

# 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)  
Graduate Program in Biological Sciences (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**

1993-1994. Systems and Network Administrator. Politehnica University Bucharest, Romania  
1994-1995. Teaching Assistant. Johns Hopkins University  
1995-2000. Research Assistant. Johns Hopkins University  
2000-2005. Bioinformatics Scientist. The Institute for Genomic Research  
2004-2005. Consultant. Helicos Biosciences Corporation  
2005-2006. Assistant Research Scientist. University of Maryland, UMIACS  
2006-2011. Assistant Professor. University of Maryland, Department of Computer Science  
2011-2012, 2013-2014. Interim Director. Center for Bioinformatics and Computational Biology, University of Maryland  
2011-2016. Associate Professor. University of Maryland, Department of Computer Science and Center for Bioinformatics and Computational Biology  
October 2016-October 2017. Interim Director, University of Maryland Institute for Advanced Computer Studies  
2016-present. Professor. University of Maryland, Department of Computer Science and Center for Bioinformatics and Computational Biology  
October 2017 – March 2018. Associate Chair for Undergraduate Studies, Department of Computer Science  
August 2017- 2020. co-Director, Center for Health Related Informatics and Bioimaging  
March 2018 – October 2018. Interim Director, University of Maryland Institute for

Advanced Computer Studies.  
November 2018 – present. Director, University of Maryland Institute for Advanced  
Computer Studies

### **Awards/honors**

2014 – Thompson Reuters top 1% most cited researcher over past 10 years.  
2015 – University of Maryland Department of Computer Science Teaching Award  
2018 – Clarivate Analytics Highly Cited Researcher  
2019 – Fellow of the Association for Computing Machinery (ACM)  
2022 – Fellow of the International Society for Computational Biology and Bioinformatics  
(ISCB)

### **Professional society membership**

2006 – present. Association for Computing Machinery (ACM)  
2008 – present. International Society for Computational Biology and Bioinformatics  
(ISCB)  
2019 – present. American Society for Microbiology (ASM)  
2019 – present. Sigma Xi (invited)

### **Publications**

**Google Scholar:** <https://scholar.google.com/citations?user=4glkLD0AAAAJ>

**ORCID:** <https://orcid.org/0000-0001-9617-5304>

**MyNCBI:** <https://www.ncbi.nlm.nih.gov/myncbi/mihai.pop.1/bibliography/public/>

### **Papers in Refereed Journals**

The following marks apply:

\* - 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**. *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.
  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. Astrovskaia\*, 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. Astrovskaya\*, 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.
71. Morris, A., J.N. Paulson\*, H. Talukder, L. Tipton, H. Kling, L. Cui, A. Fitch, **M. Pop**, K.A. Norris, and E. Ghedin, *Longitudinal analysis of the lung microbiota of cynomolgous macaques during long-term SHIV infection*. Microbiome, 2016. 4(1): p. 38.PMC4939015

