

## Curtis Huttenhower

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

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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

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### Education

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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

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### Awards, Honors, and Scholarships

- ISCB Overton Prize (Harvard School of Public Health, 2015)
- eLife Sponsored Presentation Series early career award (Harvard School of Public Health, 2014)
- 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

- HMS Systems Biology Program (2011-Present)
- Broad Institute, Associate Member (2010-Present)
- Harvard Microbial Sciences Initiative (2010-Present)
- MGH Center for the Study of Inflammatory Bowel Diseases (2010-Present)
- HSPH Program in Biological Sciences in 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 - 2014

- <http://huttenhower.sph.harvard.edu/bio508>
- 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.

### Introduction to Data Structures and Algorithms (BIO514)

Harvard School of Public Health, Boston, MA

Spring 2014

- Analysis of algorithms for biostatisticians and computational biologists. Introduces the basic concepts of data structure modeling, algorithmic efficiency, runtime and space analysis, and common algorithm design patterns. Also provides an overview of numerical analysis algorithms and approximations for solving common mathematical and statistical computing challenges.

### Introduction to Systems Biology (BI410/510)

University of Oregon, Eugene, OR

Fall 2014

- Introduction to systems biology, including overviews of systems concepts, dynamical and stochastic systems, biological network analysis, and quantitative metabolic and regulatory modeling.

### 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**

### Advisory Boards/Directorships

Steering Committee, NIAID Genomic Centers for Infectious Diseases, 2014-Present

Scientific Advisory Board, American Microbiome Institute, 2014-Present

Co-Director, Center for Characterizing the Gut Microbial Ecosystem in Inflammatory Bowel Disease, 2013-Present

Scientific Advisory Board, Seres Health, 2013-Present

Co-Chair, Publications, Analysis, and Metabolic Reconstruction, NIH Human Microbiome Project, 2010-2012

### Editorial Boards

Genome Biology, Associate Editor, 2011-Present

Microbiome, Associate Editor, 2011-Present

BMC Bioinformatics, Associate Editor, 2010-Present

### 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, 2015

Life Sciences Society, 2009-2010

Genetics Society of America, 2007-2009

### Referee

Nature, Science, NEJM, Cell, PNAS, Nature Biotechnology, Nature Medicine, 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 (advisees in italics)

