Benjamin Furman, PhD

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Professional Summary

- A thorough bioinformatician with diverse experience, from evolutionary genomics of amphibians, to the analysis of actionable cancer biomarkers, to aiding in the discovery of novel therapeutics
- Having worked in both academia and biotech startups, within clinical and research settings, I enjoy diving deep into data to answer novel questions

Professional Experience

Imagia Canexia Health   **June 2020 – August 2023**
Senior Bioinformatician   Jan 2023 – Aug 2023
Data Scientist   Jan 2021 – Dec 2022
Bioinformatician   Jun 2020 – Dec 2020

- Point person for analysis/visualization through dashboards and detailed analytical reports of in-house data including real world clinical data from a Canada-wide cancer ctDNA sequencing project, longitudinal patient monitoring, and general quality control
- Established core bioinformatics analysis codebase, developed and expanded custom Nextflow pipelines and Python packages for multiple objectives including assessing tumour mutational burden, semi-automated performance validation, general tooling and quality assurance
- Worked closely with laboratory specialists on assay development and regulatory approval (CAP/CLIA/CE-IVD) for both amplicon-based and hybrid capture targeted cancer panels (FFPE and ctDNA)
- Jointly deployed bioinformatic pipelines with software teams in a distributed, cloud-based framework to deliver SaaS
- Résumé screening, interviews, and hiring of co-workers and direct reports; managed a team for internal/external support

Key accomplishments: Development and certification of several new product versions, multiple publications with collaborators, maintained key pharmaceutical funding with custom data analyses and reports

Adapsyn Biosciences   **September 2019–May 2020**
Independent Contractor

- Developed custom Python packages for large-scale genome mining to find genomic drivers of drug resistance and genome-derived therapeutics
- Executed general data science tasks and statistical analyses
- Performed targeted literature reviews

Key accomplishments: Resulted in analytical tools that will be implemented company-wide for continued efforts in drug discovery

University of British Columbia   **November 2018–May 2020**
Postdoctoral Research Fellow

- Conducted multi-population whole genome analyses assessing recombination rate variation
- Demonstrated utility of a novel analytical method to understand the interaction between sex-biased gene expression and selection
- Lab-wide bioinformatic and statistical analyses for co-workers

Key accomplishments: First authored three (one published, two unpublished) and contributed to another three papers.

Skills

Programming

- Proficient in Python, tidyverse/base R, Bash, SQL, (some Perl), for biological analyses and big data manipulation/visualization
- Experience developing interactive dashboards with both Python/Dash, R/Shiny
- Accustom to working with Git version control, CI/CD environments automated code review and testing workflows
- Code deployment on Unix clusters and cloud computing (AWS)

Analysis

- Capable of thorough, detailed analysis to maintain clinical accreditation
- Knowledgeable in model fitting (linear, generalized, and mixed model), non-/parametric statistics
- Skillful with custom pipeline development for genomic analyses, (Nextflow)

- Thorough understanding of both non-/model genome/transcriptome analyses (e.g., somatic and germline variant calling, expression analyses) and tooling (e.g., samtools, bwa, GATK) for a variety of sequencing types (Illumina, RAD/GBS, 10X, PacBio)
- Familiarity with public human genomics databases
- Experienced with GWAS, parent–offspring inheritance, evolutionary, and population genetic analyses
- Basic wetlab experience (DNA/RNA extraction, PCR, Sanger sequence prep)

Communication, Mentorship, Teamwork

- Accustom to working in an agile framework (Jira) and remote work
- Hiring and guiding teammates and managing a small team, previously mentoring grad students
- Proficient in scientific writing and presentation, with nine first authored publications
- Involved in coordination of international collaborations for fieldwork in remote and foreign locations

Education

Ph.D., Evolutionary Genomics — 2012–2018
McMaster University, transferred from M.Sc. with distinction — Hamilton, ON, Canada

B.Sc., Specialization in Animal Biology — 2008–2012
University of Alberta, graduated with distinction, first class standing — Edmonton, AB, Canada

Research Experience

Ph. D. Dissertation – Laboratory of Dr. Ben Evans, McMaster University

- Evolutionary genomic and genetic analyses of polyploid African clawed frogs (*Xenopus*)
- Discovered and characterized novel sex chromosomes through whole & reduced genome sequencing of lab-reared families, genotype–phenotype association tests, and recombination rate analyses
- Uses multi-species transcriptome data and custom analytical pipelines to study the impact of whole genome duplication on selection at the gene level
- Redefined multiple species boundaries and determined the impact of cross species hybridization with mutli-locus sequence data
- Conducted four field collection excursions with a multi-national team in foreign countries to collect samples for projects

Key accomplishments: Published six first author papers and three middle author publications

Select Publications (17 total, nine first author), Google Scholar link here

Furman, B. L. S., Baran, E., Brahmbhatt, S., Chan, B., Nip, K. M., Kense, A., Murphy, B., Funari, V., Huntsman, D. G., Miller, R., et al. (2023) Liquid biopsy testing in metastatic or advanced breast cancer patients during the COVID-19 pandemic (poster abstract). *Cancer Research* 83(7 Supplement), 5590–5590.

McGuire, A. L., McConechy, M. K., Melosky, B. L., English, J. C., Choi, J. J., Peng, D., Yee, J., **Furman, B. L. S.**, Aguirre Hernandez, R., Feijao, P., et al. (2022) The Clinically Actionable Molecular Profile of Early versus Late-Stage Non-Small Cell Lung Cancer, an Individual Age and Sex Propensity-Matched Pair Analysis. *Current Oncology* 29(4), 2630–2643.

Furman, B. L. S., Metzger, D. C., Darolti, I., Wright, A. E., Sandkam, B. A., Almeida, P., Shu, J. J., and Mank, J. E. (2020) Sex chromosome evolution: so many exceptions to the rules. *Genome biology and evolution* 12(6), 750–763.

Furman, B. L. S. and Evans, B. J. (2018) Divergent evolutionary trajectories of two young, homomorphic, and closely related sex chromosome systems. *Genome Biology and Evolution* 10(3), 742–755.