72. Ghurye, J.S.\*, V. Cepeda-Espinoza\*, and **M. Pop**, *Metagenomic Assembly: Overview, Challenges and Applications*. The Yale Journal of Biology and Medicine, 2016. 89(3): p. 353-362.
73. Davison, M., T.J. Treangen, S. Koren, **M. Pop**, and D. Bhaya, *Diversity in a Polymicrobial Community Revealed by Analysis of Viromes, Endolysins and CRISPR Spacers*. PLOS ONE, 2016. 11(9): p. e0160574.
74. Del Canto, F., M. O'Ryan, M. Pardo, A. Torres, D. Gutiérrez, L. Cádiz, R. Valdés, A. Mansilla, R. Martínez, D. Hernández, B. Caro, M.M. Levine, D.A. Rasko, C.M. Hill\*, **M. Pop**, O.C. Stine, and R. Vidal, *Chaperone-Usher Pili Loci of Colonization Factor-Negative Human Enterotoxigenic Escherichia coli*. Frontiers in Cellular and Infection Microbiology, 2017. 6(200).
75. Chopyk, J., S. Chattopadhyay, P. Kulkarni, E. Claye, K.R. Babik, M.C. Reid, E.M. Smyth, L.E. Hittle, J.N. Paulson, R. Cruz-Cano, **M. Pop**, S.S. Buehler, P.I. Clark, A.R. Sapkota, and E.F. Mongodin, *Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens*. Microbiome, 2017. 5(1): p. 22.
76. Chopyk, J., S. Chattopadhyay, P. Kulkarni, E.M. Smyth, L.E. Hittle, J.N. Paulson, **M. Pop**, S.S. Buehler, P.I. Clark, E.F. Mongodin, and A.R. Sapkota, *Temporal Variations in Cigarette Tobacco Bacterial Community Composition and Tobacco-Specific Nitrosamine Content Are Influenced by Brand and Storage Conditions*. Front Microbiol, 2017. 8: p. 358. PMC5339245
77. Ghurye, J.\*, **M. Pop**, S. Koren, D. Bickhart, and C.-S. Chin, *Scaffolding of long read assemblies using long range contact information*. BMC Genomics, 2017. 18(1): p. 527. PMC5508778
78. Nathan D. Olson, Todd J. Treangen\*, Christopher M. Hill\*, Victoria Cepeda-Espinoza\*, Jay Ghurye\*, Sergey Koren, **Mihai Pop**. *Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes*. Briefings in Bioinformatics. 2017.
79. Chung, M., J. Krueger, and **M. Pop**, *Identification of microbiota dynamics using robust parameter estimation methods*. Math Biosci, 2017. 294: p. 71-84.
80. Sczyrba, A., P. Hofmann, et al. (67 authors), *Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software*. Nat Methods, 2017.
81. Olson, N.D.^#, T.J. Treangen, C.M. Hill, V. Cepeda-Espinoza#, J. Ghurye#, S. Koren, and **M. Pop\***, *Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes*. Brief Bioinform, 2017.
82. Shah, N.^#, S.F. Altschul, and **M. Pop\***, *Outlier detection in BLAST hits*. Algorithms Mol Biol, 2018. 13: p. 7.
83. Kulkarni, P., N.D. Olson, J.N. Paulson, **M. Pop**, C. Maddox, E. Claye, R.E. Rosenberg Goldstein, M. Sharma, S.G. Gibbs, E.F. Mongodin, and A.R. Sapkota, *Conventional wastewater treatment and reuse site practices modify bacterial community structure but do not eliminate some opportunistic pathogens in reclaimed water*. Sci Total Environ, 2018. 639: p. 1126-1137.
84. Meisel, J.S., D.J. Nasko, et al., *Current progress and future opportunities in applications of bioinformatics for biodefense and pathogen detection: report from the Winter Mid-Atlantic Microbiome Meet-up, College Park, MD, January 10, 2018*. Microbiome, 2018. 6(1): p. 197. PMC6219074
85. Zhu, L., M. Torres, W.Q. Betancourt, M. Sharma, S.A. Micallef, C. Gerba, A.R. Sapkota, A.

- Sapkota, S. Parveen, F. Hashem, E. May, K. Kniel, **M. Pop**, and S. Ravishankar, *Incidence of fecal indicator and pathogenic bacteria in reclaimed and return flow waters in Arizona, USA*. *Environmental Research*, 2019. 170: p. 122-127.
86. Panthi, S., A.R. Sapkota, et al., *Pharmaceuticals, herbicides, and disinfectants in agricultural water sources*. *Environ Res*, 2019. 174: p. 1-8.
87. Shah, N.\*, J.S. Meisel\*, and **M. Pop**, *Embracing Ambiguity in the Taxonomic Classification of Microbiome Sequencing Data*. *Frontiers in Genetics*, 2019. 10(1022).
88. Sakowski, E., Uritskiy, G., et al., *Current State of and Future Opportunities for Prediction in Microbiome Research: Report from the Mid-Atlantic Microbiome Meet-up in Baltimore on 9 January 2019*. *mSystems*, 2019. 4(5): p. e00392-19.
89. Chopyk, J., D.J. Nasko, et al., *Metagenomic analysis of bacterial and viral assemblages from a freshwater creek and irrigated field reveals temporal and spatial dynamics*. *Science of The Total Environment*, 2019: p. 135395.
90. Bickhart, D.M., M. Watson, et al., *Assignment of virus and antimicrobial resistance genes to microbial hosts in a complex microbial community by combined long-read assembly and proximity ligation*. *Genome Biology*, 2019. 20(1): p. 153.
91. Ghurye, J.\*, T. Treangen, M. Fedarko\*, W.J. Hervey, and **M. Pop**, *MetaCarvel: linking assembly graph motifs to biological variants*. *Genome Biology*, 2019. 20(1): p. 174.
92. Chopyk, J., D.J. Nasko, S. Allard, A. Bui, T. Treangen, **M. Pop**, E.F. Mongodin, and A.R. Sapkota, *Comparative metagenomic analysis of microbial taxonomic and functional variations in untreated surface and reclaimed waters used in irrigation applications*. *Water Research*, 2020. 169: p. 115250.
93. Kulkarni, P., N.D. Olson, et al., *Zero-Valent Iron Sand Filtration Can Reduce Human and Plant Pathogenic Bacteria While Increasing Plant Growth Promoting Bacteria in Reclaimed Water*. *Frontiers in Environmental Science*, 2020. 8(203).
94. Mitchell, K., J.J. Brito, et al., *Benchmarking of computational error-correction methods for next-generation sequencing data*. *Genome Biology*, 2020. 21(1): p. 71.
95. Chopyk, J., D.J. Nasko, S. Allard, A. Bui, **M. Pop**, E.F. Mongodin, and A.R. Sapkota, *Seasonal dynamics in taxonomy and function within bacterial and viral metagenomic assemblages recovered from a freshwater agricultural pond*. *Environmental Microbiome*, 2020. 15(1): p. 18.
96. Worley, J.N., K. Javkar\*, et al., *Genomic Drivers of Multidrug-Resistant Shigella Affecting Vulnerable Patient Populations in the United States and Abroad*. *mBio*, 2021. 12(1).
97. Shah, N\*., E.K. Molloy, **M. Pop**, and T. Warnow, *TIPP2: metagenomic taxonomic profiling using phylogenetic markers*. *Bioinformatics*, 2021.
98. Muralidharan, H.S.\*, N. Shah\*, J.S. Meisel, and **M. Pop**, *Binnacle: Using Scaffolds to Improve the Contiguity and Quality of Metagenomic Bins*. *Front Microbiol*, 2021. 12: p. 638561.
99. Commichaux, S.\*, N. Shah\*, J. Ghurye\*, A. Stoppel, J.A. Goodheart, G.G. Luque, M.P. Cummings, and **M. Pop**, *A critical assessment of gene catalogs for metagenomic analysis*. *Bioinformatics*, 2021. 37(18): p. 2848-2857.
100. Medvedev, P. and **M. Pop**, *What do Eulerian and Hamiltonian cycles have to do with genome assembly?* *PLoS Comput Biol*, 2021. 17(5): p. e1008928.
101. Commichaux, S.\*, K. Javkar\*, et al., *Evaluating the accuracy of Listeria monocytogenes assemblies from quasimetagenomic samples using long and short reads*. *BMC Genomics*, 2021.



