# Benjamin Furman

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## Professional Summary

- Currently operating in both 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 developing tools for the field of biotechnology, aiding in the discovery of novel therapeutics

## 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

## 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, LaTeX, 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