

Curtis Huttenhower

Associate Professor of Computational Biology and Bioinformatics
Department of Biostatistics, School of Public Health, Harvard University

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Academic Appointments

July 2009 - Present	<i>Department of Biostatistics, Harvard School of Public Health</i>
April 2013 - Present	Associate Professor of Computational Biology and Bioinformatics
July 2009 - March 2013	Assistant Professor of Computational Biology and Bioinformatics

Education

November 2008 - June 2009	<i>Lewis-Sigler Institute for Integrative Genomics, Princeton University</i> Supervisor: Dr. Olga Troyanskaya Postdoctoral Researcher
August 2004 - November 2008	<i>Computer Science Department, Princeton University</i> Adviser: Dr. Olga Troyanskaya Ph.D. in Computer Science, November 2008; M.A., June 2006
August 2002 - May 2004	<i>Language Technologies Institute, Carnegie Mellon University</i> Adviser: Dr. Eric Nyberg M.S. in Language Technologies, December 2003
August 1998 - November 2000	<i>Rose-Hulman Institute of Technology</i> B.S. summa cum laude, November 2000 Majored in Computer Science, Chemistry, and Math; Minored in Spanish
August 1996 - May 1998	<i>Simon's Rock College of Bard</i> A.A., May 1998

Awards, Honors, and Scholarships

- Presidential Early Career Award for Scientists and Engineers (Harvard School of Public Health, 2012)
- NSF CAREER award (Harvard School of Public Health, 2010)
- Quantitative and Computational Biology Program Training Fellowship (Princeton University, 2006-2008)
- Association of Princeton Graduate Alumni Teaching Award (Princeton University, 2006)
- Addison-Wesley Computer Science Award (Rose-Hulman Institute of Technology, 2000)
- William Albert Noyes, Sr. Award in Chemistry (Rose-Hulman Institute of Technology, 2000)
- EDS Computer Science Scholarship (Rose-Hulman Institute of Technology, 1998)
- Acceleration to Excellence Program full two-year scholarship (Simon's Rock College of Bard, 1996)

Academic Affiliations

- Systems Biology Program, Harvard Medical School (2011-Present)
- Broad Institute (2010-Present)
- NIH Human Microbiome Project: co-chair, Publications; co-chair, Whole-Genome Shotgun Analysis and Metabolic Reconstruction; member, Steering (2010-2012)
- Harvard Microbial Sciences Initiative (2010-Present)
- Center for the Study of Inflammatory Bowel Diseases (2010-Present)
- Program in Biological Sciences in Public Health, Harvard School of Public Health (2009-Present)
- Dana-Farber/Harvard Cancer Center (2009-Present)

Teaching Experience

Genomic Data Manipulation (BIO508)

Harvard School of Public Health, Boston, MA

Spring 2010 - 2013

- Introduction to tools and techniques needed to obtain, analyze, and interpret modern genome-scale data. Includes a brief overview of Python and statistical methods for high-dimensional data, geared toward biological investigators interpreting their own data or integrating it with results from public repositories.

Instructor

The Johns Hopkins University Center for Talented Youth, Baltimore, MD

June 2006 - August 2006, June 2005 - August 2005, June 2004 - August 2004, June 2000 - August 2000,

Supervisor: Dr. Ronald Bridwell

- Instructed students aged 12-16 in introductory CS. Developed, prepared, and presented complete curricula covering an introduction to the field and to the theory of computation; authored two course textbooks.

Mentor

Princeton Summer Undergraduate Research Experience through The Leadership Alliance, Princeton, NJ

June 2007 - August 2007, Supervisor: Dean David Redman

- Mentored undergraduate students individually and in groups to prepare them for academic careers.

Industry Experience

Software Design Engineer

Microsoft, Redmond, WA

January 2001 - August 2002, Supervisor: Dr. Douglas Potter

- Worked on the Microsoft Natural Language Development Platform, including spelling/grammar checking, language detection software, and a novel morphological processing environment.

Additional Academic Experience

Editorial Boards

Genome Biology, Associate Editor, 2011-Present

Microbiome, Associate Editor, 2011-Present

BMC Bioinformatics, Associate Editor, 2010-Present

Seminar and Conference Organization

Microbiome Research in the Boston Area (MiRiBA), 2011-Present

Emerging Technologies for Translational Bioinformatics symposium co-chair, 2011

Human Microbiome Project Virtual Analysis Jamboree chair, 2011-2012

Princeton Program in Integrative Information, Computer and Application Sciences (PICASso), 2007-2009

Academic Society Memberships

International Society for Computational Biology, 2007-Present

Poster Committee, 2009; Late-Breaking Research Committee, 2010; Education Committee, 2009-Present;

Program Committee, 2012

Life Sciences Society, 2009-2010

Genetics Society of America, 2007-2009

Referee

Nature, NEJM, PNAS, Nature Biotechnology, Nature Methods, Molecular Systems Biology, Genome Research, ISME J, Genome Biology, Nucleic Acids Research, PLoS Computational Biology, Microbiome, Bioinformatics, Journal of Bioinformatics and Computational Biology, BMC Genomics, BMC Bioinformatics, Genomics

