

Cecilia Noecker

Assistant Professor
Department of Biological Sciences
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Lab website: **noeckerlab.github.io**

EDUCATION

Ph.D., Genome Sciences
University of Washington, Seattle, WA March 2019
Dissertation: Metabolic modeling-based tools for integrative microbiome data analysis
Advised by Elhanan Borenstein
Certificate programs in Advanced Data Science and Computational Molecular Biology
GPA 3.79

B.A., Biology, Statistics concentration
St. Olaf College, Northfield, MN May 2012
summa cum laude, with Distinction in Statistics
GPA 3.92

PROFESSIONAL APPOINTMENTS

Assistant Professor 2023–
Department of Biological Sciences, Minnesota State University, Mankato

Adjunct Faculty Spring 2023
Pre-professional Health Academic Program, California State University - East Bay
• Instructor for BIOL 433: Microbial Ecology.

Postdoctoral Scholar 9/2019–8/2023
Turnbaugh Lab, University of California San Francisco, San Francisco, CA
• Characterized a novel nutrient niche and metabolic strategy in the human gut microbiome.
• Developed and applied new approaches to study strain variation in human gut bacteria.

Senior Fellow 2019
Graduate Assistant/Fellow 2013-2019
Borenstein Lab, University of Washington, Seattle, WA
• Developed and applied methods for analysis, visualization, and interpretation of multi-omic microbiome data using metabolic models.

Research Intern 2013
Computational Oncology Group, Sage Bionetworks, Seattle, WA
• Contributed data visualization and analysis to a framework for modeling cancer drug sensitivity.

Fulbright Research Fellow 2012-2013
Ramos-Castañeda Lab, National Institute of Public Health, Cuernavaca, Mexico

- Studied associations between human immune polymorphisms and dengue severity in a Mexican population.

TEACHING EXPERIENCE

Assistant Professor 2023–
 Minnesota State University, Mankato

- BIOL 476: Microbial Physiology and Genetics
- BIOL 270: General Microbiology lab
- BIOL 479: Molecular Biology

Adjunct Faculty Spring 2023
 BIOL 433: Microbial Ecology at California State University - East Bay

- Instructor of record for this course. Developing new curriculum on animal-associated microbial communities, experimental design, and project-based assessments.

Microbiome Analysis Workshop Instructor 2019–
 Organized, developed, and facilitated customized workshops on microbiome data analysis for learners of diverse life stages and backgrounds.

- BMS270: Fundamentals of Microbiome Research, UCSF – intro to metagenomics and metabolomics for biomedical Ph.D. students (2021, 2022)
- Invited remote workshop on metagenomics, University of Utah (2021)
- 5-part intro workshop on bioinformatics and data science for UCSF affiliates, offered during COVID-19 lab shutdown (2020)
- Invited workshop on multi-omics, Sheba Medical Center, Tel Aviv, Israel (2019)

Software and Data Carpentry Certified Instructor 2018–

- Taught lessons on R for Ecology, Unix shell, and Python; positive student feedback.

Teaching Assistant 2016–2017
 University of Washington, Seattle, WA

- Genome Informatics: Developed and led weekly tutorial sections, wrote and graded homework assignments. Designed and led a sequence analysis workshop, “Diagnosing GI infections from metagenomic data”, materials available on GitHub.
- Introductory Genetics and Genomics: Led interactive quiz sections, graded homework and exams.

GRE Prep Instructor 2016
 Genome Sciences Summer Undergraduate Research Program, University of Washington, Seattle, WA

Academic Assistant 2008–2012
 St. Olaf Academic Support Center, Northfield, MN

- Led workshops on study skills and time management.
- Tutored students in math, science and Spanish.

RESEARCH MENTORING EXPERIENCE

UCSF-CCSF Inclusive Mentoring Fellow 2021–2022

Mentee: Lu (Liz) Guo, City College of San Francisco Biotechnology Certificate Program
Project: Biogeography and comparative genomics of *Eggerthella lenta*
Currently: completing her B.S. in Chemical Biology at UC Berkeley

Turnbaugh lab Ph.D. student mentoring

2020–

- Mentee: Janice Goh, UCSF Pharmacological Sciences and Pharmacogenomics Ph.D.
Project: Effects of the gut microbiome on host drug clearance
Currently: Ph.D. student, Saba Lab, UCSF
- Mentee: Kai Trepka, UCSF Medical Scientist Training Program (M.D./Ph.D.)
Project: Ecological interactions among human gut microbes in health and disease
- Mentee: Rachel Rock, UCSF Biomedical Sciences Ph.D.
Project: Statistical analysis of gut microbial strains, host sex, and autoimmune disease

Code Club

2020–

Founder and facilitator of a monthly code review and/or tutorial on tools and concepts in bioinformatics and statistics for Turnbaugh lab members and other biomedical trainees at UCSF.

