

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 bioinformatician and data scientist with ten years of experience beyond the PhD. 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 manage multiple projects and direct reports. Proficient in human and microbial bioinformatics, and software development. Expertise in machine learning, with the ability to rapidly master new domains.
- Results-oriented bioinformatician and data scientist with ten years of experience beyond the PhD. Proficient in human and microbial bioinformatics, and software development. Expertise in machine learning, with the ability to rapidly master new domains. Capable of writing pipelines and performing data analysis using R, Python, and Nextflow. Experience leading software development and data engineering projects. Effective leader and clear communicator with the ability to manage multiple projects and direct reports.
- Broadly-trained data scientist with ten years of experience beyond the PhD. Established cloud-based infrastructure for SeqCoast genomics, where I developed data and bioinformatics pipelines to enable efficient genomic data processing and delivery. At Amplify Bio, maintained and improved numerous bioinformatics pipelines with diverse architectures. Also led the data science group at Federation Bio, where I oversaw projects in bioinformatics, machine learning, and software development. Passionate about building data tools to enable scientific breakthroughs.

Experience

- **Senior Bioinformatics Scientist**, Amplify Bio *March 2024 - December 2024*
 - Developed and maintained bioinformatic pipelines to enable neoantigen identification and TCR discovery for T-cell receptor therapies
 - Led customization of Benchling LIMS to streamline workflows and enhance data management for programs in TCR discovery and mRNA-based therapeutic development
 - Developed processes to maintain chain of custody and chain of identity during discovery of personalized TCRs
- **Technical Advisor**, SeqCoast Genomics *January 2024 - Present*
 - Provide strategic guidance on bioinformatics, data pipelines, and cloud-based infrastructure, to enable efficient genomic data processing and delivery to clients
- **Data Scientist I, Data Scientist II, Sr Data Scientist**, Federation Bio, Inc *May 2019 - July 2023*
 - Built and led group of three data scientists. Established priorities, managed timelines, and provided mentorship, enabling the team to support multiple research programs in metabolism, immunology, and oncology
 - Partnered with CMC, translational medicine, clinical science, and regulatory affairs to advance discovery programs into clinical development, by serving as technical expert in microbiome science and data science
 - Communicated findings to internal and external stakeholders, in the form of research presentations, memos, and regulatory filings
 - Established a functional definition of the healthy human microbiome, and designed the first-ever metabolically-complete synthetic microbiome replacement therapy
 - Designed novel microbiome therapies with multiple mechanisms of action to correct gut dysbiosis and to treat metabolic and immune-mediated diseases
 - Provided guidance on experimental design to ensure safety, efficacy, and engraftment of microbiome therapies in human and animal models
 - Developed and implemented novel algorithms for annotation of bile acid and short-chain fatty acid production, improving FedBio's ability to predict metabolic capabilities of new bacterial strains
 - Integrated multiple sources of experimental and bioinformatic data to ensure FedBio's bacterial strains were safe for oral administration
 - Developed machine learning algorithms to detect FedBio's strains in murine and human fecal samples, improving the limit of detection 10-fold and enabling pharmacokinetic analysis of FedBio's microbiome therapies

- Validated a GMP-compliant bioinformatic method to confirm identity of master cell banks, drug substance, and drug product, releasing 100s of MCBs over a 9-month period
- Led internal and external cross-functional teams in development and qualification of bioanalytical assays, ensuring concentration and composition of FedBio's drug product could be quantified with accuracy and precision
- Collaborated on sample collection and statistical analysis plans for Phase 1 trial of FedBio's lead asset, enabling pharmacokinetic analysis and biomarker discovery
- Oversaw analysis of flow cytometry data to characterize immunogenicity of microbial strains
- Led development of a machine learning algorithm to predict immune response of microbial strains
- Coordinated selection of epitopes to be engineered into antigen-presenting microbial strains
- Collaborated with IT to develop and deploy a scientific computing environment, enabling a team of three data scientists to deliver reproducible and shareable analyses for 100s of projects
- Built bioinformatics infrastructure on AWS, enabling terabase-scale analysis of next-generation sequencing datasets
- Optimized bioinformatics pipelines to handle a 100% year-over-year increase with 80% decrease in turnaround time, and upgraded pipelines to ensure availability of state-of-the-art methods
- Oversaw development of 6+ software tools to enable data analysis and visualization by a team of twenty wet-lab scientists
- Launched laboratory informatics program using Benchling ELN/LIMS, enabling lineage tracking of 1000s of cell lines
- Established templates and training for reporting of study outcomes, thereby accelerating filing of regulatory documentation

Skills

- Human bioinformatics: bulk and single-cell RNA-Seq (transcriptomics), neoantigen identification and prioritization, T-cell receptor (TCR) and V(D)J sequencing, tumor characterization, variant calling
- Microbial bioinformatics: 16S rRNA sequencing, amplicon sequencing, genome assembly, genome annotation, metagenomic assembly and binning, metagenome profiling, RNA-Seq, transcriptomics
- Computational biology: differential equation modeling, genome-scale modeling, Lotka–Volterra models, machine learning, systems biology, time-series modeling
- Software development: AWS, Bash, Benchling, CI/CD, Docker, Git, Github, Jupyter, Linux, Nextflow, package development, Posit Connect, Posit Workbench, Python, Quarto, R, RStudio, R markdown, Shiny, SQL, testing, VS Code
- Soft skills: leadership, cross-functional collaboration, communication, writing, presentations
- 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, Posters, and Publications

- Fett, C, Win Y, **Hamilton J**, Rosoff H, Bronevetsky Y, Garcia C, Wong A, Pan Z, Velazquez VM, Kunkel EJ, and A Conroy. (2024) *Adapting T cells for the Tumor Microenvironment (TME) During Manufacturing for Improved Anti-Tumor Potency*. International Society for Cell & Gene Therapy.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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.
- 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 acl*. mSystems. 2(4): e00091-17. doi:10.1128/mSystems.00091-17.
- 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.
- Hamilton JJ**, Calixto Contreras M[†], and JL Reed. (2015) *Thermodynamics and H₂ Transfer in a Methanogenic, Syntrophic Community*. PLoS Computational Biology. 11(7): e1004364. doi:10.1371/journal.pcbi.1004364.
- 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.
- 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.
- 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