

Jennifer Fouquier

Curriculum Vitae

Gmail address: jennietf

SUMMARY

- Ten years of designing and developing scientific software tools for analyzing and visualizing biological data with an emphasis on microbiome applications
- Ten years of “wet lab” research and development experience in biotechnology and academic research laboratories with a focus on molecular biology
- Interdisciplinary background with a desire to improve computational methods using biological data

SKILLS

Programming, and Markup Languages: Python, R, JavaScript, HTML/Jade, CSS, Markdown, Java

Software, Bioinformatics, and Technical Skills:

- Next-generation sequence analysis, and microbiome research
- Quantitative Insights Into Microbial Ecology (QIIME) 1 & 2
- Laboratory Information Management Systems (LIMS)
- Integrated development environments (IDEs)
- Git version control <https://github.com/JTFouquier>
- Web development using Django framework (frontend and backend)
- Javascript/JQuery
- BASH/Unix shell
- Databases/MySQL
- Matlab
- Microsoft Word, Excel, and PowerPoint
- Mac, Windows, Linux OS (Mac preferred)
- Pep8, unit testing, and other software engineering skills

Soft Skills:

- Creative, inquisitive, and open-minded
- Strong work ethic developed from academic and industrial roles
- Outgoing, friendly, and confident
- Enjoys different personalities and cultures
- Scientific outreach & volunteering
- Strong leadership skills and tendency to initiate changes
- Willing to admit faults and ask questions as needed

EDUCATION

PhD in Computational Bioscience Aug 2018 – May 2024 (expected)
University of Colorado Anschutz Medical Campus, Aurora, CO

M.S. in Bioinformatics, San Diego State University, San Diego, CA (3.76 GPA) May 2015
- Specialization in molecular analysis of indoor fungal diversity (“mycobiome”)

B.S. in Microbiology, University of California at San Diego, La Jolla, CA Jun 2007

A.A. in Liberal Arts and Sciences at Palomar College, San Marcos, CA Jun 2005

EXPERIENCE

University of Colorado Anschutz Medical Campus, Aurora, CO Sep 2017 – present
Student researcher (1 year) PhD student (current) Lozupone Laboratory

- Performs 16S rRNA gene region analyses of gut samples from autism spectrum disorder cohort to look at microbial diversity changes and their relationship to factors such as diet and autism severity
- Performs computational analyses with an emphasis on longitudinal aspects of the project using Quantitative Insights into Microbial Ecology 2, R programming, and Python

Freelance Bioinformatics Programmer, Broomfield, CO

Sep 2016 – Dec 2017

- Microbiome bioinformatics consulting work (remote) for Second Genome, San Francisco, CA.
- Independent programming projects related to past projects or new interests
- Tutored three professionals on Python for school or professional development

The Scripps Research Institute, La Jolla, CA

Jun 2015 – Jun 2016

Bioinformatics Programmer III, Su Laboratory

- Developed software for Mark2Cure.org, a website that invites volunteers to annotate scientific abstracts to help researchers find clues for rare disease research within an overwhelming collection of scientific literature; improves upon advances in natural language processing
- Developed relationship identification application and HTML-guided user training for Mark2Cure.org using Django web framework
- Programmed backend and frontend using Python, Javascript/JQuery, or HTML/Jade depending on the scope of the feature or bug
- Created a visual, interactive word cloud of user contribution using Data Driven Documents (D3) and Mark2Cure APIs
- Improved data mapping in MyGene.info gene annotation website using mygene-py client
- Implemented data-loading protocol for visualizing RNA-seq gene-expression data using Django framework for BioGPS.org
- Worked effectively in team-programming environment to implement user feedback
- Improved unit testing for software QC
- Documented project installation steps and usage in README documents
- Used virtual environments for developing multiple projects as necessary (MyGene, BioGPS, and Mark2Cure)

AltheaDx, Inc., La Jolla, CA

Jan 2015 – Jun 2015

LIMS Developer

- Wrote scripts to analyze data derived from genetic testing and pharmacogenetic algorithms used for personalized medical treatment
- Validated and tested the Laboratory Information Management System (LIMS) for software production releases
- Added features and fixed bugs in algorithms and LIMS system, reported issues and suggestions as necessary to improve software report quality
- Analyzed data using simulated patient genotypes to ensure proper algorithm behavior

