

Joseph McGirr, PhD

Bioinformatics Scientist

✉ email: josephmcgirr@gmail.com

🐦 twitter: @mcgirr_joe

🌐 website: joemcgirr.github.io

🐙 github: @joemcgirr

Summary

I'm a bioinformatics scientist working in research and development at Thermo Fisher Scientific. I specialize in:

- **Experimental Design** -- I work closely with molecular biologists to design efficient experiments.
- **Data Analysis** -- I process large data sets on high performance computing clusters, perform analyses using modern data science tools, and communicate interpretations that drive decisions on product development.
- **Pipeline Development** -- I build workflows that automate repetitive processes and create html reports with interactive visualizations, enabling molecular biologists to quickly explore their results.
- **Algorithm Development** -- I write tools to perform a variety of analyses and work closely with software developers to implement them into production level code.

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**
- Collaborated in teams with a broad range of expertise to bring quality products to market under fast-paced deadlines, including the CytoScan HD Accel chromosomal microarray.
 - Contributed to multiple incubation projects as lead bioinformatics scientist.
 - Used next generation sequencing experiments to improve microarray sample preparation protocols.
 - Developed tools implemented in Axiom Analysis Suite to automate complex workflows and improve copy number genotyping with Axiom microarray products.
 - Wrote software specifications and research documentation required for product commercialization.
- 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.

Technical Skills

Code: R, SQL, python, bash.

Computing: SLURM scheduling, Rmarkdown/Jupyter/Quarto, DbVisualizer, Amazon EC2, 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.

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

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*.

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*.

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