

Uncovering Epidemics: *serofoi*, an R package to estimate the historical Force-of-Infection

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Abstract

As part of the Epiverse, a global collaborative initiative for research software development in epidemiology, particularly TRACE-LAC for Latin America and the Caribbean, *serofoi* is an R package developed to estimate the Force-of-Infection (FoI) of a given pathogen from age-disaggregated population-based cross-sectional serosurveys. The FoI represents the rate at which susceptible individuals become infected in a population, and it is a crucial concept in the mathematical modelling of infectious diseases. Unlike traditional approaches that assume a constant FoI, *serofoi* offers the flexibility of implementing both constant and time-varying models. This flexibility allows for the identification and characterisation of disease spread dynamics over time. By untangling the underlying mechanisms of the prevalence of IgG antibodies, which indicate prior and cumulative exposure to the pathogen, *serofoi* can be applied to uncover hidden epidemics, clarify true incidence, and determine the effectiveness of control interventions for various infectious diseases. These diseases include vector-borne diseases such as Dengue, Chikungunya, Chagas disease, alphaviruses, and others. The package provides researchers and public health officials with powerful tools for data visualisation, model comparison, and fitting processes, all within a Bayesian framework.

Introduction

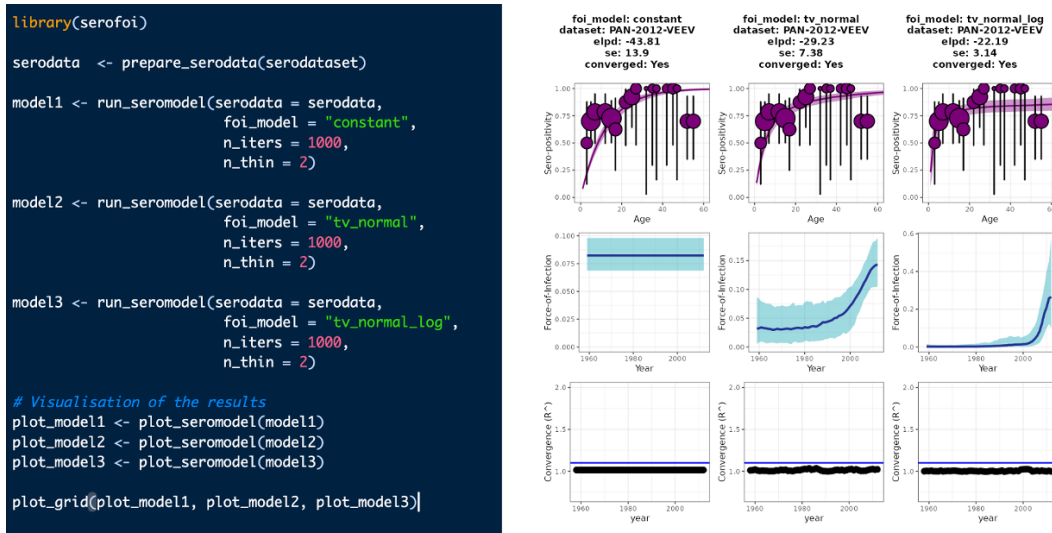
When informing public health response about the spread of a disease, it is crucial to estimate not only the number of individuals infected up to a specific point in time but also the speed at which the disease spreads. Age-disaggregated population-based cross-sectional serological surveys provide a means to estimate the historical Force of Infection (FoI), a vital concept in mathematical modelling of infectious diseases. The FoI represents the rate at which susceptible individuals become infected over a given time period.

The FoI is often assumed to be constant over time, although this may not necessarily be the case. Identifying whether the FoI follows a constant or time-varying trend is important for understanding and characterising the spread of a disease in a specific population. *Serofoi v 0.0.9* offers the possibility to implement a constant model and two time-varying models, enabling the identification and characterisation of time-varying trends. Additionally, it provides tools for visualisation and model comparison, which aid in identifying the most suitable model for the given dataset. To assess how well the different FoI models mathematically represent the seroprevalence data, a fitting process is implemented using a Bayesian framework. *Serofoi* utilises the Rstan package, which implements a variant of Hamiltonian Monte Carlo (HMC) algorithm which allows Markov chain Monte Carlo sampling from the posterior distribution of parameters and provides Bayesian metrics for model comparison.

Usage

Serofoi is a versatile tool that can be applied to any infectious disease for which IgG antibodies can be measured, including arboviruses (such as dengue, Zika, chikungunya, etc.), Chagas disease, alphaviruses, and many others. These antibodies are typically produced by the immune system in response to an infection, and their presence in the blood can indicate previous exposure to the pathogen. *serofoi v0.0.9* is specifically designed for serosurveys that meet the following inclusion criteria: a) They are population-based cross-sectional surveys (not hospital-based). b) They specify individuals' age or age group. c) They indicate the diagnostic test(s) used. d) They identify the location and year of sample collection.

By using serofoi, users can easily visualise the performance of different models and select the best-fitted model to uncover the temporal trend of the Force of Infection (FoI) over time.



Outlook

Future versions of the package will include models allowing for waning immunity, age-dependent FoI, and congenital transmission. The source code and further documentation of the package can be found at <https://github.com/epiverse-trace/serofoi>.

Conclusion

serofoi is a package intended to provide researchers and public health officials in Latin America and the world with high-level modelling tools for the characterisation and assessment of the spread of infectious diseases. By enabling the estimation of time-varying FoI, serofoi contributes to the evaluation of the impact that public health interventions have on the spread of diseases, enhances serological research and facilitates equitable access to epidemiological research tools.