22(1): p. 389.

102. Javkar, K.\*, H. Rand, et al., *Whole-Genome Assessment of Clinical Acinetobacter baumannii Isolates Uncovers Potentially Novel Factors Influencing Carbapenem Resistance*. *Frontiers in Microbiology*, 2021. **12**: p. 2826.
103. Braccia, D.J.\*, X. Jiang, M. Pop, and A.B. Hall, *The Capacity to Produce Hydrogen Sulfide (H<sub>2</sub>S) via Cysteine Degradation Is Ubiquitous in the Human Gut Microbiome*. *Frontiers in Microbiology*, 2021. **12**(3193).
104. Balaji, A., Kille, B., Kappell, A.D. et al. *SeqScreen: accurate and sensitive functional screening of pathogenic sequences via ensemble learning*. *Genome Biol* 2022, **23**: p 133.
105. Malayil, L. et al. *Variations in Bacterial Communities and Antibiotic Resistance Genes Across Diverse Recycled and Surface Water Irrigation Sources in the Mid-Atlantic and Southwest United States: A CONSERVE Two-Year Field Study*. *Environ Sci Technol*, 2022, **56**, 15019–15033.
106. Braccia, D.J.\*, Minabou Ndjite, G., Weiss, A., Levy, S., Abeysinghe, S., Jiang, X., **Pop, M.**, and Hall, B. *Gut Microbiome-Wide Search for Bacterial Azoreductases Reveals Potentially Uncharacterized Azoreductases Encoded in the Human Gut Microbiome*. *Drug Metab Dispos*, 2023, **51**, 142–153.
107. Javkar, K.\*, Rand, H., Strain, E., and **Pop, M.** *PRAWNS: compact pan-genomic features for whole-genome population genomics*. *Bioinformatics*, 2023, **39**.
108. Luan, T.\*, Muralidharan, H.S.\*, Alshehri, M.\*, Mittra, I.\*, and **Pop, M.** *SCRAPT: an iterative algorithm for clustering large 16S rRNA gene data sets*. *Nucleic Acids Res*, 2023, **51**, e46.
109. Commichaux, S. et al. *Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation*. *BMC Genomics*, 2023, **24**, 165.
110. Muralidharan, H.S.\*, Fox, N.Y.\*, and **Pop, M.** *The impact of transitive annotation on the training of taxonomic classifiers*. *Front. Microbiol.*, 2024, **14**, 1240957.