Publications

1. Langille MG*, Zaneveld J*, Caporaso JG, McDonald D, Knights D, Reyes JA, Clemente JC, Burkpile DE, Vega Thurber RL, Knight R, Beiko RG, **Huttenhower C**. "Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences." *Nature Biotechnology*, 2013 Sep;31(9):814-21
2. Lee S, Cantarel B, Henrissat B, Gevers D, Birren BW, **Huttenhower C**, Ko G. "Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota." *ISME J*, 2013 Oct 10
3. *Tickle TL, Segata N, Waldron L, Weingart U, **Huttenhower C***. "Two-stage microbial community experimental design." *ISME J*, 2013 Aug 15
4. *Segata N, Boernigen D, Morgan XC, **Huttenhower C***. "PhyloPhlAn is a new method for improved phylogenetic and taxonomic placement of microbes." *Nature Communications*, 2013 Aug 14;4:2304
5. *Boernigen D, Pers TH, Thorrez L, **Huttenhower C**, Moreau Y, Brunak S*. "Concordance of gene expression in human protein complexes reveals tissue specificity and pathology." *Nucleic Acids Research*, 2013 Oct 1;41(18):e171
6. Smeekens SP, **Huttenhower C**, Riza A, van de Veerdonk FL, Zeeuwen PL, Schalkwijk J, van der Meer JW, Xavier RJ, Netea MG, Gevers D. "Skin Microbiome Imbalance in Patients with STAT1/STAT3 Defects Impairs Innate Host Defense Responses." *J. Innate Immunity*, 2013 Jun 22
7. Glass K, **Huttenhower C**, Quackenbush J, Yuan GC. "Passing messages between biological networks to refine predicted interactions." *PLoS ONE*, 2013 May 31;8(5):e64832
8. Larson JL, **Huttenhower C**, Quackenbush J, Yuan GC. "A tiered hidden Markov model characterizes multi-scale chromatin states." *Genomics*, 2013 Jul;102(1):1-7
9. Koren O, Knights D, Gonzalez A, *Waldron L, Segata N, Knight R, **Huttenhower C**, Ley RE*. "A guide to enterotypes across the human body: meta-analysis of microbial community structures in human microbiome datasets." *PLoS Computational Biology*, 2013 e1002863
10. Ballarini A*, *Segata N**, **Huttenhower C**[†], Jousson O[†]. "Simultaneous quantification of multiple bacteria by the BactoChip microarray designed to target species-specific marker genes." *PLoS ONE*, 2013 e55764
11. *Ganzfried BF, Riester M, Haibe-Kains B, Risch T, Tyekucheva S, Jazic I, Wang XV, Ahmadifar M, Birrer MJ, Parmigiani G, **Huttenhower C**, Waldron L*. "curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome." *Database*, 2013 bat013
12. *Waldron L*, Ogino S*, Hoshida Y, Shima K, McCart Reed AE, Simpson PT, Baba Y, Nosho K, Segata N, Vargas AC, Cummings MC, Lakhani SR, Kirkner GJ, Giovannucci E, Quackenbush J, Golub TR, Fuchs CS, Parmigiani G, **Huttenhower C***. "Expression Profiling of Archival Tumors for Long-term Health Studies." *Clinical Cancer Research*, 2012
13. Zhang YJ, Ioerger TR, **Huttenhower C**, Long JE, Sasseti CM, Sacchetti JC, Rubin EJ. "Global Assessment of Genomic Regions Required for Growth in *Mycobacterium tuberculosis*." *PLoS Pathogens*, 2012, 8(9):e1002946
14. *Morgan XC*, Tickle TL*, Sokol H*, Gevers D, Devaney KL, Ward DV, Reyes JA, Shah SA, LeLeiko N, Snapper SB, Bousvaros A, Korzenik J, Sands BE, Xavier RJ, **Huttenhower C***. "Dysfunction of the Intestinal Microbiome in Inflammatory Bowel Disease and Treatment." *Genome Biology*, 2012, 13:R80, [highlighted in Genome Biology 2012, 13:169](#)
15. *Segata N, Waldron L, Ballarini A, Narasimhan V, Jousson O, **Huttenhower C***. "Metagenomic microbial community profiling using unique clade-specific marker genes." *Nature Methods*, 2012 Jun 10. doi: 10.1038/nmeth.2066, [highlighted in Nature Methods 9, 793–794](#)

