop**. *Better Metagenomic Assembly Through the Combination of de novo and Comparative Assemblies*. International Human Microbiome Congress, Vancouver, BC, Canada. March 9-11, 2011.

Invited talks (last 3 years)

1. *From one genome to many: how cheap sequencing is changing genomics*. Picasso seminar series. Princeton University, Princeton, NJ. February 2009.
2. *What can you do with millions of short sequences*. Biotechnology High Performance Computing Software Application Institute workshop. US Army Medical Research and Materiel Command, Ft. Detrick, MD. March 2009.
3. *Keeping up with DNA technologies*. Bioinformatics Technology Forum. University of Maryland, Shady Grove. Rockville, MD. March 2009.
4. *Human metagenomics: challenges and promises*. Dana Farber Cancer Institute. Boston, MA. May 2009.
5. *Commodity computing in genomics research*. Clue PI meeting. Mountain View, CA. October 2009.
6. *Map-guided scaffolding and assembly*. Medicago Informatics Meeting, JCVI, Rockville, MD. November 2009.
7. *DNA technologies: promises and computational challenges*. George Mason University, Fairfax, VA. February 2010.
8. *Analyzing next-generation metagenomic data*. JCVI, Rockville, MD. February 2010.
9. *DNA assembly and analysis tools in a cloud environment using next generation sequence data*. NHGRI/NIH Cloud Computing Meeting. Bethesda, MD. March 2010.

10. *What can you do with billions of short DNA sequences*. Indiana University. April 2010.
11. *How next generation sequencing technologies are changing metagenomics*. Argonne National Labs. April 2010.
12. *DNA technologies: promises and computational challenges*. U. of Wisconsin. April 2010.
13. *First steps towards automated metagenomic assembly*. International Human Microbiome Congress. St. Louis, MO, August 2010.
14. *Genome assembly from non-traditional data*. Single Cell Genomics Workshop. Boothbay Harbor, ME. September 2010.
15. *Challenges in metagenomic assembly*. 1st IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS). Orlando, FL. February 2011.
16. *Can you assemble whole genomes from next generation sequencing data?* Workshop on Computational Advances for Next Generation Sequencing (CANGS 2011). Orlando, FL. February 2011.
17. *Assembling and understanding microbial communities*. Cold Spring Harbor Laboratories. April 2011.
18. *Genome assembly reborn: new challenges in microbial reconstruction*. American Society for Microbiology General Meeting. New Orleans, LA, May 2011.
19. *Assembling and understanding microbial communities*. Notre Dame University, South Bend, IN. July 2011.

Software packages

1. AMOS - a modular open-source assembly package <http://amos.sourceforge.net>
2. BAMBUS - genome scaffolding software. <http://amos.sourceforge.net/docs/bambus>.
3. Figaro - statistical vector trimming for shotgun sequencing projects. <http://amos.sourceforge.net/Figaro>.
4. SOMA - scaffolding of genome data using optical maps. <http://www.cbcb.umd.edu/soma>.
5. MetaStats - statistical software for comparing metagenomic libraries <http://metastats.cbcb.umd.edu>
6. MetaPath - statistical software for comparing metagenomic data-sets at the pathway level. <http://www.cbcb.umd.edu/~boliu/metapath>
7. ARDB - antibiotic resistance genes database <http://arbd.cbcb.umd.edu>
8. Bowtie - sequence aligner for short-read sequencing data <http://bowtie-bio.sf.net>
9. Crossbow - SNP calling pipeline relying on cloud computing resources <http://bowtie-bio.sf.net/crossbow>
10. Metapath - statistical software for identifying differentially abundant pathways in metagenomic data-sets. <http://cbcb.umd.edu/software/metapath/>
11. Metaphyler - software for estimating the taxonomic composition of a community from whole-metagenomic data. <http://cbcb.umd.edu/software/metaphyler>
12. DNAClust - software for rapid clustering of DNA sequences. <http://dnaclust.sf.net>

Editorial/Review Duties

Editorial Boards

- BMC Bioinformatics - section editor (2010 -) manage editorial activities for ~40 academic editors.

- Biological Procedures Online - editorial board member (2007 - 2008)

Reviewer for journals

Annals of Mathematics and Artificial Intelligence, Bioinformatics, BioMed Central journals (BMC Bioinformatics, BMC Plant Biology, BMC Genomics, Genome Biology), Biotechniques, Chemical Reviews, Computer Programs and Methods in Biomedicine, Genome Research, IEEE Transactions on Nanobioscience, Journal of Computational Biology, Molecular Ecology, Molecular Biology and Evolution, Nature Review Genetics, Nature Methods, Nucleic Acids Research, PLoS Computational Biology, PLoS One.