### 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. Ghurye, J\* and **M. Pop**, *Better Identification of Repeats in Metagenomic Scaffolding*, in Algorithms in Bioinformatics: 16th International Workshop, WABI 2016, Aarhus, Denmark, August 22-24, 2016. Proceedings, M. Frith and N.C. Storm Pedersen, Editors. 2016, Springer International Publishing: Cham. p. 174-184.
  13. Brian Brubach\*, Jay Ghurye\*, Aravind Srinivasan and **Mihai Pop**. *Better Greedy Sequence Clustering with Fast Banded Alignment*. in Algorithms in Bioinformatics: 17th International Workshop, WABI 2017, Boston, MA, August 21-23, 2017.
  14. Nidhi Shah\*, Stephen Altschul and **Mihai Pop**. *Outlier detection in BLAST hits*. in Algorithms in Bioinformatics: 17th International Workshop, WABI 2017, Boston, MA, August 21-23, 2017.
  15. Albin, D., D. Nasko, et al. *SeqScreen: a biocuration platform for robust taxonomic and biological process characterization of nucleic acid sequences of interest*. in 2019 IEEE International Conference on Bioinformatics and Biomedicine (BIBM). 2019.
  16. B. Stacy, J. Hauzel, M. Lindvall, A. Porter and **M. Pop**, *Metamorphic Testing in Bioinformatics Software: A Case Study on Metagenomic Assembly*, in 2022 IEEE/ACM 7th International Workshop on Metamorphic Testing (MET), 2022, pp. 31-33.

## 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
9. Gene Myers, **Mihai Pop**, Knut Reinert, Tandy Warnow. *Next generation sequencing (Dagstuhl seminar 16351)*. *Dagstuhl Reports* 6(8). 2017.
10. Altschul, S.F. and **M. Pop**, *Sequence Alignment*, in *Handbook of Discrete and Combinatorial Mathematics*, K.H. Rosen, Editor. 2017, CRC Press: Boca Raton, FL.

### Other publications

1. **M. Pop**. *We are what we eat: how the diet of infants affects their gut microbiome*. *Genome Biology* 13, 152. 2012. **Research highlight**
2. **M. Pop** and S. L. Salzberg. *Use and mis-use of supplemental material in science publications*. *BMC Bioinformatics*., 16:237. 2015. **Editorial**
3. Shah, N., M.G. Nute, T. Warnow, and **M. Pop**, *Misunderstood parameter of NCBI BLAST impacts the correctness of bioinformatics workflows*. *Bioinformatics*, 2018. **Letter to the editor**
4. Cagle, R., P. Ramachandran, E. Reed, S. Commichaux, M.K. Mammel, D.W. Lacher, D. Miller, S. Lindley, **M. Pop**, M.C. Bazaco, B. Wolpert, E.A. Strain, S. Aker, J. Feely, and A. Ottesen, *Microbiota of the Hickey Run Tributary of the Anacostia River*. *Microbiol Resour Announc*, 2019. 8(12).PMC6430318. **Data set announcement**
5. Treangen, T.J. and **M. Pop**, *You can't always sequence your way out of a tight spot: Next-generation sequencing holds great promise for pathogen detection, but the devil is in the details*. *EMBO Rep*, 2018. 19(12).PMC6280640. **Invited perspective**
6. **M. Pop**. *Introducing genome assembly to the general public through interactive word games*. **Short presentation at ISMB 2020**.

### Contracts and Grants

#### Current

1. December 1, 2019 – June 30, 2024 (\$2,644,000, Pop PI). NIH R01-AI-100947. *Algorithms and software for the assembly of metagenomic data*.
2. February 1, 2023 – January 31, 2025 (\$500,000, Pop PI). University of Maryland. *Grand*

*challenges: A center of excellence in microbiome sciences*

3. June 1, 2022 – May 31, 2025 (\$439,615). NSF CNS2149868. REU Site: *Undergraduate Bioinformatics Research in Data Science for Genomics*

### **Completed**

4. Jan 1, 2007- Sep 31, 2010 (\$980,123, PI). Henry Jackson Foundation. *Assembly and gene finding algorithms for genome sequences generated by pyrosequencing.*
5. 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.*
6. 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.*
7. Sep 24, 2008 – Jul 31, 2012 (\$780,000, PI). NIH. R01-HG004885: *Assembly and analysis software for exploring the human microbiome.*
8. 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*
9. May 1, 2009 – April 30, 2013. (\$183,175, PI on subcontract to U. Wisc.) NIH R01-HG-000225. *New physical methodologies for genomic analysis.*
10. 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.*
11. 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*
12. 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.*
13. 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.*
14. 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.*
15. 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).*
16. Sep 1, 2011 – Aug 31, 2015 (\$492,809, PI). National Science Foundation IIS-1117247 *III: Small: Genome Assembly Using Sparse Sequence Information.*
17. Sep 16, 2011 – Nov 15, 2011. (\$75,000, PI). Lockheed Martin Corporation *Genomics collaboration*
18. Sep 1, 2012 – Jun, 30, 2016. (\$183,175, PI on subcontract to U. Wisc.) NIH R01-HG-000225. *New physical methodologies for genomic analysis.*
19. Mar 21, 2013 – Feb 28, 2017. (\$1,779,715, PI). NIH R01-AI-100947 *Algorithms and Software for the Assembly of Metagenomic Data.*
20. Sept 1, 2013 – Aug 31, 2018 (\$18,700,000, Key personnel). NIH P50-CA-180523 *Rapid Response Characterization of New and Manipulated Tobacco Products*
21. Oct 23, 2015 – Aug 25, 2018 (\$210,792, PI). NRL. *High performance tools for metagenomic data*

