Joseph McGirr, PhD
Bioinformatics Scientist

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Professional Summary
Bioinformatics scientist with expertise in genomics, large-scale biological data analysis, and pipeline development. Experienced with modern data science tools and statistical methods. Skilled in cross-functional collaboration, communication, and translating complex data into actionable insights.

Education
University of North Carolina, Chapel Hill	2015-2020	Ph.D. Biology
University of Colorado, Colorado Springs	2010-2014	B.S. Biology *magna cum laude*

Experience
2021 – Current: Staff Scientist, Bioinformatics, Thermo Fisher Scientific, Emeryville, CA
- Act as lead bioinformatics scientist on multiple R&D incubation projects analyzing diverse datasets (NGS, microarray, public databases) to develop novel genotyping assays and improve existing protocols.
- Collaborate with precision medicine researchers to design assays targeting disease-causing variants.
- Design pipelines in cloud-based Linux environments using parallelization to efficiently execute reproducible analyses and automate genotyping reports.
- Build regression and classification models applied to genotyping datasets to predict assay performance.
- Collaborate with software engineers to incorporate prototype scripts into production-level code and write customer-facing documentation.
- Design interactive Shiny dashboards that query databases and create automated reports for QC tracking.
- Choose study sample cohorts for product validation experiments and work with sensitive human research subject data from large biobank initiatives while complying with regulations and company policies.
- Interpret genotyping results from clinical assays to ensure accurate diagnoses with IVD products.
- Foster a supportive team culture by mentoring new hires and establishing cross-division workflows.
- Present research at the American Society for Human Genetics Conference.
- Recognized by management with the highest annual performance rating across multiple years.

2020 – 2021:   Postdoctoral Researcher, University of California, Davis, CA
- Analyzed whole-genome sequencing from hundreds of individuals to identify genetic variation contributing to disease risk and population collapse.
- Created robust pipelines for variant calling and troubleshooting sequencing anomalies.

2015-2020:   PhD Student, University of North Carolina, Chapel Hill, NC
- Used a multi-omics approach to identify novel candidate genes influencing craniofacial development and designed gene editing experiments to validate them *in vivo*.
- Completed graduate coursework in computational genomics, statistical modeling, and genetics.

Technical Skills
Programming: R, Python, SQL, Bash, GitHub, Slurm, Shiny, Quarto/Rmarkdown/Jupyter, Positron/Rstudio.
Statistics: Hypothesis testing, predictive models for regression and classification, feature selection, cross-validation, exploratory data analysis, principal component analysis, genome-wide association mapping.
NGS: Whole-genome and transcriptome alignment, variant calling, and annotation. Experience with Illumina / Ion Torrent platforms and industry-standard tools (BWA, STAR, Trinity, GATK, PLINK, samtools, DESeq2).
Microarray: SNP, indel, and copy number genotyping on Thermo Fisher microarrays.
Bench: Experimental design. CRISPR/Cas9 gene editing. PCR. DNA/RNA extraction.

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

Evidence of positive polygenic selection following a series of environmental and demographic disasters in Pacific herring. Tisthammer KH, **McGirr JA**, et al. 2025 *In Review.*

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.*