Taylor K. Paisie **(419)672-1850**
tpaisie91@gmail.com
Bioinformatics Engineer
Atlanta, GA

Education

University of Cape Town Cape Town, South Africa
PhD in Bioinformatics *October 2024-Present*

- Dissertation Project: Surveillance and evolution of *Vibrio cholerae* in Haiti and Africa

University of Florida Gainesville, FL
MS in Genetics and Genomics *August 2015-December 2021*

- Phylodynamaics of *Vibrio cholerae* in Haiti
- Phylodynamics of *Vibrio cholerae* in the Democratic Republic of Congo

Florida State University Tallahassee, FL
B.Sc. in Biological Science *Graduated December 2013*

- Concentration: Molecular and cell biology
- Minors: Chemistry and criminology

Research Experience

Bioinformatics Engineer, ORISE Fellow Atlanta, GA
Center for Disease Control *September 2023-Present*

- Developing and maintaining various internal bacterial genomics pipelines
- Building Docker containers for bioinformatics tools

Bioinformatics Engineer Brooklyn, NY
Biotia, Inc. *March 2022-Jan 2023*

- Developing and maintaining our COVID-DX and BIOTIA-DX software for analyzing samples from patients for metagenomic analysis
- Maintaining and working with laboratory data to develop clinical and research metagenomic tests

Bioinformatics Scientist Gainesville, FL
Emerging Pathogens Institute, University of Florida *January 2022-March 2022*

- Performing and maintaining genomic surveillance pipelines for real-time analysis of SARS-CoV-2 in Florida and Alachua county
- Automatizing workflows and pipelines for analyzing NGS data

Graduate Research Assistant Gainesville, FL
Emerging Pathogens Institute, University of Florida *April 2016-December 2021*

- Graduate research assistant in Dr. Marco Salemi's laboratory studying phylogenetic analysis of infectious diseases.

- The main research for my thesis included the phylodyanmics and ongoing evolution of *Vibro cholerae*.

Laboratory Technician Gainesville, FL
Genetics Institute, University of Florida *July 2014-July 2015*

- I worked on projects involving the gene UBASH3A and studied the effect UBASH3A has on type 1 diabetes
- My position included techniques such as bacteria and tissue culturing, Western blotting, DNA and RNA extraction, PCR, designing PCR primers, cloning and sequencing, and various other laboratory duties

Laboratory Technician Tallahassee, FL
Department of Earth Science, Florida State University *May 2013-July 2014*

- I worked on a project involving the microbial ecology of the carnivorous pitcher plant *Sarracenia purpurea*
- My position included techniques such as DNA and RNA extraction, PCR, qPCR, next-generation sequencing, bioinformatics, and other various laboratory techniques

Research Assistant Tallahassee, FL
Department of Biology, Florida State University *March 2012-August 2013*

- I worked on a project in an evolutionary genetics laboratory studying the allometry of *Drosophila melanogaster*
- My position included imaging *Drosophila melanogaster* wings, analyzing wing pictures, transferring *Drosophila melanogaster*, making *Drosophila melanogaster* food, and various other upkeep duties

Research Assistant Mountain View, CA
Exobiology Branch, NASA Ames Research Center *January 2013-April 2013*

- I worked on a project involving the cyanobacterium, ESFC-1, which was isolated from a microbial mat
- My position included performing PCR, qPCR, DNA and RNA extraction, and various other laboratory duties

Directed Individual Study Tallahassee, FL
Department of Biology, Florida State University *December 2011-August 2012*

- I worked on a project in an evolutionary genetics laboratory that studied the effect certain genes have on *Drosophila melanogaster* wings
- My position included knocking down numerous genes and imaging the wings to see the effect of the knock down on *Drosophila melanogaster* wings

Professional Affiliations

Data Carpentry Instructor Gainesville, FL
University of Florida Informatics Institute *April 2019*

- Developed my teaching abilities, both through the Instructor training course I attended to certify as an Instructor and through regular teaching
- Gained greater insight into and knowledge of the tools taught at workshops (git, Unix shell, Python and R)

- Managed interpersonal interactions with a wide range of learners from all backgrounds
- Gained useful perspectives and adaptability through teaching audiences with different levels of skill
- Developed research and teaching insights by instructing learners in disciplines other than my own
- Volunteered my time to help teach others computing, data, and information skills because I believe in the importance of these skills to foster research
- Learned better time management to stay on top of all my commitments
- deepened my understanding of equity and inclusion principles through Data Carpentry's ethos and Code of Conduct

Webmaster of Women in Science and Engineering Gainesville, FL
University of Florida *August 2019 - August 2020*

- In charge of developing and maintaining the Women in Science and Engineering website
- Planning and helping with workshops involved in the community