16. **Huttenhower C***, Gevers D*, Knight R, The Human Microbiome Project Consortium, White O. "Structure, function and diversity of the healthy human microbiome." *Nature*, 2012 486(7402):207-14 [cover article, highlighted in Nature](#). 2012 Jun 13; 486(7402)
17. Methé BA, Nelson KE, Pop M, Creasy HH, Giglio MG, **Huttenhower C**, The Human Microbiome Project Consortium, White O. "A framework for human microbiome research." *Nature*, 2012 486(7402):215-21
18. Abubucker S, *Segata N*, Goll J, Schubert AM, IZARD J, Cantarel BL, Rodriguez-Mueller B, Zucker J, Thiagarajan M, Henrissat B, White O, Kelley ST, Methé B, Schloss PD, Gevers D, Mitreva M, **Huttenhower C**. "Metabolic reconstruction for metagenomic data and its application to the human microbiome." *PLoS Computational Biology*, 2012 Jun;8(6):e1002358
19. Faust K*, *Sathirapongsasuti F**, Raes J†, **Huttenhower C†**. "Microbial Co-occurrence Relationships in the Human Microbiome." *PLoS Computational Biology*, Jul;8(7):e1002606
20. *Segata N*, Haake SK, Mannon P, Lemon KP, *Waldron L*, Gevers D, **Huttenhower C**, IZARD J. "Composition of the adult digestive tract bacterial microbiome based on seven mouth surfaces, tonsils, throat and stool samples." *Genome Biology*, 2012 Jun 14;13(6):R42
21. Goll J, Thiagarajan M, Abubucker S, **Huttenhower C**, Yooseph S, Methé BA. "A case study for large-scale human microbiome analysis using JCVI's Metagenomics Reports (METAREP)." *PLoS ONE*, 2012;7(6):e29044
22. Aagaard K, Riehle K, Ma J, *Segata N*, Mistretta TA, Coarfa C, Raza S, Rosenbaum S, Van den Veyver I, Milosavljevic A, Gevers D, **Huttenhower C**, Petrosino J, Versalovic J. "A metagenomic approach to characterization of the vaginal microbiome signature in pregnancy." *PLoS ONE*, 2012;7(6):e36466
23. Merrick CJ, **Huttenhower C**, Buckee C, Amambua-Ngwa A, Gomez-Escobar N, Walther M, Conway DJ, Duraisingh MT. "Epigenetic Dysregulation of Virulence Gene Expression in Severe Plasmodium falciparum Malaria." *J Infect Dis*. 2012 Apr 12.
24. Yamauchi M, Morikawa T, Kuchiba A, Imamura Y, Qian ZR, Nishihara R, Liao X, *Waldron L*, Hoshida Y, **Huttenhower C**, Chan AT, Giovannucci E, Fuchs C, Ogino S. Assessment of colorectal cancer molecular features along bowel subsites challenges the conception of distinct dichotomy of proximal versus distal colorectum." *Gut*. 2012 Mar 17
25. Morikawa T, Tanaka N, Kuchiba A, Nosho K, Yamauchi M, Hornick JL, Swanson RS, Chan AT, Meyerhardt JA, **Huttenhower C**, Schrag D, Fuchs CS, Ogino S. "Predictors of Lymph Node Count in Colorectal Cancer Resections: Data From US Nationwide Prospective Cohort Studies." *Arch Surg*. 2012
26. *Waldron L*, Pintilie M, Tsao MS, Shepherd FA, **Huttenhower C***, Jurisica I*. "Optimized application of penalized regression methods to diverse genomic data." *Bioinformatics*. 2011 Dec 15;27(24):3399-406
27. *Segata N*, **Huttenhower C**. "Toward an efficient method of identifying core genes for evolutionary and functional microbial phylogenies." *PLoS ONE* 2011;6(9):e24704
28. Kostic AD, Gevers D, Pédamallu CS, Michaud M, Duke F, Earl AM, Ojesina AI, Jung J, Bass AJ, Tabernero J, Baselga J, Liu C, Shivdasani RA, Ogino S, Birren BW, **Huttenhower C**, Garrett WS, Meyerson M. "Genomic analysis identifies association of *Fusobacterium* with colorectal carcinoma." *Genome Res* 2011
29. Sczesnak A, *Segata N*, Qin X, Gevers D, Petrosino JF, **Huttenhower C**, Littman DR*, Ivanov II*. "The genome of Th17 cell-inducing segmented filamentous bacteria reveals extensive auxotrophy and adaptations to the intestinal environment." *Cell Host and Microbe* 2011 Sep 15;10(3):260-72
30. *Segata N*, IZARD J, *Waldron L*, Gevers D, *Miropolsky L*, Garrett WS, **Huttenhower C**. "Metagenomic biomarker discovery and explanation." *Genome Biology* 2011, Jun 24;12(6):R60 [cover article](#)
31. Ballal SA, Gallini CA, *Segata N*, **Huttenhower C**, Garrett WS. "Host and gut microbiota symbiotic factors: lessons from inflammatory bowel disease and successful symbionts." *Cellular Microbiol* 2011, 13(4):508-17

32. Morikawa T, Baba Y, Yamauchi M, Kuchiba A, Nosho K, Shima K, Tanaka N, **Huttenhower C**, Frank DA, Fuchs CS, Ogino S. "STAT3 Expression, Molecular Features, Inflammation Patterns, and Prognosis in a Database of 724 Colorectal Cancers." *Clin Cancer Res* 2011, 17(6):1452-62
33. Wardwell LH, **Huttenhower C**, Garrett WS. "Current concepts of the intestinal microbiota and the pathogenesis of infection." *Curr Infect Dis Rep* 2011, 13(1):28-34
34. Park CY, Hess DC, **Huttenhower C***, Troyanskaya OG*. "Simultaneous Genome-Wide Inference of Physical, Genetic, Regulatory, and Functional Pathway Components." *PLoS Computational Biology* 2010, 6(11)
35. Pop A*, **Huttenhower C***, Iyer-Pascuzzi A, Benfey PN, Troyanskaya OG. "Integrated functional networks of process, tissue, and developmental stage specific interactions in *Arabidopsis thaliana*." *BMC Systems Biology* 2010, 4:180
36. *Sathirapongsasuti JF*, Sathira N, Suzuki Y, **Huttenhower C**, Sugano S. "Ultraconserved cDNA segments in the human transcriptome exhibit resistance to folding and implicate function in translation and alternative splicing." *Nucleic Acids Research* 2011, 39(6):1967-79
37. Tanaka N, **Huttenhower C**, Nosho K, Baba Y, Shima K, Quackenbush J, Haigis KM, Giovannucci EL, Fuchs CS, Ogino S. "Novel Application of Structural Equation Modeling to Correlation Structure Analysis of CpG Island Methylation in Colorectal Cancer." *American Journal of Pathology* 2010, 177(6):2731-40
38. Baba Y, Nosho K, Shima K, **Huttenhower C**, Tanaka N, Hazra A, Giovannucci EL, Fuchs CS, Ogino S. "Hypomethylation of the IGF2 DMR in Colorectal Tumors, Detected by Bisulfite Pyrosequencing, is Associated with Poor Prognosis." *Gastroenterology* 2010, 139(6):1855-64
39. **Huttenhower C**, Hofmann O. "A quick guide to large scale genomic data mining." *PLoS Computational Biology* 2010, 6(5)
40. Baba Y, **Huttenhower C**, Nosho K, Tanaka N, Shima K, Hazra A, Schernhammer ES, Hunter DJ, Giovannucci EL, Fuchs CS, Ogino S. "Epigenomic diversity of colorectal cancer indicated by LINE-1 methylation in a database of 869 tumors." *Molecular Cancer* 2010, 9:125
41. **Huttenhower C***, Mehmood SO*, Troyanskaya OG. "Graphle: Interactive exploration of large, dense graphs." *BMC Bioinformatics* 2009, 10(417)
42. **Huttenhower C***, Mutungu KT*, Indik N, Yang W, Schroeder M, Forman JJ, Troyanskaya OG[†], Collier HA[†]. "Detailing regulatory networks through large scale data integration." *Bioinformatics* 2009, 25(24):3267-74
43. **Huttenhower C***, Hibbs MA*, Myers CL*, Caudy AA, Hess DC, Troyanskaya OG. "The impact of incomplete knowledge on evaluation: an experimental benchmark for protein function prediction." *Bioinformatics* 2009, 25(18):2404-10
44. Chikina MD, **Huttenhower C**, Troyanskaya OG[†], Murphy CT[†]. "Global prediction of tissue-specific gene expression and context-dependent gene networks in *Caenorhabditis elegans*." *PLoS Computational Biology* 2009, 5(6)
45. **Huttenhower C***, Haley EM*, Hibbs MA, Dumeaux V, Barrett DR, Collier HA[†], Troyanskaya OG[†]. "Exploring the human genome with functional maps." *Genome Research* 2009, 19(6):1093-106
46. Hess DC, Myers CL*, **Huttenhower C***, Hibbs MA*, Hayes AP, Paw J, Clore JJ, Mendoza RM, San Luis B, Nislow C, Giaever G, Costanzo M, Troyanskaya OG[†], Caudy AA[†]. "Computationally driven, quantitative experiments discover genes required for mitochondrial biogenesis," *PLoS Genetics* 2009, 5(3)
47. Hibbs MA*, Myers CL*, **Huttenhower C***, Hess DC, Li K, Caudy AA, Troyanskaya OG. "Directing experimental biology: a case study in mitochondrial inheritance," *PLoS Computational Biology* 2009, 5(3)
48. Airoidi EM*, **Huttenhower C***, Gresham D, Lu C, Broach JR, Botstein D[†], Troyanskaya O[†], "Predicting the rate of cellular growth from gene expression states," *PLoS Computational Biology* 2009, 5(1)

