

# ERIC ALAN FRANZOSA, PH.D.

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Updated: 22 June 2017

## APPOINTMENTS

1/2015 – present **Research Associate**  
Harvard T. H. Chan School of Public Health (Biostatistics Dept.), Boston, MA  
Broad Institute, Cambridge, MA  
Supervisor: Curtis Huttenhower  
*Duties include mentoring trainees and staff, overseeing collaborative projects, assisting with grant preparation, and lecturing/delivering workshops on bioinformatics*

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10/2012 – 12/2014 **Postdoctoral Fellow**  
Harvard T. H. Chan School of Public Health (Biostatistics Dept.), Boston, MA  
Broad Institute, Cambridge, MA  
Supervisor: Curtis Huttenhower  
*Research in computational analysis of human-associated microbial communities*

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6/2011 – 9/2012 **Postdoctoral Associate**  
Boston University (Bioinformatics Program), Boston, MA  
Supervisor: Yu Xia (now at Dept. of Bioengineering, McGill University)  
*Research in computational analysis of host-virus protein-protein interactions*

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## EDUCATION

9/2006 – 5/2011 **Ph.D. Bioinformatics**  
Boston University (Bioinformatics Program), Boston, MA  
Advisor: Yu Xia (now at Dept. of Bioengineering, McGill University)  
*Dissertation: Determinants of Protein Evolution: from Residues to Networks*

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9/2002 – 5/2006 **B.Sc. Biophysics**  
Brown University, Providence, RI  
Advisor: David Rand, Dept. of Ecology and Evolutionary Biology  
*Honors thesis: Patterns of Evolution in Human Mitochondrial tRNAs*

## TEACHING EXPERIENCE

### Course leader:

- Genomic Data Manipulation (BIO508 / BST281).  
Harvard T. H. Chan School of Public Health, Boston, MA.  
*Lecture/lab course for graduate students. Introduces 'omics data types, the technologies that produce them, and methods for analysis. Introduces computer programming in Python. 5 hours instruction/week.*  
Spring 2016; Spring 2017.
- Applications in Bioinformatics (BF527).  
Boston University, Boston, MA.  
*Lecture/lab course for senior undergraduate and graduate students. Covers biological data analysis with a strong emphasis on sequence analysis. Introduces computer programming in Python. 5 hours instruction/week.*  
Fall 2009; Fall 2010.

### Workshop leader:

- "Meta'omic Analysis for Microbial Communities." *BroadE Workshop Series*; Cambridge, M; 11/1/2016.
- "Introduction to shotgun meta'omic analysis." *Strategies and Techniques for Analyzing Microbial Population Structure (Marine Biological Laboratory)*; Woods Hole, MA; 8/11-12/2016.
- "Introduction to shotgun meta'omic analysis." *CFAR Workshop on Metagenomics (Harvard University)*; Boston, MA. 9/15/2015.
- "The Human Microbiome in Health and Disease." *Harvard Catalyst: Introduction to Network Medicine*; Cambridge, MA; 11/14/2014.
- "Introduction to Metagenomics." *CFAR Workshop on Metagenomics and Transcriptomics (Harvard University)*; Boston, MA; 9/17/2014.
- "Computational metagenomics techniques and challenges." *Intelligent Systems for Molecular Biology (ISMB)*; Boston, MA; 7/12/2014.
- "A Tour of the bioBakery: Computational Tools for Microbial Community Analysis." *Program in Quantitative Genomics Short Course (Harvard University)*; Boston, MA; 3/4/2014.
- "Meta'omic Analysis with MetaPhlAn & LEfSe." *Workshop on New Methods for Phylogenomics and Metagenomics (Univ. of Texas, Austin)*; Austin, TX; 2/17/2013.
- "Computational methods for meta'omic analyses: Identifying microbial species and functional roles." *COBRA group meeting (Broad Institute)*; Cambridge, MA; 9/18/2012.
- "How to present." *Bioinformatics Program Retreat (Boston University)*; Westminister, MA; 5/22/2010.

### Guest lectures:

- "Regular expressions" in Genomic Data Manipulation (BIO508). Harvard T. H. Chan School of Public Health; Boston, MA; 2/23/2015.
- "Dynamic Programming" in Algorithms and Data Structures (BIO514). Harvard T. H. Chan School of Public Health; Boston, MA; 2/20/2015.
- "Bioinformatics and the human microbiome." MITES Summer Program. Cambridge, MA; 7/9/2014.
- "Computational Genomics" in Genomic Data Manipulation (BIO508). Harvard T. H. Chan School of Public Health; Boston, MA; 4/2/2014.