1. Mima K, Sukawa Y, Nishihara R, Qian ZR, Yamauchi M, Inamura K, Kim SA, Masuda A, Nowak JA, Noshu K, *Kostic AD*, Giannakis M, Watanabe H, Bullman S, Milner DA, Harris CC, Giovannucci E, Garraway LA, Freeman GJ, Dranoff G, Chan AT, Garrett WS, **Huttenhower C**, Fuchs CS, Ogino S. "Fusobacterium nucleatum and T Cells in Colorectal Carcinoma." *JAMA Oncol.* 2015 Jun 4
2. *Börnigen D*, Moon YS, *Rahnavard G*, *Waldron L*, *McIver L*, *Shafquat A*, *Franzosa EA*, *Miropolsky L*, *Sweeney C*, *Morgan XC*, Garrett WS, **Huttenhower C**. "A reproducible approach to high-throughput biological data acquisition and integration." *PeerJ.* 2015 Mar 31;3:e791
3. Asnicar F, *Weingart G*, *Tickle TL*, **Huttenhower C**, *Segata N*. "Compact graphical representation of phylogenetic data and metadata with GraPhlAn." *PeerJ.* 2015 Jun 18;3:e1029
4. Anahtar MN, Byrne EH, Doherty KE, Bowman BA, Yamamoto HS, Soumillon M, Padavattan N, Ismail N, Moodley A, Sabatini ME, Ghebremichael MS, Nusbaum C, **Huttenhower C**, Virgin HW, Ndung'u T, Dong KL, Walker BD, Fichorova RN, Kwon DS. "Cervicovaginal bacteria are a major modulator of host inflammatory responses in the female genital tract." *Immunity.* 2015 May 19;42(5):965-76
5. *Franzosa EA*, Huang K, Meadow JF, Gevers D, Lemon KP, Bohannon BJ, **Huttenhower C**. "Identifying personal microbiomes using metagenomic codes." *Proc Natl Acad Sci U S A.* 2015 Jun 2;112(22):E2930-8 highlighted in Proc Natl Acad Sci U S A. 2015 Jun 2;112(22):6778-9
6. *Morgan XC*, Kabakchiev B, *Waldron L*, Tyler AD, *Tickle TL*, Milgrom R, Stempak JM, Gevers D, Xavier RJ, Silverberg MS, **Huttenhower C**. "Associations between host gene expression, the mucosal microbiome, and clinical outcome in the pelvic pouch of patients with inflammatory bowel disease." *Genome Biol.* 2015 Apr 8;16(1):67
7. *Yasuda K*, *Oh K*, *Ren B*, *Tickle TL*, *Franzosa EA*, Wachtman LM, Miller AD, Westmoreland SV, Mansfield KG, Vallender EJ, Miller GM, Rowlett JK, Gevers D, **Huttenhower C**, *Morgan XC*. "Biogeography of the intestinal mucosal and lumenal microbiome in the rhesus macaque." *Cell Host Microbe*, 2015 Mar 11;17(3):385-91 cover article
8. Haberman Y, *Tickle TL*, Dexheimer PJ, Kim MO, Tang D, Karns R, Baldassano RN, Noe JD, Rosh J, Markowitz J, Heyman MB, Griffiths AM, Crandall WV, Mack DR, Baker SS, **Huttenhower C**, Keljo DJ, Hyams JS, Kugathasan S, Walters TD, Aronow B, Xavier RJ, Gevers D, Denson LA. "Pediatric Crohn's disease patients exhibit specific ileal transcriptome and microbiome signature." *J Clin Invest*, 2015 Mar 2;125(3):1363
9. Pelle KG\*, *Oh K\**, Buchholz K, *Narasimhan V*, *Joice R*, Milner DA, Brancucci NM, Ma S, Voss TS, Ketman K, Seydel KB, Taylor TE, Barteneva NS, **Huttenhower C**†, Marti M†. "Transcriptional profiling defines dynamics of parasite tissue sequestration during malaria infection." *Genome Med*, 2015 Feb 27;7(1):19
10. *Kostic AD*, Gevers D, Siljander H, Vatanen T, Hyötyläinen T, Hämäläinen AM, Peet A, Tillmann V, Pöhö P, Mattila I, Lähdesmäki H, *Franzosa EA*, Vaarala O, de Goffau M, Harmsen H, Ilonen J, Virtanen SM, Clish CB, Orešič M, **Huttenhower C**, Knip M; DIABIMMUNE Study Group, Xavier RJ. "The Dynamics of the Human Infant Gut Microbiome in Development and in Progression toward Type 1 Diabetes." *Cell Host Microbe*, 2015 Feb 11;17(2):260-73
11. *Knights D*, Silverberg MS, Weersma RK, Gevers D, Dijkstra G, Huang H, Tyler AD, van Sommeren S, Imhann F, Stempak JM, Huang H, Vangay P, Al-Ghalith GA, Russell C, Sauk J, Knight J, Daly MJ, **Huttenhower C**, Xavier RJ. "Complex host genetics influence the microbiome in inflammatory bowel disease." *Genome Med*, 2014 Dec 2;6(12):107
12. Zhao SD, Parmigiani G, **Huttenhower C**, *Waldron L*. "Más-o-menos: a simple sign averaging method for discrimination in genomic data analysis." *Bioinformatics*, 2014 Nov 1;30(21):3062-9
13. Bernau C, Riester M, Boulesteix AL, Parmigiani G, **Huttenhower C**, *Waldron L*, Trippa L. "Cross-study validation for the assessment of prediction algorithms." *Bioinformatics*, 2014 Jun 15;30(12):i105-12
14. *Franzosa EA*, *Morgan XC*, *Segata N*, *Waldron L*, *Reyes J*, Earl AM, Giannoukos G, Boylan MR, Ciulla D, Gevers D, IZARD J, Garrett WS, Chan AT, **Huttenhower C**. "Relating the metatranscriptome and metagenome of the human gut." *Proc Natl Acad Sci*, 2014 Jun 3;111(22):E2329-38
15. Tong M, McHardy I, Ruegger P, Goudarzi M, Kashyap PC, Haritunians T, Li X, Graeber TG, *Schwager E*, **Huttenhower C**, Fornace AJ Jr, Sonnenburg JL, McGovern DP, Borneman J, Braun J. "Reprogramming of gut

