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# KEVIN A. BOYD

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## PROFESSIONAL SUMMARY

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Hardworking data scientist and bioinformatics analyst with extensive experience analyzing complex biological datasets, developing NGS pipelines, and applying machine learning models to genomics research. Proven track record supporting multiple Principal Investigators by delivering high quality analyses for publications, securing grant funding, developing automated workflows, and training lab members in downstream analytics. Result focused and efficient in performing statistical analyses with multiple programming languages. A motivated, detail-oriented team player with a passion for coding and biological sciences.

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## EDUCATION

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**Master of Science:** Data Science, December 2023  
**Southern Methodist University** – Dallas, TX

**Bachelor of Science:** Microbiology, May 2016  
**University of Oklahoma** – Norman, OK

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## WORK HISTORY

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**Senior Bioinformatics Analyst**, 2024 to Current

**Oklahoma Medical Research Foundation (OMRF)** – Dr. Linda Thompson, Oklahoma City, OK

- Lead genomic analyses for 8 different Principal Investigators (PIs).
- Developed and deployed 6 custom Snakemake NGS workflows to improve reproducibility, reduce processing time, and better utilize resource allocation.
- Led training for 7 lab members to efficiently run workflows on a SLURM-based HPC system.
- Delivered analytical support that directly contributed to 5 manuscripts, 3 publications and 14 successful grant submissions.
- Routinely presented experimental findings to various teams and collaborators.

**Bioinformatics Analyst**, 2021 to 2023

**Oklahoma Medical Research Foundation (OMRF)** – Dr. Linda Thompson, Oklahoma City, OK

- Conducted Bulk RNA-seq, scRNA-seq, ChIP-seq, Cut&Run, and Cut&Tag analyses for 12 PIs.
- Analyzed microscopy imagery using both conventional and machine learning methodologies.
- Optimized pipelines/scripts to run samples in parallel to reduce processing time and increase efficiency in Illumina sequencing workflows.
- Collaborated with researchers to perform analyses used in 6 successful grants.

**Senior Laboratory Technician**, 2019 to 2021

**Oklahoma Medical Research Foundation (OMRF)** – Dr. Chris Sansam Lab, Oklahoma City, OK

- Performed drug screens with transcriptional inhibitors to study DNA replication.
- Optimized protocols, performed DNA/RNA extractions, ran RT-qPCRs, and analyzed data sets.
- Designed, optimized, and performed genome wide CRISPR Knockout and Activation screens.
- Managed zebrafish colony by performing health checks, generating new transgenic lines, and sustaining genetic variability.
- Trained new lab members, mentored students, and optimized protocols.
- Maintained cancer cell lines, performed In Situ Hybridization experiments, cloned genes, made variants, and microinjected morpholinos and RNAs.

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## SKILLS

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### Programming and Platforms

- Windows, MacOS, Linux
- Python
- R
- Bash
- SQL
- C++
- RegEx
- HTML
- Command Line
- Spark
- Hadoop
- Slurm
- GitHub
- Singularity
- AWS

### Bioinformatic / Data Science Tools

- FastQC / MultiQC / Fastq-Screen
- BWA / Bowtie2
- STAR / HISAT2
- Fastp / Cutadapt / Trimmomatic
- MACS2 / SICER
- SAMtools / Bedtools / Deeptools
- IGV (Integrative Genomics Viewer)
- IPA (Ingenuity Pathway Analysis)
- FIJI (ImageJ)
- TensorFlow / Scikit-learn / Matplotlib / Seaborn
- Tidyverse / ggplot2 / DESeq2 / edgeR / limma
- GenomicRanges / pheatmap / plotly / DiffBind
- 10x Genomics scRNA-seq / Cell Ranger / Seurat
- ApE
- Snakemake

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## PUBLICATIONS

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Qin, W., Lin, S.-J., Zhang, Y., Huang, K., Petree, C., Boyd, K., Varshney, P., & Varshney, G. K. (2025). Rationally designed TadA-derived cytosine editors enable context-independent zebrafish genome editing. *Advanced Science*. <https://doi.org/10.1002/advs.202509800>

Hossain, M. S., Sansam, C. G., Wittig, K. A., Noble, T. D., Boyd, K. A., & Sansam, C. L. (2025). Dynamic regulation of origin firing factors links CDK activity to dormant origin activation. *bioRxiv [Preprint]*. <https://doi.org/10.1101/2025.06.10.657920>

Boyd, K. A., Mitra, R., Santerre, J., & Sansam, C. L. (2023). Deep learning image analysis to isolate and characterize different stages of S-phase in human cells. *SMU Data Science Review*, 7(3), Article 7.