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Education

Ph.D. Computer Science 1989, Harvard University, Cambridge, MA
M.Phil. 1984, M.S. 1982, Computer Science, Yale University, New Haven, CT
B.A. *cum laude* English 1980, Yale University

Research Areas: Genomics, bioinformatics, gene finding, genome assembly, sequence analysis.

Academic and Professional Experience

2011-present	Professor, Department of Medicine and the McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University. Joint appointments as Professor in the Department of Biostatistics, Bloomberg School of Public Health, and in the Department of Computer Science, Whiting School of Engineering.
2012-present	Director, Center for Computational Biology, Johns Hopkins University.
2005-2011	Director, Center for Bioinformatics and Computational Biology, University of Maryland Institute for Advanced Computer Studies
2005-2011	Horvitz Professor, Department of Computer Science, University of Maryland. (On leave of absence 2011-2012.)
1997-2005	Senior Director of Bioinformatics (2000-2005), Director of Bioinformatics (1998-2000), and Investigator (1997-2005), The Institute for Genomic Research (TIGR).
1999-2006	Research Professor, Departments of Computer Science and Biology, Johns Hopkins University
1989-1999	Associate Professor (1996-1999), Assistant Professor (1989-1996), Department of Computer Science, Johns Hopkins University. On leave 1997-99.
1988-1989	Associate in Research, Graduate School of Business Administration, Harvard University. Consultant to Ford Motor Co. of Europe and to N.V. Bekaert (Kortrijk, Belgium).
1985-1987	Research Scientist and Senior Knowledge Engineer, Applied Expert Systems, Inc., Cambridge, MA. Designed expert systems for financial services companies.

Awards, honors, and editorial boards

- Winner, Benjamin Franklin Award for Open Access in the Life Sciences, 2013
- Fellow, American Association for the Advancement of Science
- Fellow, International Society for Computational Biology
- Board of Scientific Counselors, National Center for Biotechnology Information, NIH, 2003-2008
- Member, International Advisory Committee, International Nucleotide Sequence Database Collaboration (comprising GenBank, EMBL, and DDBJ), 2005-present
- Member, Biodata Management and Analysis Study Section, NIH, 2007-2011
- Co-winner (with Ben Langmead, Cole Trapnell, and Mihai Pop) of *Genome Biology* Award for Best Research Paper of 2009
- Named as one of BioMed Central's "Hot 100 authors," December 2007
- Chosen for ISIHighlyCited.com, an online directory of the most highly cited researchers of the past 20 years
- Ranked among scientists for "The Hottest Research of 1999-2000," based on number of highly-cited papers (tied for 2nd in list of 13), by the Institute for Scientific Information.

- NIH Career Award, 1996-1998
- 2009-present: Editorial Advisory Board, *Genome Biology*, BioMed Central Publishers
- 2009-present: Editorial Board, *Genome Research*, Cold Spring Harbor Laboratory Press
- 2003-present: Editorial Board, *BMC Biology*, BioMed Central Publishers
- 2008-present: Editorial Board, *Biology Direct*, BioMed Central Publishers
- 2008-present: Member, *Faculty of 1000*, Bioinformatics section
- 2002-present: Associate Editor, *Journal of Computational Biology*, Mary Ann Liebert Publishers
- 2008-2012: Board of Reviewers, *PLoS Currents Influenza*, Public Library of Science
- 2006-present: Editorial Board, *PLoS ONE*, Public Library of Science
- 2001-2006: Associate Editor, *Bioinformatics*, Oxford University Press
- 2003-present: Editorial Board, *BMC Genomics*, BioMed Central Publishers
- 2003-present: Editorial Board, *BMC Bioinformatics*, BioMed Central Publishers
- 2005-present: Editorial Board, *Evolutionary Bioinformatics*, Libertas Academica Ltd
- 1999-2003: Editorial Board, *Gene*, Elsevier Science Publishers.
- 2002-2006: Editorial Board, *Applied Bioinformatics*, Open Mind Journals Ltd
- 1997-2000: Editorial Board, *Pattern Analysis and Applications*, Springer-Verlag Publishers
- 1995-2002: Editorial Board, *Artificial Intelligence Review*, Kluwer Academic Publishers

Articles in Refereed Journals and Book Chapters (h-index: 102)