- microbiome energy metabolism by the FUT2 Crohn's disease risk polymorphism." *ISME J*, 2014 Nov;8(11):2193-206
16. Riestler M, Wei W, Waldron L, Culhane AC, Trippa L, Oliva E, Kim SH, Michor F, **Huttenhower C**, Parmigiani G, Birrer MJ. "Risk Prediction for Late-Stage Ovarian Cancer by Meta-analysis of 1525 Patient Samples." *JNCI*, 2014 Apr 3
  17. Waldron L, Haibe-Kains B, Culhane AC, Riestler M, Ding J, Wang XV, Ahmadifar M, Tyekucheva S, Bernau C, Risch T, Ganzfried BF, **Huttenhower C**, Birrer M, Parmigiani G. "Comparative Meta-analysis of Prognostic Gene Signatures for Late-Stage Ovarian Cancer." *JNCI*, 2014 Apr 3
  18. Gevers D, Kugathasan S, Denson LA, Vázquez-Baeza Y, Van Treuren W, Ren B, Schwager E, Knights D, Song SJ, Yassour M, Morgan XC, Kostic AD, Luo C, González A, McDonald D, Haberman Y, Walters T, Baker S, Rosh J, Stephens M, Heyman M, Markowitz J, Baldassano R, Griffiths A, Sylvester F, Mack D, Kim S, Crandall W, Hyams J, **Huttenhower C**, Knight R, Xavier RJ. "The treatment-naive microbiome in new-onset Crohn's disease." *Cell Host and Microbe*, 2014 Mar 12;15(3):382-92 [cover article](#)
  19. Rooks MG, Veiga P, Wardwell-Scott LH, Tickle T, Segata N, Michaud M, Gallini CA, Beal C, van Hylckama-Vlieg JE, Ballal SA, Morgan XC, Glickman JN, Gevers D, **Huttenhower C**, Garrett WS. "Gut microbiome composition and function in experimental colitis during active disease and treatment-induced remission." *ISME J*, 2014 Feb. 6
  20. Huang K, Brady A, Mahurkar A, White O, Gevers D, **Huttenhower C**, Segata N. "MetaRef: a pan-genomic database for comparative and community microbial genomics." *Nucleic Acids Research*, 2014 Jan;42:D617-24
  21. Scher JU, Sczesnak A, Longman RS, Segata N, Ubeda C, Bielski C, Rostron T, Cerundolo V, Pamer EG, Abramson SB, **Huttenhower C**, Littman DR. "Expansion of intestinal *Prevotella copri* correlates with enhanced susceptibility to arthritis." *eLife*, 2013 Nov 5;2:e01202, [highlighted](#) in *Nature Reviews Microbiology* 2014 Jan;12(1):5 and *Nature Reviews Rheumatology* 2014 Jan;10(1):2
  22. Langille MG<sup>\*</sup>, Zaneveld J<sup>\*</sup>, Caporaso JG, McDonald D, Knights D, Reyes JA, Clemente JC, Burkepile 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
  23. McHardy IH, Goudarzi M, Tong M, Ruegger PM, Schwager E, Weger JR, Graeber TG, Sonnenburg JL, Horvath S, **Huttenhower C**, McGovern DP, Fornace AJ Jr, Borneman J, Braun J. "Integrative analysis of the microbiome and metabolome of the human intestinal mucosal surface reveals exquisite inter-relationships." *Microbiome*, 2013 Jun 5;1(1):17
  24. Morrow AL, Lagomarcino AJ, Schibler KR, Taft DH, Yu Z, Wang B, Altaye M, Wagner M, Gevers D, Ward DV, Kennedy MA, **Huttenhower C**, Newburg DS. "Early microbial and metabolomic signatures predict later onset of necrotizing enterocolitis in preterm infants." *Microbiome*, 2013 Apr 16;1(1):13
  25. Joice R<sup>\*</sup>, Narasimhan V<sup>\*</sup>, Montgomery J, Sidhu AB, Oh K, Meyer E, Pierre-Louis W, Seydel K, Milner D, Williamson K, Wiegand R, Ndiaye D, Daily J, Wirth D, Taylor T, **Huttenhower C**<sup>†</sup>, Marti M<sup>†</sup>. "Inferring developmental stage composition from gene expression in human malaria." *PLoS Computational Biology*, 2013 Dec;9(12):e1003392
  26. Zhang YJ, Reddy MC, Ioerger TR, Rothchild AC, Dartois V, Schuster BM, Trauner A, Wallis D, Galaviz S, **Huttenhower C**, Sacchettini JC, Behar SM, Rubin EJ. "Tryptophan biosynthesis protects mycobacteria from CD4 T-cell-mediated killing." *Cell*, 2013 Dec 5;155(6):1296-308
  27. 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
  28. Tickle TL, Segata N, Waldron L, Weingart U, **Huttenhower C**. "Two-stage microbial community experimental design." *ISME J*, 2013 Aug 15
  29. 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
  30. 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