- “4D Organization of Cells” in Molecular Biology and Biochemistry: Molecules and Processes (BF571). Boston University; Boston, MA; 10/6/2011 and 12/4/2012.

**Teaching assistantships:**

- Genetic Analysis (BI47); Brown University; Providence, RI; Fall 2005.
- Calculus I (MA7); Brown University; Providence, RI; Fall 2004.
- Introduction to Chemistry (CH33); Brown University; Providence, RI; Fall 2003.

**Other teaching experience:**

- Curriculum developer, Genetic Analysis (BI47); Brown University; Providence, RI; Summer 2005.  
*(Revised lecture presentations and produced associated study guides.)*
- Team leader, Providence Science Outreach program; Providence, RI; Spring 2004-Spring 2005.  
*(Led weekly science demonstrations in 5th grade classrooms.)*

## PUBLICATIONS

### Top 5 peer-reviewed publications:

1. [Franzosa EA](#), Huang K, Meadow JF, Gevers D, Lemon KP, Bohannan BJM, Huttenhower C. Identifying personal microbiomes using metagenomic codes. *Proceedings of the National Academy of Sciences USA*, 112: E2930–E2938 (2015).  
[F1000 recommended; Highlighted in “This Week in PNAS” and *The Boston Globe*, 5/11/2015]
2. [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. *Nature Reviews Microbiology*, 13:360-372 (2015).  
[Highlighted in *Current Opinion in Biotechnology*, 37:182-189 (2016) as “●● of outstanding interest.”]
3. [Franzosa EA](#), Morgan XC, Segata N, Waldron L, Reyes J, Earl AE, Giannoukos G, Boylan M, Ciulla D, Gevers D, Izard J, Garrett WS, Chan AT, Huttenhower C. Relating the metatranscriptome and metagenome of the human gut. *Proceedings of the National Academy of Sciences USA*, 111:E2329-E2338 (2014).
4. [Franzosa EA](#), Xia Y. Structural principles within the human-virus protein-protein interaction network. *Proceedings of the National Academy of Sciences USA*, 108:10538-10543 (2011).  
[Highlighted in “This Week in PNAS” and *Frontiers in Microbiology*, 2:186 (2011).]
5. [Franzosa EA](#), Xia Y. Structural determinants of protein evolution are context-sensitive at the residue level. *Molecular Biology and Evolution*, 26:2387-95 (2009).  
[Highlighted in *Current Opinion in Structural Biology*, 20:385-389 (2010) as “●● of outstanding interest.”]

### Other peer-reviewed publications:

6. Levin BJ, Huang YY, Peck SC, Wei Y, Martínez-del Campo A, Marks JA, [Franzosa EA](#), Huttenhower C, Balskus EP. A prominent glyceryl radical enzyme in human gut microbiomes metabolizes trans-4-hydroxy-L-proline. *Science*. 10: eaai8386 (2017).
7. Hill JH, [Franzosa EA](#), Huttenhower C, Guillemin K. A conserved bacterial protein induces pancreatic beta cell expansion during zebrafish development. *eLife*. 13:e20145 (2016).
8. Schirmer M, Smeekens SP, Vlamakis H, Jaeger M, Oosting M, [Franzosa EA](#), ter Horst R, Jansen T, Jacobs L, Bonder MJ, Kurilshikov A. Linking the human gut microbiome to inflammatory cytokine production capacity. *Cell*. 167:1125-36 (2016).
9. Netea MG, Joosten LA, Li Y, Kumar V, Oosting M, Smeekens S, Jaeger M, Ter Horst R, Schirmer M, Vlamakis H, Notebaart R, Pavelka N, Aguirre-Gamboa RR, Swertz MA, Tunjungputri RN, van de Heijden W, [Franzosa EA](#), Ng A, Graham D, Lassen K, Schraa K, Netea-Maier R, Smit J, de Mast Q, van de Veerdonk F, Kullberg BJ, Tack C, van de Munckhof I, Rutten J, van der Graaf J, Franke L, Hofker M, Jonkers I, Platteel M, Maatman A, Fu J, Zhernakova A, van der Meer JW, Dinarello CA, van der Ven A, Huttenhower C, Koenen H, Joosten I, Xavier RJ, Wijmenga C. Understanding human immune function using the resources from the Human Functional Genomics Project. *Nature Medicine*, 22:831-3 (2016).
10. Yassour M, Vatanen T, Siljander H, Hämäläinen AM, Härkönen T, Ryhänen SJ, [Franzosa EA](#), Vlamakis H, Huttenhower C, Gevers D, Lander ES, Knip M, DIABIMMUNE Study Group, Xavier RJ. Natural history of the infant gut microbiome and impact of antibiotic treatment on bacterial strain diversity and stability. *Science Translational Medicine*, 8:343ra81 (2016).
11. Vatanen T, Kostic AD, d’Hennezel E, Siljander H, Franzosa EA, Yassour M, Kolde R, Vlamakis H, Arthur TD, Hämäläinen AM, Peet A, Tillmann V, Uibo R, Mokurov S, Dorshakova N, Ilonen J, Virtanen SM, Szabo SJ, Porter JA, Lähdesmäki H, Huttenhower C, Gevers D, Cullen TW, Knip M, DIABIMMUNE Study Group,