49. **Huttenhower C**, Troyanskaya OG. "Assessing the functional structure of genomic data," *Bioinformatics* 2008, 24(13):i330-8
50. **Huttenhower C**, Schroeder M, Chikina MD, Troyanskaya OG. "The Sleipnir library for computational functional genomics," *Bioinformatics* 2008, 24(13):1559-61
51. Brauer MJ, **Huttenhower C***, Airoidi EM*, Rosenstein R, Matese JC, Gresham D, Boer VM, Troyanskaya OG, Botstein D. "Coordination of growth rate, cell cycle, stress response, and metabolic activity in yeast," *Molecular Biology of the Cell* 2008, 19(1):352-67
52. Hibbs MA, Hess DC, Myers CL, **Huttenhower C**, Li K, Troyanskaya OG, "Exploring the functional landscape of gene expression: directed search of large microarray compendia," *Bioinformatics* 2007, 23(20):2692-9
53. **Huttenhower C**, Flamholz AI, Landis JN, Sahi S, Myers CL, Hibbs MA, Siemens NO, Troyanskaya OG, Collier HA. "Nearest Neighbor Networks: clustering expression data based on gene neighborhoods." *BMC Bioinformatics* 2007, 8(250)
54. Chi A*, **Huttenhower C***, Geer LY, Coon JJ, Syka JE, Bai DL, Shabinowitz J, Burke DJ, Troyanskaya OG, Hunt DF. "Analysis of phosphorylation sites on proteins from *Saccharomyces cerevisiae* by electron transfer dissociation (ETD) mass spectrometry." *PNAS* 2007, 104(7):2193-8
55. Sealfon RS, Hibbs MA, **Huttenhower C**, Myers CL, Troyanskaya OG. "GOLEM: an interactive graph-based gene-ontology navigation and analysis tool," *BMC Bioinformatics* 2006, 7(443)
56. **Huttenhower C**, Hibbs MA, Myers CL, Troyanskaya OG. "A scalable method for integration and functional analysis of multiple microarray data sets," *Bioinformatics* 2006, 22(23):2890-7
57. Myers CL, Barrett DR, Hibbs MA, **Huttenhower C**, Troyanskaya OG. "Finding function: evaluation methods for functional genomic data," *BMC Genomics* 2006, 7(1)
58. **Huttenhower C**, Troyanskaya OG. "Bayesian data integration: a functional perspective," *Proceedings of the Computational Systems Bioinformatics Conference* 2006, 341-51
59. Nyberg E, Mitamura T, Callan J, Carbonell J, Frederking R, Collins-Thompson K, Hiyakumoto L, Huang Y, **Huttenhower C**, Judy S, Ko J, Kupse A, Lita L, Pedro V, Svoboda D, Van Durme B. "The JAVELIN question-answering system at TREC 2003: a multi-strategy approach with dynamic planning." 2003
60. **Huttenhower C**, Kinley A. "Development of an intelligent system for organic compound analysis." *Proceedings of the Eleventh Midwest Artificial Intelligence and Cognitive Science Conference* 2000, 85-92
61. **Huttenhower C**, Sherman G. "Extending cwatsets to higher dimensions: an examination of the statistical properties of cwatsets with dimension greater than two." *Spring meeting of the Indiana Section of the Mathematical Association of America* 2000

Book Chapters, Invited Articles, and Technical Reports

- *Boernigen D, Morgan XC, Franzosa EA, Ren B, Xavier RJ, Garrett WS, **Huttenhower C**. "Functional profiling of the gut microbiome in disease-associated inflammation." *Genome Medicine*, 2013 Jul 31;5(7):65*
- *Segata N, Boernigen D, Tickle TL, Morgan XC, Garrett WS, **Huttenhower C**. "Computational meta'omics for microbial community studies." *Molecular Systems Biology*, 2013 May 14;9:666*
- *Brown J, de Vos WM, Distefano PS, Doré J, **Huttenhower C**, Knight R, Lawley TD, Raes J, Turnbaugh P. "Translating the human microbiome." *Nat. Biotechnology* 2013, 31(4):304-8*
- *Morgan XC, **Huttenhower C**. "Human microbiome analysis." *PLoS Computational Biology*, 2013 8(12):e1002808*
- *Morgan XC, **Huttenhower C**. "Biodiversity and Functional Genomics in the Human Microbiome." *Trends in Genetics*, 2013 29(1):51-8*
- *Gevers D, Pop M, Schloss P, **Huttenhower C**. "Bioinformatics for the Human Microbiome Project" *PLoS Computational Biology*, 2012 8(11):e1002779*