31. 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
32. 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
33. 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
34. 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
35. 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
36. 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
37. Waldron L\*, Ogino S\*, Hoshida Y, Shima K, McCart Reed AE, Simpson PT, Baba Y, Noshio 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
38. Zhang YJ, Ioerger TR, **Huttenhower C**, Long JE, Sasseti CM, Sacchettini JC, Rubin EJ. "Global Assessment of Genomic Regions Required for Growth in Mycobacterium tuberculosis." *PLoS Pathogens*, 2012, 8(9):e1002946
39. 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
40. 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
41. **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)
42. 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
43. 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
44. Faust K\*, Sathirapongsasuti F\*, Raes J†, **Huttenhower C**†. "Microbial Co-occurrence Relationships in the Human Microbiome." *PLoS Computational Biology*, Jul;8(7):e1002606
45. 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
46. Goll J, Thiagarajan M, Abubucker S, **Huttenhower C**, Yooseph S, Methe BA. "A case study for large-scale human microbiome analysis using JCVI's Metagenomics Reports (METAREP)." *PLoS ONE*, 2012;7(6):e29044
47. 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

48. 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.
49. 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
50. 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
51. *Waldron L*, Pintilie M, Tsao MS, Shepherd FA, **Huttenhower C**<sup>\*</sup>, Jurisica I<sup>\*</sup>. "Optimized application of penalized regression methods to diverse genomic data." *Bioinformatics*. 2011 Dec 15;27(24):3399-406
52. *Segata N*, **Huttenhower C**. "Toward an efficient method of identifying core genes for evolutionary and functional microbial phylogenies." *PLoS ONE* 2011;6(9):e24704
53. Kostic AD, Gevers D, Pedomallu 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
54. Sczesnak A, *Segata N*, Qin X, Gevers D, Petrosino JF, **Huttenhower C**, Littman DR<sup>\*</sup>, Ivanov II<sup>\*</sup>. "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
55. *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\*](#)
56. 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
57. 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
58. 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
59. Park CY, Hess DC, **Huttenhower C**<sup>\*</sup>, Troyanskaya OG<sup>\*</sup>. "Simultaneous Genome-Wide Inference of Physical, Genetic, Regulatory, and Functional Pathway Components." *PLoS Computational Biology* 2010, 6(11)
60. Pop A<sup>\*</sup>, **Huttenhower C**<sup>\*</sup>, 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
61. *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
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65. 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

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67. **Huttenhower C\***, Mutungu KT\*, Indik N, Yang W, Schroeder M, Forman JJ, Troyanskaya OG<sup>†</sup>, Collier HA<sup>†</sup>. "Detailing regulatory networks through large scale data integration." *Bioinformatics* 2009, 25(24):3267-74
68. **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
69. Chikina MD, **Huttenhower C**, Troyanskaya OG<sup>†</sup>, Murphy CT<sup>†</sup>. "Global prediction of tissue-specific gene expression and context-dependent gene networks in *Caenorhabditis elegans*." *PLoS Computational Biology* 2009, 5(6)
70. **Huttenhower C\***, Haley EM\*, Hibbs MA, Dumeaux V, Barrett DR, Collier HA<sup>†</sup>, Troyanskaya OG<sup>†</sup>. "Exploring the human genome with functional maps." *Genome Research* 2009, 19(6):1093-106
71. 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<sup>†</sup>, Caudy AA<sup>†</sup>. "Computationally driven, quantitative experiments discover genes required for mitochondrial biogenesis." *PLoS Genetics* 2009, 5(3)
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85. **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



86. **Huttenhower C**, Sherman G. "Extending cwtsets to higher dimensions: an examination of the statistical properties of cwtsets 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