1. D. Kim, G. Pertea, C. Trapnell, H. Pimentel, R. Kelley, and S.L. Salzberg. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biology* 2013, **14**:R36.
2. A. Zimin, G. Marçais, D. Puiu, M. Roberts, S.L. Salzberg, and J.A. Yorke. The MaSuRCA genome assembler. *Bioinformatics* (2013), in press.
3. T. Magoc, S. Pabinger, S. Canzar, X. Liu, Q. Su, D. Puiu, L.J. Tallon, and S.L. Salzberg. GAGE-B: An Evaluation of Genome Assemblers for Bacterial Organisms. *Bioinformatics* **29**:14 (2013), 1718-1725.
4. J.T. Leek and S.L. Salzberg. Sequestration: inadvertently killing biomedical research to score political points. *Genome Biology* 2013, **14**:109.
5. J.L. Wegrzyn, B.Y. Lin, J.J. Zieve, W.M. Dougherty, P.J. Martínez-García, M. Koriabine, A. Holtz-Morris, P. deJong, M. Crepeau, C.H. Langley, D.Puiu, S.L. Salzberg, D.B. Neale, K.A. Stevens. Insights into the Loblolly Pine Genome: Characterization of BAC and Fosmid Sequences. *PLoS ONE*, in press (2013).
6. T. Magoc, D. Wood, and S.L. Salzberg. EDGE-pro: Estimated Degree of Gene Expression in Bacterial Genomes. *Evolutionary Bioinformatics* 9 (2013) 127-136.
7. B. Langmead and S.L. Salzberg. Fast gapped-read alignment with Bowtie 2. *Nature Methods* 9 (2012), 357-359.
8. The Heliconius Genome Consortium. Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature* **487**, 94-98 (2012). doi:10.1038/nature11041.
9. S.L. Salzberg. The perils of gene patents. *Clinical Pharmacology & Therapeutics* 91:6 (2012), 969-971.
10. C. Trapnell, A. Roberts, L. Goff, G. Pertea, D. Kim, D.R. Kelley, H. Pimental, S.L. Salzberg, J.L. Rinn, and L. Pachter. Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. *Nature Protocols* 7:3 (2012), 562-578.
11. S.L. Salzberg A.M. Phillippy, A. Zimin, D. Puiu, T. Magoc, S. Koren, T. Treangen, M.C. Schatz, A.L. Delcher, M. Roberts, G. Marçais, M. Pop, and J.A. Yorke. GAGE: a critical evaluation of genome assemblies and assembly algorithms. *Genome Research*, 22:3 (2012), 557-567.
12. T.J. Treangen and S.L. Salzberg. Repetitive DNA and next-generation sequencing: computational challenges and solutions. *Nature Reviews Genetics* 13, 36-46 (2012).
13. D.E. Wood, H. Lin, A. Levy-Moonshine, R. Swaminathan, Y.-C. Chang, B.P. Anton, L. Osman, M. Steffen, S. Kasif, and S.L. Salzberg. Thousands of missed genes found in bacterial genomes and their analysis with COMBEX. *Biology Direct* 2012, **7**:37.

14. A.V. Zimin, D.R. Kelley, M. Roberts, S.L. Salzberg, and J.A. Yorke. Mis-assembled segmental duplications in two versions of the *Bos taurus* genome. *PLoS ONE* 7(8): e42680 (2012).
15. D.R. Kelley, B. Liu, A.L. Delcher, M. Pop, and S.L. Salzberg. Gene prediction with Glimmer for metagenomic sequences augmented by classification and clustering. *Nucleic Acids Research* 40:1 (2012), e9. doi:10.1093/nar/gkr1067.
16. M.C. Schatz, A.M. Phillippy, D.D. Sommer, A.L. Delcher, D. Puiu, G. Narzisi, S.L. Salzberg, and Mihai Pop. Hawkeye & AMOS: Visualizing and assessing the quality of genome assemblies. *Briefings in Bioinformatics*, 2011, doi:10.1093/bib/bbr074.
17. D. Kim and S.L. Salzberg. TopHat-Fusion: an algorithm for discovery of novel fusion transcripts. *Genome Biology* (2011), 12:R72. **Highly accessed.**
18. T. Magoč and S.L. Salzberg. FLASH: Fast Length Adjustment of Short Reads to Improve Genome Assemblies. *Bioinformatics* 27:21 (2011), 2957-2963.
19. M. Pertea, G.M. Pertea, and S.L. Salzberg. Detection of lineage-specific evolutionary changes among primate species. *BMC Bioinformatics* 2011, 12:274. **Highly accessed.**
20. A.J. Bogdanove, R. Koebnik, H. Lu, A. Furutani, S.V. Angiuoli, P.B. Patil, M. Van Sluys, R.P. Ryan, D.F. Meyer, S.-W. Han, G. Aparna, M. Rajaram, A.L. Delcher, A.M. Phillippy, D. Puiu, M.C. Schatz, M. Shumway, D.D. Sommer, C. Trapnell, F. Benahmed, G. Dimitrov, R. Madupu, D. Radune, S. Sullivan, G. Jha, H. Ishihara, S.-W. Lee, A. Pandey, V. Sharma, M. Sriariyanun, B. Szurek, C.M. Vera-Cruz, K.S. Dorman, P.C. Ronald, V. Verdier, J.M. Dow, R.V. Sonti, S. Tsuge, V. Brendel, P.D. Rabinowicz, J.E. Leach, F.F. White, and S.L. Salzberg. Two new complete genome sequences offer insight into host and tissue specificity of plant pathogenic *Xanthomonas spp.* *J. Bacteriology* 193:19 (2011), 5450-64.
21. J. Enk, R. Debruyne, A. Devault, C.E. King, T. Treangen, D. O'Rourke, S.L. Salzberg, D. Fisher, R. MacPhee, and H. Poinar. Complete Columbian mammoth mitogenome suggests interbreeding with woolly mammoths. *Genome Biology* (2011), 12:R51. **Highly accessed.**
22. A. Brady and S. Salzberg. PhymmBL expanded: confidence scores, custom databases, parallelization and more. *Nature Methods* 8, 367 (2011). doi:10.1038/nmeth0511-367.
23. L. Florea, A. Souvorov, T.S. Kalbfleisch, and S.L. Salzberg (2011). Genome assembly has a major impact on gene content: A comparison of annotation in two *Bos taurus* assemblies. *PLoS ONE* 6(6), e21400. doi:10.1371/journal.pone.0021400.
24. S.V. Angiuoli, J.C. Dunning Hotopp, S.L. Salzberg and H. Tettelin. Improving pan-genome annotation using whole genome multiple alignment. *BMC Bioinformatics* 2011, 12:272. **Highly accessed.**
25. D.A. Rasko, P. Worsham, T.G. Abshire, S.T. Stanley, J.D. Bannan, M.R. Wilson, R. 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. *Proc. Natl. Acad. Sci. USA* 102:12(2011), 5027-32.
26. V Shulaev, DJ Sargent, RN Crowhurst, TC Mockler, O Folkerts, AL Delcher, P Jaiswal, K Mockaitis, A Liston, SP Mane, P Burns, TM Davis, JP Slovin, N Bassil, RP Hellens, C Evans, T Harkins, C Kodira, B Desany, OR Crasta, RV Jensen, AC Allan, TP Michael, JC Setubal, J-M Celton, DJG Rees, KP Williams, SH Holt, JJR Rojas, M Chatterjee, B Liu, H Silva, L Meisel, A Adato, SA Filichkin, M Troggio, R Viola, T-L Ashman, H Wang, P Dharmawardhana, J Elser, R Raja, HD Priest, DW Bryant Jr, SE Fox, SA Givan, LJ Wilhelm, S Naithani, A Christoffels, DY Salama, J Carter, EL Girona, A Zdepki, W Wang, RA Kerstetter, W Schwab, SS Korban, J Davik, A Monfort, B Denoyes-Rothan, P Arus, R Mittler, B Flinn, A Aharoni, JL Bennetzen, SL Salzberg, AW Dickerman, R Velasco, M Borodovsky, RE Veilleux, and KM Folta. The genome of woodland strawberry (*Fragaria vesca*). *Nature Genetics* 43(2011), 109-116.
27. S.V. Angiuoli and S.L. Salzberg. Mugsy: Fast multiple alignment of closely related whole genomes. *Bioinformatics* (2011), 27(3), 334-342.
28. R.J. Roberts, Y.-C. Chang, Z. Hu, J.N. Rachlin, B.P. Anton, R.M. Pokrzywa, H.-P. Choi, L.L. Faller, J. Guleria, G. Housman, N. Klitgord, V. Mazumdar, M.G. McGettrick, L. Osmani, R. Swaminathan, K.R. Tao, S. Letovsky, D. Vitkup, D. Segrè, S.L. Salzberg, C. Delisi, M. Steffen, and S. Kasif. COMBEX: a project to accelerate the functional annotation of prokaryotic genomes. *Nucleic Acids Research* (2011) January; 39(Database issue):D11-D14. doi: 10.1093/nar/gkq1168.

