

**Brandi Cantarel**  
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## EDUCATION

### **Ph.D. University of Virginia May 2006**

- Structural and Computational Biology, Biophysics
- Thesis: Reconstruction of Ancient Evolution, Protein Domains and Phylogenies
- Laboratory of William Pearson

### **M.S. University of Virginia December 2005**

Major: Biochemistry and Molecular Genetics

### **B.S. University of Maryland Baltimore County December 2000**

Major: Biochemistry

## RESEARCH EXPERIENCE

### 2016-present **Assistant Professor, Research, University of Texas, Southwestern, Dallas TX, Bioinformatics Department**

- Develop Clinical Sequencing Analysis pipeline
- Develop Core NGS pipelines (Germline Mutation, Somatic Mutation, RNAseq, Methylseq)
- Comparison of human exome and microbiome profiles to identify biomarkers in disease.
- Develop NGS analysis tools and web browsing for researchers
- Develop Bioinformatics Courses for graduate students, post-docs and researchers

### 2015-2016 **Computational Biologist, University of Texas, Southwestern, Dallas TX, Bioinformatics Core Facility**

- Development of Bioinformatics Core Resources

### 2013-2015 **Research Associate (Lead Bioinformatics Scientist NGS), Baylor Scott and White**

- Manages all NGS Bioinformatics Core projects and development
- Training in Bioinformatics: Graduate Students and Post-Docs

### 2009-2013 **Research Associate (Non-Tenure-Track Faculty), University of Maryland, Baltimore, Institute for Genome Sciences.**

- HMP Jumpstart Project, Scientific Coordinator Data Analysis Working Group, Sub-Chair: Genes of Interest
- Human Genomic and Human Microbiome Studies (16S, Metatranscriptomics, Metagenomics) in Longevity, Metabolic Disease, Oral Health and Crohn's Disease
- Managed 1 Bioinformatics Engineer and Trained Graduate Students and Post-Docs

### 2007-2009 **Postdoctoral Fellow, CNRS in Laboratory of Bernard Henrissat**

- Software and Web Development for the Carbohydrate Active Enzyme (CAZy) Database
- Fungal Genomics, Microbial Genomics and Human Gut Microbiome Studies
- Managed 2 Bioinformatics Engineers

### 2006-2007 **Postdoctoral Fellow, University of Utah in Laboratory of Mark Yandell**

- Software Development, Eukaryotic Genome Annotation, MAKER

## TEACHING

2015 Lecturer, Programming for Biology, CSHL

2009-2012 IGS Genomics Workshop (4 lectures/year), University of Maryland, Baltimore

2011 Lecturer, Computational and Comparative Genomics, CSHL

2011 Lecturer, PERL (2 lectures), University of Maryland, Baltimore

2011 Biotechnology 102 (2 credits) Adjunct Faculty, Baltimore City Community College

2003-2007 Teaching Assistant, Computational and Comparative Genomics, CSHL

### **ABSTRACTS AND PRESENTATIONS (2011 to Present)**

1. Abstract: May 2013 The Biology of Genomes, CSHL, Cold Spring Harbor, NY, BAYSIC: A Bayesian Method for Genomic Variation Integration.
2. Abstract October 2012 Personal Genomes and Medical Genomics, CSHL, Cold Spring Harbor, NY  
Integrating multiple variant calling packages into an improved consensus variant discovery system
3. Abstract: May 2012 The Biology of Genomes, CSHL, Cold Spring Harbor, NY, Carbohydrate Active Enzymes in the Human Microbiome.
4. **Presentation:** April 2012 International Human Microbiome Consortium, Paris, France  
Identification of Crohn's Signatures in the Human Gut Microbiota by Meta-omics.
5. **Invited Talk:** April 2011 Genoscope Evry France  
The Role of the Human Gut Microbiome in Obesity and Crohn's Disease
6. **Presentation:** 2011 International Human Microbiome Consortium, Vancouver, Canada  
Metagenomic Analysis of the Structure and Function of the Human Gut Microbiota in Crohn's Disease.
7. Abstract: 2011 International Human Microbiome Consortium, Vancouver, Canada  
The Role of the Gut Microbiota in Obesity in the Amish

### **PROFESSIONAL ACTIVITIES**

Editorial Board for BioMed Research International

Reviewer for research articles in (i) Plos, (ii) BMC, (iii) FEBS Letters and (iv) Translational Research