Borenstein lab mentoring

2019

- Mentee: Efrat Muller, Tel Aviv University Bioinformatics Ph.D.
Project: Analysis of microbiome-metabolome studies

HONORS, AWARDS AND FELLOWSHIPS

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| Trainee Pilot Award, UCSF Benioff Center for Microbiome Medicine (\$10,000) | 2021–2022 |
| Ruth L. Kirschstein NRSA F32 Postdoctoral Fellowship, NIGMS | 2021–2023 |
| UCSF Microbial Pathogenesis and Host Defense T32 Training Grant | 2019–2020 |
| Young Investigator Award, Sage Assembly | 2018 |
| University of Washington-NSF IGERT Fellowship in Big Data Science | 2014–2016 |
| First Prize, Washington Research Foundation Pitch Competition (\$250) | 2016 |
| Young Scientist Travel Award, Multi-omics for Microbiomes Conference (\$1,000) | 2015 |
| Pacific Science Center Science Communication Fellow | 2015 |
| NSF Graduate Research Fellowship Honorable Mention | 2014, 2015 |
| U.S.-Mexico Fulbright Student Research Fellow (\$12,000) | 2012–2013 |
| St. Olaf-NSF Center for Interdisciplinary Research Fellow | 2011–2012 |
| Minnesota State Academics-Arts-Athletics Scholar | 2008–2012 |

PUBLICATIONS

*indicates equal contribution/co-first author

In review

1. Escalante, V., R. Nayak, **C. Noecker**, A. Deutschbauer, and P.J. Turnbaugh. Human gut bacteria fortify their cell surface to escape the off-target effects of statins. In review at *Molecular Microbiology*. 2023.
2. Li, X., L. Xu, B. Demaree, **C. Noecker**, J.E. Bisanz, D.W. Weisgerber, C. Modavi, P.J. Turnbaugh, and A.R. Abate. Microbiome single cell atlases generated with a commercial instrument. *bioRxiv*. doi:10.1101/2023.08.08.551713, 2023.