*assembly and analysis. (cooperative agreement: N00173162C001)*

22. 2016 (\$9,600, PI). REU Supplement to NSF IIS-1513615 to support two undergraduate summer interns.
23. Sep 1, 2015 – Aug 31, 2019 (\$373,288, co-PI). NSF III:CIF:Medium: Collaborative Research: Scalable and Highly Accurate Methods for Metagenomics
24. March 1, 2016 – Feb 28, 2020. (\$10,000,000, Sapkota PI, I was 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.

### **Invited talks (last 3 years)**

1. *Embracing ambiguity when characterizing microbes*. Bringing Artificial Intelligence to the Bedside workshop, Purdue, IN, April 2021.
2. *Embracing ambiguity when characterizing microbes*. ISMB 2021, July 2021.
3. *Using computers to understand microbial communities*. Department of Veterinary Medicine, Virginia-Maryland College of Veterinary Medicine, College Park, MD, September 2021.
4. *Making uncertainty explicit when analyzing microbiomes*. Institute for Bioinformatics and Medical Informatics, University of Tübingen, Germany, February 2022.
5. *Making uncertainty explicit when analyzing microbiomes*. Institute for Mathematical and Statistical Innovation, University of Chicago, February 2022.
6. *Handling analytic challenges in microbiome science*. Rutgers University, Camden, NJ. October 2023
7. *Overcoming analytic challenges in microbiome science*. US FDA. Microbiome Working Group webinar. October 2023.
8. *Overcoming analytic challenges in microbiome science*. Johns Hopkins University, Baltimore, MD. April 2024.

### **Outreach (last 3 years)**

2021, 2022, 2023, 2024 – Organized booth on computational microbiome analysis at Maryland Day – annual open house that brings > 80K visitors to campus each year

2021, 2022, 2023 – Judged posters and presentations at the Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS)

March 2023 – *Getting down and dirty with Bacteria*. Science on Tap, College Park, MD – part of monthly lecture series for popularizing science

March 2023 – Deschis la cercetare (Open for research) – Romanian videocast for popularizing science. <https://www.youtube.com/watch?v=8-0iFoAJBy0>

### **Software packages**

\* - software primarily developed in my lab.

#### **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>
10. \*MetaCompass – reference guided assembly for metagenomics  
<https://github.com/marbl/MetaCompass>
11. \*MetaCarvel – scaffolding and structural variant discovery for metagenomics  
<https://github.com/marbl/MetaCarvel>
12. \*MetagenomeScope – visualization of metagenomic assembly graphs  
<http://mgsc.umiacs.io>
13. SeqScreen – software for assessing the biological threat potential of short DNA sequences.  
<https://gitlab.com/treangenlab/seqscreen>
14. TIPP2 – taxonomic classification and profiling tool based on phylogenetic principles.  
(collaboration with Warnow lab at UIUC). <https://github.com/smirarab/sepp/blob/tipp2>
15. \*Binnacle – scaffold-based binning for metagenomic assemblies.  
<https://github.com/marbl/binnacle>
16. \*Atlas – taxonomic classification tool that enables the exploration of the ambiguity in classification. <https://github.com/marbl/ATLAS>

### **Alignment software**

17. Bowtie – sequence aligner for short-read sequencing data  
<http://bowtie-bio.sf.net>
18. Crossbow – SNP calling pipeline relying on cloud computing resources  
<http://bowtie-bio.sf.net/crossbow>
19. \*DNAClust – software for rapid clustering of DNA sequences.  
<http://dnacust.sf.net>
20. \*PRAWNS – software for multiple alignment of bacterial genomes with the goal of discovering biomarkers associated with phenotype.  
<https://github.com/KiranJavkar/PRAWNS>

21. \*SCRAPT – software for iterative clustering of large volumes of DNA sequences.  
<https://github.com/hsmurali/SCRAPT>.

