Joshua J. Hamilton

San Francisco Bay Area, CA, USA joshamilton@gmail.com 913-269-7789
https://www.linkedin.com/in/joshamilton/ https://github.com/joshamilton

Professional Summary

- Results-oriented data scientist harnessing complex data to improve the human condition, with eight years of experience beyond the PhD. I built and led the data science group at Federation Bio, where I was responsible for designing, leading, and executing data science projects from discovery to early clinical development. Effective leader and clear communicator with the ability to prioritize competing objectives and align projects accordingly.

Experience

- **Data Scientist I, Data Scientist II, Sr Data Scientist**, Federation Bio, Inc *2019-present*
  - Established, built, and led data science group. Managed research associates and scientists. Mentored cross-functionally.
  - Led design and execution of data science efforts across the portfolio, including data analysis, bioinformatics, software development, data management, data engineering, and cloud computing for programs in microbiome, immunology, and oncology
  - Served as technical expert in microbiome science, and partnered with CMC, translational medicine, clinical science, and regulatory affairs to advance discovery programs into clinical development
  - Authored documents to support regulatory filings
  - Identified, screened, selected, and managed contractors and CROs
  - Led internal and external cross-functional teams in development and qualification of bioanalytical assays
  - Designed and built bioinformatics pipelines for genome assembly, genome annotation, and metagenomic profiling, using Nextflow, Docker, R, and Python
  - Built and optimized cloud computing infrastructure, powered by AWS
  - Launched laboratory informatics program by implementing Benchling ELN/LIMS and establishing best practices for data management and documentation
- **Postdoctoral Research Associate**, UW-Madison *2014-2019*
  - Identified molecular interactions within microbial communities, using a combination of experimental and computational methods, including:
    - Experimental: high-throughput experimental screens, metabolomics, genomics, and transcriptomics
    - Computational: bioinformatics (genome-centric metagenomics and metatranscriptomics), metabolic modeling, and differential equations modeling
  - Led development of genomic, transcriptomic, and metabolomic assays, authored laboratory protocols, and identified external service providers and collaborators
  - Mentored graduate students in bioinformatics and software development, and fostered adoption of good data management practices among laboratory members and collaborators
  - Participated in build out of anaerobic microbiology lab, including anaerobic chambers and liquid handling robots
  - Developed algorithm for improved species-level taxonomic assignment within microbiomes
- **Graduate Research Assistant**, UW-Madison *2009-2014*
  - Published multiple metabolic reconstructions and genome-scale metabolic models
  - Developed algorithm to identify functional differences between microbes using comparative genomics and metabolic modeling
  - Incorporated thermodynamic information into metabolic models using chemoinformatic group contribution methods

Skills

- Soft skills: leadership, cross-functional collaboration, communication, writing, presentations
- Programming and Software Development: R, Python, Git, Github, Nextflow, Docker, AWS
- Bioinformatics: genome assembly, genome annotation, metagenomic assembly and binning, metagenome profiling, 16S rRNA sequencing, amplicon sequencing
- Drug development: drug discovery, assay development, preclinical research, translational research, early clinical development

Education

- **University of Wisconsin-Madison (UW-Madison)** — Madison, WI
  Ph.D., Chemical Engineering — *2014*
- **Case Western Reserve University (CWRU)** — Cleveland, OH
  B.S., Chemical Engineering — *2009*