San Diego State University, San Diego, CA

Aug 2012 – Jun 2015

Bioinformatics Graduate Student, Kelley Laboratory

- Programmed for research and classes using Python, Java, command-line, R, Matlab, QIIME (Quantitative Insights Into Microbial Ecology), Git, and test-driven development (TDD)
- Created barcoded fungal amplicons via PCR and obtained over three million sequence reads using next generation sequencing (NGS) technology
- Performed eukaryotic ITS1 rRNA gene amplicon sequence analyses using QIIME
- Received award from American Society of Microbiology to give oral presentation at the general meeting in Boston (2014)
- Gave oral presentations and poster presentations at six conferences within two years

- Designed ghost-tree bioinformatics tool to create hybrid-gene phylogenetic trees to improve fungal diversity analyses for microbiome research in collaboration with software engineers at Northern Arizona University
- Co-chaired student-organized biotech club (Biomedical Technology Students Association) 2013-2014; hosted weekly speakers, biotech company tours, and science events for college and grade-school students
- Supervised and mentored three undergraduate students throughout their research projects; co-authored a paper with one of these students

Cypher Genomics, Inc., La Jolla, CA

May 2014 – Jul 2014

Intern, Development and Software Testing

- Tested genome interpretation software
- Reported bugs and recommended features using Atlassian/JIRA Project Management tools
- Performed research on competitive market for human genomic interpretation space
- Presented findings on competitive market to improve software quality and user experience (UX)

- Designed platform comparison analyses using human genomes to determine concordance and discrepancies in variant reporting
- Improved collaborative company relationships with academic and clinical scientists
- Experienced working at a fast-paced, start-up bioinformatics company which was acquired by Human Longevity Inc. in 2015

Fate Therapeutics, Inc., San Diego, CA

Jul 2011 – Aug 2012

Research Associate II, Molecular Biology and Technology

- Performed cord blood transplant experiments in mice by performing bone marrow ablation and subsequent treatment with small molecule *ex vivo*-modulated hematopoietic stem cells (HSCs)
- Prepared cells for flow cytometry assays for antibody based detection of surface markers on human HSCs

- Analyzed flow cytometry data with FlowJo
- Ran microarray experiments to measure human gene expression
- Extracted and quantified DNA and RNA from human tissue, animal tissue and human cell lines
- Performed quantitative PCR and digital PCR

Quadrants Scientific, Inc., Rancho Bernardo, CA

Feb 2010 – Dec 2010

Microbiologist

- Completed microbiological tests including: viable and non-viable surface and air environmental monitoring, bioburden, microbial enumeration testing, antimicrobial effectiveness testing, population verification, water coliform, and microscopic fungal identification
- Tested quantitative endotoxin via chromogenic and turbidimetric methods. Completed training

- seminar and training on *Limulus* amebocyte lysate (LAL) background and technique
- Performed analytical testing including: Wet chemistry identification of raw materials, total organic carbon (TOC), Fourier transform infrared (FTIR) spectroscopy, conductivity, residue on ignition, and residue on evaporation

AVIVA Biosciences, Sorrento Valley, CA

Nov 2007 – Feb 2010

Research Associate

- Performed electrophysiological experiments including cardiac contraction, and action potential using coronary arteries, papillaries and purkinje fibers from donated human hearts
- Performed Langendorff apparatus experiments
- Analyzed electrophysiology experiments using specialized electrophysiology software
- Interpreted data, performed documentation and wrote professional customer reports
- Ran robotic instruments for high throughput screening of pharmaceuticals to test for IC50 on stably transfected cell lines expressing sodium and potassium cardiac ion channels
- Optimized organ preservation solutions for cardiac tissue to be used for in vitro pharmaceutical studies
- Passaged, isolated, transfected, and cryopreserved HEK and CHO cell lines

The Salk Institute for Biological Studies, La Jolla, CA
Molecular Neurobiology Laboratory-Heinemann
Laboratory Assistant IV

Mar 2006 – Mar 2008

- Studied transgenic mouse behavior to document acute effects of nicotine on anxiety
- Performed intraperitoneal injections, anesthesia, and euthanasia as necessary
- Studies included black/white box, elevated plus maze, and loco motor analysis
- Extracted mouse DNA and genotyped mice after performing PCR
- Assisted animal facility with cryopreservation of the laboratory's mouse lines
- Performed mini-preps to isolate bacterial DNA
- Prepared E. coli competent cells

Cliniqa Corporation, San Marcos, CA
Laboratory Assistant

Mar 2000 – Mar 2004

- Processed normal human plasma or pleural fluid into controls and calibrators used in medical diagnostic instruments according to varying protein concentration and purification standards
- Wrote and reviewed Standard Operating Procedures (SOPs)
- Performed assays on various protein and chemistry analyzer systems
- Followed Good Manufacturing Procedures (GMP), Work Instructions (WIs), and Standard Operating Procedures (SOPs)

