

# 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

October 2017 – March 2018. Associate Chair for Undergraduate Studies, Department of Computer Science

2016-present. Professor. University of Maryland, Department of Computer Science and Center for Bioinformatics and Computational Biology

August 2017- present. co-Director, Center for Health Related Informatics and Bioimaging

March 2018 – present. Interim 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

### Professional society membership

2006 – present. Association for Computing Machinery (ACM)

2008 – present. International Society for Computational Biology and Bioinformatics (ISCB)

### Publications

**Publication impact H-index: 48 (Google Scholar); 39 (Web of Knowledge)**

### **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. Pyrpassopoulos, 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. 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. Astrovszkaya\*, 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. Astrovszkaya\*, 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.

### **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.

## 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.

### 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**

### Contracts and Grants

#### Current

1. Aug 1, 2015 – Aug 31, 2017 (\$916,391, Corrada Bravo PI). NIH R01-GM-114267. *Integrative Visual and Computational Exploratory Analysis of Genomics Data*.
2. Mar 21, 2013 – Feb 28, 2017. (\$1,779,715, PI). NIH R01-AI-100947 *Algorithms and Software for the Assembly of Metagenomic Data*.
3. Sept 1, 2013 – Aug 31, 2018 (\$18,700,000, Key personnel). NIH P50-CA-180523 *Rapid Response Characterization of New and Manipulated Tobacco Products*
4. Oct 23, 2015 – Aug 25, 2018 (\$210,792, PI). NRL. *High performance tools for metagenomic data assembly and analysis*. (cooperative agreement: N00173162C001)
5. Sep 1, 2015 – Aug 31, 2019 (\$373,288, co-PI). NSF III:CIF:Medium: *Collaborative Research: Scalable and Highly Accurate Methods for Metagenomics*
6. 2016 (\$9,600, PI). REU Supplement to NSF IIS-1513615 to support two undergraduate summer interns.
7. 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*.

#### Completed

8. Jan 1, 2007- Sep 31, 2010 (\$980,123, PI). Henry Jackson Foundation. *Assembly and gene finding algorithms for genome sequences generated by pyrosequencing*.
9. 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*.
10. 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*.
11. Sep 24, 2008 – Jul 31, 2012 (\$780,000, PI). NIH. R01-HG004885: *Assembly and analysis software for exploring the human microbiome*.

12. 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*
13. May 1, 2009 – April 30, 2013. (\$183,175, PI on subcontract to U. Wisc.) NIH R01-HG-000225.  
*New physical methodologies for genomic analysis.*
14. 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.*
15. 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*
16. 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.*
17. 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.*
18. 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.*
19. 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).*
20. Sep 1, 2011 – Aug 31, 2015 (\$492,809, PI). National Science Foundation IIS-1117247  
*III: Small: Genome Assembly Using Sparse Sequence Information.*
21. Sep 16, 2011 – Nov 15, 2011. (\$75,000, PI). Lockheed Martin Corporation  
*Genomics collaboration*
22. Sep 1, 2012 – Jun, 30, 2016. (\$183,175, PI on subcontract to U. Wisc.) NIH R01-HG-000225.  
*New physical methodologies for genomic analysis.*

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

1. *Genome Assembly Forensics.* Smithsonian Institute, Washington DC, March 2014
2. *Metagenomics: beyond just scaling genomics.* University of Missouri, Columbia, MO. February 2014
3. *Mission impossible: genome assembly.* Isaac Newton Institute, Cambridge, UK. March 2014
4. *Metagenomics: beyond just scaling genomics.* Michigan State University, East Lansing, MI. May 2014
5. *Mission impossible: genome assembly.* Joint meeting of Mid-Atlantic Directors and Staff of Scientific Cores. Baltimore, MD, June 2014
6. *Beyond single pathogens.* Bioscience Day. University of Maryland, College Park. November 2014.
7. *Beyond single pathogens.* University of Delaware, Newark DE, March 2015
8. *Beyond single pathogens.* University of Maryland, Baltimore County, Baltimore, MD. April 2015
9. *Beyond single pathogens.* Indiana University, Bloomington, IN, April 2015.
10. *Testing Scientific Software in Bioinformatics.* Fraunhofer Institute, College Park, MD, June 2015

