

Position Title: Postdoctoral Research Associate in Comparative Genomics

We are seeking a dynamic and highly motivated postdoctoral candidate to join our team who is interested in applying cross-species multiomics approaches, including the powerful single cell or nuclei technology, to comparatively understand natural models of human disease. Research in the Warren group is directed toward using species that exhibit phenotypes that mimic human disease states but that are adaptations for the species' specific environment. Through the diverse use of a comparative toolbox of non-traditional model organisms, evolutionary medicine, coupled with sequencing and gene editing technologies, has provided a conceptual framework to study these adaptations, thus providing indispensable biological insight. Our group is dynamic and interactive, and most projects require close teamwork among senior scientists, graduate students, postdocs, and staff promoting excellent opportunities for acquiring new skills.

Project

Natural models of human disease represent species that exhibit phenotypes that mimic human disease states but that are adaptations for the species' specific environment. Species in which traits have naturally evolved in response to extreme environmental stressors offer unique and complementary models in this sense. A type of remarkable genetic resilience occurs, resulting in disease-like phenotypes, but they are not sick. Amongst these emerging models, natural trait alterations in the Mexican cavefish *Astyanax mexicanus*, has offered incredible insight into many adaptive phenotypes with disease relevance. We collaborate with several laboratory groups in the *A. mexicanus* community that are taking advantage of this model to investigate the unique molecular mechanisms underlying obesity, sleep disorders, diabetes, heart regeneration, and many other phenomena. Using a comparative genomics toolbox the Warren lab in collaboration with members of this community offers a framework to study these fascinating adaptations, thus providing indispensable biological insight into trait origins.

Summary of Duties and Responsibilities

Successful candidates should be highly innovative and motivated individuals with general experience in comparative genomics, transcriptome analysis and bioinformatics. She or he primary responsibilities include producing, analyzing, and publishing high-throughput bioinformatics data generated on a NIH funded project using cutting-edge techniques. Our group has already produced single nuclei data sets of several species that each reveal novel cell types and their associated molecular circuitry. We have access to genomics and bioinformatics cores at University of Missouri as well as state-of-the-art genetically edited fish in a collaboration with the Stowers Institute and Texas AM University. The successful applicant will have the opportunity for further training in translational research, in vivo model systems, infectious disease model systems, and a range of immunological techniques.

The candidate is expected to have a PhD with experience in bioinformatics and Next Generation Sequencing data analysis, knowledge of current best practices in transcriptomics, proficiency in UNIX command line and high-performance computing, script writing skills using at least one language (R, Python or Perl), and documented proficiency in verbal and written communication in English. The successful candidate will be self-motivated and have the capacity for independent

evaluation of the literature. Prior knowledge in primary cell or nuclei isolation, molecular biology methods, and single cell approaches would be an added benefit.

The University of Missouri offers an excellent salary and benefits package. This position is funded for 3 years. Interested applicants should send a brief statement of interest and curriculum vitae with contact information for two references to the Principal Investigator.

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