29. S.L. Salzberg and M. Pertea. Do-it-yourself genetic testing. *Genome Biology* (2010), 11:404.
30. D.R. Kelley, M.C. Schatz, and S.L. Salzberg. Quake: quality-aware detection and correction of sequencing errors. *Genome Biology* (2010), 11:R116. <http://genomebiology.com/2010/11/11/R116/>.
31. D.R. Kelley and S.L. Salzberg. Clustering metagenomic sequences with interpolated Markov models. *BMC Bioinformatics* 11:544 (2010). <http://www.biomedcentral.com/1471-2105/11/544>
32. M.C. Schatz, B. Langmead, and S.L. Salzberg. Cloud computing and the DNA data race. *Nature Biotechnology* **28**, 691-693 (2010) doi:10.1038/nbt0710-691.
33. M.C. Schatz, A.L. Delcher, and S.L. Salzberg. Assembly of large genomes using second-generation sequencing. *Genome Research* **20**, 1165-1173 (2010). doi:10.1101/gr.101360.109
34. C. Trapnell, B.A. Williams, G. Pertea, A. Mortazavi, G. Kwan, M.J. van Baren, S.L. Salzberg, B.J. Wold, and L. Pachter. Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. *Nature Biotechnology* **28**, 511-515 (2 May 2010).
35. T.R. Miller, A.L. Delcher, S.L. Salzberg, E. Saunders, J.C. Detter, and R.U. Halden. Genome sequence of the dioxin-mineralizing bacterium *Sphingomonas wittichii* RW1. *J. Bacteriology* **192** (2010), 6101-2.
36. S.L. Salzberg. Recent advances in RNA sequence analysis. *F1000 Biology Reports* **2010**, 2:64.
37. M. Pertea and S.L. Salzberg. Between a chicken and a grape: estimating the number of human genes. *Genome Biology* (2010), 11:206, doi:10.1186/gb-2010-11-5-206.
38. R.A. Dalloul, J.A. Long, A.V. Zimin, L. Aslam, K. Beal, L. Blomberg, D.W. Burt, O. Crasta, R.P.M.A. Crooijmans, K. Cooper, R.A. Coulombe, S. De, M.E. Delany, J.B. Dodgson, J.J. Dong, C. Evans, P. Flicek, L. Florea, O. Folkerts, M.A.M. Groenen, T.T. Harkins, J. Herrero, S. Hoffmann, H.-J. Megens, A. Jiang, P. de Jong, P. Kaiser, H. Kim, K.-W. Kim, S. Kim, D. Langenberger, M.-K. Lee, T. Lee, S. Mane, G. Marcais, M. Marz, A.P. McElroy, T. Modise, M. Nefedov, C. Notredame, I.R. Paton, W.S. Payne, G. Pertea, D. Prickett, D. Puiu, D. Qiao, E. Raineri, S.L. Salzberg, M.C. Schatz, C. Scheuring, C.J. Schmidt, S. Schroeder, E.J. Smith, J. Smith, T.S. Sonstegard, P.F. Stadler, H. Tafer, Z. Tu, C.P. Van Tassell, A.J. Vilella, K. Williams, J.A. Yorke, L. Zhang, H.-B. Zhang, X. Zhang, Y. Zhang, and K.M. Reed. Multi-platform next generation sequencing of the domestic turkey (*Meleagris gallopavo*): genome assembly and analysis. *PLoS Biology* (2010), 8(9): e1000475. doi:10.1371/journal.pbio.1000475.
39. X. Deng, A.M. Phillippy, Z. Li, S.L. Salzberg, and W. Zhang. Probing the pan-genome of *Listeria monocytogenes*: new insights into intraspecific niche expansion and genomic diversification. *BMC Genomics* (2010), 11:500.
40. S.L. Salzberg. Mind the gaps. *Nature Methods* **7:2** (2010), 105-106.
41. D.R. Kelley and S.L. Salzberg. Detection and correction of false segmental duplications caused by genome mis-assembly. *Genome Biology* (2010), 11:R28. doi:10.1186/gb-2010-11-3-r28
42. B. Langmead, M.C. Schatz, J. Lin, M. Pop, and S.L. Salzberg. Searching for SNPs with cloud computing. *Genome Biology* (2009) **10**:R134. doi:10.1186/gb-2009-10-11-r134. **Highly accessed.**
43. A. Brady and S.L. Salzberg. Phymm and PhymmBL: Metagenomic phylogenetic classification with interpolated Markov models. *Nature Methods*, **6:9** (2009), 673 – 676.
44. A.V. Zimin, A.L. Delcher, L. Florea, D.A. Kelley, M.C. Schatz, D. Puiu, F. Hanrahan, G. Pertea, C.P. Van Tassell, T.S. Sonstegard, G. Marcais, M. Roberts, P. Subramanian, J.A. Yorke, and S.L. Salzberg. A whole-genome assembly of the domestic cow, *Bos taurus*. *Genome Biology* (2009), **10**:R42. **Highly accessed.**
45. C. Kingsford, N. Nagarajan and S.L. Salzberg. 2009 Swine-Origin Influenza A (H1N1) Resembles Previous Influenza Isolates. *PLoS ONE* **4:7** (2009), e6402. (doi:10.1371/journal.pone.0006402)
46. M. Berriman, B.J. Haas, P.T. LoVerde, R.A. Wilson, G.P. Dillon, G.C. Cerqueira, S.T. Mashiyama, B. Al-Lazikani, L.F. Andrade, P.D. Ashton, M.A. Aslett, D.C. Bartholomeu, G. Blandin, C.R. Caffrey, A. Coghlan, R. Coulson, T.A. Day, A. Delcher, R. DeMarco, A. Djikeng, T. Eyre, J.A. Gamble, E. Ghedin, Y. Gu, C. Hertz-Fowler, H. Hirai, Y. Hirai, R. Houston, A. Ivens, D.A. Johnston, D. Lacerda, C.D. Macedo, P. McVeigh, Z. Ning, G. Oliveira, J.P. Overington, J. Parkhill, M. Pertea, R.J. Pierce, A.V. Protasio, M.A. Quail, M.-A. Rajandream, J. Rogers, M. Sajid, S.L. Salzberg, M. Stanke, A.R. Tivey, O. White, D.L. Williams, J. Wortman, W. Wu, M. Zamanian, A. Zerlotini, C.M. Fraser-Liggett, B.G. Barrell, and N.M. El-Sayed. The genome of the blood fluke *Schistosoma mansoni*. *Nature* **460** (2009), 352-358.

