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, HTML
- **Bioinformatics Analysis:** GATK, miRNA-Seq, scRNA-seq, scATAC-seq, eQTL, Multiomics analysis
- **Machine Learning and Data Analysis:** TensorFlow, Keras, NumPy, Pandas, Sklearn, Tidyverse
- **Workflow Management and Scaling:** NextFlow, Snakemake, Anaconda, HPC, Git
- **Database:** MySql

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*

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, EMBLEBI) as well as GWAS variants associated with Crohn's disease.

- Performed cross-tissue analysis using eQTL findings and GTEx database; found overlap among several tissues
  - O-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 inhibiters either specific or broad spectrum.

RECENT PUBLICATIONS:
- **Haltom, J. A**., Trovao, N. S., Guarnieri, J. W., Pan, V., Singh, U., Tsoy, S., … Wurtele, E. S. **(2025)**. Importance of De Novo Gene Evolution to Emerging Viral Threats: The ORF10 Strain-Restricted Orphan Gene of SARS-CoV-2 Promotes Pathogenesis. *Molecular Biology and Evolution*, *42*(10), msaf211.

- Galeano, D., Imrat, **Haltom, J.**, et al. **(2024)**. sChemNET: a deep learning framework for predicting small molecules targeting microRNA function. *Nature Communications, 15*(1), 9149.

- Guarnieri, J. W., **Haltom, J. A.**, et al. **(2024)**. SARS-CoV-2 mitochondrial metabolic and epigenomic reprogramming in COVID-19. *Pharmacological Research, 204*, 107170.

- McDonald, J. T., Kim, J., Farmerie, L., Johnson, M. L., Trovao, N. S., Arif, S., … **Haltom, J. A.**, et al. **(2024)**. Space radiation damage rescued by inhibition of key spaceflight associated miRNAs. *Nature Communications, 15*(1), 4825.

- Guarnieri, J. W., Dybas, J. M., Fazelinia, H., Kim, M. S., Frere, J., Zhang, Y., … **Haltom, J. A.**, et al. **(2023)**. Core mitochondrial genes are down-regulated during SARS-CoV-2 infection of rodent and human hosts. *Science Translational Medicine, 15*(708), eabq1533.

GRANTS & AWARDS
- **Teaching Excellence Award**   *May 2022*
  - Outstanding teaching accomplishments in a graduate program, 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
- NASA GeneLab   *October 2022 - Present*
- Member, COVID-19 International Research Team (COV-IRT).   *Mar 2021 – Present*
- Cyclone Martial Arts Club, Taekwondo/ Judo, Iowa State University   *May 2017 – Oct 2022*