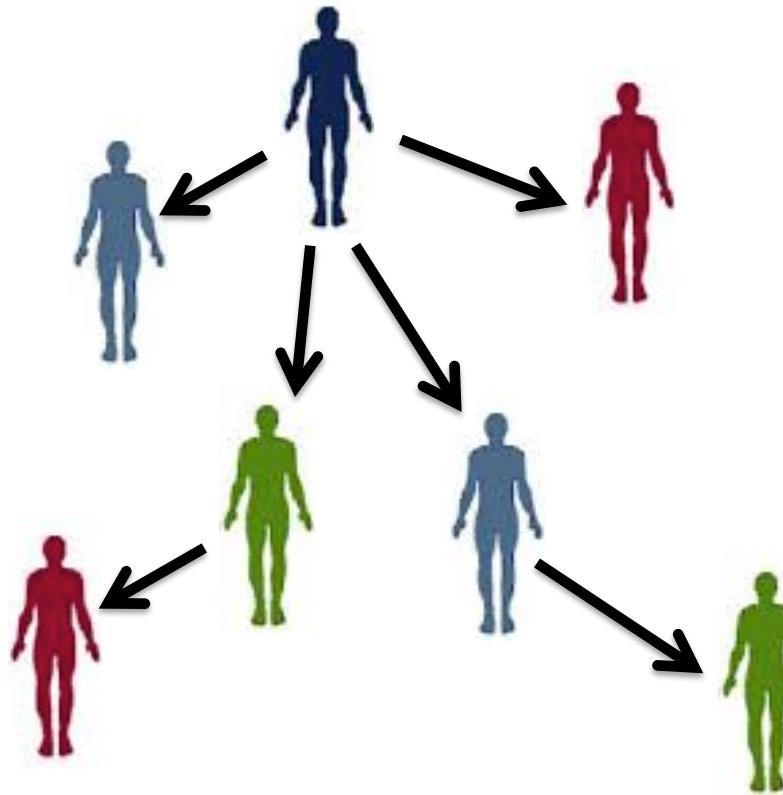


SCOTTI: Inferring transmission with the Structured Coalescent

Nicola De Maio, Chieh-Hsi Wu, Daniel Wilson



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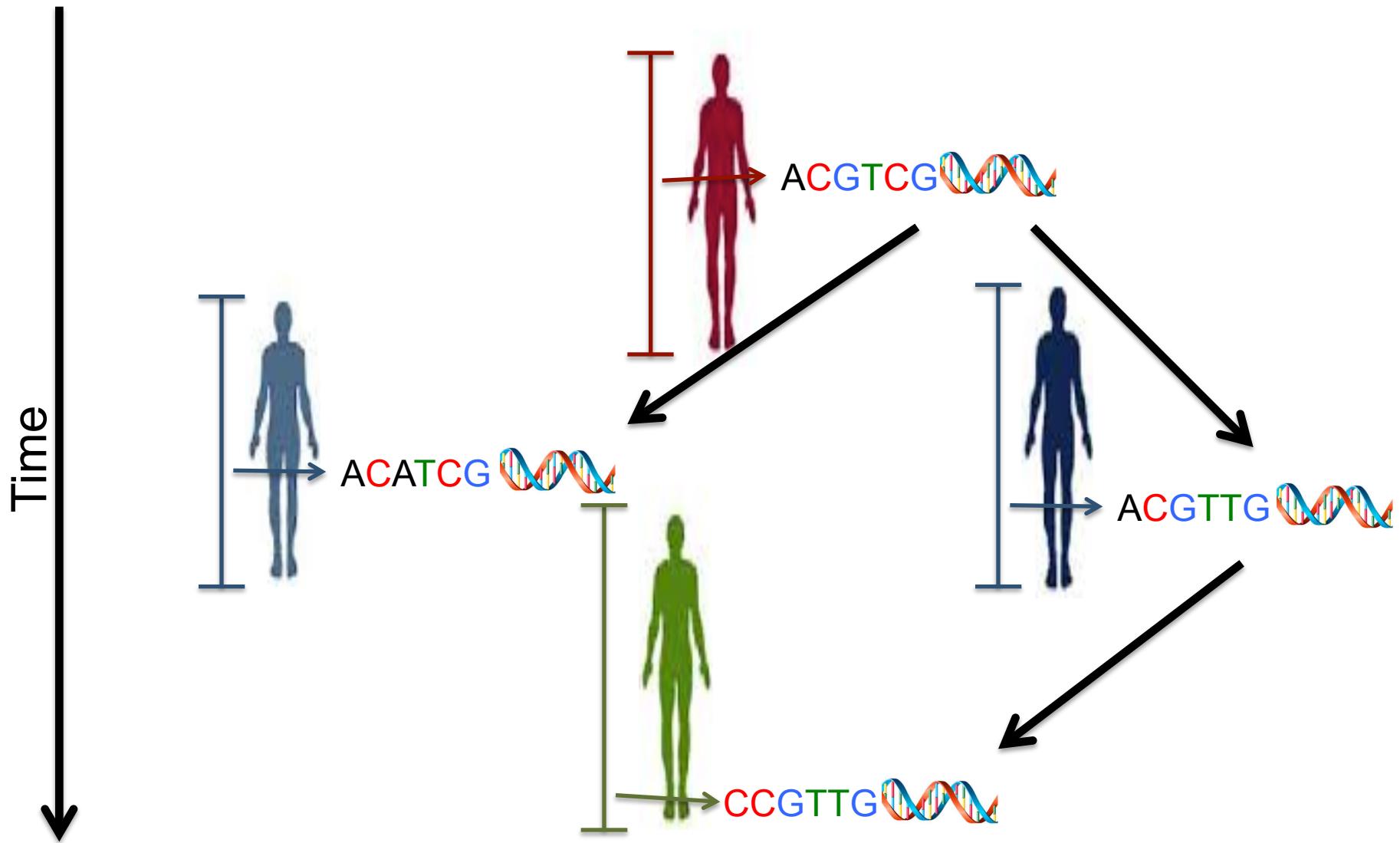
NHS

