

Modelling the spread of MRSA

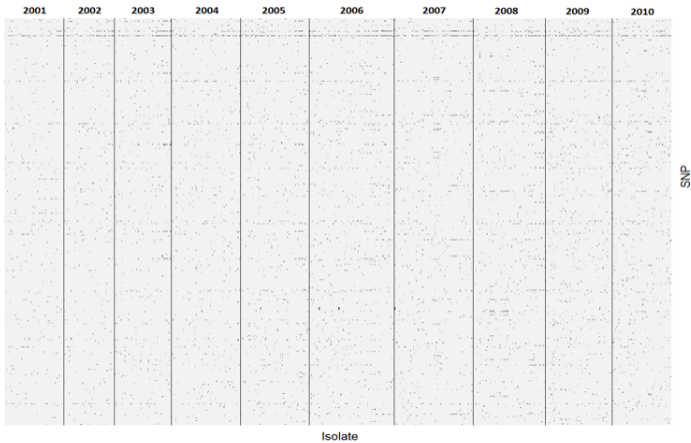
Alex, Dick, Ed, Emma, John, Sandra, Thomas

ITT8

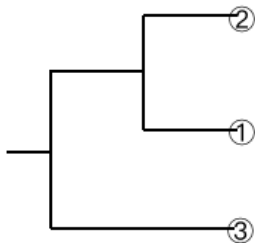
June 15, 2018

The problem

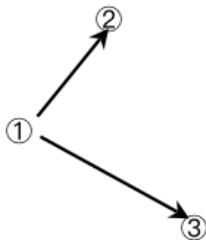
Database: 1022 isolates; 5469 loci; 46 hospitals