Reviewer for MétaProgramme INRA "Meta-omics for microbial ecosystems" 2011

### **SPECIAL SKILLS**

- Programming Skills in PERL
- Relational Database, MySQL and Statistical Scripting, R
- Knowledge in MAC OSX/UNIX working environments
- Experience in HTML and Web-Interface design with CGI
- Experience in Variant Marker Discovery Applications – BWA, Samtools, Freebayes, PLINK, VAAST
- Experience in Biological Computer Applications – BLAST, FASTA, PHYLIP, MSA, etc
- Knowledge of Biological Databases, KEGG, NCBI, UNIPROT, SCOP, PDB, CATH, etc
- Knowledge of programming with open source software – BIOPERL, BioConductor and CPAN
- Experience in Software Development (MAKER, BAYSIC)
- Experience in Genome Annotation and Meta-Genomic Analysis
- Experience in Transcriptomics Analysis using TopHat2, HiSAT, StringTie, Ballgown, DESeq2, edgeR
- Experience in Large Scale Analysis
- Prior genetics and biochemistry laboratory experience

### **PUBLICATIONS**

#### **\*\* Co-first or first author**

1. Kathania M, Khare P, Zeng M, Cantarel B, Zhang H, Ueno H, Venuprasad K. Itch inhibits IL-17-mediated colon inflammation and tumorigenesis by ROR- $\gamma$ t ubiquitination. Nat Immunol. 2016 Jun 20. doi: 10.1038/ni.3488. [Epub ahead of print] PubMed PMID: 27322655.
2. Ohne Y, Silver JS, Thompson-Snipes L, Collet MA, Blanck JP, Cantarel BL, Copenhaver AM, Humbles AA, Liu YJ. IL-1 is a critical regulator of group 2 innate lymphoid cell function and plasticity. Nat Immunol. 2016 Apr 25. doi:

- 10.1038/ni.3447. [Epub ahead of print] PubMed PMID: 27111142.
3. Banchereau R, Hong S, Cantarel B, Baldwin N, Baisch J, Edens M, Cepika AM, Acs P, Turner J, Anguiano E, Vinod P, Kahn S, Obermoser G, Blankenship D, Wakeland E, Nassi L, Gotte A, Punaro M, Liu YJ, Banchereau J, Rossello-Urgell J, Wright T, Pascual V. Personalized Immunomonitoring Uncovers Molecular Networks that Stratify Lupus Patients. *Cell*. 2016 Mar 30. pii: S0092-8674(16)30264-1. doi: 10.1016/j.cell.2016.03.008. [Epub ahead of print] PubMed PMID: 27040498.
  4. Venuprasad K, Theivanthiran B, Cantarel B. Intra-tracheal Administration of *Haemophilus influenzae* in Mouse Models to Study Airway Inflammation. *J Vis Exp*. 2016 Mar 2;(109). doi: 10.3791/53964. PubMed PMID: 26967704.
  5. \*\*Cantarel BL, Lei Y, Weaver D, Zhu H, Farrell A, Benstead-Hume G, Reese J, Finnell RH. Analysis of archived residual newborn screening blood spots after whole genome amplification. *BMC Genomics*. 2015 Aug 13;16(1):602. doi: 10.1186/s12864-015-1747-2. PubMed PMID: 26268606; PubMed Central PMCID: PMC4535253.
  6. \*\*Cantarel BL, Waubant E, Chehoud C, Kuczynski J, DeSantis TZ, Warrington J, Venkatesan A, Fraser CM, Mowry EM. Gut Microbiota in Multiple Sclerosis: Possible Influence of Immunomodulators. *J Investig Med*. 2015 Mar 14. [Epub ahead of print] PubMed PMID: 25775034.
  7. Seedorf, H, Griffin, NW, Ridaura, VK, Reyes, A, Cheng, J, Rey, FE, Smith, MI, Simon, GM, Scheffrahn, RH, Woebken, D, Spormann, AM, Van Treuren, W, Ursell, LK, Pirrung, M, Robbins-Pianka, A, Cantarel, BL, Lombard, V, Henrissat, B, Knight, R, Gordon, JI (2014). Bacteria from Diverse Habitats Colonize and Compete in the Mouse Gut. *Cell*, 159(2), 253–266. doi:10.1016/j.cell.2014.09.008
  8. \*\*Cantarel BL, Weaver D, McNeill N, Zhang J, Mackey AJ, Reese J. BAYSIC: a Bayesian method for combining sets of genome variants with improved specificity and sensitivity. *BMC Bioinformatics*. 2014 Apr 12;15:104. doi:10.1186/1471-2105-15-104
  9. Torey Looft, Heather K Allen, Brandi L Cantarel, Uri Y Levine, Darrell O Bayles, David P Alt, Bernard Henrissat, and Thaddeus B Stanton.(2014) Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. *ISME J*. <http://dx.doi.org/10.1038/ismej.2014.12>
  10. Reese J, Christenson MK, Leng N, Saha S, Cantarel B, Lindeberg M, Tamborindeguy C, MacCarthy J, Weaver D, Trease AJ, Ready SV, Davis VM, McCormick C, Haudenschild C, Han S, Johnson SL, Shelby KS, Huang H, Bextine BR, Shatters RG, Hall DG, Davis PH, Hunter WB. Characterization of the Asian Citrus Psyllid Transcriptome. *J Genomics* 2013; 2:54-58.
  11. Mongodin EF, Casjens SR, Bruno JF, Xu Y, Drabek EF, Riley DR, Cantarel BL, Pagan PE, Hernandez YA, Vargas LC, Dunn JJ, Schutzer SE, Fraser CM, Qiu WG, Luft BJ. Inter- and intra-specific pan-genomes of *Borrelia burgdorferi* sensu lato: genome stability and adaptive radiation. *BMC Genomics*. 2013 Oct 10;14(1):693.
  12. Lee S, Cantarel B, Henrissat B, Gevers D, Birren BW, Huttenhower C, Ko G. (2013) Gene-targeted metagenomic analysis of glucan-branching enzyme gene profiles among human and animal fecal microbiota. *ISME J*. 2013 Oct 10. doi: 10.1038/ismej.2013.167.
  13. \*\*Erickson AR, Cantarel BL, Lamendella R, Darzi Y, Mongodin EF, et al. (2012) Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. *PLoS ONE* 7(11): e49138. doi:10.1371/journal.pone.0049138
  14. \*\*Zupancic ML, Cantarel BL, Liu Z, Drabek EF, Ryan KA, et al. (2012) Analysis of the Gut Microbiota in the Old Order Amish and Its Relation to the Metabolic Syndrome. *PLoS ONE* 7(8): e43052. doi:10.1371/journal.pone.0043052