Selected Patents and Publications

14. Swem LR, Kumar P, Bhalla A, Tripathi SA, Parmar A, **Hamilton JJ**, Brumbaugh AR, Ricci DP, Layman HRW, Ciglar AM, Berleman J, Walters Z, Jacoby K, Youngblut ND, Grauer A, Drabant Conley E, Romasko H (2023) *Microbial consortia*. US Patent Application No. 18/060,831.
13. Swem L, Ricci D, Brumbaugh AR, Cremin J, **Hamilton JJ**, Tripathi S, Wong L, Romasko H, Bracken R, Drabant Conley E. (2023) *Microbial consortia for the treatment of disease*. US Patent Application No. 17/906,060.
12. Ricci D, **Hamilton JJ**, Tripathi S, Brumbaugh A, Cremin J, Ou N, Layman H, and L Swem. (2022) *Creation of Rationally Designed and Metabolically Active Microbiome Consortia for Treatment of Enteric Hyperoxaluria*. Kidney International Reports. 7(2): S204-S205. doi:10.1016/j.ekir.2022.01.490.
11. Clark RL, Connors B, Stevenson DM, Hromada SE, **Hamilton JJ**, Amador-Noguez D, and OS Venturelli. (2021) *Design of synthetic human gut microbiome assembly and function*. Nature Communications. 12: 3254. doi:10.1038/s41467-021-22938-y.
10. Scarborough MJ, **Hamilton JJ**, Erb EA, Donohue TJ, and DR Noguera. (2020) *Diagnosing and Predicting Mixed-Culture Fermentations with Unicellular and Guild-Based Metabolic Models*. mSystems. 5(5):e00755-20. doi:10.1128/mSystems.00755-20.
9. Cao X*, **Hamilton JJ***, and OS Venturelli. (2019) *Understanding and Engineering Distributed Biochemical Pathways in Microbial Communities*. Biochemistry. 58(2): 94-107. doi:10.1021/acs.biochem.8b01006.
8. Scarborough MJ, Lawson CE, **Hamilton JJ**, Donohue TJ, and DR Noguera. (2018) *Metatranscriptomic and Thermodynamic Insights into Medium-Chain Fatty Acid Production Using an Anaerobic Microbiome*. mSystems. 3(6): e00221-18. doi:10.1128/mSystems.00221-18.
7. Rohwer RR, **Hamilton JJ**, Newton, RJ, and KD McMahon. (2018) *TaxAss: Leveraging a Custom Freshwater Database Achieves Fine-Scale Taxonomic Resolution*. mSphere. 3(5): e00327-18. doi:10.1128/mSphere.00327-18.
6. **Hamilton JJ**, Garcia SL, Brown BS†, Oyserman BO, Moya F, Bertilsson S, Malmstrom RR, Forest KT, and KD McMahon. (2017) *Metabolic Network Analysis and Metatranscriptomics Reveals Auxotrophies and Nutrient Sources of the Cosmopolitan Freshwater Microbial Lineage acI*. mSystems. 2(4): e00091-17. doi:10.1128/mSystems.00091-17.
5. Lawson CE, Wu S, Bhattacharjee AS, **Hamilton JJ**, McMahon KD, Goel R, and DR Noguera. (2017) *Metabolic network analysis reveals microbial community interactions in anammox granules*. Nature Communications. 8: 15416. doi:10.1038/ncomms15416.
4. **Hamilton JJ**, Calixto Contreras M†, and JL Reed. (2015) *Thermodynamics and H_2 Transfer in a Methanogenic, Syntrophic Community.* PLoS Computational Biology. 11(7): e1004364. doi:10.1371/journal.pcbi.1004364.
3. **Hamilton JJ** and JL Reed. (2014) *Software platforms to facilitate reconstructing genome-scale metabolic networks*. Environmental Microbiology. 16(1): 49-59. doi:10.1111/1462-2920.12312.
2. **Hamilton JJ**, Dwivedi V†, and JL Reed. (2013) *Quantitative Assessment of Thermodynamic Constraints on the Solution Space of Genome-Scale Metabolic Models*. Biophysical Journal. 105(2): 512-522. doi:10.1016/j.bpj.2013.06.011.
1. **Hamilton JJ** and JL Reed. (2012) *Identification of Functional Differences in Metabolic Networks Using Comparative Genomics and Constraint-Based Models*. PLoS ONE. 7(4): e34670. doi:10.1371/journal.pone.0034670.

* indicates equal contribution
† indicates an undergraduate student author