- Xavier RJ. Variation in Microbiome LPS Immunogenicity Contributes to Autoimmunity in Humans. *Cell*, 165:1551 (2016).
12. Yassour M, Lim MY, Yun HS, Tickle TL, Sung J, Song YM, Lee K, [Franzosa EA](#), Morgan XC, Gevers D, Lander ES, Xavier RJ, Birren BW, Ko GP, Huttenhower C. Sub-clinical detection of gut microbial biomarkers of obesity and type 2 diabetes. *Genome Medicine*, 8:1 (2016).
  13. Kaminski J, Gibson MK, [Franzosa EA](#), Segata N, Dantas G, Huttenhower C. High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. *PLoS Computational Biology*, 11:e1004557 (2015).
  14. Truong DT, [Franzosa EA](#), Tickle TL, Scholz M, Weingart G, Pasolli E, Tett A, Huttenhower C, Segata N. MetaPhlan2 for enhanced metagenomic taxonomic profiling. *Nature Methods*, 12:902-903 (2015).
  15. 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*, 3:e791 (2015).
  16. Yasuda K, Oh K, Ren B, Tickle TL, [Franzosa EA](#), Wachtman LM, Miller AD, Westmoreland SV, Mansfield KG, Vallender EJ, Miller GM, Rowlett KR, Gevers D, Huttenhower C, Morgan XC. Biogeography of the Intestinal Mucosal and Luminal Microbiome in the Rhesus Macaque. *Cell Host & Microbe*, 17:385-391 (2015).
  17. 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*, 17:260-273 (2015).
  18. Rolland T, Taşan M, Charloteaux B, Pevzner SJ, Zhong Q, Sahni N, Yi S, Lemmens I, Fontanillo C, Mosca R, Kamburov A, Ghiassian SD, Yang X, Ghamsari L, Balcha D, Begg BE, Braun P, Brehme M, Broly MP, Carvunis AR, Convery-Zupan D, Corominas R, Coulombe-Huntington J, Dann E, Dreze M, Dricot A, Fan C, [Franzosa E](#), Gebreab F, Gutierrez BJ, Hardy MF, Jin M, Kang S, Kiros R, Lin GN, Luck K, MacWilliams A, Menche J, Murray RR, Palagi A, Poulin MM, Rambout X, Rasla J, Reichert P, Romero V, Ruyssinck E, Sahalie JM, Scholz A, Shah AA, Sharma A, Shen Y, Spirohn K, Tam S, Tejada AO, Trigg SA, Twizere JC, Vega K, Walsh J, Cusick ME, Xia Y, Barabási AL, Iakoucheva LM, Aloy P, De Las Rivas J, Tavernier J, Calderwood MA, Hill DE, Hao T, Roth FP, Vidal M. A Proteome-scale map of the human interactome network. *Cell*, 159:1212-1226 (2014).
  19. Huttenhower C, Knight R, Brown CT, Caporaso JG, Clemente JC, Gevers D, [Franzosa EA](#), Kelley ST, Knights D, Ley RE, Mahurkar A, Ravel J, White O. Advancing the Microbiome Research Community. *Cell*, 159:227-230 (2014).
  20. Garamszegi S, [Franzosa EA](#), Xia Y. Signatures of pleiotropy, economy and convergent evolution in a domain-resolved map of human-virus protein-protein interaction networks. *PLoS Pathogens*, 9:e1003778 (2013).
  21. [Franzosa EA](#), Xue R, Xia Y. Quantitative residue-level structure-evolution relationships in the yeast membrane proteome. *Genome Biology and Evolution*, 5:734-744 (2013).
  22. [Franzosa EA](#), Xia Y. Independent effects of protein core size and expression on structure-evolution relationships at the residue level. *PLoS ONE*, 7:e46602 (2012).
  23. [Franzosa EA](#), Xia Y. Structural models for host-pathogen protein-protein interactions: assessing coverage and bias. *Pacific Symposium on Biocomputing*, 17:287-298 (2012).
  24. [Franzosa EA](#), Albančse V, Frydman J, Xia Y, McClellan AJ. Heterozygous yeast deletion collection screens reveal essential targets of Hsp90. *PLoS ONE*, 6:e28211 (2011).

