OpenMalaria, a simulator of malaria transmission and morbidity, and the use of BOINC for high-throughput computing

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Abstract

Malaria is an infectious disease, spread through mosquito bites, and responsible for substantial morbidity and mortality, principally in sub-Saharan Africa. In the last decade significant reductions in transmission and burden have been achieved; these gains, however, now face the twin threats of decreased funding for control and the development of resistance to both drugs and mosquito-targeting interventions.

Mathematical models can be useful in planning the deployment of current interventions and developing new tools. We present an agent-based model of malaria in humans, OpenMalaria [1], which includes demography, heterogeneity, dynamics of individual infections, and acquired immunity [2, 3], and is linked to a population-based model of seasonal malaria transmission in mosquitoes [4].

The OpenMalaria code is open source under the GNU Public License, and has been developed since 2004 in collaboration between the Swiss TPH and the Liverpool School of Tropical Medicine. It relies on several free software tools, among them Berkeley’s volunteer computing platform (BOINC), the C++ Boost libraries and the GNU Scientific Library.

OpenMalaria allows the simulation of the deployment of multiple control interventions concurrently with independent decay rates and functions, and outputs both transmission levels and clinical event statistics. Examples of intervention scenarios include combinations such as insecticidal treated nets along with improvements in access to official health care [5], or the introduction of vaccines in a setting with existing coverage of indoor residual spraying [6]. Outputs include predictions of effectiveness in reducing number of clinical cases (sicknesses and deaths), disability-adjusted life years, prevalence (detectible infections), and inoculation rates.

The talk will first focus on an overview of our malaria model before moving on to discuss how we use the BOINC computing platform to cope with large experiments (involving tens of thousands to millions of individual simulations, each involving tens to hundreds of thousands of agents) and parameter uncertainty (genetic algorithms to improve a statistical measure of fitness).

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References


