

# Marcus W. Fedarko

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## SUMMARY

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I'm a postdoc at the University of Maryland. I develop methods to help researchers study microbiome sequencing data in high resolution, with a focus on data visualization and metagenome assembly.

## EDUCATION

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PH.D., Computer Science <b>University of California, San Diego</b>	9/2018–6/2025 La Jolla, CA
M.S., Computer Science <b>University of California, San Diego</b>	9/2018–6/2022 La Jolla, CA
B.S. WITH HIGH HONORS, Computer Science <b>University of Maryland</b>	9/2014–5/2018 College Park, MD

## RESEARCH EXPERIENCE

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POSTDOCTORAL ASSOCIATE <b>University of Maryland</b>	10/2025–Present College Park, MD
GRADUATE STUDENT RESEARCHER <b>University of California, San Diego</b>	9/2018–10/2025 La Jolla, CA
RESEARCH INTERN <b>University of Maryland</b>	6/2016–8/2018 College Park, MD

## TEACHING EXPERIENCE

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TEACHING ASSISTANT <b>University of California, San Diego</b>	La Jolla, CA
• <b>CSE 185:</b> Advanced Bioinformatics Laboratory	3/2025–6/2025
• <b>CSE 181:</b> Molecular Sequence Analysis	1/2025–3/2025 1/2024–3/2024
• <b>CSE 282:</b> Introduction to Bioinformatics Algorithms	1/2025–3/2025 1/2023–3/2023 1/2022–3/2022 1/2021–3/2021
COURSE ASSISTANT <b>Marine Biological Laboratory</b>	Woods Hole, MA
• <b>STAMPS:</b> Strategies and Techniques for Analyzing Microbial Population Structures	7/2018–8/2018
• <b>MOLE:</b> Workshop on Molecular Evolution	7/2018
TEACHING ASSISTANT <b>University of Maryland</b>	College Park, MD

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## OTHER PROGRAMMING / WRITING EXPERIENCE

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SOFTWARE DEVELOPER <i>Bioinformatics Algorithms</i> (Compeau & Pevzner)	7/2025–10/2025 Remote
STUDENT STAFF WRITER University of Maryland Department of Computer Science	1/2015–9/2017 College Park, MD
STUDENT INTERN Axiometric	5/2013–8/2014 Columbia, MD
INTERN SOFTWARE ENGINEER Battlefield Telecommunications Systems	7/2012–8/2012 Columbia, MD

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## SUBMITTED PAPERS

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2. **Fedarko MW**, Ghurye J, Treangen T, and Pop M (2026). “Hierarchical decomposition and visualization of sequence assembly graphs with MetagenomeScope.”
1. Zhang Z, **Fedarko MW**, Bankevich A, and Pevzner PA (2025). “Haplotype-mixed assembly of long and accurate reads.”

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## PEER-REVIEWED PAPERS

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7. **Fedarko MW**, Kolmogorov M, and Pevzner PA (2022). “Analyzing rare mutations in metagenomes assembled using long and accurate reads.” *Genome Research*, 32(11-12):2119–2133.
6. Cantrell K\*, **Fedarko MW\***, 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, Swafford 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.” *mSystems*, 6(2):e01216-20. (\* = contributed equally)
5. Huey SL, Jiang L, **Fedarko MW**, 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.” *mSphere*, 5(5):e00731-20.
4. **Fedarko MW**, 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.” *NAR Genomics and Bioinformatics*, 2(2):lqaa023.
3. Sanders JG, Nurk S, Salido RA, Minich J, Xu ZZ, Martino C, **Fedarko M**, 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.” *Genome Biology*, 20(1):226.
2. Ghurye J, Treangen T, **Fedarko M**, Hervey WJ, and Pop M (2019). “MetaCarvel: linking assembly graph motifs to biological variants.” *Genome Biology*, 20(1):174.
1. Meisel JS, Nasko DJ, Brubach B, Cepeda-Espinoza V, Chopyk J, Corrada-Bravo H, **Fedarko M**, Ghurye J, Javkar K, Olson ND, Shah N, Allard SM, Bazinet AL, Bergman NH, Brown A, Capo-

raso 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 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