25. Wang Y\*, [Franzosa EA\\*](#), Zhang XS, Xia Y. Protein evolution in yeast transcription factor subnetworks. *Nucleic Acids Research*, 38:5959-69 (2010).
26. Xia Y, [Franzosa EA](#), Gerstein MB. Integrated assessment of genomic correlates of protein evolutionary rate. *PLoS Computational Biology*, 5:e1000413 (2009).  
[Highlighted in *Current Opinion in Structural Biology*, 21:441-446 (2011) as “● of special interest.”]

**Book chapters, invited reviews, & conference proceedings:**

27. Börnigen 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*, 5: 65 (2013).
28. [Franzosa EA](#), Garamszegi S, Xia Y. Toward a three-dimensional view of protein networks between species. *Frontiers in Microbiology*, 3: 428 (2012).
29. Linghu B, [Franzosa EA](#), Xia Y. Construction of functional linkage gene networks by data integration. *Methods in Molecular Biology*, 939: 215-232 (2013).
30. [Franzosa EA](#), Lynagh KJ, Xia Y. Structural correlates of protein melting temperature. *Proceedings of the Fourth International Beilstein Symposium on Experimental Standard Conditions of Enzyme Characterizations*, 99-106 (2009)
31. [Franzosa EA](#), Linghu B, Xia Y. Computational reconstruction of protein-protein interaction networks: algorithms and issues. *Methods in Molecular Biology*, 541:89-100 (2009).
32. [Franzosa EA](#), Xia Y. Structural perspectives on protein evolution. *Annual Reports in Computational Chemistry*, 4:3-21 (2008).

## RESEARCH PRESENTATIONS

### Conferences:

- Introduction to Microbiome Data Visualization. *BioVis*; Baltimore, MD; 10/23/2016.
- Functionally profiling metagenomes and metatranscriptomes at species-level resolution. *Intelligent Systems for Molecular Biology (ISMB)*; Orlando, FL; 7/10/2016.
- Identifying personal microbiomes using metagenomic codes. *Computational System for Integrative Genomics (CSIG)*; Philadelphia, PA; 4/4/2016.
- Informatics for the Human Microbiome in Health & Disease. *Information Technology and Bioinformatics Workshop for the Helmsley IBD Research Network*; Pasadena, CA; 9/29/2015.
- Identifying personal microbiomes using metagenomic codes. *BioC (Bioconductor Annual Meeting)*; Seattle, WA; 7/22/2015.
- Stable Identifiability of the Human Microbiome based on Metagenomic Hitting Sets. *Intelligent Systems for Molecular Biology (ISMB)*; Boston, MA; 7/15/2014.
- Relating the metatranscriptome & metagenome of the human gut. *Intelligent Systems for Molecular Biology (ISMB)*; Berlin, Germany; 7/21/2013.
- Transmission & alteration of the human microbiome by urban public transportation systems. *Microbiology of the Built Environment (MicroBE)*; Boulder, CO; 5/23/2013.
- Structural models for host-pathogen protein-protein interactions: assessing coverage and bias. *Pacific Symposium on Biocomputing (PSB)*; Kona, Hawaii; 1/5/2012.
- Integrated assessment of genomic correlates of protein evolutionary rate. *International Workshop on Bioinformatics and Systems Biology (IWBSB)*; Kyoto, Japan; 7/28/2010.