- Gevers D, Knight R, Petrosino JF, Huang K, McGuire AL, Birren BW, Nelson KE, White O, Methe BA*, **Huttenhower C***. "The Human Microbiome Project: a community resource for the healthy human microbiome." *PLoS Biology*, *PLoS Biol.* 2012 Aug;10(8):e1001377
- *Waldron L*, Simpson PT, Parmigiani G, **Huttenhower C**. "Report on emerging technologies for translational bioinformatics: a symposium on gene expression profiling for archival tissues." *BMC Cancer*. 2012 Mar 29;12(1):124
- Yamauchi M, Lochhead P, Morikawa T, **Huttenhower C**, Chan AT, Giovannucci E, Fuchs C, Ogino S. "Colorectal cancer: a tale of two sides or a continuum?" *Gut*. 2012 Apr 5
- Adams D, Berger B, Harismendy O, **Huttenhower C**, Liu SX, Myers C, Oshlack A, Rinn J, Walhout M. "Genomics in 2011: challenges and opportunities." *Genome Biol.* 2011 Dec 28;12(12):137
- **Huttenhower C**. "Computational biology: plus c'est la même chose, plus ça change." *Genome Biology*, 2011 Aug 23;12(8):307
- *Waldron L*, Collier HA, **Huttenhower C**. "Integrative Approaches for Microarray Data Analysis." *Methods in Molecular Biology*, 2012;802:157-82
- Livstone MS, Oughtred R, Heinicke S, Vernot B, **Huttenhower C**, Durand D, Dolinski K. "Inferring protein function from homology using the Princeton Protein Orthology Database (P-POD)." *Curr Protoc Bioinformatics* 2011, 6:6.11
- **Huttenhower C**, Myers CL, Hibbs MA, Troyanskaya OG. "Computational analysis of the yeast proteome: understanding and exploiting functional specificity in genomic data." *Methods in Molecular Biology* 2009, 548:273-93
- **Huttenhower C**, Troyanskaya OG. "Analysis of large genomic data collections." Princeton University Doctoral Thesis 2008
- **Huttenhower C**, Nyberg E. "FLOOD: a planning framework for reasoning with linguistic data," Carnegie Mellon University Language Technologies Institute Master's Thesis 2003

Invited Presentations

- "Interaction of Host Gene Expression and the Human Gut Microbiome in Pouchitis," INFORMS Annual Meeting. Minneapolis, MN, 2013 (presented by Levi Waldron)
- "The Human Microbiome Project and beyond: Next steps in understanding health and targeting disease," NCI Symposium on Inflammation, Microbiota, and Cancer. Bethesda, MD, 2013
- "Adding depth to human microbiome studies with multi'omic data integration," International Human Microbiome Congress. Hangzhou, China, 2013
- "Gut microbiome function in inflammatory disease," FASEB Gastrointestinal Tract XV: Epithelia, Microbes, Inflammation and Cancer meeting. Steamboat Springs, CO, 2013
- "Functional analysis of human microbiome metagenomes, metatranscriptomes, and multi'omics," NIH Microbiome Sciences: Vision for the Future workshop. Bethesda, MD, 2013
- "The Human Microbiome Project and beyond: From microbial surveys to mechanisms of interaction in the human microbiome," Gordon Research Conference on Applied and Environmental Microbiology. South Hadley, MA, 2013
- "From Microbial Surveys to Mechanisms of Interaction in the Gut Microbiome," Gordon Research Conference on Mucosal Health and Disease. Easton, MA, 2013
- "From Microbial Surveys to Mechanisms of Interaction in the Human Microbiome," Memorial Sloan Kettering Cancer Center seminar. New York, NY, 2013
- "Bug bytes: bioinformatics for the human microbiome in health and disease," Canadian Student Health Research Forum. Alberta, Canada, 2013