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48. Cole Trapnell, Lior Pachter, and Steven L. Salzberg. TopHat: Discovering splice junctions with RNA-Seq. *Bioinformatics* 25 (2009), 1105-1111. **Selected by *Bioinformatics* as the best Next Generation Sequencing paper in the journal (2008-2009).**
49. Cole Trapnell and Steven L. Salzberg. How to map billions of short reads onto genomes. *Nature Biotechnology* 27:5 (2009), 455-457.
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51. A.M. Phillippy, K. Ayanbule, N.J. Edwards, and S.L. Salzberg. Insignia: a DNA signature search web server for diagnostic assay development. *Nucleic Acids Research* 37 (2009), W229-W234.
52. S.L. Salzberg, D. Puiu, D.D. Sommer, V. Nene, and N.H. Lee. The genome sequence of *Wolbachia* endosymbiont of *Culex quinquefasciatus* JHB. *J. Bacteriology* 191:5 (2009). 1725.
53. J. Ravel, L. Jiang, S.T. Stanley, M.R. Wilson, R.S. Decker, T.D. Read, P. Worhsam, P.S. Keim, S.L. Salzberg, C.M. Fraser-Liggett, and D.A. Rasko. The complete genome sequence of *Bacillus anthracis* Ames "Ancestor." *J. Bacteriology* 191:1 (2009), 445-446.
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56. J.M. Carlton, J.H. Adams, J.C. Silva, S.L. Bidwell, H. Lorenzi, E. Caler, J. Crabtree, S.V. Angiuoli, E.F. Merino, P. Amedeo, Q. Cheng, R.M.R. Coulson, B.S. Crabb, H.A. del Portillo, K. Essien, T.V. Feldblyum, C. Fernandez-Becerra, P.R. Gilson, A.H. Gueye, X. Guo, S. Kang'a, T.W.A. Kooij, M. Korsinczky, E.V.-S. Meyer, Vish Nene, I. Paulsen, O. White, S.A. Ralph, Q. Ren, T.J. Sargeant, S.L. Salzberg, C.J. Stoeckert, S.A. Sullivan, M.M. Yamamoto, S.L. Hoffman, J.R. Wortman, M.J. Gardner, M.R. Galinski, J.W. Barnwell, and C.M. Fraser-Liggett. Comparative genomics of the neglected human malaria parasite *Plasmodium vivax*. *Nature* 455 (2008), 757-763.
57. E.V. Shakirov, S.L. Salzberg, M. Alam, and D.E. Shippen. Analysis of *Carica papaya* Telomeres and Telomere-Associated Proteins: Insights into the Evolution of Telomere Maintenance in Brassicales. *Tropical Plant Biology* (2008) doi:10.1007/s12042-008-9018-x.
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1. S.L. Salzberg and T. Warnow (editors). *Algorithms in Bioinformatics: 9th International Workshop, WABI 2009*. ISBN: 978-3-642-04240-9. Berlin: Springer-Verlag, 2009.
2. S.L. Salzberg, D. Searls, and S. Kasif (editors). *Computational Methods in Molecular Biology*. Amsterdam: Elsevier Science B.V., 1998.
3. S.L. Salzberg. *Learning with Nested Generalized Exemplars*. Norwell, MA: Kluwer Academic Publishers, 1990.

