

Joseph McGirr, PhD

Bioinformatics Scientist

✉ email: josephmcgirr@gmail.com

🐦 twitter: @mcgirr_joe

🌐 website: joemcgirr.github.io

🔗 github: @joemcgirr

Summary

I'm a bioinformatics scientist specializing in genetics and population biology. I have experience analyzing diverse biological data sets from microarray, whole genome sequencing, and RNA sequencing. I earned my Ph.D. in biology from the University of North Carolina and have published research in prominent journals including *Molecular Biology and Evolution*, *Evolution Letters*, and *PNAS*. I am passionate about learning, developing, and applying advanced bioinformatics approaches to answer questions at the intersection of basic and applied research.

Education

University of North Carolina, Chapel Hill	2015-2020	Ph.D. Biology
University of Colorado, Colorado Springs	2010-2014	B.S. Biology <i>magna cum laude</i>

Experience

2021 - Staff Scientist, Bioinformatics, Thermo Fisher Scientific, Emeryville, CA

- Design and develop tools implemented in Axiom Analysis Suite to automate complex workflows and improve copy number genotyping with Axiom microarray products.
- Use next generation sequencing experiments to improve microarray sample preparation protocols.
- Design custom microarray products for human genotyping based on unique customer requirements.
- Write software specifications and research documentation required for product commercialization.
- Collaborate in teams with a broad range of expertise to bring quality products to market under fast-paced deadlines.

2020 - 2021 Postdoctoral Researcher, University of California, Davis, CA

- Analyzed whole genome sequences from hundreds of individuals and performed temporal genomic contrasts to identify genetic variation contributing to disease and limiting population growth.
- Investigated the genetic basis of saltwater to freshwater evolutionary transitions by measuring cross-species differential gene expression in response to osmotic stress.

2015-2020 PhD Student, University of North Carolina, Chapel Hill, NC

- Research on the genetic basis of adaptive traits and reproductive isolation in newly formed species.
- Identified novel candidate genes influencing craniofacial development.
- Taught labs in evolution, animal behavior, anatomy, and course-based undergraduate research.

Selected Publications

full list at: <https://scholar.google.com/citations?user=BaXHXekAAAAJ&hl=en>

A vertebrate adaptive radiation is assembled from an ancient and disjunct spatiotemporal landscape. Richards EJ, **McGirr JA**, et al. 2021 *Proceedings of the National Academy of Sciences* doi.org/10.1073/pnas.2011811118

Few fixed variants between trophic specialist pupfish species reveal candidate *cis*-regulatory alleles underlying rapid craniofacial divergence. **McGirr JA** and Martin CH. 2020. *Molecular Biology and Evolution*.

doi.org/10.1093/molbev/msaa218

Ecological divergence in sympatry causes gene misregulation in hybrids. **McGirr JA** and Martin CH. 2020.

Molecular Ecology. doi.org/10.1111/mec.15512

Technical Skills

Code: R, SQL, python, bash.

Computing: SLURM scheduling, Rmarkdown, Jupyter, DbVisualizer, Amazon EC2, LSF, Snakemake, git.

Statistics: Linear and mixed models, classical stats, GWAS.

Next Gen Sequencing: Illumina whole genome and transcriptome alignment, annotation, and SNP calling with BWA, STAR, Trinity, GATK, samtools, ANGSD and R-Bioconductor packages.

Microarray: SNP, indel, and copy number genotyping on Thermo Fisher microarray products. Improvements to copy number genotyping algorithms. Custom microarray designs.

Bench: Designed and performed CRISPR/Cas9 gene editing experiments. PCR. DNA/RNA extraction.