- "High-precision functional profiling of metagenomes and metatranscriptomes," Enterics Research Investigational Network Cooperative Research Center meeting. Traverse City, MI, 2013
- "From microbial surveys to mechanisms of interaction in the human microbiome," 113th Meeting of the American Society for Microbiology. Denver, CO, 2013
- "Cataloging genes and pathways in the human microbiome," Genomic Standards Consortium Workshop. Bethesda, MD, 2013
- "From microbes to microbiota and back: using thousands of genomes to understand thousands of metagenomes," Harvard School of Public Health Bioinformatics Core Forum. Boston, MA, 2013
- "High-precision functional profiling of metagenomes and metatranscriptomes using unique marker sequences," Janelia Farms Biological Sequence Analysis and Probabilistic Models conference. Ashburn, VA, 2013
- "From microbes to microbiota and back: using thousands of genomes to understand thousands of metagenomes," Symposium and Workshop on New Methods for Phylogenomics. Austin, TX, 2013
- "Computational methods for meta'omic characterization of the human microbiome," Los Alamos National Laboratory Center for Nonlinear Studies seminar. Los Alamos, NM, 2013
- "From microbial surveys to mechanisms of interaction in the human microbiome," Keystone Gut Microbiome conference. Taos, NM, 2013
- "Planning for functional microbial community analysis in IBD genetics," Inflammatory Bowel Disease Genetics Consortium meeting. Bethesda, MD, 2013
- "Bug bytes: Computational analysis methods for microbial communities," University of Oregon BioBE center seminar. Eugene, OR, 2013
- "From microbial surveys to mechanisms of interaction in the human microbiome," University of Colorado at Boulder BioFrontiers Institute seminar. Boulder, CO, 2013
- "Predicting biomolecular mechanisms in complex specific functional relationship networks," University of Chicago seminar. Chicago, IL, 2013 (presented by Daniela Boernigen)
- "Detailing the human microbiome with meta'omics," New England Primate Research Center. Southboro, MA, 2012
- "A meta'omic microscope: detailing the human microbiome," Broad Institute annual retreat. Boston, MA, 2012
- "Post-Human Microbiome Project: Predicting the Next Decade of Research," Center for the Study of Inflammatory Bowel Disease workshop. Boston, MA, 2012
- "Computational methods for meta'omic characterization of the human microbiome," Forsyth Institute seminar. Cambridge, MA, 2012
- "Computational methods for meta'omic characterization of the human microbiome," Procter and Gamble BioFusion Symposium. Cincinnati, OH, 2012
- "Bug bytes: Computational analysis methods for microbial communities," Army Research Office workshop on the skin microbiome. Boulder, CO, 2012
- "Personalized Medicine, Bioinformatics, and Biotechnology," Saint Francis University Science Day. Loretto, PA, 2012
- "The Human Microbiome, Or: How I Learned to Stop Worrying and Love Metagenomic Sequencing," Harvard Systems Biology Program annual retreat. Portsmouth, NH, 2012
- "Meta'omic Characterization of Microbial Community Function in Health and Disease," Mount Sinai School of Medicine Department of Health Evidence and Policy Grand Rounds. New York, NY, 2012
- "Bug bytes: Computational analysis methods for microbial communities," Carnegie Mellon Lane Center for Computational Biology seminar. Pittsburgh, PA, 2012
- "Identifying species, strains, and functional roles in metagenomes and metatranscriptomes," 19th International Meeting on Microbial Genomics at Lake Arrowhead. Lake Arrowhead, CA, 2012

- "Meta'omic characterization of microbial community function in health and disease," American Society for Microbiology Conference on Beneficial Microbes. San Antonio, TX, 2012
- "Microbial community bioinformatics: identifying species, strains, and functions in the human microbiome," US-Russia Workshop on the Human Microbiome. Moscow, Russia, 2012
- "Bug bytes: bioinformatics for metagenomics and microbial community analysis," Lewis-Sigler Institute for Integrative Genomics seminar. Princeton, NJ, 2012
- "Bug bytes: bioinformatics for metagenomics and microbial community analysis," 8th International Purdue Symposium on Statistics. West Lafayette, IN, 2012
- "Identifying Species, Strains, and Functional Roles in the Microbiome," 112th Meeting of the American Society for Microbiology. San Francisco, CA, 2012
- "Reducing microbial unemployment: functional roles in the human microbiome," Biogen Idec symposium on mucosal immunology. Cambridge, MA, 2012
- "Reducing microbial unemployment: functional roles in the human microbiome," Broad Metabolic Initiative seminar. Cambridge, MA, 2012
- "Bug bytes: computational methods for microbial community analysis," Woods Hole Marine Biology Laboratory seminar. Woods Hole, MA, 2012
- "Reducing microbial unemployment: functional roles in the human microbiome," International Human Microbiome Congress. Paris, France, 2012
- "Understanding the role of NFkB systems biology in prostate cancer using pathway reconstruction," Prostate Cancer SPORE. Boston, MA, 2012 (presented by Daniela Boernigen)
- "Computational tools for functional analysis of microbial communities," Cloud Computing for the Microbiome Workshop. Boulder, CO, 2012
- "Gene expression profiling of archival tissues for long-term health studies," Program in Molecular and Genetic Epidemiology. Boston, MA, 2012 (presented by Levi Waldron)
- "Reducing microbial unemployment: functional roles in the human microbiome," New York University Medical School seminar. New York, NY, 2012
- "Functional Aspects of the Intestinal Microbiome in Inflammatory Bowel Disease and Treatment," Crohn's and Colitis Foundation of America symposium. Ft. Lauderdale, FL, 2012
- "Reducing microbial unemployment: functional roles in the human microbiome," MIT Computer Science and Artificial Intelligence Laboratory seminar. Cambridge, MA, 2012
- "Charting the function of microbes and microbial communities," University of Idaho Initiative for Bioinformatics and Evolutionary Studies (IBEST) seminar. Moscow, IA, 2011
- "Functional and structural diversity in the human microbiome," Vanderbilt University Center for Human Genetics Research symposium. Nashville, TN, 2011
- "Microbial community function and diversity in the Human Microbiome Project," Harvard University Microbial Sciences Initiative seminar. Cambridge, MA, 2011
- "Personalized Medicine, Bioinformatics, and Biotechnology," Saint Francis University Science Day. Loretto, PA, 2011
- "Functional metagenomics of the human microbiome in health and disease," University of North Carolina at Charlotte seminar. Charlotte, NC, 2011
- "Large scale genomic data integration for functional metagenomics," Keynote address at the Student Council Symposium of the 19th Annual International Conference on Intelligent Systems for Molecular Biology. Vienna, Austria, 2011
- "Metagenomic biomarker discovery and the human microbiome," Microbial Systems (and Beyond) Seminar @ Parsons Laboratory, MIT. Boston, MA, 2011 (presented by Nicola Segata)