Blogs

- <http://blogs.forbes.com/stevensalzberg/> (A featured writer at *Forbes* magazine, a major business-oriented publisher, since January 2010)
- <http://genome.fieldofscience.com> (since 2007)

Research Grants (PI is Salzberg unless otherwise indicated)

9/21/2011-8/31/2014 National Institutes of Health, NHGRI, "Computational gene modeling and genome sequence assembly", R01 HG006677, \$1,910,827 (\$469,084 direct costs, year 1).

7/6/2011-4/30/2014 National Institutes of Health, NHGRI, "Alignment Software for Second-Generation Sequencing," R01 HG006102, \$2,122,212 (\$1,459,353 direct costs).

2/1/2011-1/31/2016 U.S. Dept. of Agriculture, National Institute of Food and Agriculture, "Loblolly Pine Genome Project, Award 2011-67009-30030, \$1,981,737. (Overall award: \$14,994,424) **PI:** David Neale, UC Davis.

3/25/08-2/28/13 National Institutes of Health, "Bioinformatics software for analyzing microbial genomes," R01 GM083873, \$1,107,000 (\$738,000 direct costs).

2/1/09-1/31/12 U.S. Department of Agriculture National Research Initiative, "Assembly and Annotation of Agricultural Genomes," 2008-04049, \$906,098.

6/1/07-9/20/11 National Institutes of Health, "Computational gene modeling and genome sequence assembly," R01 LM006845, \$2,398,178.

7/1/09-5/31/2012 National Institutes of Health, "Computational gene modeling and genome sequence assembly," R01 LM006845-Supplement, \$250,000 (\$167,333 direct costs). This ARRA supplement adds support for one postdoctoral fellow to R01 LM006845.

9/24/08-7/31/11 National Institutes of Health, "Assembly and analysis software for exploring the human microbiome," R01 HG004885, \$891,000. **PI:** Mihai Pop.

10/1/09-9/30/2011 National Institutes of Health, "SciBay: A New Methodology for Scientific Collaboration and Gene Function Determination," RC2-GM092602, \$305,995 (subcontract). **PI:** Martin Steffen, Boston University.

4/1/09-3/31/14 National Institutes of Health, "Genomic Sequencing Centers for Infectious Diseases," HHSN2722009000009C, \$471,186 (subcontract). **PI:** Claire Fraser-Liggett, Univ. of Maryland School of Medicine.

12/29/06-1/30/09 Department of Homeland Security, "Bioinformatics tools for Rapid Pathogen Detection and Analysis," award NBCH207002, \$4,973,420.

4/1/09-3/31/11 National Science Foundation, "Algorithms for the analysis of data from massively-parallel genome sequencing." IIS-0844494, \$379,919. **PI:** Mihai Pop.

6/1/2008-5/31/2009 Burroughs Wellcome Fund (subcontract to University of Pittsburgh), "Brugia Malayi: Proposal to Complete Assembly and Annotation of the Genome," \$40,000. **PI:** Elodie Ghedin.

5/4/05-9/3/06 Homeland Security Advanced Research Projects Agency (HSARPA), "Bioinformatics tools for Rapid Pathogen Detection and Analysis," award W81XWH-05-2-0051, \$2,094,428.

1/1/07-12/31-09 Henry M. Jackson Foundation (Naval Medical Research Center), "Assembly and gene finding algorithms for genome sequences generated by pyrosequencing," \$1,154,879. **PI:** Mihai Pop.

9/30/02-9/29/06 National Institutes of Health, "Computational gene modeling and genome sequence assembly," R01 LM06845-04, \$2,667,000.

9/1/03-2/29/08 National Institutes of Health, "Bioinformatics software for analyzing microbial genomes," R01 LM007938-01, \$779,500 (500,000 direct).

7/1/04 – 6/30/09 National Institutes of Health (NIAID), "Bioinformatics Resource Centers for Biodefense and Emerging/Re-emerging Infectious Diseases," Contract HHSN266200400038C, \$21,078,000. **PI:** Owen White.

7/1/04 – 9/30/06 National Science Foundation, "Sequencing of Xanthomonas pathovars enabling a broad comparative genomics approach to understanding vascular and non-vascular bacterial diseases of dicots and monocots, MCB-0412260, \$400,376 (320,301 direct). Subcontract to Iowa State (full award was \$736,336), **PI:** Adam Bogdanove.

09/30/03-09/29/08 National Institutes of Health, "Network for Large-scale Sequencing of Microbial Genomes," NIH-N01-AI-30, \$65,042,611. **PI:** C.M. Fraser.

11/10/03-10/31/06 National Institutes of Health, "TIGR/JTC Large Scale Sequencing Production Center," U54-HG003068-01, \$27,200,000. **P.I.:** J.C. Venter.

2/1/03-1/31/06 National Science Foundation, "Bioinformatics Analysis of Regulatory Sites in Genomic DNA Sequences," DBI-0234704, \$310,191.

9/1/03-8/31-05 National Science Foundation, "A high-speed network connection for genomics research," ANI-0333537, \$183,035.

1/1/02-12/31/05 National Institutes of Health (NIAID), "Comprehensive Sequencing of Bacillus anthracis," N01-AI-15447, \$5,557,421. **PI:** C.M. Fraser.

8/15/01-8/14/05 National Science Foundation, "Pre-mRNA splicing signals in Arabidopsis," MCB-0114792, \$371,903. Subcontract from Univ. of Maryland (full award was \$1,010,298). **PI:** Stephen Mount.

8/15/03-7/31/05 National Science Foundation, "2003 and 2004 Computational Genomics Conferences," DBI-0314206, \$29,500.