- *Franzosa EA, Hsu T, Sirota-Madi A, Shafquat A, Abu-Ali G, Morgan XC, **Huttenhower C***. "Sequencing and beyond: integrating molecular 'omics' for microbial community profiling." *Nat Rev Microbiol*. 2015 Jun;13(6):360-72
- *Joice R, Yasuda K, Shafquat A, Morgan XC, **Huttenhower C***. "Determining microbial products and identifying molecular targets in the human microbiome." *Cell Metab*, 2014 Nov 4;20(5):731-41
- **Huttenhower C**, *Kostic AD, Xavier RJ*. "Inflammatory bowel disease as a model for translating the microbiome." *Immunity*, 2014 Jun 19;40(6):843-54
- **Huttenhower C**, Knight R, Brown CT, Caporaso JG, Clemente JC, Gevers D, *Franzosa EA, Kelley ST, Knights D, Ley RE, Mahurkar A, Ravel J; Scientists for Advancement of Microbiome Research, White O*. "Advancing the microbiome research community." *Cell*, 2014 Oct 9;159(2):227-30
- *Shafquat A, Joice R, Simmons SL, **Huttenhower C***. "Functional and phylogenetic assembly of microbial communities in the human microbiome." *Trends in Microbiology*, 2014 Mar 4. pii: S0966-842X(14)00023-7
- *Morgan XC, **Huttenhower C***. "Meta'omic Analytic Techniques for Studying the Intestinal Microbiome." *Gastroenterology*, 2014 S0016-5085(14)00140-1
- *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, Vernet 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

- "Biogeography of the intestinal and lumenal microbiome in the rhesus macaque." Bowling Green University Biological Sciences seminar. Bowling Green, OH, 2015 (presented by Xochitl Morgan)
- "High-precision functional profiling of the gut microbiome for characterization during inflammatory disease." University of Pittsburgh Immunology seminar. Pittsburgh, PA, 2015
- "Understanding microbial community function and the human microbiome in health and disease." Overton Prize keynote address at the 23rd Annual International Conference on Intelligent Systems for Molecular Biology. Dublin, Ireland, 2015
- "Microbial communities in the Boston MBTA mass transit system." MetaSUB First International Summit on Metagenomics and Metadesign of Subways and Urban Biomes. New York, NY, 2015
- "From microbes to molecules: detailing function in integrated multi'omics." New York Academy of Sciences Advances in Human Microbiome Science. New York, NY, 2015
- "High-precision meta'omic profiling for gut microbial biogeography." EMBO Symbiomes: Systems Biology of Host-Microbiome Interactions. Pultusk, Poland, 2015
- "Characterizing the gut microbial ecosystem for diagnosis and therapy in inflammatory bowel disease." 115th Meeting of the American Society for Microbiology. New Orleans, LA, 2015
- "Strategies for analysis of big datasets." Digestive Disease Week. Washington, DC, 2015
- "Identifying personal microbiomes using metagenomic codes." Dana-Farber Cancer Institute Biostatistics seminar. Boston, MA, 2015 (presented by Eric Franzosa)
- "Identifying personal microbiomes using metagenomic codes." BioC Bioconductor annual meeting. Seattle, WA, 2015 (presented by Eric Franzosa)
- "Diet-Linked Gut Microbiome Risk Factors in Colorectal Carcinogenesis." Starr Cancer Consortium annual retreat. Cold Spring Harbor, NY, 2015
- "High-precision functional profiling of microbial communities and the human microbiome." Wellcome Trust Workshop on Applied Bioinformatics and Public Health Microbiology. Hinxton, UK, 2015
- "Identifying personal microbiomes using metagenomic codes." Canadian Institute for Health Research International Speaker Seminar Series. Toronto, Canada, 2015
- "High-precision functional profiling of microbial communities and the human microbiome." Canadian Institute for Health Research STAGE seminar. Toronto, Canada, 2015
- "MetaPhlAn: High-precision profiling of microbial communities and the human microbiome." Illumina BaseSpace Worldwide Developer Conference. Cambridge, MA, 2015
- "Towards systems-level functional profiling of microbial communities and the human microbiome." University of Pennsylvania Microbiology seminar. Philadelphia, PA, 2015
- "High-precision Functional Profiling of Microbial Communities and the Human Microbiome." 41st Annual Northeast Bioengineering Conference. Albany, NY, 2015
- "High-precision functional profiling and integration of metagenomes and metatranscriptomes." International Human Microbiome Congress workshop on Integrated 'Omics for Microbiome Analyses. Luxembourg, Luxembourg, 2015
- "Drivers of microbial ecology in the human gut." University of Otago Microbiology and Immunology seminar. Dunedin, New Zealand, 2015 (presented by Xochitl Morgan)