Published peer-reviewed research

1. **Noecker, C.**, J. Sanchez, J.E. Bisanz, V. Escalante, M. Alexander, K. Trepka, A. Heinken, Y. Liu, D. Dodd, I. Thiele, B. DeFelice, and P.J. Turnbaugh. Systems biology elucidates the distinctive metabolic niche of the human gut bacterium *Eggerthella lenta*. *PLOS Biology*. doi:10.1371/journal.pbio.3002125, 2023.
2. Upadhyay, V., R. Suryawanshi, P. Tasoff, M. McCavitt-Malvido, G.R. Kumar, V. Wong Murray, **C. Noecker**, J.E. Bisanz, Y. Hswen, C.Y. Ha, B. Sreekumar, I.P. Chen, S.V. Lynch, M. Ott, S. Lee, and P.J. Turnbaugh. Mild SARS-CoV-2 infection results in long-lasting microbiota instability. *mBio*. doi:10.1128/mbio.00889-23, 2023.
3. Dong, X., B. Guthrie, M. Alexander, **C. Noecker**, L. Ramirez, N. Glasser, P. J. Turnbaugh, and E. Balskus. Genetic manipulation of the human gut bacterium *Eggerthella lenta* reveals a widespread family of transcriptional regulators. *Nature Communications*. doi:10.1038/s41467-022-33576-3, 2022.
4. **Noecker, C.**, A. Eng, E. Muller, and E. Borenstein. MIMOSA2: A metabolic network-based tool for inferring mechanism-supported relationships in microbiome-metabolome data. *Bioinformatics*. doi:10.1093/bioinformatics/btac003, 2022.
5. Ang, Q.Y., D.L. Alba, V. Upadhyay, J.E. Bisanz, J. Cai, H.L. Lee, E. Barajas, G. Wei, **C. Noecker**, A.D. Patterson, S.K. Koliwad, and P.J. Turnbaugh. The East Asian gut microbiome is distinct from colocalized white subjects and connected to metabolic health. *eLife*. doi:10.7554/eLife.70349, 2021.
6. Buffington, S.A., S.W. Dooling, M. Sgritta, **C. Noecker**, O.D. Murillo, D.F. Felice, P.J. Turnbaugh and M.Costa-Mattioli. Dissecting the contribution of host genetics and the microbiome in complex behaviors. *Cell*. doi:10.1016/j.cell.2021.02.009, 2021.
7. Shouval, R., A. Eshel, B. Dubovski, A.A. Kuperman, I. Danylesko, J. Fein, S. Fried, M. Geva, E. Kouniavski, E. Muller, **C. Noecker**, E. Borenstein, Y. Louzoun, A. Nagler, and O. Koren. Patterns of salivary microbiota injury and oral mucositis in recipients of allogeneic hematopoietic stem cell transplantation. *Blood Advances*. doi:10.1182/bloodadvances.2020001827, 2020.
8. Bisanz, J., P. Soto-Perez, **C. Noecker**, A.A. Aksenov, K.N. Lam, G.E. Kenney, E.N. Bess, H.J. Haiser, T.S. Kyaw, F.B. Yu, V.M. Rekdal, C.W.Y. Ha, S. Devkota, E.P. Balskus, P.C. Dorrestein, E. Allen-Vercoe, and P. Turnbaugh. A genomic toolkit for the mechanistic dissection of intractable human gut bacteria. *Cell Host & Microbe*. doi:10.1016/j.chom.2020.04.006, 2020.
9. **Noecker, C.**, H.-C. Chiu, C.P. McNally, and E. Borenstein. Defining and evaluating microbial contributions to metabolite variation in microbiome-metabolome association studies. *mSystems*. doi:10.1128/mSystems.00579-19, 2019.
10. Sharon, G., N.J. Cruz, D. Kang, M.J. Gandal, Y.-M. Kim, E.M. Zink, C.P. Casey, L.M. Bramer, N.G. Isern, D.W. Hoyt, **C. Noecker**, E. Borenstein, J. Jansson, T.O. Metz, D.H. Geschwind, R. Krajmalnik-Brown, and S.K. Mazmanian. Human microbiomes from autism spectrum disorder promote behavioral symptoms in mice. *Cell*. doi:10.1016/j.cell.2019.05.004, 2019.
11. Rebollar, E., A. Gutierrez-Preciado, **C. Noecker**, A. Eng, M.C. Hughey, D. Medina, J.B. Walke, E. Borenstein, R.V. Jensen, L. K. Belden, and R.N. Harris. The functional repertoire of the skin microbiome of the frog *Craugastor fitzingeri*: Inferring potential bacterial-host-pathogen interactions from metagenomic data. *Frontiers in Microbiology*. doi:10.3389/fmicb.2018.00466, 2018.

12. Eng, A.*, C.P. McNally*, **C. Noecker***, W. Gagne-Maynard and E. Borenstein. BURRITO: An interactive multi-omic tool for visualizing taxa-function relationships in microbiome data. *Frontiers in Microbiology*. doi:10.3389/fmicb.2018.00365, 2018.
13. Mosites, E., M. Sammons, E. Otiang, A. Eng, **C. Noecker**, O. Manor, S. Hilton, T. Mwangi, C. Onyango, G. Garland-Lewis, D. Call, K. Njenga, J. Wasserheit, J. Zambriski, J. Walson, J. Montgomery, E. Borenstein, R. Omore and P. Rabinowitz. Microbiome sharing between children, livestock and household surfaces in Western Kenya. *PLOS ONE*. doi:10.1371/journal.pone.0171017, 2017.
14. Snijders, A.M., S.A. Langley, Y.-M. Kim, C.J. Brislawn, **C. Noecker**, E.M. Zink, S.J. Fansler, C.P. Casey, D.R. Miller, Y. Huang, G.H. Karpen, S.E. Celniker, J.B. Brown, E. Borenstein, J.K. Jansson, T.O. Metz, and J.-H. Mao. Influence of early life exposure, host genetics and diet on the mouse gut microbiome and metabolome. *Nature Microbiology*. 2:16221, doi:10.1038/nmicrobiol.2016.221, 2017.
15. **Noecker, C.**, A. Eng, S. Srinivasan, C. Theriot, V. Young, J. Jansson, D. Fredricks and E. Borenstein. Metabolic model-based integration of microbiome taxonomic and metabolomic profiles elucidates mechanistic links between ecological and metabolic variation. *mSystems*. 1(1):e00013-15, doi:10.1128/mSystems.00013-15, 2016.
16. **Noecker, C.**, K. Schaefer, K. Zaccheo, Y. Yang, J. Day and V. Ganusov. Simple mathematical models do not accurately predict early SIV dynamics. *Viruses*. 7(3):1189-1217, doi:10.3390/v7031189, 2015.
17. **Noecker, C.**, I.Y. Amaya-Larios, M. Galeana-Hernandez, J. Ramos-Castaneda, and R.A. Martinez-Vega. Contrasting associations of polymorphisms in Fc γ RIIa and DC-SIGN with the clinical presentation of dengue infection in a Mexican population. *Acta Tropica*. 138:15-22, doi:10.1016/j.actatropica.2014.05.021, 2014.
18. **Noecker, C.** and P. Roback. New insights on the tendency of NCAA basketball officials to even out foul calls. *Journal of Quantitative Analysis in Sports*. 8:3, doi:10.1515/1559-0410.1402, 2012.

