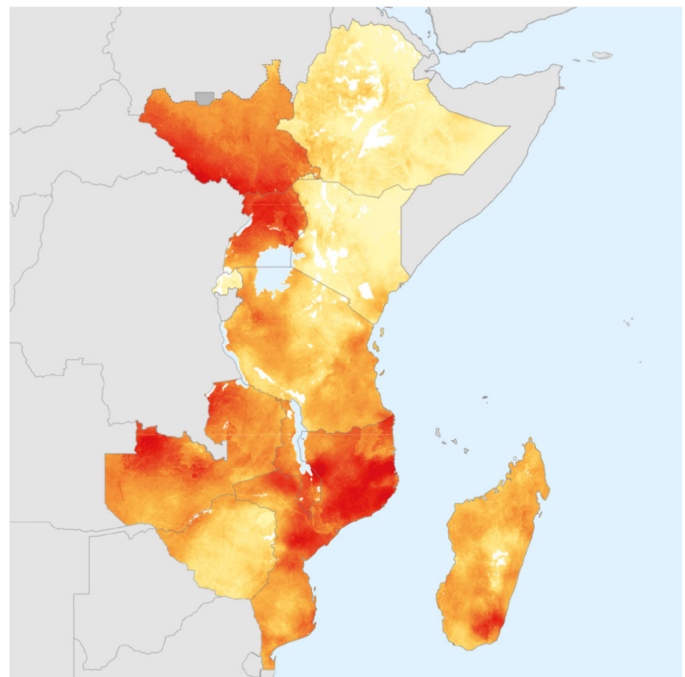


Training program in *Computational Biophysics*

TFG proposal

Estimating malaria transmission flow, importation, and exportation across Mozambique, combining human mobility and parasite genomics

Malaria remains one of the most devastating infectious diseases globally, causing hundreds of thousands of deaths annually and imposing a significant burden on public health systems, particularly in low- and middle-income countries. Precise estimates of malaria incidence are critical to tailor malaria control and elimination interventions. **Understanding the role of malaria importation and identifying what areas are acting as sinks or sources of transmission is key** to improving the characterisation of malaria incidence beyond local reports, especially in low-transmission settings where malaria importation can contribute to sustaining transmission.



P. falciparum parasite rate, East and Southern Africa
2023, World Health Organization

Project details

Objectives

The main objective of the project is to improve and apply a **new Bayesian approach to classify reported cases as local or imported** in different areas of Mozambique and **identify which provinces are acting as sinks or sources of transmission**, in cooperation with researchers from Mozambique.

Methods

Travel reports, epidemiological data, and parasite genetic data of infected individuals will be combined to provide individual classifications into local or imported infections. Importation rates will be obtained at the population level and combined with malaria incidence estimates to infer the rates of importation and exportation of infections at each province. Risk factor and



correlation analyses will be applied to identify potential risk factors of importation and their imprint on parasite genetic populations.

Activities

- Reading literature about malaria genomic surveillance and importation
- Explore and use methods to estimate importation
- Defining new approaches to quantify transmission flow across Mozambique
- Writing and testing code in R
- Validating the output of the code and comparing it with other software
- Develop and use visualisation tools for the interpretation of the results
- Attend regular online meetings with collaborators from Mozambique to discuss the analysis and results
- Promote collaborative work with other researchers from the Manhica Health Research Centre (CISM)
- **Carry out a 1-month stay at Manhica (Mozambique)** to develop the analysis together with another researcher from CISM, after asking for funding support from *Centre de Cooperació al Desenvolupament* of the UPC
- Publishing a repository of the codes
- Writing and defending the bachelor's thesis

Supervisors and host research groups

- Dr. Arnau Pujol Vallribera, junior research leader at the Institut de Salut Global de Barcelona (ISGlobal, <https://www.isglobal.org/en/malaria-physiopathology>).
- Dr. Daniel López (BIOCOM-SC, <https://biocomsc.upc.edu/en>).

Valued characteristics of the candidates

- Programming knowledge, especially R
- Knowledge in statistics and visualisation tools
- Commitment to collaborate (remotely and in person) with researchers from Mozambique with a cooperative spirit
- 4th course student of Engineering Physics or Data Science and Engineering

Practical information

Financial opportunities: The group will support the candidate to apply for a project at the *Centre de Cooperació al Desenvolupament*, so that the travel to Manhica can be funded. The selected student will also be considered as a candidate for an INIREC fellowship (<https://talenthub.upc.edu/en/jobs/r0-predocctoral>, awarded subject to the availability of funds).

Application: Send your CV and motivation letter to arnau.pujol@isglobal.org and daniel.lopez-codina@upc.edu **before September 20th**, 2025. Interviews for this position will be conducted in October.

Further information: You can contact Arnau Pujol (arnau.pujol@isglobal.org) or Daniel López (daniel.lopez-codina@upc.edu) to ask for more details.