

CURRICULUM VITAE

Mihai Pop

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Department affiliations:

Department Computer Science
Center for Bioinformatics and Computational Biology, 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)

Rank: 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

2016-present. Professor. University of Maryland, Department of Computer Science and Center for Bioinformatics and Computational Biology
2011-2016. Associate Professor. University of Maryland, Department of Computer Science and Center for Bioinformatics and Computational Biology
2011-2012, 2013-2014. Interim Director. Center for Bioinformatics and Computational Biology, University of Maryland
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

Awards/honors

2015 – University of Maryland Department of Computer Science Teaching Award
2014 – Thompson Reuters top 1% most cited researcher over past 10 years.

Publications

Publication impact H-index: 44 (Google Scholar); 32 (Web of Knowledge)

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.Ghedini, 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. Pyrpasopoulos, 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**. *DNA-CLUST: 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.
44. Salzberg, S.L., A.M. Phillippy, A.V. Zimin, D. Puiu, T. Magoc, S. Koren, . . . J.A. Yorke, *GAGE: A critical evaluation of genome assemblies and assembly algorithms*. Genome Research, 2011.
45. Ye, C., Z. Ma, C. Cannon, **M. Pop**, and D. Yu, *Exploiting sparseness in de novo genome assembly*. BMC Bioinformatics, 2012. 13(Suppl 6): p. S1. (**conference version also listed below**)
46. Liu, B., L.L. Faller, N. Klitgord, V. Mazumdar, M. Ghodsi, D.D. Sommer, . . . S. Amar, *Deep*

- sequencing of the oral microbiome reveals signatures of periodontal disease. PLoS ONE, 2012. 7(6): p. e37919.
47. Lin, H.C.*, S. Goldstein, L. Mendelowitz*, S. Zhou, J. Wetzel, D.C. Schwartz, and **M. Pop**, AGORA: Assembly Guided by Optical Restriction Alignment. BMC Bioinformatics, 2012. 13: p. 189.
 48. Del Canto, F., D.J. Botkin, P. Valenzuela, V. Popov, F. Ruiz-Perez, J.P. Nataro, M.M. Levine, O.C. Stine, **M. Pop**, A.G. Torres, R. Vidal, Identification of Coli Surface Antigen 23, a Novel Adhesin of Enterotoxigenic Escherichia coli. Infect Immun, 2012. 80(8): p. 2791-801.
 49. Human Microbiome Project Consortium (**2nd author**), A framework for human microbiome research. Nature, 2012. 486(7402): p. 215-21.
 50. Human Microbiome Project Consortium, Structure, function and diversity of the healthy human microbiome. Nature, 2012. 486(7402): p. 207-14.
 51. Gevers, D., **M. Pop**, P.D. Schloss, and C. Huttenhower, Bioinformatics for the Human Microbiome Project. PLoS Comput Biol, 2012. 8(11): p. e1002779.
 52. Treangen, T.J., S. Koren*, D.D. Sommer*, B. Liu*, I. Astrovsкая*, B. Ondov, A.E. Darling, A.M. Phillippy, and **M. Pop**, MetAMOS: a modular and open source metagenomic assembly and analysis pipeline. Genome Biol, 2013. 14(1): p. R2.1. **Highly accessed**
 53. Nagarajan, N. and **M. Pop**, Sequence assembly demystified. Nat Rev Genet, 2013. 14(3): p. 157-67.
 54. M.C. Schatz, A.M. Phillippy, D.D. Sommer, A.L. Delcher, D. Puiu, G. Narzisi, S.L. Salzberg, **M. Pop**. Hawkeye and AMOS: visualizing and assessing the quality of genome assemblies. Briefings in Bioinformatics. 14(2):213-224. 2013. PMC3603210
 55. Lindsay, B., B. Ochieng, et al., Quantitative Polymerase Chain Reaction for Detection of Shigella Improves Ascertainment of Shigella Burden in Children with Moderate to Severe Diarrhea in Low Income Countries. Journal of Clinical Microbiology, 2013. 51(6) 1740-1746.
 56. Bishop-Lilly, K.A., H. Ge, A. Butani, B. Osborne, K. Verratti, V. Mokashi, N. Nagarajan, **M. Pop**, T.D. Read, and A.L. Richards, Genome sequencing of four strains of Rickettsia prowazekii, the causative agent of epidemic typhus, including one flying squirrel isolate. Genome announcements, 2013. 1(3). PMC3695431 **genome announcement**
 57. Lindsay, B., **M. Pop**, et al. (52 authors), Alternative Methods of Bacterial Pathogen Detection: Culture, GoldenGate(R), Universal Biosensor(R), 16S rRNA-Gene Survey. J Clin Microbiol, 2013.
 58. Ghodsi, M.*, C.M. Hill*, I. Astrovsкая*, H. Lin*, D.D. Sommer*, S. Koren, and **M. Pop**, De novo likelihood-based measures for comparing genome assemblies. BMC Res Notes, 2013. 6(1): p. 334.
 59. Nijkamp, J.F.*, **M. Pop**, M.J. Reinders, and D. de Ridder, Exploring variation-aware contig graphs for (comparative) metagenomics using MaryGold. Bioinformatics, 2013.
 60. Paulson, J.N.*, O.C. Stine, H.C. Bravo, and **M. Pop**, Differential abundance analysis for microbial marker-gene surveys. Nature Methods, 2013. 10(12)
 61. Koren, S.*, T. Treangen, C. M.Hill*, **M. Pop**, and A. Phillippy, Automated ensemble assembly and validation of microbial genomes. BMC Bioinformatics, 2014. 15(1): p. 126. **highly accessed.**
 62. **Pop, M.**, A.W. Walker, et al. (35 authors), Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. Genome Biol, 2014.