Reviews and commentaries

1. **Noecker, C.***, C.P. McNally*, A. Eng* and E. Borenstein. High-resolution characterization of the human microbiome. *Translational Research*. doi:10.1016/j.trsl.2016.07.012, 2016.
2. **Noecker, C.** and E. Borenstein. Getting personal about nutrition. *Trends in Molecular Medicine*. doi:10.1016/j.molmed.2015.12.010, 2016.

PRESENTATIONS

Invited Talks

- “Ecology and evolution of the cardenolide-metabolizing gut bacterium *Eggerthella lenta*.” Symposium on diverse mechanisms of adaptation to natural toxins, Berlin, Germany. 2023
- “Modeling gut microbial metabolism across scales.” Having IMPACTT: Advancing Microbiome Research Symposium, Canmore, Alberta, Canada. 2023
- “Survival strategies in the gut: Using genomes to decipher the metabolism and evolution of a common human-associated microbe”. Seminar, Minnesota State University - Mankato, Mankato, MN. 2023

- “Survival strategies in the gut: Using genomes to decipher the metabolism of a common human-associated microbe”. Seminar, Carthage College, Kenosha, WI. 2022
- “Survival strategies in the gut: Using genomes to decipher the metabolism of a common human-associated microbe”. Seminar, Elmhurst University, Elmhurst, IL. 2022
- “Tools for analyzing the metabolism of microbes and microbiomes.” University of Puerto Rico, San Juan, Puerto Rico. Virtual talk due to COVID-19 pandemic. 2020
- “Using metabolic models to integrate microbiomes and metabolomes.” Invited conference talk, Intelligent Systems for Molecular Biology. Virtual meeting due to COVID-19 pandemic. 2020
- “Metabolism and systems biology of the gut bacterium *Eggerthella lenta*.” SRI International, Menlo Park, CA. 2020

Conference Talks

- “Local and global profiling of genome variation in a prevalent human gut microbe.” ASM Microbe, Houston, TX. 2023
- “Defining and evaluating microbiome contributions to metabolic variation.” Conference on Constraint-Based Reconstruction and Analysis (COBRA), Seattle, WA. 2018
- “MIMOSA: An integrative framework for linking ecological and metabolic microbiome variation.” International Human Microbiome Consortium Congress, Houston, TX. 2016
- “MIMOSA: An integrative framework for linking ecological and metabolic microbiome variation.” University of Washington Computational Molecular Biology Symposium, Seattle, WA. 2016
- “Integrative, mechanistic, multi-omic analysis of the vaginal microbiome.” Mayo Clinic Individualizing Medicine Conference, Rochester, MN. 2015
- “Theory of early SIV/HIV infection.” Undergraduate Research Conference in Mathematics and Biology, Knoxville, TN. 2011

Selected Conference Posters

- “Systems biology illuminates an alternative metabolic niche in the human gut microbiome.” Lake Arrowhead Microbial Genomics Meeting, Lake Arrowhead, CA. 2022
- “Metabolic profile of the prevalent gut bacterium *Eggerthella lenta*.” Conference on Beneficial Microbes, Madison, WI. 2022
- “Metabolic model-based evaluation of taxon-metabolite links in microbiomes.” Conference on Beneficial Microbes, Madison, WI. 2018
- “Model-based analysis of microbiome taxon-metabolite relationships.” Sage Assembly, Seattle, WA. 2018
- “Integrative, mechanistic multi-omic analysis of taxa and metabolites elucidates links between ecological and metabolic variation.” PNNL Multi-omics for Microbiomes Conference, Kennewick, WA. 2015
- “Integrative multi-omic analysis of microbiome taxa and metabolites reveals community metabolic trends and putative mechanistic links.” META Center Symposium on Host-Microbe Systems Biology, Eugene, OR. 2015
- “Contrasting associations of immune polymorphisms with the clinical presentation of dengue infection in a Mexican population.” American Society of Tropical Medicine and Hygiene Annual Meeting, Washington, D.C. 2013

OUTREACH

Scientist Interviewee 2018–
Skype a Scientist

Science Communication Fellow and Volunteer 2013–2019
Pacific Science Center, Seattle, WA

- Regular “Meet a Scientist” contributor, facilitating an informal educational activity for museum visitors on diet-microbiome metabolic interactions.
- Featured Scientist in 2015 “Meet your Microbes!” exhibit.

