Joseph McGirr, PhD

Bioinformatics Scientist

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Professional Summary

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

- **Data Analysis and Interpretation:** Processing large biological datasets on high-performance clusters. Conducting analyses with modern data science tools and statistical methods. Communicating interpretations that guide product development decisions.
- **Pipeline and Algorithm Development:** Building workflows that automate complex processes. Creating applications and reports with interactive visualizations that enable scientists to explore their results. Working with software developers to implement my tools in user-facing programs.
- **Cross-Functional Collaboration:** Representing bioinformatics on teams directing new product introductions and incubation projects. Presenting at scientific conferences and departmental seminars. Collaborating with scientists internally to design experiments. Collaborating with external scientists to design products specific to their research applications.

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

- Collaborate in teams with a broad range of expertise to bring products to market under fast-paced deadlines, including the CytoScan HD Accel chromosomal microarray and the SwiftArrayStudio Microarray Analyzer.
- Contribute to multiple R&D incubation projects as lead bioinformatics scientist.
- Compile information on clinically important genetic variants from public databases and scientific literature to inform microarray designs for custom research applications.
- Use NGS experiments to improve existing microarray protocols and develop novel genotyping assays.
- Write tools implemented in Axiom Analysis Suite to improve copy number genotyping on Axiom microarrays.
- Present research and represent microarray R&D at the American Society for Human Genetics Conference.
- Develop QC thresholds and statistical tests used by our manufacturing team to qualify new reagent lots.
- Author performance specifications and research documentation supporting product validation and commercialization.
- Troubleshoot instrument and assay failures to improve customer experience.
- Maintain high visibility and impact as a remote employee through consistent virtual communication and quarterly visits to the home office.

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

- Identified novel candidate genes influencing craniofacial development that have since been validated *in vivo*.
- Researched the genetic basis of adaptive traits and reproductive isolation in newly formed species.

Technical Skills

Programming: R, SQL, Python, Bash, Git, SLURM, Shiny, Quarto/Rmarkdown/Jupyter, Positron.
Statistics: Hypothesis testing, prediction and classification modeling, feature selection, PCA, GWAS.
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 (power analysis, randomized and factorial designs). CRISPR/Cas9 gene editing. PCR. DNA/RNA extraction.
Publications: Six first-author publications. Full list: https://scholar.google.com/citations?user=BaXHXekAAAAJ&hl