Modelling the spread of MRSA

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

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June 15, 2018

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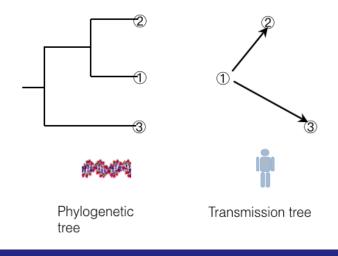
The problem

Database: 1022 isolates; 5469 loci; 46 hospitals

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Isolate

The problem

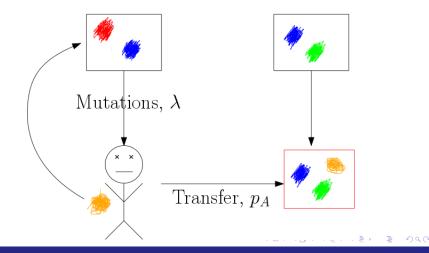


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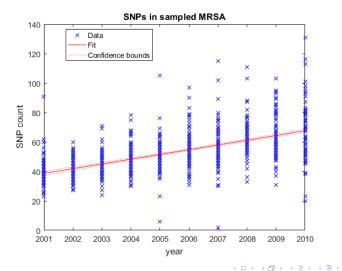
Our model



Hospital B

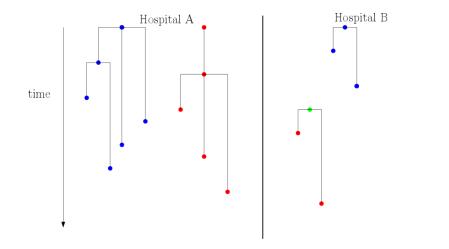


Simulations



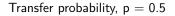
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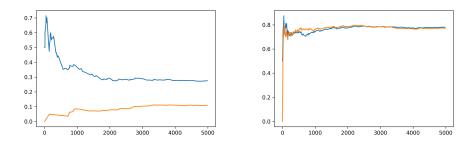
Simulations



Simulation

Transfer probability, p = 0.2





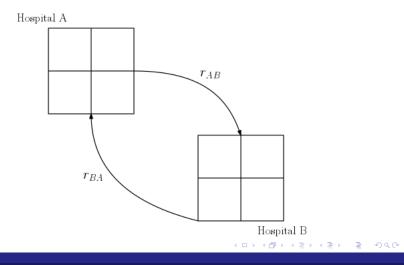
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Assumptions

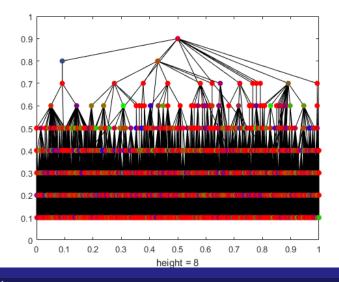
- Only one site mutates at each mutation time.
- Each mutation occurs in a new place.
- Only one infection at a time.
- No mutations occur during transfer.
- Person equally likely to be affected by each strain.

SIS model

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



SIS model



• 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 intial 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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