- "The Integrative 'HMP2' Human Microbiome Project (iHMP)." International Human Microbiome Congress. Luxembourg, Luxembourg, 2015
- "High-precision functional profiling of microbial communities and the human microbiome." Simons Foundation Symposium on Genomics in Single Cells and Microbiomes. New York, NY, 2015
- "A Tour of the bioBakery: Computational Tools for Microbial Community Analysis." Broad Institute Medical and Population Genetics seminar. Cambridge, MA, 2015 (presented by Eric Franzosa)
- "Exploring host-microbe relationships in the mucosa." Broad Institute Medical and Population Genetics seminar. Cambridge, MA, 2015 (presented by Xochitl Morgan)
- "The human microbiome and biomarker discovery." Harvard CATALYST Understanding Biomarker Science workshop. Boston, MA, 2015
- "Towards systems-level functional profiling of microbial communities and the human microbiome." Channing Division of Network Medicine Theodore L. Badger Lecture. Boston, MA, 2015
- "Characterizing the gut microbial ecosystem for diagnosis and therapy in inflammatory bowel disease." Keystone Symposium on Gut Microbiota Modulation of Host Physiology. Keystone, CO, 2015
- "The microbiome in IBD and analysis methods for microbial communities." International Inflammatory Bowel Disease Genetics Consortium meeting. Barcelona, Spain, 2015
- "An Introduction to Microbial Community Analyses." Evomics and Genomics workshop. Cesky Krumlov, Czech Republic, 2015
- "High-specificity methods for profiling microbial communities and the human microbiome." University of Oregon Computer Science colloquium. Eugene, OR, 2014
- "Metagenomics, metatranscriptomics, and multi-omic integration." Massachusetts General Hospital Center for the Study of Inflammatory Bowel Disease research symposium. Boston, MA, 2014
- "High-precision methods for metagenomic and metatranscriptomic profiling." New York University Medical School seminar. New York, NY, 2014
- "Computational Approaches to Microbiome Analysis." ADA/JDRF Diabetes and the Microbiome Research Symposium. Chicago, IL, 2014
- "Gut microbial epidemiology and biogeography." University of Washington Genome Sciences seminar. Seattle, WA, 2014
- "High-precision profiling of microbial communities and the human microbiome." University of Oregon Institute for Theoretical Sciences seminar. Eugene, OR, 2014
- "Initial results from the Microbiome Quality Control Project pilot phase (MBQC-pilot)." Microbiome Quality Control Project workshop. Gaithersburg, MD, 2014
- "Identifying personal microbiomes using metagenomic codes." Statistical and Applied Mathematical Sciences Institute Bioinformatics Opening Workshop. Research Triangle Park, NC, 2014
- "Known knowns and known unknowns in host-associated microbial communities," META Center for Systems Biology symposium. Eugene, OR, 2014
- "The human microbiome and microbial community studies," The Education Cooperative Summer Science Institute. Dover, MA, 2014
- "Computational Approaches for the Human Microbiome in Health and Disease," 12th Biennial Congress of the Anaerobe Society of the Americas. Chicago, IL, 2014
- "An introduction to the microbiome and quantitative methods for microbial community analysis," HSPH Biostatistics Summer Program in Quantitative Sciences. Boston, MA, 2014
- "An introduction to the microbiome and methods for microbial community analysis," Harvard/MIT Minority Introduction to Engineering, and Science. Boston, MA, 2014
- "An introduction to metagenomics," Strategies and Techniques for Analyzing Microbial Population Structure. Woods Hole, MA, 2014
- "Identifiability of the Human Microbiome," Dalhousie University Centre for Comparative Genomics and Evolutionary Bioinformatics and Microbiome User Group. Halifax, Canada, 2014