15(6): p. R76.PMC 4072981. **highly accessed.**

63. Nguyen, N.-p., S. Mirarab, B. Liu*, **M. Pop**, and T. Warnow, *TIPP: taxonomic identification and phylogenetic profiling*. *Bioinformatics*, 2014. 30(24): p. 3548-3555.
64. Mendelowitz, L.* and **M. Pop**, *Computational methods for optical mapping*. *GigaScience*, 2014. 3(1): p. 33. **review**
65. Almeida, M.*, A. Hebert, A.-L. Abraham, S. Rasmussen, C. Monnet, N. Pons, C. Delbes, V. Loux, J.-M. Batto, P. Leonard, S. Kennedy, S. Ehrlich, **M. Pop**, M.-C. Montel, F. Irlinger and P. Renault, *Construction of a dairy microbial genome catalog opens new perspectives for the metagenomic analysis of dairy fermented products*. *BMC Genomics*, 2014. 15(1): p. 1101.
66. Brianna, L., Oundo, J., et al. (28 authors), *Microbiota That Affect Risk for Shigellosis in Children in Low-Income Countries*. *Emerging Infectious Disease Journal*, 2015. 21(2): p. 242.
67. Mendelowitz*, L.M., D.C. Schwartz, and **M. Pop**, *Maligner: a fast ordered restriction map aligner*. *Bioinformatics*, 2015.
68. Almeida, M.*, **M. Pop**, E. Le Chatelier, E. Prifti, N. Pons, A. Ghozlane, and S. Dusko Ehrlich. *Capturing the most wanted taxa through cross-sample correlations*. *ISME J*. 2016.
69. Nguyen, N-P, T. Warnow, **M. Pop**, B. White. *A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity*. *NPJ Biofilms and Microbiomes*. 2:p. 16004. 2016.
70. **Pop, M.**, J.N. Paulson*, S. Chakraborty, I. Astrovskaya*, B.R. Lindsay, S. Li, H.C. Bravo, C. Harro, J. Parkhill, A.W. Walker, R.I. Walker, D.A. Sack, and O.C. Stine, *Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic Escherichia coli and subsequent ciprofloxacin treatment*. *BMC Genomics*, 2016. 17(1): p. 1-11.

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.**
9. Ye, C., Z. Ma, C. Cannon, **M. Pop**, and D. Yu, *Exploiting sparseness in de novo genome assembly*. RECOMB-seq, Barcelona, Spain. April 2012.
10. C.M. Hill*, C.H. Albach*, S.G. Angel*, **M. Pop**. *K-mulus: Strategies for BLAST in the cloud*. 10th International Conference on Parallel Processing and Applied Mathematics (PPAM) Warsaw, Poland, September 2013.
11. C.M. Hill*, Irina Astrovskaya*, Howard Huang*, Sergey Koren, Todd Treangen, Atif Memon, and **Mihai Pop**. *De novo likelihood-based measures for comparing metagenomic assemblies*. IEEE International Conference on Bioinformatics and Biomedicine (BIBM) Shanghai, China, December 2013.
12. J. Ghurye*, **M. Pop**. *Better identification of repeats in metagenomic scaffolding*. Workshop on Algorithms in Bioinformatics (WABI). Aarhus, Denmark, August 2016.

