Joshua J. Hamilton

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Professional Summary

- Bioinformatician/data scientist with leadership and management experience in cancer immunotherapy and microbiome therapeutics. Expertise in human and microbial bioinformatics, machine learning, software development, and cloud-based systems architecture. Enjoy interdisciplinary collaboration and team-building to discover life-changing therapies for patients. Passionate about educating colleagues in data best practices to facilitate data-driven decision making.

Experience

- **Senior Bioinformatics Scientist**, Amplify Bio *March 2024 - December 2024*
  - Developed and maintained bioinformatic pipelines to enable neoantigen identification, tumor characterization, 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

15. 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.
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