11. *Metagenomics Assembly: the devil is in the details*. MicroSeminar – <https://microseminar.wordpress.com/> (new online seminar series). August 2015
12. *Reconstructing genomes from metagenomic samples: promises and challenges*. J. Craig Venter Institute, La Jolla, CA. September 2015.
13. *Metagenomic assembly: the devil is in the details*. UCSD, La Jolla, CA. September 2015
14. *Reconstructing genomes from metagenomic samples: promises and challenges*. Institute Pasteur, Paris, France. October 2015
15. *Computational Challenges in Microbiome Research* – IEEE International Conference on Bioinformatics and Biomedicine, Washington DC, November 2015. **Keynote presentation**
16. *Reconstructing genomes from metagenomic samples*. US-UK Microbiome Workshop, UCSD, La Jolla, CA, March 2016.
17. *Unravelling how the microbiome impacts health and disease*. Department of Computer Science, University of Illinois, Urbana Champaign, October 2016.
18. *Computational Challenges in Microbiome Research* – Symposium on Frontiers in Big Data, University of Illinois, Urbana Champaign, September 2016. **Keynote presentation**
19. *Unravelling how the microbiome impacts health and disease*. University of William and Mary, Williamsburg, VA, October 2016.
20. *Computational challenges in microbiome research*. NCBI, NIH, Bethesda, MD, December 2016.
21. *Metagenomics analysis at the strain level resolution*. Radcliffe Institute, Harvard, Cambridge, MA, June 2017.
22. *Challenges and opportunities in computational microbiome-ology*. German Conference on Bioinformatics. Tübingen, Germany, September 2017. **Keynote presentation**
23. *Characterizing and quantifying the world's microbiota*. US NIST, Gaithersburg, MD, September 2017
24. *Computational challenges in quantifying the microbiome and its impact on human health*. Johns Hopkins University, Baltimore, MD, November 2017.

## **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://dnaclust.sf.net>

### **Databases**

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

### **Editorial/Review Duties**

#### **Editorial Boards**

- Microbiome – associate editor (2012 - )
- PeerJ Computer Science – associate editor (2015 - )
- Metagenomics – Mathematical, Statistical and Computational Methods – Editorial Advisory Board member (2015 - )
- IEEE Transactions on Computational Biology and Bioinformatics – associate editor (2015 – 2017)
- BMC Bioinformatics – section editor (2010 – 2016) manage editorial activities for ~40 academic editors.
- Biological Procedures Online – editorial board member (2007 - 2008)

#### **Reviewer for journals**

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

### **Conference Program Committees**

CBGI 2003, ISMB 2004, ECCB 2005, ISMB 2005, CSB 2006, ISBRA 2007, ISMB/ECCB 2007, ISBRA 2008, ISMB 2008, BIBM 2008, BICoB 2009, ISBRA 2009, ISMB/ECCB 2009, BIBM 2009, ISBRA 2010, WABI 2010, ECCB 2010, ICCAB 2011, ACM BCB 2011, PSB 2012, ICCABS 2012, WABI 2012, ACM BCB 2012, RECOMB SEQ 2014, RECOMB SEQ 2015, WABI 2015, ACM BCB 2016, ACM BCB 2017, WABI 2017, ISMB/ECCB 2017

### **Conferences Organized**

RECOMB-Seq 2014 (co-chair)

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.

### **Teaching**

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

- Fall 2013. CMSC701 – *Computational genomics*. 21 students
- Spring 2014. CMSC424 – *Database Design*. 50 students.
- Fall 2014. CMSC 701 – *Computational Genomics*. 30 students
- Fall 2014. CMSC 828Q – *Lectures in bioinformatics*. 3 students
- Spring 2015. CMSC 423 – *Bioinformatic algorithms, databases, and tools*. 51 students
- Fall 2015. CMSC701 – *Computational Genomics*. 37 students
- Spring 2016. CMSC131 – *Object oriented programming I*. 152 students
- Fall 2016. CMSC701 – *Computational genomics*. 37 students.
- Fall 2016. CMSC423 – *Bioinformatics*. 52 students.
- Fall 2017. CMSC423 – *Bioinformatics*. 78 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.

2017 – present, 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.