Books

1. Pop, M., & Touzet, H. (Eds.). (2015). *Algorithms in Bioinformatics: 15th International Workshop, WABI 2015*: Springer.

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
7. M. Almeida#, **M. Pop***^ . *High-Throughput Sequencing as a Tool for Exploring the Human Microbiome*. in Metagenomics for Microbiology, Elsevier, J. Izard ed; 2014.
8. Simpson, J.T. and **Pop, M**. *The theory and practice of genome sequence assembly*. in Annual Review of Genomics and Human Genetics, vol. 16: 153-172. 2015 doi: 10.1146/annurev-genom-090314-050032

Contracts and Grants

Current

1. March 1, 2016 – Feb 28, 2020. (\$10,000,000, Sapkota PI, I am head of the data core with a budget of \$767,000) *CONSERVE: A Center of Excellence at the Nexus of Sustainable Water Reuse, Food, and Health.*
2. 2016 (\$9,600, PI). REU Supplement to NSF IIS-1513615 to support two undergraduate summer interns.
3. Sep 1, 2015 – Aug 31, 2019 (\$373,288, co-PI). NSF III:CIF:Medium: *Collaborative Research: Scalable and Highly Accurate Methods for Metagenomics*
4. Oct 23, 2015 – Oct 22, 2016 (\$210,792, PI). NRL. *High performance tools for metagenomic data assembly and analysis. (cooperative agreement: N00173162C001)*
5. Mar 21, 2013 – Feb 28, 2017. (\$1,779,715, PI). NIH R01-AI-100947 *Algorithms and Software for the Assembly of Metagenomic Data.*
6. Sep 1, 2012 – Jun, 30, 2016. (\$183,175, PI on subcontract to U. Wisc.) NIH R01-HG-000225. *New physical methodologies for genomic analysis.*

Completed

1. Sep 1, 2011 – Aug 31, 2015 (\$492,809, PI). National Science Foundation IIS-1117247 III: *Small: Genome Assembly Using Sparse Sequence Information.*
2. Sep 23, 2009 – Jul 31, 2015. (\$380,604, PI on subcontract to U. Pittsburgh). NIH U01-HL-098962. *Pathogenesis of obstruction/emphysema and the microbiome (POEM) in HIV.*
3. Jan 1, 2011 – Oct 31, 2014. (\$653,925, PI on subcontract to UM. School of Medicine). Bill and Melinda Gates Foundation. *Metagenomics-Based Discovery of New Viral Pathogens Causing Diarrheal Disease.*
4. Apr 1, 2009 – Mar 31, 2013 (\$380,000, PI). National Science Foundation. IIS-0844494 *Algorithms for the analysis of data from massively-parallel genome sequencing*
5. Sep 1, 2008 – Aug 31, 2013 (\$445,358, PI). National Science Foundation. IIS-0812111 III-CXT- *Small: Graphs to Diversity: extracting genomic variation from sequence graphs.*
6. May 1, 2009 – April 30, 2013. (\$183,175, PI on subcontract to U. Wisc.) NIH R01-HG-000225. *New physical methodologies for genomic analysis.*
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 24, 2008 - Jul 31, 2012 (\$780,000, PI). NIH. R01-HG004885: *Assembly and analysis software for exploring the human microbiome.*
9. Sep 16, 2011 – Nov 15, 2011. (\$75,000, PI). Lockheed Martin Corporation *Genomics collaboration*
10. 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.*
11. 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.*
12. 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.*

13. 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*
14. Jan 1, 2007- Sep 31, 2010 (\$980,123, PI). Henry Jackson Foundation. *Assembly and gene finding algorithms for genome sequences generated by pyrosequencing.*

Invited talks (last 3 years)