9/15/99-2/28/03 National Science Foundation, "KDI: Intelligent Computational Genomic Analysis," KDI-9980088, \$795,000. Subcontract from Boston Univ (full award was \$1,700,000). **PI:** Simon Kasif.

9/1/99–9/30/02 National Institutes of Health, "Computational Modeling of Genes and Gene Structure," R01 LM06845-01, \$820,323.

9/1/01-6/30/02 National Science Foundation, "The Fifth Annual Computational Genomics Conference at TIGR," DBI-0120900, \$24,803.

8/25/99–7/31/02 National Science Foundation, "Interpolated Markov Models for DNA Sequence Analysis," IIS-9902923, \$330,000. (Co-PI: Arthur Delcher.)

8/1/01–7/31/04 National Science Foundation, "The Development of a Prokaryotic Annotation Engine" (PI: Owen White), DBI-0110270, \$900,000.

7/1/01–6/30/04 Department of Energy, "Continuation of the Comprehensive Microbial Resource" (PI: Owen White), DE-FG02-01ER63203, \$2,047,000.

3/15/00–2/28/05 NIH/NIAID, "Trypanosoma cruzi genome project at TIGR," (PI: N. El-Sayed), U01-AI45038, \$3,820,617.

7/1/96–6/30/00 National Human Genome Research Institute, National Institutes of Health, "Computational Techniques for Genomic Analysis," K01-HG00022-01, \$335,190. (Career Award)

7/1/99–6/30/04 Burroughs Wellcome Fund, "The Hopkins Program in Computational Biology," (PIs: G. Rose and M. Paulaitis), \$2,567,050. (This training grant established a joint Hopkins/TIGR training program.)

11/1/98–10/31/02 National Science Foundation, "Generation of a Tomato EST Database," (PI: E. Kirkness), \$3,246,725.

3/1/99–2/28/01 Department of Energy, "Development of a Comprehensive Microbial Resource," (PI: Owen White), DE-FC02-95ER61962 (Supplement), \$411,184.

8/15/96–7/31/00 National Science Foundation, "Finding Genes in DNA using Machine Learning Algorithms," IRI-9530462. \$214,497.

3/1/98–8/31/99 Merck Genome Research Institute, "Computational Analysis of Intergenic Regions in Microbial Genomes," \$120,000. (PI: H.O. Smith; Co-PIs: S. Salzberg, O. White.)

12/1/96–11/30/97 Pfizer Central Research (Department of Molecular Sciences), "Probabilistic Methods for Pattern Discovery in Biological Sequence Data." \$52,606.

3/1/93–2/28/97 National Science Foundation, "Knowledge Discovery for Molecular Biology: Algorithms and Experiments," IRI-9223591. \$197,698.

4/1/95–3/31/96 National Science Foundation SGER, "A Proposal to Study the Applicability of Astronomical Image Processing Methods to Low Contrast Digital Images," AST-9520463, \$49,986.

5/1/95–4/30/96 National Science Foundation, "Distributed Data Mining in Large Databases," CDA-9421531, \$50,000. (Co-PIs: S. Kasif, E. Brill, and K. Fasman.)

10/1/91–3/31/96 National Science Foundation, "A Geometric Framework for the Exploration and Analysis of Astrophysical Data," IRI-9116843, \$539,553. (PI: M. Goodrich; Co-PIs: S. Salzberg and H. Ford (Dept. of Physics and Astronomy).)

6/1/93–12/1/93 National Science Foundation, Research Experience for Undergraduates award, supplement to Grant IRI-9116843, \$4,000.

3/1/91–2/28/96 National Science Foundation, CISE Institutional Infrastructure grant, "A Facility for Experimental Exploration and Validation," CDA-9015667, \$1,476,147. (PI: G. Masson.)

Software Systems Developed and Released

The following systems have been widely distributed and are all free, open-source software.

1. Glimmer is a system for finding genes in microbial DNA. First released in 1997, Glimmer has become the world's leading bacterial gene finder, distributed to thousands of labs and institutions worldwide.
2. GlimmerHMM (formerly GlimmerM) is a system for finding genes in eukaryotic genomes, including the human genome, the malaria parasite *Plasmodium falciparum*, the model plant *Arabidopsis thaliana*, rice (*O. sativa*), *Theileria parva*, and others.
3. Bowtie is a system for very rapid alignment of short DNA sequence reads to a reference genome such as the human genome. Bowtie passed 70,000 downloads in October 2011.
4. Tophat and Cufflinks are systems for alignment of RNA-seq reads across splice junctions, and for assembly and quantitation of full-length transcripts from these alignments.
5. MUMmer, in its 3rd major release, is a system for alignment of the DNA sequences of entire genomes and chromosomes. Source code and executables have been freely available since 1999.
6. JIGSAW is a system that integrates the results of multiple gene finders and cDNA and protein sequence alignment programs to predict protein coding genes in eukaryotic genomes, including the human genome and the model organisms *C. elegans* and *D. melanogaster*.
7. AMOS is an open-source genome assembly framework and software system comprising multiple genome assembly modules that are widely used for assembly of whole-genome shotgun data, including a scaffolder (Bambus), a comparative assembler (AMOS-Cmp), and an efficient small-scale assembler (Minimus).
8. AutoEditor is a system for automatically correcting the sequencing errors in large-scale genome sequencing projects. It is able to correct 85% of sequencing errors fully automatically.
9. VEIL and MORGAN were two early human gene finders, using Hidden Markov Models and decision trees respectively. These two systems were released in 1996 and 1997.
10. OC1 is a multivariate decision tree induction system. OC1 was applied to classification of data from molecular biology, astronomy, and numerous other application domains.