National Institute for
Health Research

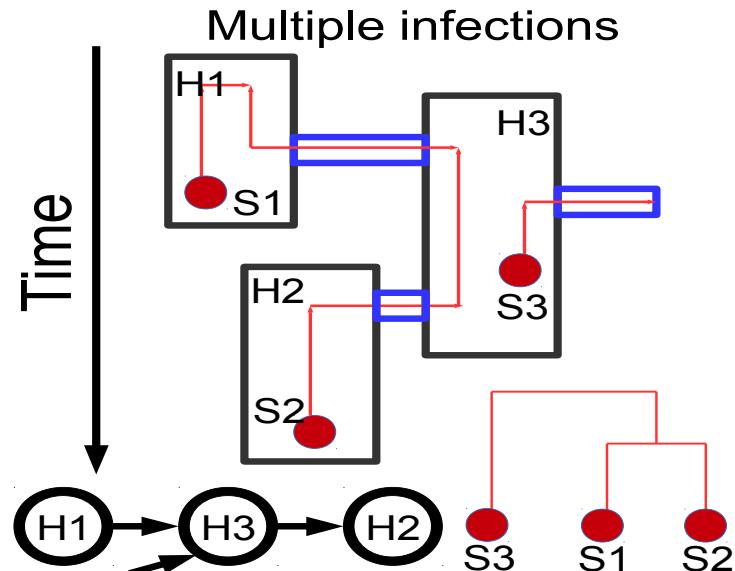
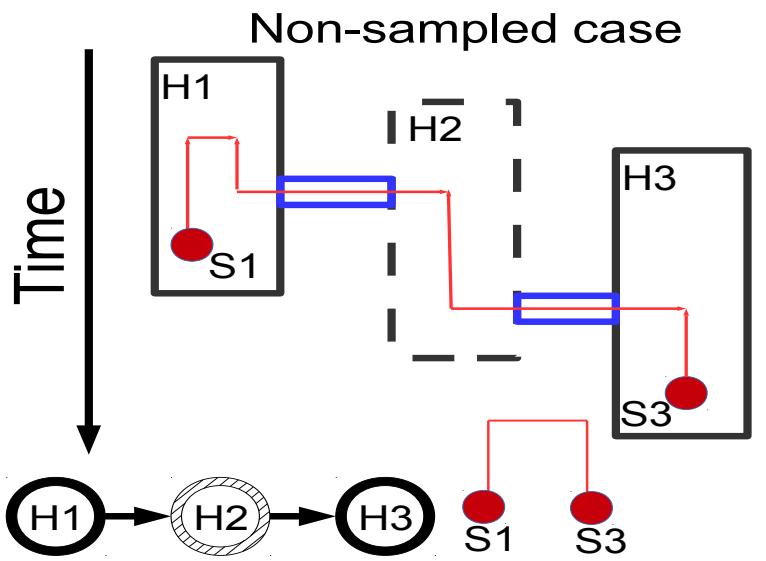