PUBLICATIONS

- J Fouquier**, N Moreno Huizar, J Donnelly, C Glickman, DW Kang, J Maldonado, RA Jones, K Johnson, JB Adams, R Krajmalnik-Brown, C Lozupone. The gut microbiome in autism: study-site effects and longitudinal analysis of behavior change. *Msystems*, 2021. 6(2): p. e00848-20.
- E Yamada, CG Martin, N Moreno-Huizar, **J Fouquier**, CP Neff, SL Coleman, JM Schneider, J Huber, NM Nusbacher, M McCarter, TB Campbell, CA Lozupone, BE Palmer. Intestinal microbial communities and *Holdemanella* isolated from HIV+/- men who have sex with men increase frequencies of lamina propria CCR5+ CD4+ T cells. *Gut microbes*, 2021. 13(1): p. 1997292.
- AJS Armstrong, K Quinn, **J Fouquier**, S X Li, JM Schneider, NM Nusbacher, KA Doenges, S Fiorillo, TJ Marden, J Higgins, N Reisdorph, TB Campbell, BE Palmer, CA Lozupone. Systems Analysis of Gut Microbiome Influence on Metabolic Disease in HIV-Positive and High-Risk Populations. *Msystems*, 2021. 6(3): p. e01178-20.
- G Tsueng, M Nanis, **JT Fouquier**, M Mayers, BM Good, AI Su. Applying citizen science to gene, drug and disease relationship extraction from biomedical abstracts; **Feb 2020**; *Bioinformatics*.

Bolyen, JR Rideout, MR Dillon, NA Bokulich, et al. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2; **Aug 2019**; *Nature Biotechnology*.

G Tsueng, SM Nanis, **J Fouquier**, BM Good, and AI Su. Citizen Science for Mining the Biomedical Literature. *Citizen Science: Theory and Practice*. 1(2), p.14; **Dec 2016**; DOI: 10.5334/cstp.56

J Chase, **J Fouquier**, M Zare, D Sonderegger, R Knight, ST Kelley, J Siegel, and JG Caporaso. Geography and location are the primary drivers of office microbiome composition. *mSystems*; **April 2016**; 19;1(2). DOI: e00022-16

J Fouquier, JR Rideout, E Bolyen, J Chase, A Shiffer, D McDonald, R Knight, JG Caporaso, and ST Kelley. ghost-tree: creating hybrid-gene phylogenetic trees for diversity analysis. *Microbiome*; **Feb 2016**; DOI: 10.1186/s40168-016-0153-6

J Fouquier, T Schwartz, and ST Kelley. Rapid assemblage of diverse environmental fungal communities on public restroom floors. *Indoor Air*. **Jan 2016**; DOI: 10.1111/ina.12279

J Fouquier. Master's Thesis. Ghost-tree: a bioinformatics tool for creating hybrid-gene phylogenetic trees with a detailed study of fungal communities in public restrooms. Committee members: Scott T Kelley, Elizabeth R Waters, and Richard Bizzoco. *San Diego State University* (April 2015)

SM Gibbons, T Schwartz, **J Fouquier**, M Mitchell, N Sangwan, JA Gilbert, and ST Kelley. Ecological succession and viability of human-associated microbiota on restroom surfaces. *Appl. Environ. Microbiol.* (January 2015) DOI:10.1128/AEM.03117-14

Google Scholar: <https://goo.gl/LgE42s>

ORAL PRESENTATIONS

J Fouquier* and CA Lozupone. Identifying predictors of response in longitudinal microbiome studies. National Library of Medicine (NLM) Informatics Training Conference; **Jun 2022**; Buffalo, NY

J Fouquier* and CA Lozupone. Identifying predictors of response in longitudinal microbiome studies. Global Engage 9th Microbiome and Probiotic R&D and Business Collaboration Forum; **Mar 2022**; San Diego, CA.

J Fouquier* and Gonzalez-Pena A. Environmental DNA Methods: QIIME 2 Software Training. Co-taught 2-day bioinformatics workshop; **May 2019**; Chattanooga, TN.

J Fouquier* et al., Ghost-tree software tool and Quantitative Insights into Microbial Ecology 2 (QIIME 2) plugin. Teaching and developing QIIME 2; **May 2018**; San Diego, CA.

G Tsueng, M Nanis, **J Fouquier***, M Mayers, BM Good, AI Su. Applying Citizen Science to Gene, Drug, Disease Relationship Extraction from Biomedical Abstracts. Citizen Science Association Conference CitSci2019; **Mar 2019**; Raleigh, NC.

