

## Malaria Genomic Epidemiology Postdoc (multiple positions)

A consortium of academic partners is inviting applications from highly motivated candidates for postdoctoral positions at the Experimental and Population-based Pathogen Investigation center (EPPICenter) at UC San Francisco, Johns Hopkins Bloomberg School of Public Health, or Imperial College. Ideal candidates will have experience with modeling and/or genomic analysis and will study the transmission of malaria and apply genomic use cases using data from a large malaria genomic epidemiology project in southern Africa. Successful candidates will have the option to be based at one of the three institutions in alignment with research interests and benefit from a rich and interdisciplinary research environment, working closely with Drs. Bryan Greenhouse (UCSF), Amy Wesolowski (JHBSPH) and Robert Verity (Imperial) as well as a diverse and international team of collaborators.

The fellow(s) will be expected to develop, optimize, and apply statistical and/or mathematical models using genetic, spatial, and epidemiologic data in order to further methods and implementation of malaria genomic use cases in southern Africa. These use cases include connectivity and importation as well as more established cases around drug and diagnostic resistance. Fellows will also work directly with regional and in-country partners and have a role to develop capacity and support a wide array of publications using these data. Our team is directly involved in all aspects of data generation and analysis including study design, supporting generation of laboratory data, methods development, modeling, communicating directly with malaria control programs and policy makers. The project is strongly focused on building research and technical capacity with local partners.

Competitive salary including full benefits will be provided commensurate with experience and qualifications, and the post offers ample opportunities for career development and independent work streams.

### Essential Skills

- PhD or equivalent in a relevant field
- Experience in analysis/modeling of infectious diseases and epidemiology
- Strong statistical and computational skills
- Demonstrated ability to produce independent, creative work
- Ability to work well as member of a team
- Excellent written and oral communication skills

### Helpful Skills

- Ability to analyze and interpret next generation sequencing data
- Background in laboratory genomics, ideally with some experience in pathogen genomics
- Programming experience in R or Python
- Experience in technical and computational capacity building
- Experience in primary epidemiological data collection

To Apply

Send a CV including publications, brief statement of research/career interests, and contact information for up to 3 references to Andrea Picariello at [andrea.picariello@ucsf.edu](mailto:andrea.picariello@ucsf.edu).

Applications will be evaluated on a rolling basis with a final deadline of March 31<sup>st</sup>, 2023.