

Stephen Nayfach

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<https://github.com/snayfach>

EDUCATION

2011 – University of California, San Francisco
Doctor of Philosophy in Bioinformatics
2004 – 2008 University of California, Santa Cruz
Bachelor of Science in Neuroscience

RESEARCH EXPERIENCE

2012 – Graduate Student, Pollard Lab, UCSF
2011 – 2012 Rotation Student, Pollard, Hernandez, Babbitt labs, UCSF
2010 – 2011 Clinical Data Analyst, Stanford University School of Medicine
2009 – 2010 Post-baccalaureate Fellow, National Institutes of Health

PUBLICATIONS

1. S. Nayfach and K.S. Pollard (2016). *Toward Accurate and Quantitative Comparative Metagenomics*, Cell. [doi:10.1016/j.cell.2016.08.007](https://doi.org/10.1016/j.cell.2016.08.007)
2. S. Nayfach, B. Rodriguez-Mueller, N. Garud, K.S. Pollard (2016). An integrated metagenomics pipeline for strain profiling reveals novel patterns of bacterial transmission and geography, bioRxiv. [doi:10.1101/031757](https://doi.org/10.1101/031757)
3. S. Nayfach and K.S. Pollard (2015). *Population genetic analyses of metagenomes reveal extensive strain-level variation in prevalent human-associated bacteria*, bioRxiv. [doi:10.1101/031757](https://doi.org/10.1101/031757)
4. S. Nayfach and K.S. Pollard (2015). *Average genome size estimation improves comparative metagenomics and sheds light on the functional ecology of the human microbiome*, Genome Biology. doi:[10.1186/s13059-015-0611-7](https://doi.org/10.1186/s13059-015-0611-7)
5. S. Nayfach, M.A. Fischbach, K.S. Pollard (2015). *MetaQuery: a web server for rapid annotation and quantitative analysis of specific genes in the human gut microbiome*. Bioinformatics. doi:[10.1093/bioinformatics/btv382](https://doi.org/10.1093/bioinformatics/btv382)
6. S. Nayfach, P. Bradley, S.K. Wyman, T.J. Laurent, A. Williams, J.A. Eisen, K.S. Pollard, T.J. Sharpton (2015). *Automated and accurate estimation of gene family abundance from shotgun metagenomes*. PLOS Computational Biology. doi:[10.1371/journal.pcbi.1004573](https://doi.org/10.1371/journal.pcbi.1004573)

TEACHING EXPERIENCE

2014 – Gladstone Institutes, Mentor for summer intern, Krista Kernoodle
Project focused on using shotgun metagenomes to identify genomics islands in strains of *Bacteroides vulgatus*
2014 – UCSF, Teaching Assistant, Dynamical Systems Course:
Course taught students the fundamentals of dissecting and understanding complex biological systems. I mentored a group of students as they learned to use modern genomic tools and bioinformatics to characterize sequence variation among strains of the model organism *Saccharomyces cerevisiae*

SOFTWARE

MIDAS: an integrated pipeline for estimating strain-level genomic variation from metagenomic data
<https://github.com/snayfach/MIDAS>
MicrobeCensus: fast and accurate estimation of average genome size from shotgun sequence data
<https://github.com/snayfach/MicrobeCensus>
MetaQuery: quantitative analysis of specific genes in the human gut microbiome
<http://metaquery.docpollard.org>

HONORS AND AWARDS

2016 Gladstone Institutes Award of Excellence in Science
2015 Fletcher Jones Fellowship
2014 Genentech Foundation Predoctoral Research Fellowship
2013 Achievement Rewards for College Scientists (ARCS) Foundation Award
2013 American Society for Microbiology (ASM) Travel Fellowship
2009 National Institutes of Health (NIH) Post-baccalaureate Intramural Training Award
2008 Highest Honors in Major, University of California Santa Cruz
2008 Merrill College Honors, University of California Santa Cruz
2008 Phi Beta Kappa Nominee, Santa Cruz Chapter

POSTERS AND PRESENTATIONS

“Shotgun metagenomes illuminate the diversity of bacterial populations in the human gut microbiome”
Awards of Excellence in Science and Leadership Celebration. San Francisco CA.
June 2016 (Talk)
“Uncovering the gene content and biogeography of microbial species from the human gut microbiome”
META Center Symposium. Eugene OR.
August 2015 (Talk)
“Population Structure of a Dominant Gut Symbiont from Metagenomic Data”
iPQB Annual Retreat. San Francisco, CA.
June 2014 (Poster).
“Estimation and Correction for Average Genome Size in the Human Microbiome”
Keystone Symposium: Biochemical Transformations in the Human Microbiome. Bozeman, MT.
April 2014 (Poster).
“Estimation and Correction for Average Genome Size in the Human Microbiome”
JGI User Meeting. Walnut Creek, CA.
March 2014 (Poster).
“Characterizing the Diversity and Function of the Human Microbiome Through Metagenomics”
Gladstone Institutes Annual Retreat. San Francisco, CA.
May 2013 (Poster).
“Optimal Algorithms and Parameters for Metagenome Functional Annotation”
American Society For Microbiology General Meeting. Denver, CO.
April 2013. (Poster)
“Methods for Metagenome Annotation”
Pollard-Wall-Hernandez Lab Meeting. San Francisco, CA.
February 2013 (Talk).
“Evaluating Metagenomic Sequence Classification Through Simulation”
BBC Graduate Programs Annual Retreat. Monterey, CA.
December 2012 (Poster).
“Exploring Enzyme Functional Space in the Cow Rumen”
Babbitt Lab Meeting. San Francisco, CA.
June 2012 (Talk).
“Functional Diversity of Bacterial Communities Across the Ocean’s Depths”
Pollard-Wall-Hernandez Lab Meeting. San Francisco, CA.
May 2012 (Talk).