

Benjamin Furman

furmanbens@gmail.com

289-925-2362

www.xenben.com

Professional Summary

- Currently operating in both the academic and industry fields, I am a critically thinking, productive scientist with excellent time management
 - An evolutionary biologist with over 8 years of experience performing genomic analyses to understand how fundamental aspects of biology impact genome evolution
 - A skilled bioinformatician developing tools for the field of biotechnology, aiding in the discovery of novel therapeutics
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Experience

Independent Contractor – Bioinformatics, Data Science

Adapsyn Biosciences

2019–current

- Developed custom python packages for large-scale genome mining
- Facilitated discovery of genome-derived therapeutics, focus on chemotherapy targets
- Executed general data science tasks and statistical analyses
- Performed targeted literature reviews
- Resulted in several analytical tools that will be implemented company-wide for continued efforts in drug discovery

Postdoctoral Research Fellow – Genome Evolution

University of British Columbia

2018–current

- Genomic and transcriptomic sequence analysis on vertebrates
 - Multi-population comparisons and identifying key genetic differences between sexes
 - Lab-wide bioinformatic and statistical analyses and assistance for co-workers
 - Producing 3 first author publications and contributed to 2 second authored publications within 2 years
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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

Skills

Programming

- Proficient in python, R, bash, and comfortable in perl, for bioinformatic analyses, and big data manipulation
- Adept in tidyverse and base R for analyses, data management, and visualization
- Project management, version control, and documentation with Git, GitHub, L^AT_EX, and Markdown
- Code deployment on unix clusters and cloud computing (Google Cloud, AWS)
- App development with R/Shiny for visualization of data trends and collecting user input
- Dedicated to best practices and modern techniques

Analysis

- Skilled in model fitting (linear, generalized, and mixed model), knowledgeable on parametric and non-parametric statistics

- Genome and transcriptome assembly, analysis and variant discovery
- DNA/RNA extraction, PCR, sequence preparation for Sanger and Next-Generation Sequencing
- Usage of public sequence databases (e.g., NCBI, Ensembl)
- Genotype–phenotype association, evolutionary, and population genetic analyses

Communication

- Coordinated international collaborations for fieldwork in remote and foreign locations
- Mentored XX undergraduate and XX graduate students
- Proficient in scientific writing and presentation, with 9 first, 3 second authored publications
- Static website development using Jekyll
- Microsoft Office suite and G-Suite