The problem

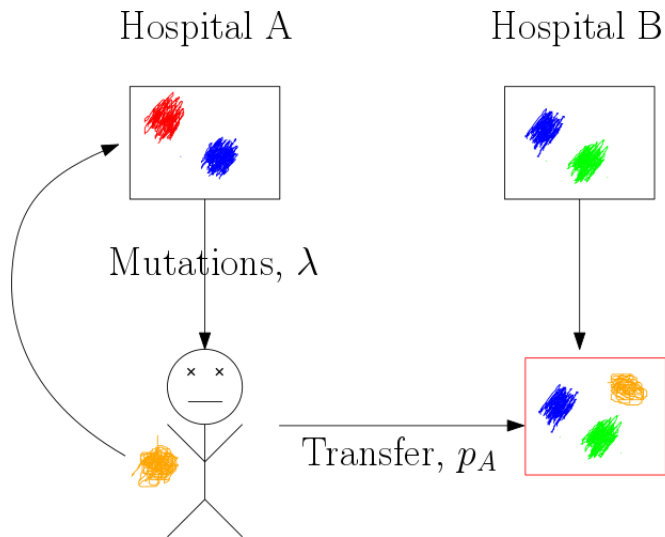


Phylogenetic
tree

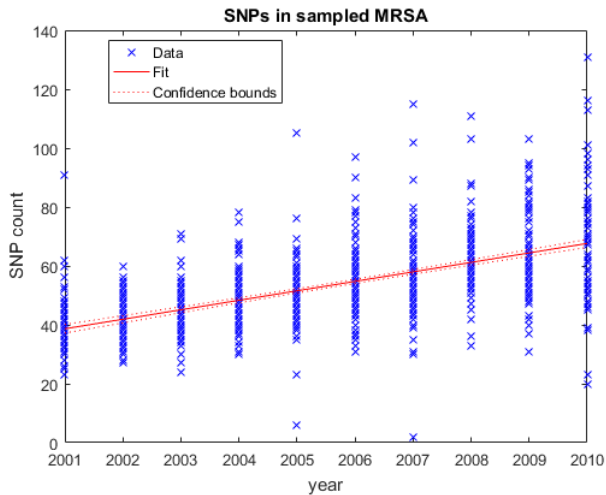


Transmission tree

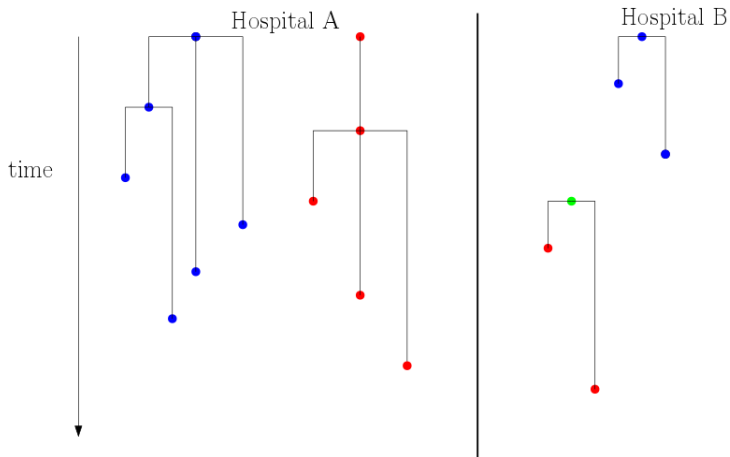
Our model



Simulations

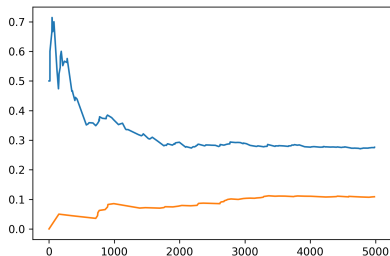


Simulations

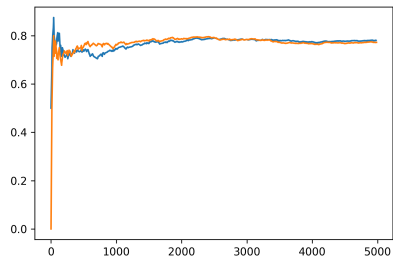


Simulation

Transfer probability, $p = 0.2$



Transfer probability, $p = 0.5$

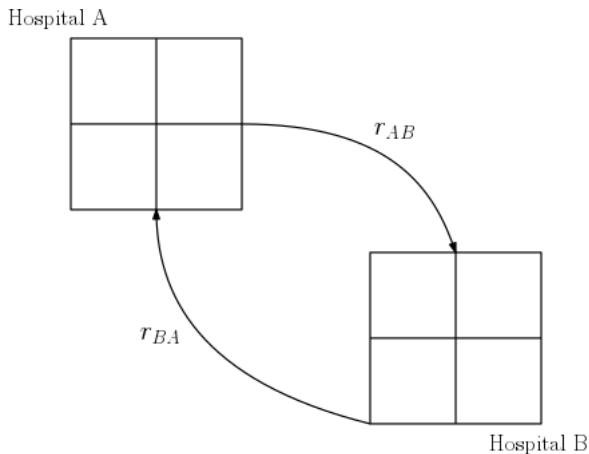


Assumptions

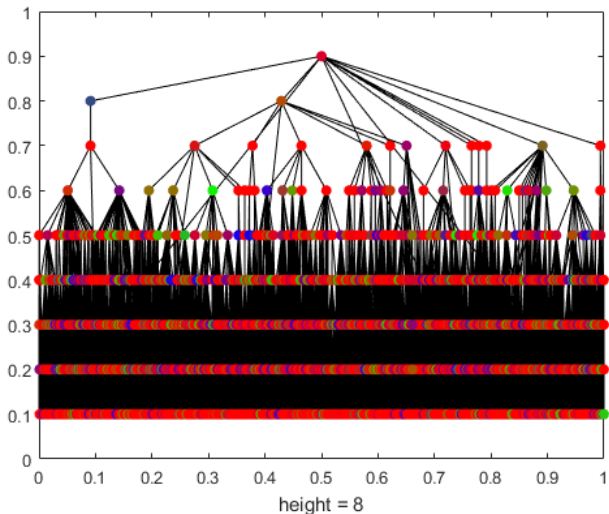
- Only one site mutates at each mutation time.
- Each mutation occurs in a new place.
- Only one infection at a time.
- No mutations occur during transfer.
- Person equally likely to be affected by each strain.

SIS model

- Each room is infected at rate λ , and recovers at rate 1.



SIS model



Future work

- Compare to current data.
- More complicated/realistic model.
 - Include death rate of a strain.
 - Different mutation rates over time/hospital/strain.
 - Different transfer probabilities according to distances between hospitals.
 - Infect a person with a strain proportional to population of the strain.
- Theoretical results on mixing times and steady states.
- Use simulations and theoretical results to study genealogies of initial strains.
 - Do one or two strains go on to live forever with others dying out?
 - Is there a threshold probability for settling of proportions of strains?

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