Professional Service

- 2011-present: Fellow, Institute for Science in Medicine (Board of Directors 2012-2014)
- 2010: Organizing committee, Beyond the Genome conference, October 2010.
- 2009: Co-chair, WABI-09, 8th Annual Workshop on Algorithms in Bioinformatics.
- 2007, 2009: Co-chair, 15th and 17th Annual International Conference on Microbial Genomics
- 2006-2011: Member, Maryland Stem Cell Research Commission
- 2008: Program Committee, Biology of Genomes Conference, Cold Spring Harbor Laboratory
- 2006-present: Advisory council member, Computer Science Department, Princeton University.
- 1999-2005: Chair or Co-chair, 3rd through 8th Annual Conferences on Computational Genomics: 1999, 2000, 2001, 2003, 2004, 2005.
- 2003-2005: Program committee, IEEE Computer Society Computational Systems Bioinformatics Conference. 2003 and 2004 Steering Committee member.
- 2005: Area chair, Intelligent Systems for Molecular Biology (ISMB), the International Conference on Computational Biology.
- 2005: Scientific organizing committee, ESF-EMBO Symposium on Comparative Genomics.
- 1996–2002: Program committee member (every year), Intelligent Systems for Molecular Biology (ISMB) conference.
- 2002-2004: External Advisory Board member, Computer Science Department, Virginia Tech.
- 2000-2003: External Advisory Board member, Center for Bioinformatics and Computational Biology, University of Maryland, College Park.

National Institutes of Health, National Science Foundation, and other scientific review panels:

- March 2012. Review panel, NIH/NHGRI Encode program.
- Nov. 2011. Chair of review panel, NIH Genomic Resources Grants for Community Resource Projects.
- July 2007-2011. Member, BDMA (Biodata Management and Analysis) study section, NIH
- June 2010. Review panel, NIH National Centers for Biomedical Computing program.
- May 2007. Review panel, NIH GCAT (Genomics, Computational Biology, and Technology) study section.
- July 2006. Review panel, NIH/NHGRI Large-scale sequencing centers program.
- May 2006. Site visit panel, Center for Cancer Research Nanobiology program, National Cancer Institute
- April 2006. Review Panel, NIH/NHGRI Genomic Database Resource program.
- May 2005. Review Panel, DOE Genomes to Life program.
- March 2005. Review Panel, NIH/NIDDK Clinical Nutrition Research Units, RFA DK-04-016.
- May 2004. Review panel, NIH National Centers for Biomedical Computing initiative.
- July 2003. Review panel, NIH/NHGRI Encyclopedia of DNA Elements (ENCODE) program.
- Mar. 2003. Review panel, NIH BISTI initiative, pre-NPEBC centers.
- Oct. 2002. NIAID Blue Ribbon Panel on Bioterrorism and Its Implications for Biomedical Research.
- Aug. 2002. NHGRI review panel, RFA HG-02-002, Model Organism Databases.
- Apr. 2002. Site visit panel, Laboratory of Experimental and Computational Biology, National Cancer Institute.
- Oct. 2001-Sept. 2002. Advisory Panel member, NSF Biological Databases and Informatics Program.
- Nov. 2001. Review Panel, NIH Biomedical Information Science and Technology Initiative (BISTI).
- April 2001. Review Panel, NSF, Information Technology Research Program.
- April 2001. Review panel NIH Genetic Sciences study section.
- Feb. 2001. Review Panel, NSF, CISE Research Infrastructure Program.
- June 2000. Genome Study Section member, NHGRI, NIH.
- March 2000. Special Study Section member, Genetic Sciences, NIH.
- July 1999. Site visit committee, National Center for Research Resources, NIH.
- Mar. 1999. SBIR/STTR review panel, Genetic Sciences Initial Review Group, NIH.
- Dec. 1998. Review Panel, NSF Digital Libraries Initiative part II.
- Aug. 1998. Review Panel, National Library of Medicine, NIH.
- Sep. 1998. Review Panel, Natl. Heart, Lung, and Blood Institute, NIH.
- October 1997. Review Panel, NSF, CISE/IRIS Research Instrumentation Program.
- November 1996. Review Panel, NSF, Knowledge Models and Cognitive Systems Program.
- June 1994. Review Panel, NSF, Research Initiation Awards, Database and Expert Systems Program.
- Apr. 1994. Review Panel, NSF, Research on Digital Libraries (a joint initiative with ARPA and NASA).
- Oct. 1993. Review Panel, NSF, CISE/IRIS Research Instrumentation Program.
- Mar. 1993. Review Panel, NSF, Research on Scientific Databases Initiative.

Other program committees and external review committees

Oct. 1998. External review committee, Functional Genomics and Bioinformatics Conf., Virginia Tech Institute of Genomics.

Program committee member, The 14th International Conference on Machine Learning (ICML-97).

Program committee member, Thirteenth National Conference on Artificial Intelligence (AAAI-96).

Program committee member, 8th IEEE International Conference on Tools with Artificial Intelligence, 1996.

Tutorial presentation, "Machine Learning Applications in Molecular Biology," ISMB-96 Conference.

Aug. 1991. Organizing committee, IJCAI Workshop on Representing Knowledge in Medical Decision Support Systems.

Referee for more than 25 journals including *Science* and *Nature*.