15. Abubucker S, Segata N, Goll J, Schubert AM, Izard J, et al. (2012) Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome. *PLoS Comput Biol* 8(6): e1002358. doi:10.1371/journal.pcbi.1002358
16. \*\*Cantarel BL, Lombard V, Henrissat B (2012) Complex Carbohydrate Utilization by the Healthy Human Microbiome. *PLoS ONE* 7(6): e28742. doi:10.1371/journal.pone.0028742 \*\* NHGRI Genome Advances of the Month (July 2012) <http://www.genome.gov/27549400>
17. The Human Microbiome Consortium (2012) The Framework for human microbiome research. *Nature* 486, 215–221 doi:10.1038/nature11209
18. The Human Microbiome Consortium (2012) Structure, function and diversity of the healthy human microbiome. *Nature* 486, 207–214. doi:10.1038/nature11234
19. \*\*Cantarel BL, Erickson AR, Verberkmoes NC, Erickson BK, Carey PA, Pan C, Shah M, Mongodin EF, Jansson JK, Fraser-Liggett CM, Hettich RL.(2011). Strategies for metagenomic-guided whole-community proteomics of complex microbial environments. *PLoS One*. 2011;6(11):e27173. <http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0027173>
20. Liu Z, Hsiao W, Cantarel BL, Drábek EF, Fraser-Liggett C. (2011) Sparse Distance Based Learning for Simultaneous Multiclass Classification and Feature Selection of Metagenomic Data. *Bioinformatics*. 2011 Oct 7. <http://bioinformatics.oxfordjournals.org/content/27/23/3242.abstract>
21. Duplessis S, Cuomo CA, Lin YC, Aerts A, Tisserant E, Veneault-Fourrey C, Joly DL, Hacquard S, Amselem J, Cantarel BL, Chiu R, Coutinho PM, Feau N, Field M, Frey P, Gelhaye E, Goldberg J, Grabherr MG, Kodira CD, Kohler A, Kües U, Lindquist EA, Lucas SM, Mago R, Mauceli E, Morin E, Murat C, Pangilinan JL, Park R, Pearson M, Quesneville H, Rouhier N, Sakthikumar S, Salamov AA, Schmutz J, Selles B, Shapiro H, Tanguay P, Tuskan GA, Henrissat B, Van de Peer Y, Rouzé P, Ellis JG, Dodds PN, Schein JE, Zhong S, Hamelin RC, Grigoriev IV, Szabo LJ, Martin F. (2011) Obligate biotrophy features unraveled by the genomic analysis of rust fungi. *Proc Natl Acad Sci U S A*. 2011 May 31;108(22):9166-71. Epub 2011 May 2.<http://www.pnas.org/content/108/22/9166.long>
22. Martin F, Kohler A, Murat C, Balestrini R, Coutinho PM, Jaillon O, Montanini B, Morin E, Noel B, Percudani R, Porcel B, Rubini A, Amicucci A, Amselem J, Anthouard V, Arcioni S, Artiguenave F, Aury JM, Ballario P, Bolchi A, Brenna A, Brun A, Buée M, Cantarel B, Chevalier G, Couloux A, Da Silva C, Denoeud F, Duplessis S, Ghignone S, Hilselberger B, Iotti M, Marçais B, Mello A, Miranda M, Pacioni G, Quesneville H, Riccioni C, Ruotolo R, Splivallo R, Stocchi V, Tisserant E, Viscomi AR, Zambonelli A, Zampieri E, Henrissat B, Lebrun MH, Paolocci F, Bonfante P, Ottonello S, Wincker P. Périgord black truffle genome uncovers evolutionary origins and mechanisms of symbiosis. *Nature*. 2010 Apr 15;464(7291):1033-8. Epub 2010 Mar 28. <http://www.nature.com/nature/journal/v464/n7291/full/nature08867.html>
23. Tasse L, Bercovici J, Pizzut-Serin S, Robe P, Tap J, Klopp C, Cantarel BL, Coutinho PM, Henrissat B, Leclerc M, Doré J, Monsan P, Remaud-Simeon M, Potocki-Veronese G. Functional metagenomics to mine the human gut microbiome for dietary fiber catabolic enzymes. *Genome Res*. 2010 Sep 14. <http://genome.cshlp.org/content/20/11/1605.long>
24. Mahowald MA, Rey FE, Seedorf H, Turnbaugh PJ, Fulton RS, Wollam A, Shah N, Wang C, Magrini V, Wilson RK, Cantarel BL, Coutinho PM, Henrissat B, Crock LW, Russell A, Verberkmoes NC, Hettich RL, Gordon JI. Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. *Proc Natl Acad Sci U S A*. 2009 Apr 7;106(14):5859-64. Epub 2009 Mar 24. <http://www.pnas.org/content/106/14/5859.long>
25. Coghlan A, Fiedler TJ, McKay SJ, Flicek P, Harris TW, Blasiar D, Consortium TN, Stein LD. (2008) nGASP - the nematode genome annotation assessment project. *BMC Bioinformatics*. 9(1):549. <http://www.biomedcentral.com/1471-2105/9/549>
26. Turnbaugh PJ, Hamady M, Yatsunencko T, Cantarel BL, Duncan A, Ley RE, Sogin ML, Jones WJ, Roe BA, Affourtit JP, Egholm M, Henrissat B, Heath AC, Knight R, Gordon JI. (2008) A core gut

