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 systems architecture. Enjoy interdisciplinary collaboration and team-building to discover life-changing therapies for patients.

Experience

- **Senior Bioinformatics Scientist**, Amplify Bio   *March 2024 - December 2024*
  - Developed and maintained bioinformatic pipelines to enable neoepitope identification, tumor characterization, and TCR discovery for T-cell receptor therapies. Ran and interpreted bioinformatic analyses for clients.
  - Characterized transcriptomic response of TCR-T cells to hypoxic growth, to guide manufacturing for improved anti-tumor potency

- **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

- **Consultant**, Federation Bio, Inc and Kanvas Biosciences, Inc   *July 2023 - August 2024*
  - Assist with orderly wind-down of Federation Bio, Inc and transfer of operations to Kanvas Biosciences, Inc

- **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
  - Designed novel microbiome therapies with multiple mechanisms of action to correct gut dysbiosis and to treat metabolic and immune-mediated diseases
  - 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
  - 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
  - Analyzed results of Phase 1 trial to identify potential biomarkers of favorable pharmacokinetics, enabling rescue of FedBio's lead asset
  - Built bioinformatics infrastructure on AWS, enabling terabase-scale analysis of next-generation sequencing datasets
  - Launched laboratory informatics program using Benchling ELN/LIMS, enabling lineage tracking of 1000s of cell lines

Skills

- Human bioinformatics: bulk and single-cell RNA-Seq (transcriptomics), HLA typing, neoepitope identification and prioritization, T-cell receptor (TCR) and V(D)J sequencing, tumor characterization, variant calling, whole-exome sequencing

- 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