- "Computational Metagenomics and the Human Microbiome", DFCI Center for Cancer Computational Biology seminar. Boston, MA, 2011
- "Metabolic Reconstruction in Microbial Communities," Beyond Sequencing conference. San Francisco, CA, 2011
- "Functional metagenomics of the human microbiome in health and disease," Massachusetts General Hospital Gastroenterology seminar. Cambridge, MA, 2011
- "Understanding the Human Microbiome through Data Integration," Bio-IT World Conference and Expo. Boston, MA, 2011
- "Large scale genomic data integration for functional metagenomics," University of Maryland, Baltimore County. Baltimore, MD, 2010
- "Personalized Medicine, Bioinformatics, and Biotechnology," Saint Francis University Science Day. Loretto, PA, 2010
- "Linking Microbiome Pathways to Disease in MetaHIT and the HMP," Center for the Study of Inflammatory Bowel Disease workshop. Boston, MA, 2010.
- "Understanding gene function in the human microbiome," Frontiers in Mucosal Immunology symposium. Boston, MA, 2010.
- "Large scale genomic data integration for functional metagenomics," Indiana University School of Informatics seminar. Bloomington, IN, 2010
- "Large scale genomic data integration for functional metagenomics," Johns Hopkins University Center for Computational Genomics seminar. Baltimore, MD, 2010
- "Supervised and unsupervised methods for large scale genomic data integration," Boston University Systems Biology seminar. Boston, MA, 2010
- "Personalized Medicine, Bioinformatics, and Biotechnology," Saint Francis University Science Day. Loretto, PA, 2009
- "Analyzing large genomic data collections," Georgia Tech - Oak Ridge National Lab International Conference on Bioinformatics. Atlanta, GA, 2009
- "Answering biological questions using large genomic data collections," Mount Sinai School of Medicine Systems Biology seminar. New York, NY, 2009
- "Microarray analysis," Cold Spring Harbor Laboratory Programming for Biology course. Cold Spring Harbor, NY, 2008
- "Integration and functional analysis of microarray datasets," Princeton Program in Integrative Information, Computer and Application Sciences (PICASs). Princeton, NJ, 2006

Presentations

- "ARepA: automated repository acquisition for standardized high-throughput data retrieval, normalization, and analysis," 21st Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Berlin, Germany, 2013 (presented by Daniela Boernigen)
- "Metagenomic inference and biomarker discovery for the gut microbiome in inflammatory bowel disease," 21st Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Berlin, Germany, 2013 (presented by Timothy Tickle)
- "Tiered meta'omic study designs and clinical covariate analysis in the microbiome," University of North Carolina at Charlotte seminar. Charlotte, NC, 2012 (presented by Timothy Tickle)
- "Predicting biomolecular mechanisms in complex-specific functional relationship networks in prostate cancer," Memorial Sloan-Kettering Cancer Center Second Annual Symposium on Systems Biology of Diversity in Cancer. New York, NY, 2012 (presented by Daniela Boernigen)
- "Computational methods for shotgun metagenomics," Bertinoro Computational Biology meeting. Bertinoro, Italy, 2012 (presented by Nicola Segata)

- "Fast and accurate metagenomic profiling of microbial community composition using unique clade-specific marker genes," 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Long Beach, CA, 2012 (presented by Nicola Segata)
- "A Predictive Gene Expression Model for quantifying Plasmodium falciparum red blood cell stages," 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Long Beach, CA, 2012 (presented by Vagheesh Narasimhan)
- "Identifying tissue specificity of protein complexes based on a global map of human expression data," 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Long Beach, CA, 2012 (presented by Daniela Boernigen)
- "Microbial community function and biomarker discovery in the human microbiome," Beyond the Genome. Boston, MA, 2011 (presented by Nicola Segata)
- "Scalable metabolic reconstruction for metagenomic data and the human microbiome," 19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria, 2011
- "Metagenomic Biomarker Discovery and Explanation," 19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria, 2011 (presented by Nicola Segata)
- "Metabolic Reconstruction for Metagenomic Data and the Human Microbiome," Keystone Symposium on Microbial Communities. Breckenridge, CO, 2011
- "Metabolic Reconstruction in Microbial Communities," International Human Microbiome Congress. Vancouver, Canada, 2011
- "Using all the data: Large scale biological data mining for functional genomics and metagenomics," 18th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2010
- "Computational methodology for microbial and metagenomic characterization using large scale functional genomic data integration," Keystone Symposium on Biomolecular Interaction Networks: Function and Disease. Quebec, Canada, 2010
- "Exploring the human genome with functional maps," 17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Stockholm, Sweden, 2009
- "Detailing regulatory networks through large scale data integration," 5th Annual RECOMB Satellite on Regulatory Genomics. Boston, MA, 2008
- "Assessing the functional structure of genomic data," 16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Toronto, Canada, 2008
- "Growth-specific programs of gene expression," 16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Toronto, Canada, 2008
- "*S. cerevisiae* mitochondria: validating predictions from microarray integration," 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria, 2007
- "Bayesian data integration: a functional perspective," Computational Systems Bioinformatics (CSB) Conference. Stanford, CA, 2006

Posters

- "The oral microbiome in head and neck cancer," Broad Institute annual retreat. Boston, MA, 2013 (presented by Boyu Ren)
- "Biogeography of the rhesus macaque gut microbiome and its metabolic response to alcohol consumption," Biology in Public Health annual retreat. Woods Hole, MA, 2013 (presented by Koji Yasuda)
- "Gene expression profiling of archival tumor tissues for long-term health studies," Broad Institute annual retreat. Boston, MA, 2012 (presented by Levi Waldron)