Supervision of Graduate Students and Postdoctoral Fellows

Ph.D. students: University of Maryland

Ben Langmead, Ph.D. 2012. Thesis advisor. Assistant Professor, Johns Hopkins University.
 Samuel Angiuoli, Ph.D. 2011. Thesis advisor. Director, Bioinformatics Software Engineering, Institute for Genome Sciences, University of Maryland.
 David Kelley, Ph.D. 2011. Thesis advisor. Postdoctoral fellow, the Broad Institute and Harvard University.
 Michael Schatz, Ph.D. 2010. Thesis advisor. Assistant Professor, Cold Spring Harbor Laboratory.
 Adam Phillippy, Ph.D. 2010. Thesis advisor. Principal Investigator, National Biodefense Analysis and Countermeasures Center (NBACC).
 Bruce (Cole) Trapnell, Ph.D. 2010. Thesis advisor. Postdoctoral fellow, the Broad Institute and Harvard University.
 Derrick Wood, Ph.D. student, enrolled 2008.
 Daehwan Kim, Ph.D. expected June 2013.
 James White, Ph.D. 2010, Applied Mathematics. Dissertation committee member.
 Jessica Miller, Ph.D. 2009, Molec. and Cell Biol. Dissertation committee member.
 Xue Wu, Ph.D. 2008. Dissertation committee member.
 Eugene Melamud, Ph.D. 2006, Molec. and Cell Biol. Dissertation committee member.

Ph.D. students: Johns Hopkins University

Jonathan Allen, Ph.D. September 2006. Thesis advisor. Research scientist, Lawrence Livermore National Laboratory.
 Mihaela Pertea, Ph.D. August 2001. Thesis advisor. Assistant Professor, Johns Hopkins University.
 John Sheppard, Ph.D. January 1997. Thesis advisor. Chaired Professor, Montana State University.
 Sreerama K. Murthy, Ph.D. October 1995. Thesis advisor. Chairman, Teqnum Consultancy Services.
 Lewis Stiller, Ph.D. June 1995. Dissertation committee member.
 Kai Ming Ting, Ph.D. December 1995, University of Sydney, Australia. External examiner.
 David Heath, Ph.D. October 1992. Dissertation committee member.
 Kathleen Romanik, Ph.D. June 1992, University of Maryland. Dissertation committee member.
 Walter Harley, Ph.D. in Psychology, June 1990. Dissertation committee member.

Postdoctoral Fellows and trainees

- Mihai Pop, Ph.D. Johns Hopkins University. Research Scientist in my group, 2000-2005. Currently an Associate Professor (tenured) at the University of Maryland, College Park
- Natalia Volfovsky, Ph.D. Hebrew University. Postdoc 1999-2002. Currently at the National Cancer Institute, Frederick, MD.
- Maria Ermolaeva, Ph.D. Moscow State University. Research Scientist in my group, 1999-2004.
- Pawel Gajer, Ph.D. Research scientist in my group, 2000-2004. Currently at Institute for Genome Sciences, University of Maryland.
- Jonathan Allen, Ph.D., Johns Hopkins University. Currently at Lawrence Livermore National Laboratory..
- Carl Kingsford, Ph.D. Princeton University. Postdoc 2006-2007. Currently an Associate Professor at Carnegie Mellon University.
- Arthur Brady, Ph.D. Tufts University. Postdoc 2008-2011. Currently a Research Scientist at the Institute for Genome Sciences, University of Maryland School of Medicine.
- Todd Treangen, Ph.D. Polytechnic Univ. of Catalonia, Barcelona. Postdoc 2010-2012. Currently a Research Scientist at the National Biodefense Analysis and Countermeasures Center, Battelle National Biodefense Institute.
- Henry Lin, Ph.D. University of California, Berkeley. Postdoc 2010-2011, currently an associate research scientist at Columbia University.

- Tanja Magoc, Ph.D. University of Texas-El Paso. Postdoc 2010-present.
- Stefan Canzar, Ph.D. Saarland University (Saarbrücken, Germany). Postdoc 2012-present.
- Stephan Pabinger, Ph.D. University of Technology, Graz (Austria). Postdoc 2012-2013.

Master's students, University of Maryland:

Derrick Wood, M.S. 2011.
 David Kelley, M.S. 2010.
 Benjamin Langmead, M.S. 2009 (co-advisor).
 Megan Smedinghoff, M.S. 2009.
 Michael Schatz, M.S. 2008.
 Adam Phillippy, M.S. 2008.

Master's students, Johns Hopkins University:

Tugba Suzek, M.S.E. 2001.
 Baris Suzek, M.S.E. 2001.
 Mihaela Pertea, M.S.E. 1998.
 Radu State, M.S.E. 1998.
 Truxton Fulton, M.S.E. 1996.
 Xin Chen, M.S.E. 1996.
 John Rachlin, M.S.E. 1994.
 Suraj Surendrakumar, M.S.E. 1992.
 Scott Cost, M.S.E. 1991.

University Service and Teaching

Courses developed and taught:

- CMSC 828G Bioinformatics for Metagenomics (Univ. of Maryland)
- CMSC 828N/H Computational Gene Finding and Genome Assembly (Univ. of Maryland)
- CS 600.439 Computational Biology (Johns Hopkins University)
- CS 600.435 Artificial Intelligence (Johns Hopkins University)
- CS 600.350 Expert Systems (Johns Hopkins University)
- CS 600.661 Machine Learning (Johns Hopkins University)
- CS 600.665 Natural Language Processing (Johns Hopkins University)

University of Maryland:

Scientific Advisory Committee, Maryland Pathogen Research Institute (MPRI)
 Information Technology Council member, 2007-2010.
 College Appointments, Promotion, and Tenure (APT) committee member, 2007-2008.

John Hopkins University:

Chair, Computer Science Dept. Graduate Admissions Committee, 1993–1995. Committee member, 1992-1996.
 Member of the Steering Committee of the Engineering Faculty Assembly, 1993–1996.
 Member of Computer Science Graduate Student-Faculty Forum, 1995–1997.
 Member of Dean's Review Committee on Academic Computing, 1993–95.
 Member of Computer Science Dept. Equipment Committee, 1990–1995.
 Member of Whiting School Dean's Committee on International Education, 1991–92.
 Manager of Computer Science Undergraduate Computing Lab, 1989–91.
 Member of Faculty Invention Committee 1989–90.