### **Databases**

22. \*ARDB – antibiotic resistance genes database  
<http://arbd.cbc.umd.edu>

### **Editorial/Review Duties**

#### **Editorial Boards**

- Metagenomics – Mathematical, Statistical and Computational Methods – Editorial Advisory Board member (2015 -)
- Microbiome – associate editor (2012 – 2018, 2020 - 2023)
- Microbiome – section editor (2018 – 2020)
- PeerJ Computer Science – associate editor (2015 – 2018)
- IEEE Transactions on Computational Biology and Bioinformatics – associate editor (2015 – 2017)
- BMC Bioinformatics – section editor (2010 – 2016) managed 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**

I regularly serve on program committees for the ISMB, RECOMB, ACM-BCB, and WABI conferences as well as other conference in the field.

#### **Conferences Organized**

2014 – RECOMB-Seq 2014 (co-chair)

2015 – WABI 2015 (program co-chair)

2016 – co-organizer of Dagstuhl seminar on Next Generation Sequencing – Algorithms, and Software For Biomedical Applications: Myers, G., **M. Pop**, K. Reinert, and T. Warnow, *Next Generation Sequencing (Dagstuhl Seminar 16351)*. Dagstuhl Reports, 2017. 6(8): p. 91-130.

2018. Co-organized – *M3 meeting on Biodefense and Pathogen detection* – College Park, MD, January 2018.

2018. Area chair – Metagenomics and Microbial Genomics – ISMB 2018. Chicago, IL, July 2018.

2018. Program co-chair – ACM-BCB 2018. Washington, DC, August 2018.

2024. Area co-chair - Metagenomics and Microbial Genomics – ISMB 2024. Montreal, QC, Canada, July 2024

## **Teaching**

### **Full-semester courses (last five years)**

- Spring 2019. CMSC701 – *Computational genomics*. 29 students
- Fall 2019. CMSC423 - *Bioinformatics*, 95 students
- Fall 2020. CMSC423 – *Bioinformatics*, 82 students
- Spring 2022. CMSC423 – *Bioinformatics*, 86 students
- Spring 2023. CMSC423 – *Bioinformatics*, 95 students
- Spring 2024. CMSC423 – *Bioinformatics*, 88 students

### **Seminars/Short courses**

Summer 2012. Metagenomics course at the University of Chile, Santiago, Chile.

Spring 2013. Assembly course at Institut Pasteur, Paris, France

2014-2017. Metagenomic assembly as part of *Strategies and Techniques for Analyzing Microbial Population Structures* course at the Marine Biological Laboratory in Woods Hole, MA.

2018. *Bow to the microbial overlords*. Session organized at the Annual Biomedical Research Conference for Minority Students (ABRCMS) introducing the field of metagenomics.

Indianapolis, IN, October 2018.

2017 – 2022, co-Director, *Strategies and Techniques for Analyzing Microbial Population Structures* course at the Marine Biological Laboratory in Woods Hole, MA. This is an intensive, hands-on, ~10 day course focusing on the analytical tools used to understand microbial community structures.

Summer 2023 – Mentoring workshop based on Entering Mentoring curriculum. University of Maryland, College Park, MD.

Fall 2023 – Mentoring workshop based on Entering Mentoring curriculum. University of Maryland, College Park, MD.

## **Advising**

### **High school**

Laura Tanase, summer intern, 2015

Shilpa Roy, intern, 2016-2017

Abbe Miller, intern, 2017-2018

Kassie Wang, summer intern, 2018, 2019

Tracy Nguyen, intern, 2018-2019

Wendy Wu, intern, 2019-2020

Chinaza Ezinne, intern, 2020-2021

Corey Wang, summer intern, 2021

Justin Tubilla, intern, 2021-2022

Nishat Olayiwola, intern, 2022-2023

### **Undergraduate**



Elaine Nsoesie. Summer intern, 2006  
Christopher Hill. 2007 – Spring 2010 (currently engineer at Google)  
Dan Sugarman. Fall 2008 – Fall 2009  
Matt Thomas, Spring 2009  
Carl Albach, Spring 2009 – Spring 2011  
Sebastian Angel, Spring 2009 – Summer 2011 (currently faculty at U. Penn)  
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)  
Andrew Consroe, Fall 2014 – Spring 2016  
Amelia Bateman, Fall 2016  
Matthew Myers, Spring 2015 – 2017  
Samina Hussain, Spring 2017  
Marcus Fedarko, Fall 2016 – 2018  
Larry Feldman, Summer 2018  
Hope Winovitch, Fall 2018  
Amnah Mahmood, Fall 2018  
Dylan Taylor, 2018 -2019  
Dmitry Leontyev, Spring 2019  
Marie Crane, Summer 2019  
Marwan Alshehri, Spring, Summer, Fall 2021  
Sho Takeshita, Summer 2021  
Alex Lee, Summer 2021  
Alyssa Pratt, Summer 2021  
Cece Zhao, Summer 2021  
Lucy Mettee, Summer 2022  
Adam Levav, Summer 2022  
Sarah Blankespoor, Summer, Fall 2023  
Raunak Vijay, Summer, Fall, 2023  
Noam Fox, Fall 2023, Spring 2024  
Vivek Agarwal, 2023-2024  
Ipsa Mitra, 2023-2024  
Anning Cui, Spring 2024  
Althea Gonzales, Spring 2024  
Aditri Gagi, Spring 2024

