

SUMMARY	Scientist uncovering connections between us and our microbial companions that impact health.	
EDUCATION	<b>University of California San Francisco</b> , San Francisco, CA <b>PhD</b> in Biological and Medical Informatics — Adviser: Katherine Pollard <ul style="list-style-type: none"> <li>Characterized coevolution statistics for predicting structural contacts between proteins.</li> </ul> <b>University of California Santa Cruz</b> , Santa Cruz, CA <b>BS</b> in Bioinformatics	2009–2015  2005–2009
EXPERIENCE	<b>Lawrence Livermore National Laboratory</b> , Livermore, CA <b>Bioinformatics Postdoc</b> <ul style="list-style-type: none"> <li><b>Compositions with 1000s of parts:</b> Analyzed shotgun metagenomes from the International Space Station crew and surfaces to understand microbial diversity under spaceflight conditions.</li> <li><b>Biomedical data with 1000s of variables:</b> Modeled blast injury microbiomes to identify potential medical interventions using patient, treatment, and genomic measurements—including antibiotic resistance markers.</li> <li><b>Multiclass classification:</b> Benchmarked performance of de Bruijn graph based search tools in detecting drug resistance genes in shotgun metagenomes.</li> <li><b>Software development:</b> Prototyped a utility to automate antimicrobial resistance detection and reporting. Delivered a library to facilitate maintenance of an in-house non-relational annotation database.</li> </ul> <b>J David Gladstone Institutes</b> , San Francisco, CA <b>Bioinformatics Fellow</b> — Supervisor: Katherine Pollard <ul style="list-style-type: none"> <li>Identified associations between environmental variables and microbial genes in human and oceanic metagenomic data.</li> </ul>	2016–present  2015–2016
TEACHING	<b>Science Education and Outreach</b> , Gladstone Institutes <i>Guest lecturer</i> Co-led lesson and hands-on activity on HIV/AIDS biology, prevention, and history for students of Balboa High School, San Francisco. <b>School of Pharmacy</b> , University of California San Francisco <i>Teaching Assistant—Biostatistics (BPS 112)</i> Developed course material, led weekly lecture discussions, held office hours, and administrated course website. <b>Integrated Program in Quantitative Biology</b> , UCSF <i>Bootcamp Bioinformatics Leader</i> Responsible for the organization and design of three-day theoretical and applied bioinformatics crash course. Prepared simulated data sets for coursework and led journal club discussions. <i>Bootcamp Instructor</i> Gave introductory lectures on probability and statistics to incoming students from diverse fields.	Dec 2014  Fall 2010  (Falls) 2010–2012
PROGRAMMING	<b>Languages:</b> · R · Python · bash · Perl · SQL · C · Java · C++ · MATLAB · Ruby <b>Markup:</b> · (R)Markdown · L <sup>A</sup> T <sub>E</sub> X · HTML5 · XML <b>Data Science:</b> · tidyverse packages · pandas · numpy · scikit-learn <b>Web/Viz.:</b> · Jekyll · JavaScript/CoffeeScript · CSS · Stylus · D3.js · plot.ly	
SELECTED PUBLICATIONS	Wyman SK, <b>Avila-Herrera A</b> , Nayfach S, Pollard KS. <i>A most wanted list of conserved microbial protein families with no known domains</i> . PLoS ONE October 2018 13(10):e0205749 Be N, <b>Avila-Herrera A</b> , Allen JE, Singh N, Checinska Sielaff A, Jaing C, Venkateswaran K. <i>Whole metagenome profiles from ISS particulates</i> . BMC Microbiome July 2017 5:81 <b>Avila-Herrera A</b> , Pollard KS. <i>Coevolutionary analyses require phylogenetically deep alignments and better null models to accurately detect inter-protein contacts within and between species</i> . BMC Bioinformatics August 2015 16:268	
SELECTED PRESENTATIONS	<b>Avila-Herrera A</b> , Be N, Thissen J, Urbaniak C, Karouia F, Smith DJ, Mehta S, Venkateswaran K, Jaing C. <i>Building a Microbial Catalog of the International Space Station</i> . Bioinformatics for the Microbiome Symposium, September 2018. Stanford, CA <b>Avila-Herrera A</b> <i>Search strategies for antimicrobial resistance associated genes</i> . LLNL and UC Inaugural Data Science Workshop, Aug 2018. Livermore, CA <b>Avila-Herrera A</b> , Be N, Allen JE, Singh N, Checinska Sielaff A, Jaing C, Venkateswaran K. <i>Whole metagenome profiles from ISS particulates</i> . American Society for Gravitational and Space Research, Oct 2017. Seattle, WA <b>Avila-Herrera A</b> , Hernandez R, Krogan N, Pollard K. <i>Measuring correlated evolution in HIV-human protein complexes</i> . Poster. XVIth Bay Area Microbial Pathogenesis Symposium, 2013. San Francisco, CA	
OTHER	<b>Foreign Languages:</b> Fluent in Spanish and proficient in French. <b>Athletics:</b> Participated in Santa Cruz Half Marathon (2010), Marin Century (50km) (2010), and Alcatraz Challenge (2012).	

