ADRIAN FORSYTHE Ph.D.

adrian.e.forsythe@gmail.com +46 76 413 07 22 adrian-forsythe-85b40a96
AdrianForsythe adrianforsythe.github.io 0000-0003-1966-9946

RECENT EMPLOYMENT

Researcher **Department of Systematics, Uppsala University** February 2023 – Ongoing

I am working on a large meta-analysis of RNAseq data in order to identify conditions that are associated with the transposistion of transposable elements in pathogen genomes.
Right now I am working on a web app that enables exploration of large transposible elements across fungal genomes. Available at: `starbase.serve.scilifelab.se`

PostDoctoral Researcher **Department of Zoology, Uppsala University** Sept 2020 – Sept 2022

The goal of this research was to investigate the microbial ecosystems of populations in decline to understand how disruptions to microbial ecosystems can impact the function of the oral microbiome.

EDUCATION

Ph.D. in Microbiology **McMaster University, Department of Biology** Sept 2016 – Aug 2020

Thesis title: Population Genetic Investigation of the White-Nose Syndrome Pathogen, *Pseudogymonascus destructans*, in North America

M.Sc. in Microbiology **McMaster University, Department of Biology** Sept 2014 – Aug 2016

Thesis title: Genetic and environmental influences on the germination of basidiospores in the *Cryptococcus neoformans* species complex

B.Sc. in Biology, Honours **Trent University** Sept 2010 – May 2014

EXPERTISE & TECHNICAL SKILLS

Programming and HPC

`R` `python` `bash` SQL SLURM `git` GitHub

- I use `R` and `python` for all downstream data processing, statistical analysis, (interactive) visualizations, and training of machine learning models.
- I work in unix-based HPC environments in order to manage high-throughput genomics datasets
- I aim to make my work as reproducible as possible.

Data Analysis, Statistics, and Communication Skills

`dplyr` `pandas` `lme4` `tidymodels` `scikit-learn` `ggplot2` `matplotlib` `plotly` `shiny`

- I have a deep understanding of statistical methods and algorithms relevant to the analysis of biological/bioinformatics datasets.
- I am skilled at integrating genomics data with existing biological datasets, providing an informed understanding of the monitoring and treatment of infectious diseases.
- I am an effective scientific communicator, both in writing and in oral presentations.
- I have a passion for using visualizations in communicating complex concepts to an audience.

Bioinformatics Pipeline Development

`samtools` RNAseq assembly variant calling metagenomics `snakemake` Nextflow

- I have a strong background in bioinformatic methods and best-practices related to the analysis of genomic, transcriptomic, and amplicon sequencing data.
- These skills have enabled me to extract meaningful insights from complex biological datasets in the context of microbial ecology, evolution, and infectious disease control.

COLLABORATIVE PROJECTS

Probiotic Prophylaxis to treat White-Nose Syndrome **Research Project** 2019-Ongoing

My collaborators and I developed a probiotic treatment White-Nose Syndrome, a fungal disease in bats. Field trials currently underway in British Columbia, Canada.

Novel Data Streams to Track the Spread of Wildlife Disease **Research Project** 2020-Ongoing

I led an effort to create a novel method for estimating levels of human activity at remote locations impacted by White-Nose Syndrome using public data. This data was used to model and predict the spread of WNS across North America.

ACADEMIC CONTRIBUTIONS & SCHOLARSHIP

Academic Publishing Record
7 first-author papers. 139 citations, h-index = 7

Conference Organizer
I was the lead organizer for Ontario Ethology, Ecology, and Evolution 2019 conference, the largest graduate student-organized biology and psychology event in Ontario

Consultant
I was a consultant for the McMaster University chapter of the Society of Industrial and Applied Mathematics.

Academic Awards

- Joseph and Joanne Lee Ontario Graduate Scholarship 2019-2020.
- Luella K. Weresub Memorial Award for 2019 (Canadian Botany Association).
- Outstanding Research Publication in Ecology and Evolution for the 2018-2019 academic year (McMaster University).
- Outstanding Leadership Award for the 2018-2019 academic year (McMaster University, Department of Biology).
- Service to the Department Award during the 2017-2018 academic year (McMaster University, Department of Biology).

FIRST-AUTHOR PUBLICATIONS

Research Articles Published in Peer-Reviewed Academic Journals

- Forsythe, A., Fontaine, N., Bissonnette, J., Hayashi, B., Insuk, C., Ghosh, S., … Cheeptham, N. (2022). Microbial isolates with anti-*Pseudogymnoascus destructans* activities from western canadian bat wings. *Scientific Reports*.
- Moraitou, M. *., Forsythe, A. *., Fellows Yates, J. A., Brealey, J. C., Warinner, C., & Guschanski, K. (2022). Dental calculus metagenomics suggest that ecology, not host phylogeny, shapes the oral microbiome in closely related species. *MBE*.
- Forsythe, A., Vanderwolf, K. J., & Xu, J. (2021). Landscape genetic connectivity and evidence for recombination in the north american population of the white-nose syndrome pathogen, pseudogymnoascus destructans. *Journal of Fungi*, *7*(3), 182.
- Forsythe, A., Giglio, V., Asa, J., & Xu, J. (2018). Phenotypic divergence along geographic gradients reveals potential for rapid adaptation of the white-nose syndrome pathogen, pseudogymnoascus destructans, in north america. *Applied and environmental microbiology*, *84*(16), e00863–18.
- Forsythe, A., & Xu, J. (2017). The complete mitochondrial genome of the white-nose syndrome pathogen, pseudogymnoascus destructans. *Mitochondrial DNA Part B*, *2*(1), 48–49.
- Forsythe, A., Vogan, A., & Xu, J. (2016). Genetic and environmental influences on the germination of basidiospores in the cryptococcus neoformans species complex. *Scientific reports*, *6*(1), 1–12.