Teaching Experience

Workshop on Virus Evolution and Molecular Epidemiology Brasilia, Brazil
Fiocruz *August 4–9, 2023*
Workshop on Virus Evolution and Molecular Epidemiology Stellenbosch, South Africa
Stellenbosch University *August 21–26, 2023*
Workshop on Virus Evolution and Molecular Epidemiology Panama City, Panama
Ciudad del Saber *August 20–26, 2022*
Data Carpentry Workshop: Introduction to Genomics Gainesville, FL
Emerging Pathogens Institute *November 14–15, 2019*
Workshop on Virus Evolution and Molecular Epidemiology Hong Kong, China
University of Hong Kong *August 4–9, 2019*
Data Carpentry Workshop: Introduction to Genomics Gainesville, FL
Emerging Pathogens Institute *April 11–12, 2019*

Conference Presentations

Oral Presentation and Poster October 2024. "Phylodynamic Analysis of *Leptospira kirschneri* Isolates from Mice in Croatia: Whole Genome Sequencing and SNP-Based Phylogenetic Insights" AMD Days 2024. Atlanta, GA.
Oral Presentation. April 2020. "Genomic epidemiology of toxigenic *V. cholerae* O1." Micro Binfie Conference 2020. Virtual conference.
Poster. February 2020. "Molecular epidemiology of toxigenic *V. cholerae* O1 strains from the Democratic Republic of Congo." EPI Research Day. Gainesville, FL.
Poster. February 2020. "Genomic epidemiology of toxigenic *V. cholerae* O1 in Haiti: a switch from the Ogawa to Inaba serotype." EPI Research Day. Gainesville, FL.
Poster. December 2019. "Genomic epidemiology of toxigenic *V. cholerae* O1 in Haiti: a switch from the Ogawa to Inaba serotype." Epidemics 7. Charleston, SC.
Poster. November 2019. "Genomic epidemiology of toxigenic *V. cholerae* O1 in Haiti: a switch from the Ogawa to Inaba serotype." Florida Genetics Symposium 2019. Gainesville, FL.
Oral Presentation and Poster. October 2019. "A variant calling pipeline to investigate the phylodynamics and comparative genomics of bacterial pathogens." University of Florida HiPerGator Symposium 2019. Gainesville, FL.

Poster. June 2019. ”Molecular epidemiology of toxigenic *V. cholerae* O1 strains from the Democratic Republic of Congo.” ASM Microbe 2019. San Francisco, CA.
Poster. February 2019. ”Genomic epidemiology of toxigenic *V. cholerae* O1 in Haiti: a switch from the Ogawa to Inaba serotype.” College of Medicine Celebration of Research Day. Gainesville, FL.
Poster. February 2019. ”Genomic epidemiology of toxigenic *V. cholerae* O1 in Haiti: a switch from the Ogawa to Inaba serotype.” EPI Research Day. Gainesville, FL.
Poster. September 2018. ”Genomic epidemiology of toxigenic *V. cholerae* O1 in Haiti: a switch from the Ogawa to Inaba serotype.” ASM Next Generation Sequencing. Tysons Corner, VA.

Publications

Kim M, Enzler MJ, Pritt BS, Kumlien AC, Wolf MJ, Theel ES, Norgan AP, **Paisie TK**, Patel R (2024). The Brief Case: Human leptospirosis acquired in Minnesota and diagnosed using 16S ribosomal RNA gene PCR/next-generation sequencing of blood. Journal of Clinical Microbiology. https://doi.org/10.1128/jcm.00572-24.

Sabin SJ, Beesley CA, Marston CK, **Paisie TK**, Gulvik CA, Sprenger GA, Gee JE, Traxler RM, Bell ME, McQuiston JR, Weiner ZP (2024). Investigating Anthrax-Associated Virulence Genes Among Archival and Contemporary Bacillus cereus Group Genomes. Pathogens. https://doi.org/10.3390/pathogens13100884.

Alam MT, Stern SR, Frison D, Taylor K, Tagliamonte MS, Nazmus SS, **Paisie TK**, Hilliard NB, Jones RG, Iovine NM, Cherabuddi K, Mavian C, Myers P, Salemi M, Ali A and Morris JG (2023). Seafood-Associated Outbreak of ctx-Negative Vibrio mimicus Causing Cholera-Like Illness, Florida, USA. Emerging Infectious Diseases. https://doi.org/10.3201/eid2910.230486.

Paisie TK, Cash MN, Tagliamonte M, Ali A, Morris JG, Salemi M, Mavian C (2022). Molecular basis of the toxigenic Vibrio cholerae O1 serotype switch from Ogawa to Inaba in Haiti. Microbiology Spectrum. https://doi.org/10.1128/spectrum.03624-22.

Alam MT, Mavian C, **Paisie TK**, Tagliamonte MS, Cash MN, Angermeyer A, Seed KD, Camilli A, Maisha FM, Kabangwa Kakongo Senga R, Salemi M, Morris JG, Ali A (2022). Emergence and Evolutionary Response of Vibrio cholerae to Novel Bacteriophage, Democratic Republic of the Congo. Emerging Infectious Diseases. https://doi.org/10.3201/eid2812.220572.

Sayeed MA, **Paisie TK**, Alam MT, Ali A, Camilli A, Wrammert J, Khan AI, Qadri F, Salemi M, Morris JG, Nelson EJ (2022). Development of a monoclonal antibody to a vibriophage as a proxy for Vibrio cholerae detection. Infection and Immunity. https://doi.org/10.1128/iai.00161-22.