- "An introduction to the microbiome and microbial community studies," 21st Meeting of the American Society for Microbiology Conference for Undergraduate Educators. Boston, MA, 2014
- "An introduction to the human microbiome and microbial community research," Genomic Medicine and the Bioeconomy. Boston, MA, 2014
- "Host-microbiome transcriptional crosstalk and clinical outcome in a large ileal pouch-anal anastomosis (IPAA) cohort," 109th International Titisee Conference. Titisee, Germany, 2014
- "Microbiome Bioinformatics Tools: A Tutorial," Keystone Symposium on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome. Big Sky, MO, 2014 (presented by Xochitl Morgan)
- "Identifiability of the human microbiome," Keystone Symposium on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome. Big Sky, MO, 2014
- "A Tour of the BioBakery: Computational Tools for Microbial Community Analysis," Harvard School of Public Health Program in Quantitative Genomics Short Course series. Boston, MA, 2014 (presented by Eric Franzosa)
- "High-precision functional profiling and integration of metagenomes and metatranscriptomes," Weizmann Institute Systems Biology Seminar Series. Rehovot, Israel, 2013
- "Bug bytes: bioinformatics for the human microbiome in health and disease," University of Michigan Molecular and Clinical Epidemiology of Infectious Diseases (MAC-EPID) symposium. Ann Arbor, MI, 2013
- "Profiling molecular mechanism in the human microbiome with multi'omic data integration," Schepens Eye Research Institute 28th Biennial Cornea Conference. Boston, MA, 2013
- "Computational methods for meta'omic characterization of the human microbiome," Tufts Computer Science Department Colloquium Series. Medford, MA, 2013
- "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
- "An introduction to metagenomics," Strategies and Techniques for Analyzing Microbial Population Structure. Woods Hole, MA, 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 (PICASo). Princeton, NJ, 2006

## **Presentations**

- "Dynamics of multi'omic profiles of Gut Microbiota Dysbiosis during Inflammatory Bowel Disease." Statistical and Applied Mathematical Sciences Institute Workshop on Discovering Patterns in Human Microbiome Data. Research Triangle Park, NC, 2015 (presented by Alexandra Sirota-Madi)
- "Computational screens for novel gut microbial bioactive compounds." Statistical and Applied Mathematical Sciences Institute Workshop on Discovering Patterns in Human Microbiome Data. Research Triangle Park, NC, 2015 (presented by Ayshwarya Subramanian)
- "Propidium monoazide staining with 16S rRNA gene sequencing for community viability determination." Sloan Foundation Live/Dead workshop. Davis, CA, 2015 (presented by Tiffany Hsu)
- "Computational Metagenomics Techniques and Challenges," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014
- "Relating the metatranscriptome and metagenome of the human gut," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Eric Franzosa)
- "Stable identifiability of the human microbiome based on metagenomic hitting sets," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Eric Franzosa)
- "Discovering co-variation and co-exclusion patterns in compositional data from the human microbiome," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Emma Schwager)
- "A comparative meta-analysis of prognostic gene signatures for late-stage ovarian cancer," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Levi Waldron)
- "Cross-study validation for assessment of prediction models and algorithms," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Christoph Bernau)
- "Microbial carriage within an urban transportation system," 3rd Annual Sloan Foundation Conference on the Microbiology of the Built Environment. Boulder, CO, 2014 (presented by Regina Joice)

