Title: Postdoctoral Research Fellow in Bacterial Population Genomics

School: Harvard T.H. Chan School of Public Health

Department: Epidemiology / Center for Communicable Disease Dynamics

Position Description: Recognized as a leader in infectious disease epidemiology, the Center for Communicable Disease Dynamics at the Harvard T.H. Chan School of Public Health is currently seeking an exceptional and creative scientist for a post-doctoral fellowship in the lab of Dr. William P. Hanage, to develop and apply innovative analytical approaches for studying infectious disease dynamics using next-generation sequencing data. Specifically, the prospective postdoctoral fellow will be charged with developing statistical models and approaches for inferring transmission routes and bottleneck sizes using deep sequencing data. Strong quantitative and/or programming skills are required and experience in bioinformatics is an asset.

The fellow will work closely with Dr. Hanage and staff in the multidisciplinary research team based in the Center for Communicable Disease Dynamics where they will have the opportunity for professional development through interaction with other scientists applying bioinformatic, epidemiological and epidemic modeling approaches to viral, bacterial, and protozoan pathogens. They will also have opportunities to interact with leaders of bacterial evolution and infectious disease epidemiology at this institution and abroad. The fellow will have access to a wealth of resources including high-quality genomic and epidemiological data, a cutting-edge computing facility, robust analytical pipelines, the most recent sequencing and laboratory technology, and research expertise in genomics, epidemiology, mathematics, and computer science.

The position is available immediately and is funded for two years from the start date of employment, with possibility of renewal.

Basic Qualification: Applicants must have a doctoral degree in statistics, population genetics or a related field, with experience working with next-generation sequencing data. Bioinformatic skills are valuable but not essential. Candidates should have a strong quantitative background, general knowledge of infectious disease epidemiology including programming using a common language such as Perl, Python or R, as well as excellent written and oral communication skills, and the ability to work independently and with collaborators.

Additional Qualification:

Special Instructions:

Contact Information: To apply, please send a research statement, CV, contact information for three references and one sample publication by email to: whanage@hsph.harvard.edu. Applications will be considered as they arrive.

Contact Email: whanage@hsph.harvard.edu

Number of References required: 3

Applicant Documents:

1. Cover Letter
2. Curriculum Vitae
3. Statement of Research
4. One sample Publication
5. Contact information for Three References