microbiome in obese and lean twins. *Nature* 457 480-484.

<http://www.nature.com/nature/journal/v457/n7228/full/nature07540.html>

27. \*\*Cantarel BL, Coutinho PM, Rancurel C, Bernard T, Lombard V, Henrissat B (2008) The Carbohydrate-Active EnZymes database (CAZy): an expert resource for Glycogenomics. *Nucleic Acids Res* 37 D233-238. [http://nar.oxfordjournals.org/content/37/suppl\\_1/D233.long](http://nar.oxfordjournals.org/content/37/suppl_1/D233.long)
28. Lozupone CA, Hamady M, Cantarel B L, Coutinho PM, Henrissat B, Gordon JI, Knight R.(2008) The convergence of carbohydrate active gene repertoires in human gut microbes. *Proc Natl Acad Sci U S A*. 105(39) 15076-81. <http://www.pnas.org/content/105/39/15076.long>
29. \*\*Cantarel BL, Korf I, Robb SMC, Parra G, Ross E, Moore B, Holt C, Sánchez Alvarado A, and Yandell M (2007) MAKER: An Easy-to-use Annotation Pipeline Designed for Emerging Model Organism Genomes. *Genome Res*. 18(1) 188-196. <http://genome.cshlp.org/content/18/1/188.long>
30. \*\*Cantarel, BL, Morrison HG, Pearson WR. (2006) Exploring the relationship between sequence similarity and accurate phylogenetic trees. *Mol Biol Evol*. 23(11) 2090-100. <http://mbe.oxfordjournals.org/content/23/11/2090.long>
31. Sun X, Frierson HF, Chen C, Li C, Ran Q, Otto KB, Cantarel BL, Vessella RL, Gao AC, Petros J, Miura Y, Simons JW, Dong JT. (2005) Frequent somatic mutations of the transcription factor ATBF1 in human prostate cancer. *Nature Genetics*. 37(4) 407-12. <http://www.nature.com/ng/journal/v37/n4/full/ng1528.html>