

# Marcus William Fedarko

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<b>Education</b>	PH.D. CANDIDATE, Computer Science <b>University of California, San Diego</b> GPA: 3.60/4.0	9/2018–Present La Jolla, CA
	M.S., Computer Science <b>University of California, San Diego</b> GPA: 3.60/4.0	9/2018–6/2022 La Jolla, CA
	B.S. WITH HIGH HONORS, Computer Science <b>University of Maryland</b> GPA: 3.81/4.0	9/2014–5/2018 College Park, MD
<b>Refereed Publications</b>	<ol style="list-style-type: none"><li>7. <b>Fedarko MW</b>, Kolmogorov M, and Pevzner PA (2022). “Analyzing rare mutations in metagenomes assembled using long and accurate reads.” <i>Genome Research</i>, 32(11-12):2119–2133.</li><li>6. Cantrell K*, <b>Fedarko MW*</b>, Rahman G, McDonald D, Yang Y, Zaw T, Gonzalez A, Janssen S, Estaki M, Haiminen N, Beck KL, Zhu Q, Sayyari E, Morton JT, Armstrong G, Tripathi A, Gauglitz JM, Marotz C, Matteson NL, Martino C, Sanders JG, Carrieri AP, Song SJ, Swofford AD, Dorrestein PC, Andersen KG, Parida L, Kim H-C, Vázquez-Baeza Y, and Knight R (2021). “EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets.” <i>mSystems</i>, 6(2):e01216-20. (* = contributed equally)</li><li>5. Huey SL, Jiang L, <b>Fedarko MW</b>, McDonald D, Martino C, Ali F, Russell DG, Udipi SA, Thorat A, Thakker V, Ghugre P, Potdar RD, Chopra H, Rajagopalan K, Haas JD, Finkelstein JL, Knight R, and Mehta S (2020). “Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India.” <i>mSphere</i>, 5(5):e00731-20.</li><li>4. <b>Fedarko MW</b>, Martino C, Morton JT, González A, Rahman G, Marotz CA, Minich JJ, Allen EA, and Knight R (2020). “Visualizing ’omic feature rankings and log-ratios using Qurro.” <i>NAR Genomics and Bioinformatics</i>, 2(2):lqaa023.</li><li>3. Sanders JG, Nurk S, Salido RA, Minich J, Xu ZZ, Martino C, <b>Fedarko M</b>, Arthur TD, Chen F, Boland BS, Humphrey GC, Brennan C, Sanders K, Gaffney J, Jepsen K, Khosroheidari M, Green C, Liyange M, Dang JW, Phelan VV, Quinn RA, Bankevich A, Chang JT, Rana TM, Conrad DJ, Sandborn WJ, Smarr L, Dorrestein PC, Pevzner PA, and Knight R (2019). “Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads.” <i>Genome Biology</i>, 20(1):226.</li><li>2. Ghurye J, Treangen T, <b>Fedarko M</b>, Hervey WJ, and Pop M (2019). “MetaCarvel: linking assembly graph motifs to biological variants.” <i>Genome Biology</i>, 20(1):174.</li><li>1. Meisel JS, Nasko DJ, Brubach B, Cepeda-Espinoza V, Chopyk J, Corrada-Bravo H, <b>Fedarko M</b>, Ghurye J, Javkar K, Olson ND, Shah N, Allard SM, Bazinet AL, Bergman NH, Brown A, Caporaso JG, Conlan S, DiRuggiero J, Forry SP, Hasan NA, Kralj J, Luethy PM, Milton DK, Ondov BD, Preheim S, Ratnayake S, Rogers SM, Rosovitz MJ, Sakowski EG, Schliebs NO, Sommer DD, Ternus KL, Uritskiy G, Zhang SX, Pop M, and Treangen TJ (2018). “Current progress and future opportunities in applications</li></ol>	

of bioinformatics for biodefense and pathogen detection: Report from the Winter Mid-Atlantic Microbiome Meet-up, College Park, MD January 10<sup>th</sup>, 2018.” *Microbiome*, 6(1):197.

## Open-Source Software

6. **wotplot**: Library for creating and visualizing dot plot matrices.  
<https://github.com/fedarko/wotplot>
5. **strainFlye\***: Pipeline for the analysis of rare mutations in metagenomes.  
<https://github.com/fedarko/strainFlye>
4. **EMPress\***: Visualization tool for phylogenetic trees and associated data.  
<https://github.com/biocore/empres>
3. **Qurro\***: Visualization tool for log-ratios of compositional data.  
<https://github.com/biocore/qurro>
2. **pyfastg**: Library for parsing SPAdes FASTG files.  
<https://github.com/fedarko/pyfastg>
1. **MetagenomeScope**: Visualization tool for metagenome assembly graphs.  
<https://github.com/marbl/MetagenomeScope>

Projects marked with a \* character represent the “main contribution” of at least one of the refereed publications listed above.