### Seminars:

- HUMAnN2 for functionally profiling metagenomes and metatranscriptomes at species-level resolution. *NIH integrative Human Microbiome Project (iHMP) Webinar*; presented online; 5/19/2017.
- Exploring Microbiomes with DNA and RNA Sequencing. *Broad SoftEng Primer Series*; Cambridge, MA; 5/2/2016.
- Computational Tools for Microbial Community Analysis. *Broad Medical and Population Genetics Seminar*; Cambridge, MA; 2/25/2016.
- Identifying personal microbiomes using metagenomic codes. *Broad Institute Infectious Disease Initiative*; Cambridge, MA; 10/8/2015.
- A tour of the bioBakery: Computational tools for microbial community analysis. *Broad Institute Medical and Population Genetics Seminar*; Cambridge, MA; 3/5/2015.
- Identifying personal microbiomes using metagenomic codes. *Broad Institute Medical and Population Genetics Seminar*; Cambridge, MA; 9/11/2014.
- Identifiability of the Human Microbiome. *Dana Farber Cancer Institute Genomics Get-together*; Boston, MA; 11/4/2013.
- Meta'omic analysis within the HPFS cohort. *Brigham and Women's Hospital, Channing 'Omics Seminar*; Boston, MA; 10/22/2013.

- Tolerable mutations and mutational tolerance in proteins: a physical perspective. *Boston University Physical Chemistry Seminar Series*; Boston, MA; 1/27/2010.

**Posters:**

- Functionally profiling metagenomes and metatranscriptomes at species-level resolution. *Broad Institute Annual Symposium*; Boston, MA; 12/19-12/20/2016.
- Relating the metatranscriptome & metagenome of the human gut. *Broad Institute Annual Symposium*; Boston, MA; 11/17/2014.
- Protein evolution in yeast transcription factor subnetworks. *Intelligent Systems for Molecular Biology (ISMB)*; Boston, MA; 7/11/2010.
- Disorder as a determinant of evolution in protein microenvironments. *International Workshop on Bioinformatics and Systems Biology (IWBSB)*; Berlin, Germany; 6/9/2008.



## TRAINEES MENTORED

### At Harvard T. H. Chan School of Public Health

- Ji Hua (MS student; 2016)
- Jacob Lubber (PhD rotation; 2016)
- Lana Awad (MS student; 2016)
- Tiffany Hsu (PhD student; 2013-present)
- Muneeza Patel (MIT undergraduate; 2015)
- James Kaminski (MS student; 2012-15)
- Jessica Lau (PhD rotation; 2014)
- David Gootenberg (PhD rotation; 2013)
- Wesley Wong (PhD rotation; 2014)
- Yvonne Hua (PhD rotation; 2013)
- Vagheesh Narasimhan (MS student; 2012-13)

### At Boston University

- Luke Lambourne (PhD student; 2014)
- Kevin Lynagh (NSF REU visitor; 2010)
- Sharmila Jai Kumar (High School outreach; 2007)

## PROFESSIONAL ACTIVITIES

- Member, International Society for Computational Biology (2008–present)
- Invited referee for The ISME Journal, Nucleic Acids Research, Microbiome, Bioinformatics, PLoS Computational Biology, Biochemistry, and PLoS ONE.
- Co-organized joint BU Bioinformatics Program/Dept. of Microbiology seminar series (2012)
- Co-organized Annual BU Bioinformatics Program Retreat (2010)
- Co-organized Annual BU Bioinformatics Program Student Symposium (2009)
- Volunteer for BU Bioinformatics Program recruitment and open house activities (2007 – 2011)

## HONORS & AWARDS

- NSF Travel Fellowship to ISMB Boston (2014)
- F1000 Poster Prize, ISMB (2013)
- ISCB Travel Fellowship to ISMB/ECCB Berlin (2013)
- ISCB Travel Fellowship to the Pacific Symposium on Biocomputing (2012)
- Bioinformatics IGERT Fellowship, Boston University (2007)
- Graduated magna cum laude with honors in biophysics from Brown University (2006)
- James Kidwell Prize in Genetics and Population Biology, Brown University (2006)
- Karen T. Romer Undergraduate Teaching Award, Brown University (2005)