### **Master's**

Benjamin Langmead (CMSC) Spring 2008 – Summer 2009 (co-advised with Steven Salzberg.  
Ben is currently an assistant professor of Computer Science at Johns Hopkins  
University)  
Maya Zuhl (CMSC) Fall 2008 – Summer 2009  
Aiswarya Suriaprakash – 2024-

## **Doctoral**

### Current

Harihara Muralidharan (CS), 2019 -  
Tu Luan (CS), 2019 -  
Shiva Mehravaran (BISI), 2021 -  
Yuelin Liu (CS), 2021 – (co-advised with S. Cenk Sahinalp, NCI)  
Nakyung Lee (CS), 2022 -  
Rain Haworth (CS), 2022 -  
Nathalie Bonin (CS), 2023 -

### Alumni

James White (AMSC) 2007 – 2010 (James is now a freelance bioinformatician)  
Bo Liu (CBMG/CS) 2007 – 2012 (Bo has joined Square Inc.)  
Sergey Koren (CS) 2007 – 2012 (after graduation Sergey joined NBACC and is currently a  
scientists at NIH/NHGRI)  
MohammadReza Ghodsi (CS) 2008 – 2012 (Mohammad has joined Google)  
Mike Schatz (CS) 2009 – 2010 (co-advised with Steven Salzberg. Mike joined Cold Spring Harbor  
Laboratories as an assistant professor and then joined Johns Hopkins University as  
an associate professor in Computer Science)  
Brianna Lindsay (Epidemiology) 2010 – 2014 (co-advised with O. Colin Stine, after graduation  
Brianna was a scientist at Merck and then joined the University of Pennsylvania as a  
senior project coordinator)  
Joseph Paulson (AMSC) 2010 – 2015 (co-advised with Héctor Corrada Bravo, was postdoctoral  
fellow at Dana Farber Cancer Institute then joined Genentech)  
Chris Hill (CS) 2010 – 2015 (was postdoctoral fellow at U. of Washington and has then joined  
Google)  
Lee Mendelowitz (AMSC) Summer 2011 – 2015 (Lee has joined the Washington Nationals  
baseball team as an analyst)  
Jay Ghurye (CS), 2015 – 2018 (Jay has joined Dovetail Genomics)  
Victoria Cepeda Espinoza (CS), 2014 – 2020 (postdoctoral fellow at Stanford)  
Brian Brubach (CS), 2016 – 2020 (co-advised with Aravind Srinivasan) (now assistant professor  
at Swarthmore College)  
Nidhi Shah (CS), 2016 – 2021 (now at Amazon Web Services)  
Seth Commichaux (BISI), 2017 – 2022 (now at the FDA)  
Domenick Braccia (BISI), 2020 – 2022 (co-advised with Brantley Hall)  
Kiran Javkar (CS), 2017 – 2022 (now at Illumina)

### **Graduate rotation/advisory committees**

Apratim Mitra (ANSC) 2008 – Graduate Advisory Committee member  
Yuan Lee (CBMG) Spring 2009. rotation student  
Albert Yu (BISI) 2009-2014 – Graduate Advisory Committee member

Carly Muletz (BISI) 2013 – Graduate Advisory Committee member  
Steve Smith (BISI) 2014 – Graduate Advisory Committee member  
Reynold Yu (BISI) 2019-2023 – Graduate Advisory Committee member  
Dietrich Epp Schmidt (ENST) 2019-2023 – Graduate Advisory Committee member  
Dongze He (BISI) 2021-2024 – Graduate Advisory Committee member

## **Post-doctoral**

### Current

none

### Alumni

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)

Todd Treangen (Ph.D. Technical University of Catalonia) 2010-2011 (Todd is an assistant professor at Rice University)

Henry Lin (Ph.D. UC Berkeley) 2010 – 2012 (Henry is currently a senior data scientist at Ancestry)

Irina Astrovskaya (Ph.D. Georgia State University) 2011-2014 (currently a Bioinformatics Engineer at the Flatiron Institute in New York)

Mathieu Almeida (Ph.D. Université Paris-Sud Orsay) 2013 – 2017 (currently a researcher at INRA, Jouy-en-Josas, France)

Jackie Meisel (Ph.D. U. Penn) 2017 – 2020 (currently a researcher at the US FDA)

