

Benjamin Furman

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Professional Summary

- Currently working in the academic and industry fields, I am a critically thinking, productive scientist with excellent time management skills
 - 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 currently developing tools for the field of biotechnology, which aid in the discovery of novel therapeutics
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Skills

Programming

- Proficient in Python, R, Bash, and comfortable in Perl, for bioinformatic analyses, and big data manipulation
- Well versed 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
- Experience with static website development using Jekyll

Analysis

- Adept at custom pipeline development for genomic analyses

- Deep understanding of genome and transcriptome analysis (Illumina, RAD/GBS, 10X)
- Skilled in model fitting (linear, generalized, and mixed model), knowledgeable on parametric and non-parametric statistics
- Experienced with GWAS, parent-offspring inheritance, evolutionary, and population genetic analyses
- Capable of DNA/RNA extraction, PCR, Sanger sequence prep and analysis

Communication, Mentorship, Teamwork

- Excellent communication with remote team members
 - Proficient in scientific writing and presentation, with 9 first, 3 second authored publications
 - Mentored 5 undergraduate and 2 graduate students
 - Involved in coordination of international collaborations for fieldwork in remote and foreign locations
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Professional 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
- 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

- 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 and assistance for co-workers

▷ Producing 3 first author publications (2 in review, 1 in prep) within 2 years

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
- Evaluated the impact of whole genome duplication on selection at the gene level with large-scale, multi-species gene expression sequence data set and detailed analyses of molecular rates of evolution with custom analytical pipelines
- 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 these projects

▷ Published **5 first author papers** during my Ph.D., and continued work has resulted in **another first author and 2 second author publications** (1 in review).

B. Sc. Thesis – Laboratory of Dr. Cynthia Paszkowski, University of Alberta

- Assessed how urbanization impacts connectivity of frog populations and the role that artificial wetlands play in maintaining gene flow
- Conducted a fine-scale genetic analysis of a wood frogs *Lithobates sylvaticus* though microsatellite sequence analysis
- Performed field collections, DNA extractios, fragment sequencing, and analysis

▷ This project, along with others, resulted in **2 first author and 1 second author publication**.

Select Publications (6 of 12, with 9 being first author), Google Scholar link here

- 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. *In Review: Genome Biology and Evolution*.
- Furman, B. L. S.**, van der Bijl, W., Wright, A. E., and Mank, J. E. (2020) Expression variance to infer sex-specific selection on gene regulation: identifying biologically-relevant thresholds of sex-biased expression. *In Review: Genome Biology and Evolution*.
- Furman, B. L. S.**, Dang, U. J., Evans, B. J., and Golding, G. B. (2018) Divergent subgenome evolution after allopolyploidization in African clawed frogs (*Xenopus*). *Journal of Evolutionary Biology* 31(12), 1945–1958.
- 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.
- Furman, B. L. S.** and Evans, B. J. (2016) Sequential turnovers of sex chromosomes in African clawed frogs (*Xenopus*) suggest some genomic regions are good at sex determination. *Genes, Genomes and Genetics (G3)* 6(11), 3625–3633.
- Furman, B. L. S.**, Bewick, A. J., Harrison, T. L., Greenbaum, E., Gvoždík, V., Kusamba, C., and Evans, B. (2015) Pan-African phylogeography of a model organism, the African clawed frog *Xenopus laevis*. *Molecular Ecology* 24(4), 909–925.

Select Conference Presentations (3 of 11)

- Furman, B. L. S.**, van der Bijl, W., Wright, A. E., and Mank, J. E. (August 2019) Poster: Expression variance to infer sex-specific selection on gene regulation: identifying biologically-relevant thresholds of sex-biased expression. *European Society for the Study of Evolution (ESEB)* Turku, Finland.
- Furman, B. L. S.**, Song, X., and Evans, B. J. (April 2018) Poster: Divergent evolutionary trajectories of two homomorphic sex chromosome systems.. *Jacques Monod Conference “Sex uncovered: the evolutionary biology of reproductive systems”* Roscoff, France.
- Furman, B. L. S.** and Evans, B. J. (July 2016) Talk: Sequential turnovers of sex chromosomes in African clawed frogs (*Xenopus*) suggest some genomic regions are good at sex determination. *Evolution* Austin, Texas, USA.