Conference Program Committees

CBGI 2003, ISMB 2004, ECCB 2005, ISMB 2005, CSB 2006, ISBRA 2007, ISMB/ECCB 2007, ISBRA 2008, ISMB 2008, BIBM 2008, BICoB 2009, ISBRA 2009, ISMB/ECCB 2009, BIBM 2009, ISBRA 2010, WABI 2010, ECCB 2010, ICCAB 2011, ACM BCB 2011, PSB 2012.

Teaching

Courses taught in the last five years (chronological order)

- Fall 2006. CMSC 858E - *Algorithms in Biosequence Analysis*. 5 students
- Spring 2007. CMSC 423 - *Bioinformatic algorithms, databases, and tools*. 23 students.
- Spring 2008. CMSC 858P - *Algorithms in Biosequence Analysis*. 18 students.
- Spring 2008. CMSC 424 - *Database design*. 22 students.
- Fall 2008. CMSC 423 - *Bioinformatic algorithms, databases, and tools*. 20 students.
- Fall 2009. CMSC 423 - *Bioinformatic algorithms, databases, and tools*. 37 students.
- Spring 2010. CMSC 858W - *Algorithms in Biosequence Analysis*. 12 students.
- Spring 2011. CMSC424 - *Database design*. 81 students (2 sections)
- Fall 2011. CMSC131H - *Object oriented programming*. 23 students.

Course or Curriculum Development.

Fall 2006. CMSC 858 - Algorithms in Biosequence Analysis.

Redesigned second half of the course to include topics better related to the analysis of biological sequences - RNA and protein-folding. Designed a new project for the class that incorporates a project proposal and final report in addition to the actual implementation of a system.

Spring 2007. CMSC 423 - Bioinformatic algorithms, databases, and tools.

This course had been created but never taught. I updated the syllabus and developed the entire course materials (lectures, homeworks and exams, and projects).

Fall 2008. CMS 423 - Bioinformatic algorithms, databases, and tools

Updated the course according to feedback received from students. Switched to a new textbook and added new material discussing gene association studies.

Spring 2010. CMCS 858W - Algorithms in Biosequence Analysis.

Updated the syllabus to include current research topics in the field. Added a discussion of recent scientific papers and eliminated the midterm project.

Advising

Undergraduate

Elaine Nsoesie. Summer intern, 2006
Christopher Hill. 2007 - Spring 2010
Dan Sugarman. Fall 2008 - Fall 2009
Matt Thomas, Spring 2009
Carl Albach, Spring 2009 - Spring 2011
Sebastian Gomez, Spring 2009 - Summer 2011
Joshua Wetzel, Summer 2010
Petar Stojanov, Summer 2010 (co-advised with Liliana Florea)
Joseph Paulson, Spring 2010 - Summer 2010

Master's

Benjamin Langmead (CMSC) Spring 2008 - Summer 2009 (co-advised with Steven Salzberg)
Maya Zuhl (CMSC) Fall 2008 - Summer 2009

Doctoral

Bo Liu (CBMG/CS) 2007 -
Sergey Koren (CS) 2007 -
MohammadReza Ghodsi (CS) 2008 -
Chris Hill (CS) 2010 -
Joseph Paulson (AMSC) 2010 -
Lee Mendelowitz (AMSC) Summer 2011 -
Ted Gibbons (BISI) 2008 - 2010
Brianna Lindsay (Epidemiology) Summer 2010
James White (AMSC) 2007 - 2010 (James accepted a position at the Institute for Genomic Sciences at the University of Maryland School of Medicine)
Mike Schatz (CS) 2009 - 2010 (co-advised with Steven Salzberg. Mike has accepted an assistant professor position at Cold Spring Harbor Laboratories)
Yuan Lee (CBMG) Spring 2009. rotation student
Apratim Mitra (ANSC) - Graduate Advisory Committee member

Post-doctoral

Irina Astrovskaya (Ph.D. Georgia State University) 2011-
Herny Lin (Ph.D. UC Berkeley) 2010 -
Todd Treangen (Ph.D. Technical University of Catalonia) 2010-2011 (Todd is now a postdoctoral researcher at Johns Hopkins University)
Niranjan Nagarajan (Ph.D. Cornell University) 2007 - 2009. (Niranjan is now a senior research scientist in computational and mathematical biology at the Genome Institute of Singapore)

Service

Professional

- 2008 - present. Chair, Maize Genome Database Working Group
- Feb. 2009. Life Sciences Advisory Board for Opgen Inc (Gaithersburg, MD).
- 2009 - 2010. Member, DOE Systems Biology Knowledgebase Advisory Committee.