ADDITIONAL PUBLICATIONS AND PRESENTATIONS	<p>Ahmed OM, <b>Avila-Herrera A</b>, Tun KM, Serpa PH, Peng J, Parthasarathy S, Knapp J-M, Stern DL, Davis GW, Pollard KS, Shah NM. <i>Evolution of mechanisms that control mating in <b>Drosophila males</b></i>. Cell Reports May 2019 27(9):2527-2536.e4</p> <p><b>Avila-Herrera A</b>, Be N, Thissen J, Urbaniak C, Karouia F, Smith DJ, Mehta S, Venkateswaran K, Jaing C. <i>Building a Microbial Catalog of the International Space Station</i>. Poster. American Society for Gravitational and Space Research, Oct 2018. Bethesda, MD</p> <p><b>Avila-Herrera A</b>. <i>Statistical evaluation of coevolution methods for predicting inter-protein contacts</i> (Doctoral dissertation). 2015. University of California, San Francisco.</p> <p>Roan NR, Liu H, Usmani SM, Neidleman J, Müller JA, <b>Avila-Herrera A</b>, Gawanbacht A, Zirafi O, Chu S, Dong M, Kumar ST, Smith JF, Pollard KS, Fändrich M, Kirchhoff F, Münch J, Witkowska HE, Greene WC. <i>Liquefaction of semen generates and later degrades a conserved semenogelin peptide that enhances HIV infection</i>. Journal of Virology July 2014 88:13 7221-7234.</p> <p><b>Avila-Herrera A</b>, Pollard K. <i>Performance of methods used to identify coevolving residues between proteins</i>. Poster. 14th Biomedical Computation at Stanford Symposium, 2014. Stanford, CA</p>	
SERVICE	<p><b>Manuscript Review</b> · Bioinformatics · BMC Bioinform. · PLOS Comput. Biol.</p> <p><b>Early Career Panelist</b> <i>Lawrence Livermore National Laboratory</i> <i>Gladstone Institutes Graduate Student Alumni Panel</i> Shared early career experiences with undergraduate and graduate students.</p> <p><b>Peer Mentor</b> <i>Minority Graduate Student Organization, UCSF</i> Provide long-term mentorship for new students.</p>	<p>Winter 2019 Apr 2017  2012–2015</p>
PROFESSIONAL DEVELOPMENT	<p><b>National Laboratory Entrepreneurship Academy</b>, UC Davis GSM Received interactive entrepreneurship training from experts in academia, government, and industry.</p> <p><b>American Heart Association</b>, San Francisco, CA <i>Heart Walk Team Leader</i> Built a team to fundraise and participate in the 2014 Bay Area Heart Walk.</p> <p><b>CATALYST Awards Student Internship Program</b>, UCSF <i>Student Intern</i> Reviewed funding proposals with academic and industry experts in translational research for <i>unmet need</i>, <i>commercialization potential</i>, and <i>development feasibility</i>.</p> <p><b>Graduate Student Internships and Career Exploration</b>, UCSF <i>2012 Cohort</i> Participated in career exploration and professional development workshops.</p>	<p>Nov 2018  Sept 2014  Fall 2013</p>
HONORS AND AWARDS	<p>Gladstone Institute of Cardiovascular Disease Award for Excellence in Leadership UCSF Graduate Research Mentorship Fellowship National Science Foundation Graduate Research Fellowship Program (<i>Honorable Mention</i>) Minority Access to Research Careers (MARC) Fellow International Scholar Laureate Program (<i>Delegation on Engineering, China</i>)</p>	<p>2015 2011–2012 2011 2008–2009 2007</p>
ADDITIONAL LABORATORY EXPERIENCE	<p><b>Lab Rotations</b>, UCSF <b>DeRisi</b> <i>P. falciparum</i> culture, RNA-protein coimmunoprecipitation, and RNA isolation <b>Frankel</b> Quantification of intraprotein evolutionary constraints in Rev <b>Pollard</b> CRISPR detection in metagenomic data</p> <p><b>Integrated Program in Quantitative Biology Team Challenges</b>, UCSF • Microarray expression experiment and analysis • Built rudimentary fluorescence microscope</p> <p><b>Phillip Berman Lab</b>, UCSC Tested sera for immunoreactivity and automated digitization of critical biological sequence records.</p> <p><b>MARC Summer Research Institute</b>, UCSC Diketopiperazine structure determination and arthropod pathogen screening.</p>	<p>(2009–2010)     (Fall 2009, Spring 2010)   (2007–2008)  (Summer 2008)</p>
COMPUTATIONAL BIOLOGY METHODS	<p><b>Statistics:</b> · compositional data analysis · linear modeling · probabilistic graphical modeling · sparse network inference · Bayesian inference · machine learning</p> <p><b>Microbial Metagenomics:</b> · taxonomy and gene function analyses · environmental association testing · variant detection</p> <p><b>Molecular Evolution:</b> · phylogeny inference · coevolution analysis · non-neutral evolution detection · ancestral sequence reconstruction · evolution simulation</p> <p><b>Structural Biology:</b> · homology modeling · structure alignment · visualization</p>	