- "Species-Level Co-Variation and Co-Occurrence Patterns in the Human Microbiome," 19th International Meeting on Microbial Genomics at Lake Arrowhead. Lake Arrowhead, CA, 2012 (presented by Emma Schwager)
- "Assessing the gastrointestinal microbiome through metatranscriptomics in a large prospective cohort," 14th International Symposium on Microbial Ecology. Copenhagen, Denmark, 2012 (presented by Xochitl Morgan)
- "Gene expression profiling of archival tumor tissues for long-term health studies," 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Long Beach, CA, 2012 (presented by Levi Waldron)
- "Selecting microbial communities of interest based on marker gene sequence data," 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Long Beach, CA, 2012 (presented by Timothy Tickle)
- "Fast and accurate metagenomic profiling of microbial community composition using unique clade-specific marker genes," 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Long Beach, CA, 2012 (presented by Nicola Segata)
- "Microbial community membership at the species and strain level in the human gut," The Microbiome symposium. Keystone, CO, 2012 (presented by Timothy Tickle)
- "Fast and accurate metagenomic profiling of microbial community composition using unique clade-specific marker genes," International Human Microbiome Congress. Paris, France, 2012 (presented by Nicola Segata)
- "Inferring microbial community function from taxonomic composition," International Human Microbiome Congress. Paris, France, 2012 (presented by Morgan Langille)
- "Gene expression profiling of archival tumor tissues for long-term health studies," Emerging Technologies for Translational Bioinformatics symposium. Boston, MA, 2011 (presented by Levi Waldron)
- "Scalable metabolic reconstruction for metagenomic data and the human microbiome," 19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria, 2011
- "Metagenomic Biomarker Discovery and Explanation," 19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria, 2011 (presented by Nicola Segata)
- "A sequence-based method identifying core genes for evolutionary and functional microbial phylogenies," 19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria, 2011 (presented by Nicola Segata)
- "Optimized application of penalized regression methods to diverse genomic data," 19th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria, 2011 (presented by Levi Waldron)
- "Whole-genome transcriptome profiling of archival tissue blocks by DASL," Keystone Symposium on the Cancer Genome. Boston, MA, 2011 (presented by Levi Waldron)
- "Metabolic reconstruction for metagenomic data and the human microbiome," Keystone Symposium on Microbial Communities. Breckenridge, CO, 2011
- "Scalable metabolic reconstruction for metagenomic data and the human microbiome," International Human Microbiome Congress. Vancouver, Canada, 2011
- "Metagenomic Biomarker Discovery and Explanation," International Human Microbiome Congress. Vancouver, Canada, 2011 (presented by Nicola Segata)
- "Robust biomarker development through integrative analysis of gene expression arrays," Program in Quantitative Genomics symposium. Boston, MA, 2010.
- "Computational methodology for microbial and metagenomic characterization using large scale functional genomic data integration," Keystone Symposium on Biomolecular Interaction Networks: Function and Disease. Quebec, Canada, 2010
- "Biological network integration and mining for microbial community analysis," Neural Information Processing Systems (NIPS). Vancouver, Canada, 2009

- "Orthology-based functional transfer in microbial communities," RECOMB Systems Biology Satellite. Boston, MA, 2009
- "HEFalMp: Integrating 30,000 experimental conditions to predict systems-level relationships in *H. sapiens*," 17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Stockholm, Sweden, 2009
- "Assessing the functional structure of genomic data," 16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Toronto, Canada, 2008
- "Predicting growth rate from gene expression signatures," Yeast Genetics and Molecular Biology Meeting. Toronto, Canada, 2008
- "*S. cerevisiae* Mitochondria: Validating Predictions from Microarray Integration," 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Vienna, Austria, 2007
- "A General Methodology for Integration of Microarray Data," Computational Systems Bioinformatics (CSB) Conference. Stanford, CA, 2005

Software

- *PICRUST* <http://picrust.github.com>
Metagenome inference from 16S and other marker gene microbial community profiling
- *CCREPE* <http://huttenhower.sph.harvard.edu/ccrepe>
R package for significant ecological network inference in compositional data
- *ShortBRED* <http://huttenhower.sph.harvard.edu/shortbred>
Unique marker sequences for high-precision, high-throughput meta'omic functional profiling
- *MaAsLin* <http://huttenhower.sph.harvard.edu/maaslin>
Multivariate linear models for biomarker discovery in partially confounded microbial community data
- *microPITA* <http://huttenhower.sph.harvard.edu/micropita>
Experimental design for tiered studies of microbial communities and the human microbiome
- *PhyloPhlAn* <http://huttenhower.sph.harvard.edu/phylophlan>
Phylogenetic marker prediction and application to taxonomic classification of new genomes
- *GraPhlAn* <http://huttenhower.sph.harvard.edu/graphlan>
Open source scriptable visualization for tree-associated continuous and categorical data
- *MetaPhlAn* <http://huttenhower.sph.harvard.edu/metaphlan>
Rapid species-level taxonomic relative abundance profiling from metagenomic data
- *HUMAnN* <http://huttenhower.sph.harvard.edu/humann>
Efficient metabolic and functional gene and pathway reconstruction from metagenomic data
- *LEfSe* <http://huttenhower.sph.harvard.edu/lefse>
Biomarker detection for metagenomic data incorporating statistical significance and biological consistency
- *HEFalMp* <http://function.princeton.edu/hefalmp>
Functional maps of the human genome generated by integrating ~30,000 experimental results
- *Sleipnir* <http://huttenhower.sph.harvard.edu/sleipnir>
Open-source C/C++ library for large scale computational functional genomics
- *COALESCE* <http://function.princeton.edu/coalesce>
Regulatory module inference and scalable expression data biclustering
- *Graphle* <http://function.princeton.edu/graphle>
Open-source Java applet and server for interactive exploration of large biological network compendia
- *Growth Rate* <http://function.princeton.edu/growthrate>
Tools for predicting a cellular culture's growth rate based on gene expression data

- *MEFIT* <http://function.princeton.edu/mefit>
Web-based interface to integration results from ~200 *S. cerevisiae* expression conditions
- *Nearest Neighbor Networks* <http://function.princeton.edu/nnn>
Open-source Java software for clustering based on reciprocal nearest neighborhoods

Patents

- 7490034, Lexicon with sectionalized data and method of using the same
- 7617089, Method and apparatus for compiling two-level morphology rules
- Application 20040193399, System and method for word analysis
- Application 20040148170, Statistical classifiers for spoken language understanding and command/control scenarios