

**INTEREST: Inference for large-scale transmission simulator models to estimate parameters of epidemiological/evolutionary interest, and to test intervention policies *in silico* under uncertainty**

Many recent models in biology describe nature to a high degree of accuracy but are not amenable to analytical treatment. Such models can, however, be simulated on computers to study complex phenomena, such as transmission of pathogens, vectors and genes, and natural selection acting on them. [Approximate Bayesian Computation](#) (ABC) and Synthetic Likelihood (SL) are generic likelihood-free inference (LFI) techniques that offer a principled way of fitting such models to data and to quantify uncertainty about model parameters (say  $R_0$ , strength of selection, effective population size, etc). Recent advances in LFI have accelerated inference by several orders of magnitude to make it a more practically applicable tool. [ELFI software](#) by [Lintusaari et al. \(2018\)](#) makes these tools available on an open-source software platform that is under continuous further development. Several new algorithms and features are currently being added by the development team to expand the applicability of ELFI. For an example of using ABC to fit a model for pneumococcal population evolution under vaccine intervention, see [here](#). For an example of resolving transmission model identifiability for TB using ABC, see [here](#).

In this project the aim is to lay the ground for using ELFI to make inference for large-scale transmission simulator models to estimate parameters of epidemiological or evolutionary interest. This further allows testing of possible intervention policies *in silico* while accounting for uncertainty about model parameters. An example of a large-scale spatio-temporal transmission model is provided by [Di Ruscio et al \(2019\)](#), who considered transmission dynamics of MRSA simultaneously in the healthcare and community settings using a nation-wide simulator model of Norway with millions of geo-located individuals with realistic population densities and mobility patterns. Another example of a large-scale transmission model is the PopART HIV individual-based simulator by [Pickles et al \(2020\)](#). By establishing an interface and a software pipeline for fitting models at this scale of complexity using ELFI, the project will enable a wide spectrum of further applications within the PAM programme on for example parasite transmission dynamics and vector control, and the study of bacterial pathogen dissemination in communities and healthcare settings in LMICs.