A Phylodynamic Extension to Individual Level Models

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Introduction

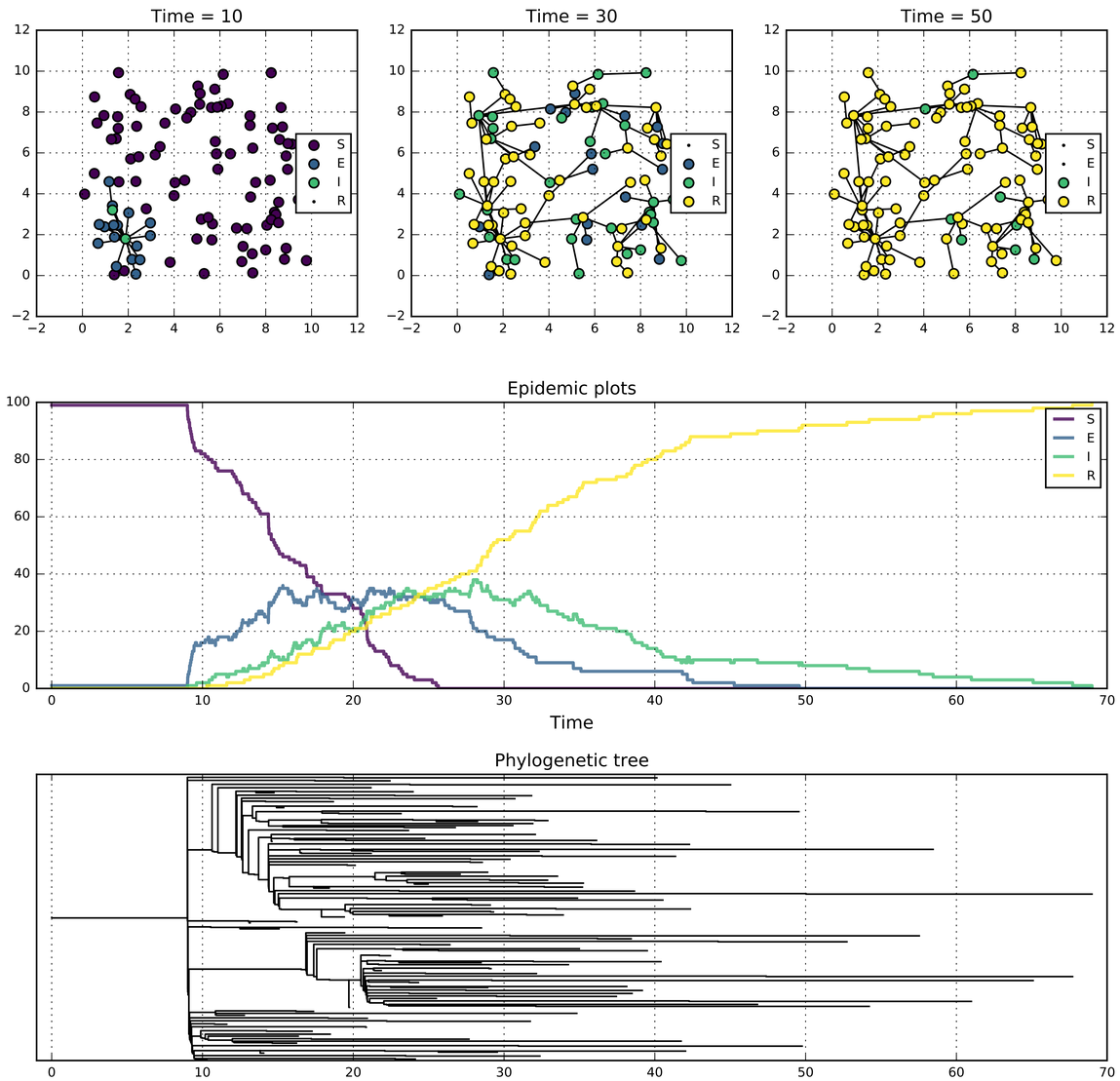
The field of phylodynamics involves the combined investigation of the dynamics of disease spread and evolution. Our newfound ability to develop and utilize statistical models of phylodynamics can be attributed to decreasing costs of computation and genetic sequencing. To apply phylodynamic models, we must conduct dense genomic sampling during epidemics. These models are most appropriate when epidemiological and evolutionary processes occur at similar timescales.

Individual level models

With the individual level model framework of infectious disease transmission of Deardon et al. (2010), functions of risk factors associated with the exposure, latency of infection, and removal of infected individuals are defined. We have extended this framework to account for source specific disease exposure as well pathogen evolution. This allows for the simultaneous simulation of epidemics and pathogen evolution, and presents opportunities for the development of specialized algorithms for Bayesian inference.

Software

The phylodynamic extension to individual level models has been built into a software package available through the Julia ecosystem called *Pathogen.jl*. Julia is a new programming language that has been developed specifically for efficiency in scientific computation applications (Bezanson et al., 2014).



Top row: The disease states of a population, and the disease transmission pathways within that population during a simulated epidemic.
Middle row: The total count of individuals in each disease state over the course of a simulated epidemic.
Bottom row: A phylogenetic tree showing the evolution of a pathogen over the course of a simulated epidemic.

Implications

With a unified framework for the modelling of pathogen spread and evolution, information contained within pathogen sequence data and within traditional epidemiological data is propagated fully between components of the phylodynamic model. With this, disease transmission pathways may be more accurately inferred, and improved predictions may be generated for the purposes of developing disease control strategies.

Current work

We are currently focused on making the extended individual level model framework and associated algorithms available in high performance software. We are also looking to apply our framework and algorithms for phylodynamic models to a wider variety of real world applications, with specific interest in RNA viruses affecting production animals.

Future work

- Simulation based methods of inference
- Self tuning computational methods for phylogenetic tree inference
- Improved models of "external" disease dynamics
- Selective pressures in pathogen evolution
- Hosts with partial immunity

References

J. Bezanson, A. Edelman, S. Karpinski, and V. B. Shah. Julia: A fresh approach to numerical computing. *arXiv preprint arXiv:1411.1607*, 2014.

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