

Jeffrey Allen Haltom

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Summary: Bioinformatician with over 13 years of experience in handling **large biological datasets** with **high-performance computing**. Strong background in **disease genomics/transcriptomics** and **molecular genetics**. Adept programmer who designs flexible pipelines that implement **parallel** computing for fast analysis. Experienced in **machine learning** and statistical analysis.

SKILLS

- **Programming:** Python, R, Bash, Java
 - **Bioinformatics Tools:** GATK, scRNA-seq, scATAC-seq, eQTL, Multiomics analysis
 - **Machine Learning and Data Analysis:** TensorFlow, Keras, NumPy, Pandas, Scikit, Tidyverse
 - **Workflow Management and Scaling:** NextFlow, Snakemake, Anaconda, HPC, Git
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EDUCATION:

- **Ph.D. in Genetics and Genomics**, Iowa State University *May 2018 – Oct 2022*
 - **B.Sc. in Biology**, Iowa State University - Cum Laude *May 2012- May 2015*
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WORK EXPERIENCE:

Senior Scientist Bioinformatician II - Children's Hospital of Philadelphia *October 2022– Present*
(Center for Mitochondrial and Epigenomic Medicine)

- Conducted single-cell multimodal analyses for projects on long COVID and neurodevelopment, uncovering key disease mechanisms.
- Applied machine learning to analyze 20,000+ whole mitochondrial genomes alongside socioeconomic and environmental metadata, identifying associations between mitochondrial haplogroups and preterm birth risk.
- Discovered mutations in SARS-CoV-2 ORF10 linked to improved clinical outcomes using data from 210,000+ COVID-19 patients.
- Computationally predicted 3D protein and 2D transcript structures for ORF10 and investigated its bioenergetic and immune effects in human cells.
- Managed and optimized operations at the PacBio sequencing facility, ensuring high-efficiency and high-quality sequencing output.
- Analyzed transcriptomic data from Arabidopsis grown on the International Space Station

Bioinformatics Graduate Research Assistant - Iowa State University *May 2021- Dec 2022*

- Developed RIAD, a novel human RNA-Seq ancestry inference tool that implements machine learning, achieving >97% accuracy; expanded to detect disease variants as well as germline and somatic mutations.
- Created a pipeline to concurrently quantify human and SARS-CoV-2 transcript expression, analyzing over 4,300 COVID-19 RNA-Seq samples and identifying novel human orphan genes linked to COVID-19.
- Collaborated with NASA on a project focused on mitigating cosmic radiation damage by inhibiting key spaceflight-associated miRNAs
- Worked with the COVID-19 International Research Team (COVIRT) to publish influential articles and enhance public datasets, aiming to uncover host infection dynamics and improve COVID-19 treatment.

Bioinformatics Experimental Intern - AbbVie Inc.*June – Aug 2020*

- Conducted eQTL analysis on ileum and rectum samples from a Crohn's disease patient cohort:
- Developed a pipeline that implements FastQTL for cis-eQTL discovery.
- Compared significant eQTL findings to known eQTL databases (DICE, eQTLGen, EMSEMBL) as well as GWAS variants associated with Crohn's disease.
- Performed cross-tissue analysis using eQTL findings and GTEx database; identified overlapping eQTLs across multiple tissues.
- AbbVie Intern Group Leader: Led and coordinated meetings with other interns to reflect on internship experience.

Bioinformatics Graduate Research Assistant - Iowa State University*July 2018 – Dec 2022*

- Developed a statistical method for predicting cancer driver somatic mutations in TCGA database based off recurrent mutations. This method utilizes a two-component mixture model along with an empirical Bayesian procedure to statistically calculate the posterior probabilities.
- Demonstrated that conservation and functional divergence analysis of gene families could identify functional residues that may cause cancer driver or drug-resistant mutations or could be used as inhibitors either specific or broad spectrum.

PUBLICATIONS:

- D. Galeano *et al.*, [sChemNET: a deep learning framework for predicting small molecules targeting microRNA function](#). *Nature Communications* 15, 9149 (2024).
- J. T. McDonald *et al.*, [Space radiation damage rescued by inhibition of key spaceflight associated miRNAs](#). *Nature Communications* 15, 4825 (2024).
- J. W. Guarnieri *et al.*, [SARS-CoV-2 mitochondrial metabolic and epigenomic reprogramming in COVID-19](#). *Pharmacological Research* 204, 107170 (2024).
- J. W. Guarnieri *et al.*, [Core mitochondrial genes are down-regulated during SARS-CoV-2 infection of rodent and human hosts](#). *Science Translational Medicine* 15, eabq1533. (2023).
- J. Haltom *et al.*, [SARS-CoV-2 Orphan Gene ORF10 Contributes to More Severe COVID-19 Disease](#). *medRxiv*, (2023).

HONORS & AWARDS

- **Teaching Excellence Award** *May 2022*
 - Outstanding teaching in the GENET 591 graduate program recognition, given to up to 10% of graduate students annually.
- **XSEDE Grant - COVID-19 HPC Consortium** *September 2021*
 - Detecting COVID -19 related human orphan gene expression in single cells with comparative genomics and data mining.

LEADERSHIP

- COVID-19 RNA-Seq data analysis in an HPC environment - *XSEDE Workshop* *March 2021*
- Genetics and Genomics Lab Boot Camp - Iowa State University *August 2018*
- Graduate Student Facilitator – BIOL 313 *August 2018*
- GDCB IT Committee Student Representative *August 2016-2017*

ACTIVITIES

- Member, COVID-19 International Research Team (COV-IRT). *Mar 2021 – Present*
- Cyclone Martial Arts Club, Taekwondo/ Judo, Iowa State University *May 2017 – Oct 2022*