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6. **wotplot**: Library for creating and visualizing dot plot matrices.  
<https://github.com/fedarko/wotplot>
5. **strainFlye** (👉<sub>7</sub>): Pipeline for the analysis of rare mutations in metagenomes.  
<https://github.com/fedarko/strainFlye>
4. **EMPress** (👉<sub>6</sub>): Visualization tool for phylogenetic trees and associated data.  
<https://github.com/biocore/empress>
3. **Qurro** (👉<sub>4</sub>): Visualization tool for log-ratios of compositional data.  
<https://github.com/biocore/qurro>
2. **pyfastg**: Library for parsing FASTG-format assembly graph files.  
<https://github.com/fedarko/pyfastg>
1. **MetagenomeScope**: Visualization tool for metagenome assembly graphs.  
<https://github.com/marbl/MetagenomeScope>

Projects marked (👉<sub>*n*</sub>) represent the “main contribution” of the *n*-th peer-reviewed paper in the list above.

## TALKS

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4. “Metagenome assembly.” 1/2024  
*Guest lecture for ESE 184 (Computational Tools for Decoding Microbial Ecosystems), California Institute of Technology.*
3. “Studying microbiomes using DNA sequencing.” 5/2023  
*Presentation to students from Kearny High School visiting UC San Diego.*
2. “Visualizing, Exploring, and Understanding Microbiome Sequencing Data.” 1/2020  
*UC San Diego CSE Research Open House.*
1. “Visualizing Metagenomic Assembly Graphs, Doing Undergrad Research at UMD, Applying to Grad Schools, and probably other stuff along the way.” 4/2018  
*Guest lecture for CMSC 396H (Undergraduate Honors Seminar), University of Maryland.*

## EDITING AND REVIEWING

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2. Textbook Editor, *Advanced Bioinformatics Algorithms* 2024
1. Peer Reviewer, *PLOS ONE* 2023

## SERVICE

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5. System Administrator, Pevzner Lab computing server 2/2023–10/2025
4. Mentor, UC San Diego Graduate Women in Computing mentorship program 10/2021–6/2024
3. Moderator, QIIME 2 forum (<https://forum.qiime2.org>) 3/2020–4/2024

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| 2. Co-organizer, UC San Diego CSE Visit Day | 1/2019–3/2024  |
| 1. Code Review (Co-)organizer, Knight Lab   | 12/2018–8/2020 |

## HONORS AND AWARDS

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|---|------------|
| 10. <b>UC San Diego:</b> Chez Bob Hackathon Award                             | 2024       |
| 9. <b>University of Maryland:</b> CMNS Dean's List                            | 2014–2018  |
| 8. <b>University of Maryland:</b> University Honors Citation                  | 2017       |
| 7. <b>University of Maryland:</b> Rita Colwell Travel Fellowship              | 2017       |
| 6. <b>University of Michigan:</b> Travel Award, EGS Workshop                  | 2017       |
| 5. <b>University of Maryland:</b> John D. Gannon Endowed Scholarship          | 2017       |
| 4. <b>University of Maryland:</b> Corporate Partners in Computing Scholarship | 2016, 2017 |
| 3. <b>Omicron Delta Kappa National Leadership Honor Society</b>               | 2016       |
| 2. <b>Northrop Grumman:</b> Scholarship for Employees' Children               | 2014       |
| 1. <b>University of Maryland:</b> Dean's Scholarship                          | 2014       |

## SKILLS

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- **Languages:** English (native), German (basic), Hindi (basic)
- **Computer Languages:** Python, JavaScript, HTML / CSS, L<sup>A</sup>T<sub>E</sub>X, Java, C, C++, ...
- **Software Libraries:** matplotlib, pandas, NumPy, SciPy, scikit-bio, Dash, Cytoscape.js, ...