Alexiev I, Mavian C, **Paisie TK**, Ciccozzi M, Dimitrova R, Gancheva A, Kostadinova A, Seguin-Devaux C, Salemi M (2022). Analysis of the Origin and Dissemination of HIV-1 Subtype C in Bulgaria. Viruses 2022, 14, 263. https://doi.org/10.3390/v14020263.

Mavian C, Tagliamonte M, Carreras BG, Bento, A, **Paisie TK**, Marini S, Cummings DA, Lednicky JA, Morris JG, Salemi M (2021). Multiple Introductions of Zika Virus in the Americas. Amer Soc Trop Med & Hygiene. Vol. 105. No. 5.

Mavian C, Pond SK, Marini S, Rife-Magalis B, Vandamme AM, Dellicour S, Samuel V. Scarpino, Houldcroft C, Villabona-Arenas J, **Paisie TK**, Trovao NS, Boucher C, Zhang Y, Scheuermann RH, Gascuel O, Lam TTY, Suchard MA, Abecasis A, Wilkinson E, de Oliveira T, Bento AI, Schmidt HA, Martin D, Hadfield J, Faria N, Grubaugh ND, Neher RA, Baele G, Lemey P, Stadler T, Albert J, Crandall KA, Leitner T, Stamatakis A, Prosperi M, Salemi M (2020). Sampling bias and incorrect rooting make phylogenetic network tracing of SARS-COV-2 infections unreliable. Proceedings of the

National Academy of Sciences. https://10.1073/pnas.2007295117.

Mavian C*, **Paisie TK***, Alam MT, Beau de Rochars VM, Nembrini S, Cash MN, Nelson EJ, Ali A, Morris JG, Salemi M (2020). Toxigenic *Vibrio cholerae* evolution and establishment of reservoirs in aquatic ecosystems. Proceedings of the National Academy of Sciences. https://10.1073/pnas.1918763117.

Ge Y, **Paisie TK**, Chen S, Concannon P (2019). UBASH3A regulates the synthesis and dynamics of T-cell receptor-CD3 complexes. The Journal of Immunology. https://doi:10.4049/jimmunol.1801338.

White SK, Mavian C, Elbadry MA, Beau de Rochars VM, **Paisie T**, Telisma T, Salemi M, Lednicky JA, Morris JG (2018). Detection and phylogenetic characterization of arbovirus dual-infections among persons during a Chikungunya Fever outbreak, Haiti 2014. PLoS Negl Trop Dis 12(5): e0006505. https://doi.org/10.1371/journal.pntd.0006505.

Blohm G, Lednicky JA, Marquez M, White SK, Loeb JC, Pacheco C, Nolan DJ, **Paisie T**, Salemi M, Rodriguez-Morales A, Morris JG, Pulliam J, Carrillo A, Plaza J, Paniz-Mondolfi A (2017). Evidence for mother-to-child transmission of Zika virus through breast milk. Clinical Infectious Diseases. https://doi.org/10.1093/cid/cix968.

Ge, Y, **Paisie TK**, Newman, JRB, McIntyre, LM, Concannon, P (2017). UBASH3A Mediates Risk for Type 1 Diabetes through Inhibition of T-Cell Receptor-Induced NF-B Signaling. Diabetes. https://doi.org/10.2337/db16-1023.

Blohm G, Lednicky JA, Marquez M, White SK, Loeb JC, Pacheco C, Nolan DJ, **Paisie T**, Salemi M, Rodriguez-Morales A, Morris JG, Pulliam J, Carrillo A, Plaza J, Paniz-Mondolfi A (2017). Complete Genome Sequences of Identical Zika Viruses in a Nursing Mother and Her Infant. Genome Announc 5:e00231-17. https://doi.org/10.1128/genomeA.00231-17.

Bonny TS, Driver JP, **Paisie T**, Salemi M, Morris JG, Shender LA, Smith L, Enloe C, Oxenrider K, Gore JA, Loeb JC, Wu C-Y, Lednicky JA. Detection of Alphacoronavirus vRNA in the Feces of Brazilian Free-Tailed Bats (Tadarida brasiliensis) from a Colony in Florida, USA (2017). Diseases. 10.3390/diseases5010007.

Cherabuddi K, Iovine, NM, Shah K, White SK, **Paisie T**, Salemi M, Lednicky, J (2016). Zika and chikungunya virus co-infection in a traveller returning from Colombia: virus isolation and genetic analysis. JMM Case Reports. http://doi.org/10.1099/jmmcr.0.005072.

Mason OU, Canter E, Gillies LE, **Paisie T**, and Roberts BJ (2016). Mississippi River plume enriches microbial diversity in the northern Gulf of Mexico. Front. Microbiol. 7:1048. doi: 10.3389/fmicb.2016.01048.

Paisie TK, Miller TE, Mason OU (2014) Effects of a Ciliate Protozoa Predator on Microbial Communities in Pitcher Plant (*Sarracenia purpurea*) Leaves. PLoS ONE 9(11): e113384. doi:10.1371/journal.pone.0113384.