1. *Can we and should we assemble metagenomes?* International Human Microbiome Congress, Paris, France. March 2012.
2. *Genome Assembly in the 21st Century.* Purdue University, West Lafayette, IN. March 2012
3. *Understanding Microbial Communities: Antibiotic Resistance and Genome Assembly.* Food and Drug Administration, Laurel, MD. March 2012
4. *Genome Assembly in the 21st Century.* NIH, Bethesda, MD. April 2012.
5. *Genome Assembly in the 21st Century.* NBACC, Frederick, MD. May 2012
6. *Can we and should we assemble metagenomes?* International Human Microbiome Congress, Paris, France. March 2012.
7. *Genome Assembly in the 21st Century.* Purdue University, West Lafayette, IN. March 2012
8. *Understanding Microbial Communities: Antibiotic Resistance and Genome Assembly.* Food and Drug Administration, Laurel, MD. March 2012
9. *Genome Assembly in the 21st Century.* NIH, Bethesda, MD. April 2012.
10. *Genome Assembly in the 21st Century.* NBACC, Frederick, MD. May 2012
11. *Towards Holistic Analyses of Metagenomic Data,* INRA, Jouy-en-Josas, France. December 2012
12. *Towards Holistic Analyses of Metagenomic Data,* INRIA, Lille, France. December 2012. **in French.**
13. *Towards Holistic Analyses of Metagenomic Data,* INRIA, Rennes, France, January 2013. **in French.**
14. *Towards Holistic Analyses of Metagenomic Data,* University of Liverpool, UK, March 2013.
15. *Performing and evaluating genome and metagenome assemblies.* Génoscope, Évry, France. March 2013. **in French**
16. *Performing and evaluating genome and metagenome assemblies.* Laboratoire d'informatique fondamentale de Lille, Lille, France. May 2013. **in French**
17. *Metagenomics: beyond just scaling genomics.* TU Delft, Netherlands, December 2013.
18. *Genome Assembly Forensics.* Smithsonian Institute, Washington DC, March 2014
19. *Metagenomics: beyond just scaling genomics.* University of Missouri, Columbia, MO. February 2014
20. *Mission impossible: genome assembly.* Isaac Newton Institute, Cambridge, UK. March 2014
21. *Metagenomics: beyond just scaling genomics.* Michigan State University, East Lansing, MI. May 2014
22. *Mission impossible: genome assembly.* Joint meeting of Mid-Atlantic Directors and Staff of Scientific Cores. Baltimore, MD, June 2014
23. *Beyond single pathogens.* Bioscience Day. University of Maryland, College Park.

November 2014.

24. *Beyond single pathogens*. University of Delaware, Newark DE, March 2015
25. *Beyond single pathogens*. University of Maryland, Baltimore County, Baltimore, MD. April 2015
26. *Beyond single pathogens*. Indiana University, Bloomington, IN, April 2015.
27. *Testing Scientific Software in Bioinformatics*. Fraunhofer Institute, College Park, MD, June 2015
28. *Metagenomics Assembly: the devil is in the details*. MicroSeminar – <https://microseminar.wordpress.com/> (new online seminar series). August 2015
29. *Reconstructing genomes from metagenomic samples: promises and challenges*. J. Craig Venter Institute, La Jolla, CA. September 2015.
30. *Metagenomic assembly: the devil is in the details*. UCSD, La Jolla, CA. September 2015
31. *Reconstructing genomes from metagenomic samples: promises and challenges*. Institute Pasteur, Paris, France. October 2015

Software packages

Assembly

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>.

Metagenomics

5. metAMOS – assembly package for metagenomic data
<http://www.cbcb.umd.edu/software/metamos>
6. MetaStats – statistical software for comparing metagenomic libraries
<http://metastats.cbcb.umd.edu>
7. MetaPath – statistical software for comparing metagenomic data-sets at the pathway level.
<http://www.cbcb.umd.edu/software/metapath>
8. Metaphyler – software for estimating the taxonomic composition of a community from whole-metagenomic data.
<http://cbcb.umd.edu/software/metaphyler>
9. MetagenomeSeq – software for association studies in metagenomic data.
<http://cbcb.umd.edu/software/metagenomeSeq>

Alignment software

10. Bowtie – sequence aligner for short-read sequencing data
<http://bowtie-bio.sf.net>

11. Crossbow – SNP calling pipeline relying on cloud computing resources
<http://bowtie-bio.sf.net/crossbow>
12. DNAClust – software for rapid clustering of DNA sequences.
<http://dnacust.sf.net>

Databases

13. ARDB – antibiotic resistance genes database
<http://ardb.cbc.umd.edu>

Editorial/Review Duties

Editorial Boards

- BMC Bioinformatics – section editor (2010 -) manage editorial activities for ~40 academic editors.
- Microbiome – associate editor (2012 -)
- PeerJ Computer Science – associate editor (2015 -)
- IEEE Transactions on Computational Biology and Bioinformatics – associate editor (2015 -)
- Metagenomics – Mathematical, Statistical and Computational Methods – Editorial Advisory Board member (2015 -)
- 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.