J Fouquier* et al. q2-ghost-tree plugin: creating hybrid-gene phylogenetic trees for diversity analysis. QIIME 2 Development workshop and 10,000 Citation Celebration; **May 2018**; La Jolla, CA.

J Fouquier*, TM Schwartz, MQ Mitchell, ST Kelley. Characterizing the Public Restroom Mycobiome Using the Internal Transcribed Spacer. Award Winner: Division Q, Environmental and General Applied Microbiology. American Society of Microbiology General Meeting, Symposium: Are We Alone? Microbial Revelations of the Built Environment; May 2014; Boston, MA.

J Fouquier*, MQ Mitchell, TM Schwartz, ST Kelley. (March 2014). Characterizing the Public Restroom Mycobiome Using the Internal Transcribed Spacer. San Diego State University Student Research Symposium, San Diego, CA.

MQ Mitchell*, **J Fouquier**, J Bell, TM Schwartz, ST Kelley. Bacterial Growth Patterns in a Public Restroom Environment. San Diego State University Student Research Symposium; Mar 2014. San Diego, CA.

* presenter

POSTER PRESENTATIONS

J Fouquier and CA Lozupone. Identifying predictors of response in longitudinal microbiome studies. Front Range Microbiome Symposium; **Apr 2022**; Fort Collins, CO.

J Fouquier and CA Lozupone. Identifying predictors of response in longitudinal microbiome studies. International Society for Computational Bioscience (ISCB) Rocky Mountain Bioinformatics Conference; **Dec 2021**; Aspen, CO.

J Fouquier and CA Lozupone. A workflow for data integration and feature selection in longitudinal microbiome studies. National Library of Medicine (NLM) Informatics Training Conference; **Jun 2021**; Virtual conference hosted by The University of Washington, Seattle, WA.

J Fouquier and CA Lozupone. A workflow for data integration and feature selection in longitudinal microbiome studies Global Engage 8th Microbiome Business Collaboration Forum; **Nov 2021**; virtual conference.

J Fouquier, JR Rideout, E Bolyen, J Chase, A Shiffer, D McDonald, R Knight, JG Caporaso, and ST Kelley*. ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. The Fourth Annual Conference on the Microbiology of the Built Environment. University of Colorado, Boulder; **Jul 2015**; Boulder, CO.

J Fouquier*, ST Kelley. Exploring the unseen world of fungal biodiversity: a hybrid-gene bioinformatics approach to creating phylogenetic trees. 27th California State University Biotechnology Symposium (CSUPERB); **Jan 2015**; Santa Clara, CA.

J Siegel*, M Zare, J Chase, **J Fouquier**, R Knight, ST Kelley, J Siegel. Impact of building science parameters on microbial communities on indoor surfaces. International Society of Indoor Air Quality and Climate. Indoor Air 2014 - 13th International Conference on Indoor Air Quality and Climate (pp. 362-364); **Jul 2014**; Hong Kong, China.

J Fouquier*, TM Schwartz, ST Kelley. Characterization of the fungal biodiversity in the Public Restroom. The Third Annual Conference on the Microbiology of the Built Environment Conference; **Jun 2014**; Boulder, CO

J Chase*, **J Fouquier**, M Zare, D Sonderegger, R Knight, ST Kelley, J Siegel, and JG Caporaso. Geography and location are the primary drivers of office microbiome composition. The Third Annual Conference on the Microbiology of the Built Environment Conference; **June 2014**; Boulder, CO

J Fouquier*, TM Schwartz, ST Kelley. The public restroom mycobiome. 26th California State University Biotechnology Symposium (CSUPERB); **Jan 2014**; Santa Clara, CA

J Fouquier*, T.M Schwartz, ST Kelley. The public restroom mycobiome. The Second Annual Conference on the Microbiology of the Built Environment Conference; **May 2013**; Boulder, CO

J Chase*, **J Fouquier**, M Zare, D Sonderegger, R Knight, ST Kelley, J Siegel, and JG Caporaso. Geography and location are the primary drivers of office microbiome composition. The Second Annual Conference on the Microbiology of the Built Environment; **May 2013**; Boulder, CO

TK Booker*, A Vlasveld, **J Fouquier**, CM Butt, SF Heinemann. Beta3-containing nicotinic receptors mediate the effects of acute nicotine on anxiety. Society for Neuroscience Conference; **Nov 2007**; San Diego, CA

* presenter

TEACHING

Led a **3-hour bioinformatics workshop**. Integrating Genetics and Social Sciences (IGSS) at the University of Colorado at Boulder; **Oct 2022**; Boulder, CO.