Grant review:

- National Institutes of Health (2005-2008 - *ad hoc* member on GGG-J panel, ~1-2 panels/year)
- National Institutes of Health (2009, 2010)
- National Cancer Institute (2008, 2009)
- National Science Foundation (2003, 2009, 2010)
- U.S. Department of Energy (2004, 2010)
- U.S. Civilian Research and Development Foundation (2006)
- U.S. Army Research and Materiel Command (2006)
- Defense Threat Reduction Agency Joint Science and Technology Office, Office for Chemical and Biological Defense. (2009)
- Research Council of Norway (2007)
- Mathematics of Information Technology and Complex Systems, Canada (2008)
- Wellcome Trust, UK. (2009)
- European Research Council (2009)

Fellowship review:

- 2007. Graduate Women in Science
- 2008. Microsoft PhD Scholarship

Meetings organized

- 2005. Co-organizer of the Fifth Annual RECOMB Satellite Meeting on DNA Sequencing Technologies and Computation. 2005, Stanford University, CA.
- 2008 Co-organizer for InformaticsMaryland 2008. Rockville, MD. January 2008.
- 2009. *Poster co-chair* for IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Washington, DC. November 1-4, 2009.
- 2010. *Member, organizing committee.* Human Microbiome Research Conference. St. Louis, MO. August 31-September 2, 2010.

Departmental committees

2006-7 - Chair, faculty search committee for Center for Bioinformatics and Computational Biology

2006-7, 2007-8, 2008-9, 2009-10 - Member, CS graduate admissions committee

2007-8, 2009-10 - Coordinator - Friday Faculty Lunches

2007-8, 2009-10 - Member, UMIACS APT committee

2007-8 - Member, faculty search committee for CBCB

2008-9, 2010-11, 2011-12 - Member, Teaching evaluation committee

2008-9 - Chair, faculty search committee for CBCB **note: committee suspended due to hiring freeze**

2010-2011 - Chair, committee to evaluate Masters student writing skills as part of Middle States Evaluation of Graduate Writing.

2011-2012 - Director search committee for CBCB.

College Committees

2007-8, 2008-9 - Member, AMSC graduate admissions committee

May 2009- May 2012 - Faculty Representative for CMPS on University Senate

2009-present - Member, Council for the Computational Biology, Bioinformatics and Genomics

concentration area within the Biological Sciences Graduate Program

Candidacy and defense committees (last 3 years)

Spring 2009 - Oral exam committee chair for James White
Spring 2009 - Oral exam committee chair for Sergey Koren
Spring 2009 - Oral exam committee member for Mike Schatz
Spring 2009 - Oral exam committee member for Adam Phillippy
Spring 2009 - MS Thesis defense committee member for Ben Langmead
Spring 2009 - Oral exam committee for Mike Schatz
Spring 2009 - Oral exam committee for Adam Phillippy
Spring 2009 - Chair, Oral exam committee for Sergey Koren
Spring 2009 - Chair, Oral exam committee for James White (AMSC)
Summer 2009 - Oral exam committee for Guillaume Marcais (AMSC)
Summer 2009 - Oral exam committee for Cole Trapnell
Summer 2009 - Chair, MS Thesis defense committee for Maya Zuhl
Summer 2009 - Thesis defense committee for Grecia Lapizco-Encinas
Fall 2009 - Graduate Advisory Committee member for Albert Yu (MOCB)
Fall 2009 - Oral exam committee for Saket Navlakha
Spring 2010 - Chair, Thesis defense committee for James White
Spring 2010 - Thesis defense committee for Cole Trapnell
Spring 2010 - Thesis defense committee for Mike Schatz
Spring 2010 - Thesis defense committee for Adam Phillippy
Summer 2010 - Oral exam committee for Chen Cao (MOCB)
Fall 2010 - Thesis defense committee for Saket Navlakha
Spring 2011 - Oral exam committee for Ben Langmead
Spring 2011 - Thesis defense committee for David Kelley
Spring 2011 - Thesis defense committee for Sam Angiouoli
Spring 2011 - Chair, Oral exam committee for Bo Liu
Summer 2011 - Oral exam committee for Rob Patro
Summer 2011 - Oral exam committee for Mohammad Ghodsi

External candidacy and defense committees

May 2010 - External advisor - Allison Regier (Notre Dame University)
June 2010 - Oral exam committee - Lina Faller (Boston University)
July 2011 - Thesis exam committee - Allison Regier (Notre Dame University)