Conferences Organized

RECOMB-Seq 2015 (co-chair)
WABI 2015 (program co-chair)

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, ICCABS 2012, WABI 2012, ACM BCB 2012, RECOMB SEQ 2014, RECOMB SEQ 2015, WABI 2015

Teaching

Courses taught in the last five years (chronological order)

- 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.
- July 2012. Metagenomics – part of ICGEB course in Santiago, Chile. ~50 students.
- March 2013. Metagenomics assembly – part of Journées des Assemblage, Institute Pasteur, Paris, France. ~40 students
- Fall 2013. CMSC701 – *Computational genomics*. 21 students

Advising

High school

Laura Tanase, summer intern, 2015

Undergraduate

Elaine Nsoesie. Summer intern, 2006

Christopher Hill. 2007 – Spring 2010 (currently graduate student in my lab)

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

Howard Huang, Summer 2013 (co-advised with Chris Hill)

Master's

Benjamin Langmead (CMSC) Spring 2008 – Summer 2009 (co-advised with Steven Salzberg)

Maya Zuhl (CMSC) Fall 2008 – Summer 2009

Doctoral

Jay Ghurye (CS), 2015 -

Victoria Cepeda Espinoza (CS), 2014 -

Senthil Kumar (BISI), Spring 2013 -

Chris Hill (CS) 2010 – 2015 (Chris is now a postdoctoral fellow at the University of Washington)

Joseph Paulson (AMSC) 2010 – 2015 (co-advised with Héctor Corrada Bravo, currently postdoctoral fellow at Dana Farber Cancer Institute)

Lee Mendelowitz (AMSC) Summer 2011 – 2015 (Lee will join the Washington Nationals baseball team as an analyst)

Brianna Lindsay (Epidemiology) 2010 – 2014 (co-advised with O. Colin Stine, Brianna has joined Merck)

Chengxi Ye (CS) 2012 – 2015 (switched advisors)

Ted Gibbons (BISI) 2008 – 2010 (switched advisors)

MohammadReza Ghodsi (CS) 2008 – 2012 (Mohammad has joined Google)

Bo Liu (CBMG/CS) 2007 – 2012 (Bo has joined Square Inc.)
Sergey Koren (CS) 2007 – 2012 (Sergey has joined NBACC)
James White (AMSC) 2007 – 2010 (James is now a freelance bioinformatician)
Mike Schatz (CS) 2009 – 2010 (co-advised with Steven Salzberg. Mike is now an assistant professor at Cold Spring Harbor Laboratories)
Yuan Lee (CBMG) Spring 2009. rotation student
Steve Smith (BISI) 2014 – Graduate Advisory Committee member
Carly Muletz (BISI) 2013 – Graduate Advisory Committee member
Albert Yu (BISI) 2009-2014 – Graduate Advisory Committee member
Apratim Mitra (ANSC) 2008 – Graduate Advisory Committee member

Post-doctoral

Mathieu Almeida (Ph.D. Université Paris-Sud Orsay) 2013 -
Irina Astrovskaya (Ph.D. Georgia State University) 2011-2014
Henry Lin (Ph.D. UC Berkeley) 2010 – 2012 (Henry has joined Columbia University)
Todd Treangen (Ph.D. Technical University of Catalonia) 2010-2011 (Todd is now a staff scientist at NBACC)
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

- 2015. NIH/NIAID Genomic Centers for Infectious Disease Steering Committee
- 2013. Newton Institute, Cambridge UK. Member of Scientific Advisory Committee for Metagenomics Programme
- 2013 – INRIA Team Evaluation Expert Panel (France)
- 2008 – 2013. 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.
- 2011 – 2012. Co-lead, Data Analysis Working Group, Human Microbiome Project
- 2011 – 2012. Lead, Assembly subgroup, Human Microbiome Project
- 2012. Morgan State University, Baltimore, MD. External reviewer of the Bioinformatics Program.