Scientific Consultant and Featured Scientist 2018-2020
Genome Sciences Education and Outreach Office, Seattle, WA

- Collaborated with NIH-supported outreach professionals to develop a lesson for high school students on human gut microbial ecology meeting NGSS standards, “The Microbiome: Food, Fiber, and Fitness” ([link](#)).

Public and Educational Presentations

- “The gut microbiome in type 2 diabetes.” High school curriculum development workshop, Genome Sciences Outreach, Seattle, WA, 2018.
- “Uncovering microbiome activities with computational modeling.” Seattle Science Slam, Seattle, WA, 2017.
- “Sharing, scavenging, and synthesizing in your gut microbiome.” Teen Science Cafe, Redmond, WA, 2017.

Introduction to Python Instructor 2017
Genome Hackers Summer Camp, University of Washington, Seattle, WA

- Developed curriculum and taught sequence analysis basics for a bioinformatics summer camp for middle school girls.

Workshop Facilitator 2015
Expand Your Horizons, Seattle, WA

- Designed and led workshops on genetics concepts and science careers for middle school girls.

DIVERSITY AND ADVOCACY

President, University of Washington Women in Genome Sciences 2016–2018

- Led organizational meetings; coordinated seminars, social events, and journal club discussions.
- Communicated information and resources to the Genome Sciences department on gender, bias, inclusion, and culture of science.
- Organized expert-led workshops on inclusive science teaching practices; preventing sexual and gender harassment in STEM; bias in citation networks; and science communication.
- 2015-2016 communications and social media officer

Department Steward, University of Washington Union of Academic Student Employees 2016–2018

ACADEMIC SERVICE

Member 2021–Present

UCSF Microbiome Data Working Group

Grant reviewer 2020–2022
UCSF Benioff Center for Microbiome Medicine Microbiome Research Program, Faculty Pilot grants

Ad hoc journal reviewer 2018–
Nature Scientific Data, Microbial Genomics, ACS Chemical Biology, mSystems, Microbiome, Genome Biology, Gut Microbes, BMC Gastroenterology, Journal of Medical Microbiology, PLOS ONE, Scientific Reports, Frontiers in Microbiology, Frontiers in Genetics, Frontiers in Cellular and Infection Microbiology, Metabolites, Microorganisms

Collaborative journal reviewer 2014–
Reviewed jointly with E. Borenstein or P. Turnbaugh for *Cell, Cell Metabolism, Cell Systems, Cell Host and Microbe, Nature, ISME J, Genome Medicine, Nature Microbiology, PLOS Computational Biology.*

Discussion leader, University of Washington Genomics Salon 2017–2018
Planned and facilitated two discussion sessions for trainees on science advocacy and science education.

Committee member, Genome Sciences Graduate Curriculum Revisions 2015–2016

PROFESSIONAL DEVELOPMENT

UCSF Inclusive Mentoring Course 2020

ComSciCon-Pacific Northwest Science Communication Workshop 2018

Software/Data Carpentry Instructor Training 2018

American Society for Microbiology Science Teaching Fellow 2017
4-month online course on best practices in curriculum design, pedagogy, and assessment in undergraduate life science education.

MEMBERSHIPS

American Society for Microbiology 2017–
Faculty of 1000 Associate Member 2015–
Phi Beta Kappa 2012–

REFERENCES

Dr. Peter J. Turnbaugh
Postdoc Advisor
Professor, Department of Microbiology and Immunology
University of California San Francisco

peter.turnbaugh@ucsf.edu

Dr. Elhanan Borenstein

Ph.D. Advisor

Professor, Blavatnik School of Computer Science and Sackler Faculty of Medicine

Head, Edmond J. Safra Center for Bioinformatics

Tel Aviv University

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Dr. M. Denise Dearing

Collaborator

Professor, School Of Biological Sciences

University of Utah

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