Inferring epidemiological parameters from summary statistics of phylogenetic trees using an ABC method

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Résumé

With the advent of affordable sequencing techniques, phylogenies are routinely generated in epidemiological studies on virus. The question is, can these really tell us more about epidemiological processes than classical incidence data?
Epidemiological models are often described by systems of differential equations, but, fundamentally they involve discrete stochastic processes: we consider a population constituted of a finite number of individuals that may contract the infectious disease (susceptible people), in which we introduce some infected people. Then, at each step, of the epidemiological process a susceptible individual can become infected or an individual infection can end.

These process can typically be modeled using an event-driven system and its outputs can be captured by a tree where branching events correspond to transmission events and tips to recovery event. Such transmission trees, which are approximated by virus phylogenies, contain more information about epidemiological processes than classical incidence data.

We created a flexible program that implements several simulation systems (from birth-death to SEIRS epidemiological processes). Each run generate many transmission trees under priors for epidemiological parameters, which we analyze in order to determine the most appropriate summary statistics. Then we perform approximate bayesian computation to infer the posterior distributions of epidemiological parameters of target trees.

We compare our method to likelihood methods and test it on real data.
This work is a first step in the understanding how phylogenies of viral sequences and ABC can inform us on epidemiological parameters for any type of epidemiological model.

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