Grant review:

- National Institutes of Health (2009, 2010, 2012, 2013, 2014, 2015)
- National Science Foundation (2003, 2009, 2010, 2012)
- Austrian Science Fund (2015)
- Canada Foundation for Innovation (2015)
- BBSRC (UK) (2014)
- U.S. Army Research and Materiel Command (2006, 2012)
- Agence Nationale de Recherche (French Research Agency) (2011, 2013)

- North Carolina Biotech Center (2011)
- U.S. Department of Energy (2004, 2010)
- National Cancer Institute (2008, 2009)
- Defense Threat Reduction Agency Joint Science and Technology Office, Office for Chemical and Biological Defense. (2009)
- Wellcome Trust, UK. (2009)
- European Research Council (2009)
- National Institutes of Health (2005-2008 – *ad hoc* member on GGG-J panel, ~1-2 panels/year)
- Mathematics of Information Technology and Complex Systems, Canada (2008)
- Research Council of Norway (2007)
- U.S. Civilian Research and Development Foundation (2006)

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.
- 2012. *Program co-chair*. ICCABS 2012. Las Vegas, NV. February 23-25, 2012
- 2012. *Track co-chair*. ACM BCB 2012. Orlando, FL. October 7-10, 2012.
- 2013-2014. *Conference chair*. RECOMB Seq 2014. Pittsburgh, PA, April 2014.
- 2015. Program co-chair. WABI 2015. Atlanta, GA, September 2015.

Departmental committees

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

2006-7, 2007-8, 2008-9, 2009-10, 2014-2015 – 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, 2013-14, 2014-2015 – 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.

2013-2014, 2014-2015 – Member, Merit Review Committee

2014-2015 – Member, Strategic Planning committee (chaired subcommittee on diversity)
2014-2015 – Member, Recruiting for Diversity committee
2014-2015 – Member, Department Council
2014-2015 – Member, UMIACS steering committee
2014-2015 – Member, UMIACS external review planning committee

College/Campus 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
Spring 2012 – UMCP-UMB SEED grant review
Spring 2014 – Student Researcher of the Year review committee
Spring 2015 – UMCP-UMB SEED grant review

Candidacy and defense committees (last 3 years)

Spring 2012 – Thesis defense committee for Louis Licamele
Summer 2012 – Oral exam committee for Derrick Wood
Summer 2012 – Chair, Oral exam committee for Lee Mendelowitz
Summer 2012 – Thesis defense committee for Rob Patro
Summer 2012 – Chair, Thesis defense committee for Sergey Koren
Summer 2012 – Chair, Thesis defense committee for Bo Liu
Summer 2012 – Chair, Thesis defense committee for Mohammad Ghodsi
Fall 2013 – Oral exam committee for Wikum Dinalakara
Summer 2014 – Thesis defense committee for Hisham Talukder
Summer 2014 – Oral exam committee for Theodoros Rekatsinas
Summer 2014 – Thesis defense Committee for Albert Yu (BISI)
Fall 2014 – Oral exam committee for Florin Chelaru
Spring 2015 – Thesis defense committee for Florin Chelaru
Spring 2015 – Thesis defense committee for Theodoros Rekatsinas
Spring 2015 – Oral exam committee for Matt Conte (BISI)
Spring 2015 – Oral exam committee for Kun Wang (BISI)
Summer 2015 – Chair, Thesis defense committee for Christopher Hill
Summer 2015 – Chair, Thesis defense committee for Joseph Paulson

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)
May 2012 – Oral exam committee – Nam Nguyen (University of Texas, Austin)

June 2013 – Thesis reader (rapporteur de thèse) and defense committee member - Mathieu Almeida (Université Paris-Sud Orsay, France)

December 2013 – Thesis defense committee – Jurgen Nijkamp (TU Delft, Netherlands)

December 2013 – Thesis reader (rapporteur de thèse) and defense committee member – Nicolas Maillet (INRIA Rennes, France)

Spring 2014 – Thesis defense committee – Nam Nguyen (University of Texas, Austin)

Spring 2014 – Thesis defense committee – Brianna Lindsay (University of Maryland, Baltimore)