Directly estimating epidemic curves from genomic data

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Phylodynamics = Phylogenetics + Epidemic Dynamics





[Grenfell et al., Science, 2004]

Population size is directly related to tree depth



Population size of N. So choose same parent with prob 1/N



Want to use compartmental models to describe epidemic curve

$$S + I
ightarrow 2I$$
 at rate $eta SI$
 $I
ightarrow R$ at rate γ



Time

Knowing model parameters is not everything



Time

An exact model for reconstructing the transmission tree and prevalence



Population dynamics estimation

Inferring SIR prevalence — parameters only



Population dynamics estimation

Inferring SIR prevalence — parameters + curve



Population dynamics estimation Inferring SIR prevalence



Incorporating incidence data





Time

PANGEA phylodynamic methods comparison exercise

Phylogenetic tree for example "Village" data set.



Software: Epilnf (working title)

View on GitHub

Epilnf

BEAST 2 package for performing exact phylodynamic inference of model parameters and prevalence.

What is EpiInf?

Epilnf is a package for performing inference of stochastic compartmental epidemiological model parameters using particle filtering to compute the prior probability density of a tree. Joint inference of prevalence trajectories is also performed.

Epilnf is currently at the early pre-release stage, so some things may not work perfectly and there is still very little in the way of documentation. Even the name may change!

Installation

To install EpiInf, follow these steps:

1. Install the most recent version of BEAST 2.

2. Open the BEAUti programme.

Visit tgvaughan.github.io/EpiInf for installation instructions.

Epilnf (working title)



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