### **Advising**

#### **High school**

Laura Tanase, summer intern, 2015

Shilpa Roy, intern, 2016-2017

Abbe Miller, intern, 2017-2018

#### **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)  
Andrew Consroe, Fall 2014 – Spring 2016  
Matthew Myers, Spring 2015 – 2017  
Samina Hussain, Spring 2017  
Marcus Fedarko, Fall 2016 – present

### **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

### **Doctoral**

#### Current

Brook Stacy (CS), 2017 -  
Saul Sarria (BISI), 2017 -  
Brian Brubach (CS), 2016 – (co-advised with Aravind Srinivasan)  
Seth Commichaux (BISI), 2017 -  
Kiran Javkar (CS), 2017 -  
Nidhi Shah (CS), 2016 -  
Jay Ghurye (CS), 2015 -  
Victoria Cepeda Espinoza (CS), 2014 -

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

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

Senthil Kumar (BISI), Spring 2013 – Fall 2016 (currently advised by Héctor Corrada Bravo)

### **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

### **Post-doctoral**

#### Current

Jackie Meisel (Ph.D. U. Penn) 2017 -

#### 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 was a staff scientist at NBACC and rejoined the University of Maryland as a Research Scientist)

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

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

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

### **Service**

#### **Professional**

- 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

- 2013 – INRIA Team Evaluation Expert Panel (France)
- 2013. Newton Institute, Cambridge UK. Member of Scientific Advisory Committee for Metagenomics Programme
- 2015 – present. NIH/NIAID Genomic Centers for Infectious Disease Steering Committee

## Grant review

- National Institutes of Health (2005-2008 – *ad hoc* member on GGG-J panel, ~1-2 panels/year)
- U.S. Civilian Research and Development Foundation (2006)
- Research Council of Norway (2007)
- Mathematics of Information Technology and Complex Systems, Canada (2008)
- 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)
- U.S. Department of Energy (2004, 2010)
- North Carolina Biotech Center (2011)
- U.S. Army Research and Materiel Command (2006, 2012)
- Agence Nationale de Recherche (French Research Agency) (2011, 2013)
- BBSRC (UK) (2014)
- Austrian Science Fund (2015)
- Canada Foundation for Innovation (2015)
- National Institutes of Health (2009, 2010, 2012, 2013, 2014, 2015, 2016)
- National Science Foundation (2003, 2009, 2010, 2012, 2017)
- Standing member on BDMA study section for the National Institutes of Health (2017-2022)

## 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 Informatics Maryland 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, 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,



May 2017.

- 2018. Co-organizer. Mid-Atlantic Microbiome Meet-up on Biodefense and Pathogen detection, College Park, January 2018.
- 2018. *Program co-chair*. ACM BCB 2018. Washington, DC, August 2018

### **Departmental committees**

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

2007-8 – Member, faculty search committee for CBCB

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

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

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.

2013-2015 – Member, Merit Review Committee

2006-10, 2014-2015 – Member, CS graduate admissions 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

2014-2017 – Member, Recruiting for Diversity committee.

2008-present – Member, Teaching Evaluation Committee

2017 – Chair, Diversity and Inclusion 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

2015 – 2016 – Member, DC@UMD Large Data Analytics Working Group

Spring 2017 – UMCP-UMB SEED grant review

2015 – 2017 – Limited Submissions Review Committee

2017 – 2019 – co-chair, Year of Data Science organization committee

### **Candidacy and defense committees (last 3 years) (in Computer Science unless otherwise marked)**

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  
Fall 2015 – Thesis defense committee for Ethar Elsaka  
Fall 2016 – Thesis defense committee for Prachi Kulkarni (SPH)  
Spring 2017 – Oral exam committee for Khoa Trinh  
Spring 2017 – PhD Defense Committee for Steven Smith (BISI)  
Spring 2017 – Thesis defense committee for Daniel Ayres (BISI)  
Spring 2017 – Chair, Oral exam committee for Jay Ghurye  
Spring 2017 – Oral exam committee for Joshua Brulé  
Summer 2017 – Chair, Oral exam committee for Victoria Cepeda  
Fall 2017 – PhD Defense Committee for Jessica Goodheart (BISI)  
Fall 2017 – Oral exam committee for Dietrich Schmidt (ENST)  
Fall 2017 – Oral exam committee for Jessica Chopyk (SPH)

**External candidacy and defense committees**

Spring 2014 – Thesis defense committee – Nam Nguyen (University of Texas, Austin)  
Spring 2014 – Thesis defense committee – Brianna Lindsay (University of Maryland, Baltimore)  
Fall 2015 – Oral exam committee – Justin Krueger (Virginia Tech)  
Fall 2016 – Oral exam committee – Michael Nute (University of Illinois, Urbana Champaign)  
Summer 2017 – Thesis defense committee – Justin Krueger (Virginia Tech)