## Outreach Presentations

3. “Studying microbiomes using DNA sequencing.” Presentation to students from Kearny High School visiting UC San Diego, 5/2023.
2. “Visualizing, Exploring, and Understanding Microbiome Sequencing Data.” UC San Diego CSE Research Open House, 1/2020.
1. “Visualizing Metagenomic Assembly Graphs, Doing Undergrad Research at UMD, Applying to Grad Schools, and probably other stuff along the way.” Guest presentation for CMSC 396H (University of Maryland undergraduate honors seminar), 4/2018.

## Service

6. Peer Reviewer, PLOS ONE 2023
5. System Administrator, Pevzner Lab computing server 2/2023–Present
4. Mentor, UC San Diego GradWIC (Graduate Women in Computing) mentorship program 10/2021–Present
3. Moderator, QIIME 2 forum (<https://forum.qiime2.org>) 3/2020–Present
2. Co-organizer, UC San Diego CSE Visit Day 1/2019–Present
1. Code Review (Co-)organizer, Knight Lab 12/2018–8/2020

## Research Experience

- GRADUATE STUDENT RESEARCHER 9/2018–Present  
**University of California, San Diego** La Jolla, CA
- Designing software for the analysis of microbiome sequencing data and other forms of “omic” data.
  - Assisting with various software and analysis projects.

- RESEARCH INTERN 6/2016–8/2018  
**University of Maryland** College Park, MD
- Designed MetagenomeScope, a visualization tool for metagenome assembly graphs.

<b>Teaching Experience</b>	TEACHING ASSISTANT	
	<b>University of California, San Diego</b>	La Jolla, CA
	<ul style="list-style-type: none"> <li>• <b>CSE 282:</b> Introduction to Bioinformatics Algorithms</li> </ul>	1/2023–3/2023 1/2022–3/2022 1/2021–3/2021
	COURSE ASSISTANT	
	<b>Marine Biological Laboratory</b>	Woods Hole, MA
	<ul style="list-style-type: none"> <li>• <b>STAMPS:</b> Strategies and Techniques for Analyzing Microbial Population Structures</li> <li>• <b>MOLE:</b> Workshop on Molecular Evolution</li> </ul>	7/2018–8/2018 7/2018
	TEACHING ASSISTANT	
	<b>University of Maryland</b>	College Park, MD
	<ul style="list-style-type: none"> <li>• <b>CMSC 330:</b> Organization of Programming Languages</li> </ul>	8/2016–12/2016
<b>Professional Experience</b>	STUDENT STAFF WRITER	1/2015–9/2017
	<b>University of Maryland Dept. of Computer Science</b>	College Park, MD
	<ul style="list-style-type: none"> <li>• Wrote and edited articles for the department’s website and other media.</li> <li>• Assisted with the logistics of various department outreach functions.</li> </ul>	
	STUDENT INTERN	5/2013–8/2014
	<b>Axiometric</b>	Columbia, MD
	<ul style="list-style-type: none"> <li>• Designed a graphical interface to an RF propagation model to assist clients in planning deployments of mesh networks of utility meters.</li> <li>• Aided in the creation and maintenance of other utility meter deployment management software.</li> </ul>	
	INTERN SOFTWARE ENGINEER	7/2012–8/2012
	<b>Battlefield Telecommunications Systems</b>	Columbia, MD
	<ul style="list-style-type: none"> <li>• Designed a web interface to monitor the connection strength of radio devices.</li> <li>• Helped integrate this functionality into the company’s existing network management user interface.</li> </ul>	
<b>Honors and Awards</b>	9. University of Maryland CMNS Dean’s List	2014–2018
	8. University of Maryland Honors College University Honors Citation	2017
	7. Rita Colwell Travel Fellowship	2017
	6. Travel Award, U. of Michigan “Explore Graduate Studies” Workshop	2017
	5. John D. Gannon Endowed Scholarship	2017
	4. Corporate Partners in Computing Scholarship	2016, 2017
	3. Omicron Delta Kappa National Leadership Honor Society	2016
	2. Northrop Grumman Scholarship for Employees’ Children	2014
	1. University of Maryland Dean’s Scholarship	2014