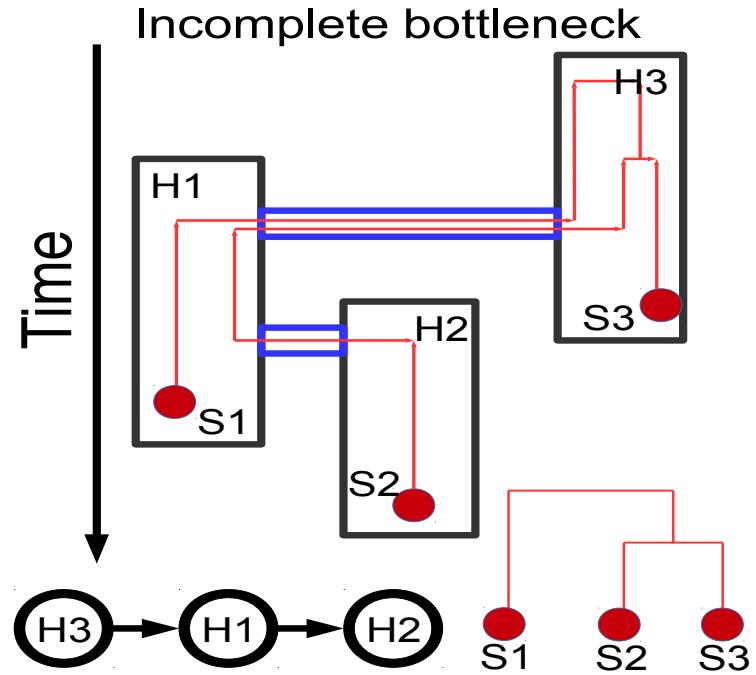
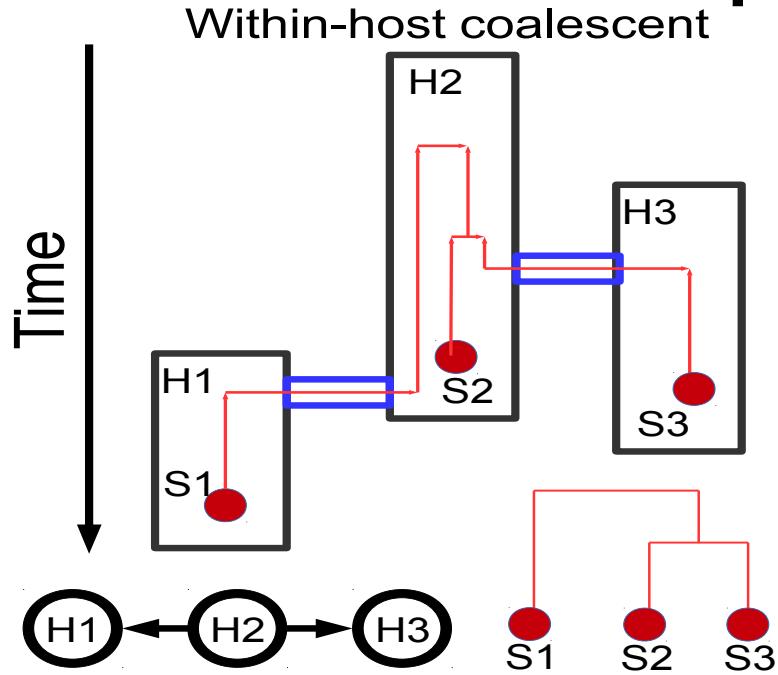


