

Postdoctoral Research Fellow

Position

Title	Postdoctoral Research Fellow
School	Harvard T.H. Chan School of Public Health
Department/Area	Epidemiology
Position Description	<p>Dr. William Hanage, PhD, Associate Professor in the Center for Communicable Disease Dynamics in the Department of Epidemiology at the Harvard T.H. Chan School of Public Health invites creative and motivated Postdoctoral Researchers to apply for positions studying bacterial population genomics. Two positions are available: one for a bioinformatics specialist to work with large genomic datasets, and the other for a theoretician/computational biologist to develop and test evolutionary models. Dr. Hanage's lab combines genomic data and theoretical approaches to improve our understanding of pathogen evolution and epidemiology. His lab has made pivotal contributions to our understanding of the response of pneumococci to vaccination, the spread of drug resistance in multiple pathogens, and the role of horizontal gene transfer in disseminating genetic innovation and speciation. He has also shown the importance of accounting for variation within infections when reconstructing transmission networks.</p> <p>The successful candidates will work closely with Dr. Hanage and staff in the multidisciplinary research team based in CCDD 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, mathematics, and computer science. The positions are funded through May 2022. Current projects include:</p> <ul style="list-style-type: none">• Using short kmers to identify pathogen strains from genomic data in real time (Collaboration with Michael Baym at Harvard Medical School).• Population genomics of bacterial pathogens including (but not limited to) <i>Streptococcus pneumoniae</i>, <i>Staphylococcus aureus</i> and <i>Mycobacterium tuberculosis</i>.• Examining the pressures leading to serotype replacement in the pneumococcus following vaccination.• Development of novel methods to detect transmission by examining polymorphisms within infections.• Predicting evolution using models of frequency dependent selection on the accessory genome (Collaboration with Marc Lipsitch).
Basic Qualifications	<p>Basic Qualification</p> <ul style="list-style-type: none">• Doctoral qualification in a relevant subject (see below for details of each position).• Significant research experience and success in publishing papers.• Strong quantitative, analytical and writing skills• Highly creative, ability to work independently and part of a team, and excited to work in a collaborative environment within the Harvard School of Public Health, and within the larger research ecosystems that Harvard and Boston have to offer.
Additional Qualifications	<p>Additional Qualifications for Theoretical Position:</p> <ul style="list-style-type: none">• Applicants must have a doctoral degree in epidemiology, mathematics, physics, ecology, evolutionary biology or a related field. Successful candidates will have very strong quantitative/statistical and/or coding skills and be very proficient in a common language such as Perl, Python or R. Experience with dynamical, ecological and epidemiological or population genetic models is useful. Successful candidates will be able to think creatively and innovate new approaches to integrate relevant data streams such as complex genomic and ecological data, antibiotic resistance, clinical data, etc. <p>Additional Qualifications for Genomics Position:</p> <ul style="list-style-type: none">• Applicants must have a doctoral degree in genomics, evolutionary biology or a related field. Candidates should have experience of bioinformatics and genomics, some general knowledge of infectious disease, with excellent written and oral communication skills, and ability to work independently and with collaborators. Experience of genome sequencing and assembly across multiple sequencing platforms will be an advantage. Should have experience in programming using a common language such as Perl, Python or R or be willing to learn.
Special Instructions	
Contact Information	<p>Interested candidates should contact Bill Hanage at whanage@hsph.harvard.edu.</p> <p>Inquiries or requests for more information can additionally be sent to whanage@hsph.harvard.edu along with a CV.</p>
Contact Email	whanage@hsph.harvard.edu
Equal Opportunity Employer	<p>We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability status, protected veteran status, gender identity, sexual orientation, pregnancy and pregnancy-related conditions or any other characteristic protected by law.</p>
Minimum Number of References Required	3
Maximum Number of References Allowed	3

Supplemental Questions

Required fields are indicated with an asterisk (*).

Applicant Documents

Required Documents
<div><div>1. Curriculum Vitae</div><div>2. Cover Letter</div><div>3. Statement of Research</div><div>4. Publication</div></div>
Optional Documents