Co-instructed **2-day bioinformatics workshop**. QIIME 2 Microbiome Analysis Workshop at The University of Tennessee. Taught microbiome analysis from raw next-generation sequence reads. **May 22-23, 2019**; Chattanooga, TN.

INVITED TALKS

Invited by to discuss fungal phylogenetic diversity analysis for “mycobiome” research at National Jewish Health Hospital; **Mar 2018**; Denver, CO.

Discussed the Mark2Cure.org website with the community of citizen scientist volunteers in a casual community setting. Citizen Science Expo Day at La Jolla Library; **Apr 2016**; La Jolla, CA (Mention Scripps.edu: <https://goo.gl/hrwKKq>)

San Diego State University Graduate Panel for Bioinformatics, Computer Science, and Computational Biology Graduate Programs. One student per graduate program was invited to discuss academic experience and answer questions. San Diego State University; Dec 2014; San Diego, CA

PRESS

“Scientists Predict Brain Drain from States that Ban Abortion.” I tweeted about my hesitation as a woman regarding relocating to states that ban abortion healthcare and interviewed with 5 news outlets. 500k views & 5,000 likes; **Jun 2022**; The Scientist. <https://www.the-scientist.com/news-opinion/scientists-predict-brain-drain-from-states-that-ban-abortion-70184>

The Scripps Research Institute team comes together with rare disease community; **Jan 2016**; The Scripps Research Institute’s News and Views Weekly Online Publication. <https://goo.gl/bjHmox>

Restrooms: not as unhealthy as you might think; **Dec 2014**; Science Daily. <https://goo.gl/xSUYUn>

Cities have individual microbial signatures; **Apr 2016**; Science Daily. <https://goo.gl/2Q59cf>

ACADEMIC AWARDS

NIH/NLM T15 Biomedical Informatics and Data Science Training Fellowship	June 2020 - current
GEN TEN, <i>runner up</i> , BIO International Convention Conference Pass Award	Jun 2014
American Society for Microbiology (ASM) Student Travel Grant	
Young Investigator Oral Presentation Award \$500	Mar 2014
National Science Foundation (NSF) Scholarship - Statistical Track in Bioinformatics	Aug 2012 – May 2014
\$20,000 towards Master’s degree	
Cal Grant Award (need based) - Full undergraduate university tuition: \$20,000	Aug 2002 - Jun 2007
California State PTA College Scholarship: \$500	Jun 2002

ASSOCIATION MEMBERSHIPS

San Diego State University Science Alumni Network (SAN)	Feb 2015 – Feb 2017
<i>Social Media Representative</i> , Feb – Sep 2015	
American Society for Microbiology (ASM)	Jan 2014 – 2016
Association for Women in Science (AWIS), San Diego Chapter	Jun 2013 – 2014
Biomedical Technology Students Association, San Diego State University	Aug 2012 – May 2014
<i>Co-Chair</i> , 2013-2014	
<i>Industry Outreach Representative</i> , 2012-2013	

OUTREACH/VOLUNTEER

Invited (for a **second time**) to teach a **full day** to 5th & 6th graders about opportunities in computer science and microbiome research at Day of Innovation. Imagine Charter School; **Feb 2023**; Firestone, CO.

Invited to volunteer at hour of code. Taught 7th and 8th graders about microbiome and computer science; **Dec 2022**; Broomfield, CO.

Invited to teach a **full day** to 5th & 6th graders about opportunities in computer science related fields for their yearly Day of Innovation; **Feb 2020**; Imagine Charter School, Firestone, CO.

Remote presentation for 7th and 8th graders on careers in bioinformatics for Hour of Code (Code.org sponsored event); **Dec 2016**; Lexington Middle School, Lexington, NE.

Presented to 5th grade students about careers in bioinformatics for Hour of Code (Code.org sponsored event). Prairie Hills Elementary School; **Dec 2016**; Thornton, CO.

Invited to give a panel discussion and short presentation about bioinformatics with middle school children for Hour of Code. Also assisted students with programming. High Tech Middle Media Arts School; **Dec 2015**; San Diego, CA.

Invited to speak to 6th-9th grade girls about future careers in STEM. The Inspired Mind Learning Center: Women in STEM night; **Feb 2015**; San Diego, CA.

PERSONAL INTERESTS

My interests include travelling, cooking, hiking, camping, SCUBA diving, snorkeling, skiing and rock climbing

WEBSITES AND SOCIAL MEDIA

Google Scholar: <https://goo.gl/LgE42s>

Github: <https://github.com/JTFouquier>

Linkedin: <https://goo.gl/4J8XK2>

Twitter: <https://twitter.com/JTFouquier>

Facebook: <https://goo.gl/brKhUw>