## **Service**

### **Professional**

- 2008-2013. Chair, Maize Genome Database Working Group
- 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
- 2013 – INRIA Team Evaluation Expert Panel (France)
- 2013. Newton Institute, Cambridge UK. Member of Scientific Advisory Committee for Metagenomics Programme
- 2015-2018. NIH/NIAID Genomic Centers for Infectious Disease Steering Committee
- 2016-2018. Scientific Advisory Board. Metacardis Project. European Union project studying the underlying causes of metabolic disease, obesity, and heart disease.
- 2015-2018. Scientific Advisory Board. Resist'Eaume Project. Suez, France.
- 2020. Scientific Advisory Board. National Center for Genome Analysis Support. University of Indiana, Bloomington, IN, USA
- 2021. Poster judge. Tapia celebration of diversity in computing (Tapia)

- 2021. Poster judge. Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS)
- 2022. Poster judge. Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS)
- 2023. Poster judge. Annual Biomedical Research Conference for Minoritized Scientists (ABRCMS)
- 2022-2024. Member of Fellows selection committee, International Society for Computational Biology (ISCB).
- 2020 - . Scientific Advisory Board. Takeda USA
- 2020 - . Scientific Advisory Board. Integrative Phenomics, Paris, France
- 2021 - . Scientific Advisory Board. DYNAMITE Project, Rice University, Houston, TX, USA
- 2023 - . External Advisory Board. Codes for Life NRT, Rutgers University, Camden, NJ, USA

### **Grant review (past 5 years)**

- Standing member on BDMA study section for the National Institutes of Health (2017-2021)
- NIH NIAID study section for the HIPC network (2021)
- US Department of Energy (2021)
- NIH New Innovator Award Program study section (2022)
- NIH K99/R00 study section (2023)

### **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.
- 2016. *Co-organizer*. Mid-Atlantic Microbiome Meet-up. College Park, MD< November 2016
- 2016. *Co-organizer*. Dagstuhl seminar on next generation sequencing - Algorithms and Software for Biomedical Applications. Dagstuhl, Germany, September 2016.
- 2017. *Co-organizer*. Mid-Atlantic Microbiome Meet-up/CAMI joint meeting. College Park, MD, May 2017.
- 2018. *Co-organizer*. Mid-Atlantic Microbiome Meet-up on Biodefense and Pathogen detection, College Park, MD, January 2018.
- 2018. *Program co-chair*. ACM BCB 2018. Washington, DC, August 2018
- 2022. *Co-organizer*. Mid-Atlantic Microbiome Meet-up on the Interaction between Academia, Industry, and Government, College Park, MD, April 2022
- 2024. *Organizer*. Symposium on Microbiome Research at the Interface of Environment,

Health, and Agriculture. College Park, MD, January 2024

- 2024. *Area co-chair*. ISMB 2024. Montreal, QC, Canada, July 2024

### **Departmental committees (past 5 years)**

2018 – present – Member, Diversity and Inclusion Committee

2021-2022 – Chair, sub-committee on Research and Scholarship for CS department unit review

### **College/Campus Committees (past 5 years)**

2020 – member, Future of Research at the University of Maryland in the post-COVID 19

2021 – member, University of Maryland strategic planning committee (subcommittee on strategic partnerships)

2022-2023 – chair, Search committee for Assistant Dean for Diversity and Strategic Initiatives

2020-present – member, College of Computer, Mathematical, and Natural Sciences Council on Diversity and Inclusion

### **Candidacy and defense committees (last 3 years)**

#### **(in Computer Science unless otherwise marked)**

Spring 2021 – Chair, Preliminary Oral Exam Committee for Kiran Javkar

Spring 2021 – Chair, PhD Defense Committee for Nidhi Shah

Fall 2021 – MS Defense Committee for Leandro Hermida (BISI)

Fall 2021 – PhD Defense Committee for Mohsen Zakeri

Spring 2022 – Chair, PhD Defense Committee for Seth Commichaux (BISI)

Summer 2022 – Chair, PhD Defense Committee for Kiran Javkar

Summer 2022 – PhD Defense Committee for Domenick Braccia (BISI)

Winter 2023 – PhD Defense Committee for Caroline Castleton (Music)

Winter 2023 – PhD Defense Committee for Dietrich Epp Schmidt (ENST)

Summer 2023 – PhD Defense Committee for Reynold Yu (BISI)

Spring 2023 – PhD Defense Committee for Dongze He (BISI)

Spring 2023 – Preliminary exam committee for Yuzhu Mao (Civil & Environmental Engineering)

### **External candidacy and defense committees**

Summer 2021 – PhD thesis defense committee – Vladimir Smirnov (University of Illinois, Urbana Champaign)