- "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

- "Diet-linked gut microbial risk factors in Colorectal Carcinogenesis," Starr Cancer Consortium annual retreat. Cold Spring Harbor, NY, 2015 (presented by Ayshwarya Subramanian)
- "The dynamics of the human infant gut microbiome in development and in progression towards Type 1 Diabetes," Keystone Symposium on Gut Microbiota Modulation of Host Physiology. Keystone, CO, 2015 (presented by Alex Kostic)
- "The effect of multiple antibiotic treatments on the development infant gut microbiome," Keystone Symposium on Gut Microbiota Modulation of Host Physiology. Keystone, CO, 2015 (presented by Moran Yassour)
- "Biogeography of the intestinal mucosal and luminal microbiome in the rhesus macaque," Keystone Symposium on Gut Microbiota Modulation of Host Physiology. Keystone, CO, 2015 (presented by Koji Yasuda)
- "Testing the hygiene hypothesis: microbiome development of infants with different lifestyles," Keystone Symposium on Gut Microbiota Modulation of Host Physiology. Keystone, CO, 2015 (presented by Tommi Vatanen)
- "Dynamics of multi-omic profiles of gut microbiota dysbiosis during inflammatory bowel disease," Keystone Symposium on Gut Microbiota Modulation of Host Physiology. Keystone, CO, 2015 (presented by Alexandra Sirota-Madi)
- "Biogeography of the intestinal mucosal and luminal microbiome in the rhesus macaque," Howard Hughes Medical Institute Science Meeting. Bethesda, MD, 2015
- "Characterizing lateral gene transfer events in microbial communities and the human microbiome," META Center for Systems Biology symposium. Eugene, OR, 2014 (presented by Tiffany Hsu)
- "Biogeography of the intestinal mucosal and luminal microbiome in the rhesus macaque," META Center for Systems Biology symposium. Eugene, OR, 2014 (presented by Koji Yasuda)
- "Discovering co-variation and co-exclusion patterns in compositional data from the human microbiome," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Emma Schwager)
- "Integration of microbiota and metabolomics data in longitudinal cohort of infants en route to type 1 diabetes," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Moran Yassour)
- "Hierarchical nonparametric association discovery in high-dimensional data with high-dimensional metadata," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Gholamali Rahnavard)
- "Relating the metatranscriptome and metagenome of the human gut," 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). Boston, MA, 2014 (presented by Eric Franzosa)
- "Microbial carriage within an urban transportation system," 3rd Annual Sloan Foundation Conference on the Microbiology of the Built Environment. Boulder, CO, 2014 (presented by Regina Joice)
- "Measuring associations between host gene expression, the mucosal microbiome, and clinical outcome in a large ileal pouch - anal anastomosis (IPAA) cohort," Keystone Symposium on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome. Big Sky, MO, 2014 (presented by Xochitl Morgan)
- "Pre-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes," Keystone Symposium on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome. Big Sky, MO, 2014 (presented by Moran Yassour)
- "Microbial carriage within an urban transportation system," Keystone Symposium on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome. Big Sky, MO, 2014 (presented by Regina Joice)
- "A prospective longitudinal analysis of the developing gut microbiome in infants en route to type 1 diabetes," Keystone Symposium on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome. Big Sky, MO, 2014 (presented by Alex Kostic)

- "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

## Meeting Organization

- Co-organizer for NSF Symposium on Computational Advances in Microbiome Research with Jillian Banfield, July 2015
- Co-organizer for EMBL Conference: The Human Microbiome with Peer Bork and Manimozhiyan Arumugam, June 2015
- Co-organizer for Keystone meeting on Exploiting and Understanding Chemical Biotransformations in the Human Microbiome with Peter Turnbaugh and Michael Fischbach, April 2014
- Program committee for the Intelligent Systems for Molecular Biology conference, June 2009 (posters), July 2010, July 2011, July 2013 (late breaking research), and July 2014 (proceedings)
- Co-organizer for the Microbiome Research in the Boston Area (MiRiBA) seminar series with Dirk Gevers, 2011-2013
- Program committee for ACM conference on Bioinformatics, Computational Biology and Biomedical Informatics, September 2013
- Organizer for the Human Microbiome Project Virtual Analysis Jamboree, January 2011 and January 2012
- Program committee for the BioVis IEEE Symposium on Biological Data Visualization, October 2012
- Organizer for Emerging Technologies for Translational Bioinformatics: a Harvard School of Public Health / Dana-Farber Cancer Institute symposium on gene expression profiling for archival tissues, August 2011

## Software

- *bioBakery* <http://huttenhower.sph.harvard.edu/biobakery>  
Integrative virtual environment for microbial community profiling and quantitative analysis
- *MetaPhlAn2* <http://huttenhower.sph.harvard.edu/metaphlan2>  
Pan-domain strain-level taxonomic profiling from metagenomic data
- *HUMAnN2* <http://huttenhower.sph.harvard.edu/humann2>  
Species-resolved rapid functional profiling of metagenomes and metatranscriptomes
- *HALLA* <http://huttenhower.sph.harvard.edu/halla>  
Nonparametric high-sensitivity hierarchical all-against-all multivariate statistical association framework

- *KneadData* <http://huttenhower.sph.harvard.edu/kneaddata>  
Quality control pipeline for read filtering, host depletion, and ribosome removal from meta'omes
- *PPANINI* <http://huttenhower.sph.harvard.edu/ppanini>  
Prioritization of important uncharacterized microbial gene families from metagenomes
- *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
- *AREPA* <http://huttenhower.sph.harvard.edu/arepa>  
Automatic biological data repository acquisition and analysis for scalable reproducible research
- *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