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Host information



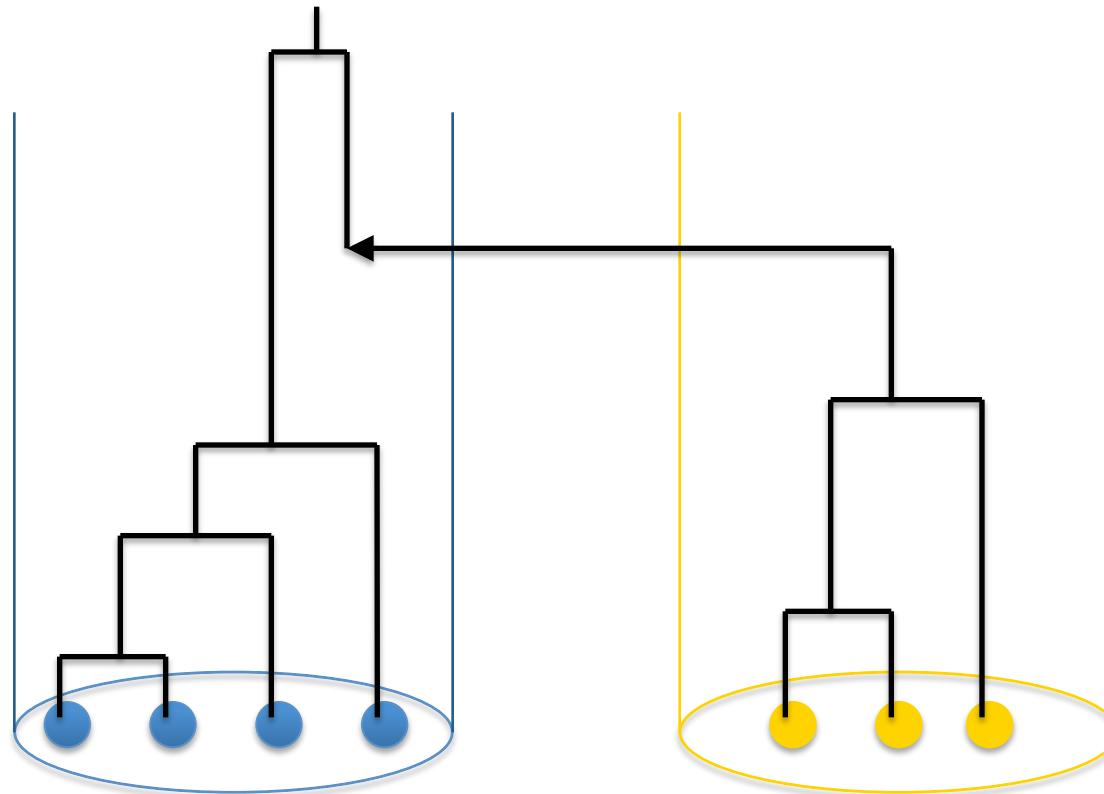
Complications



Structured coalescent

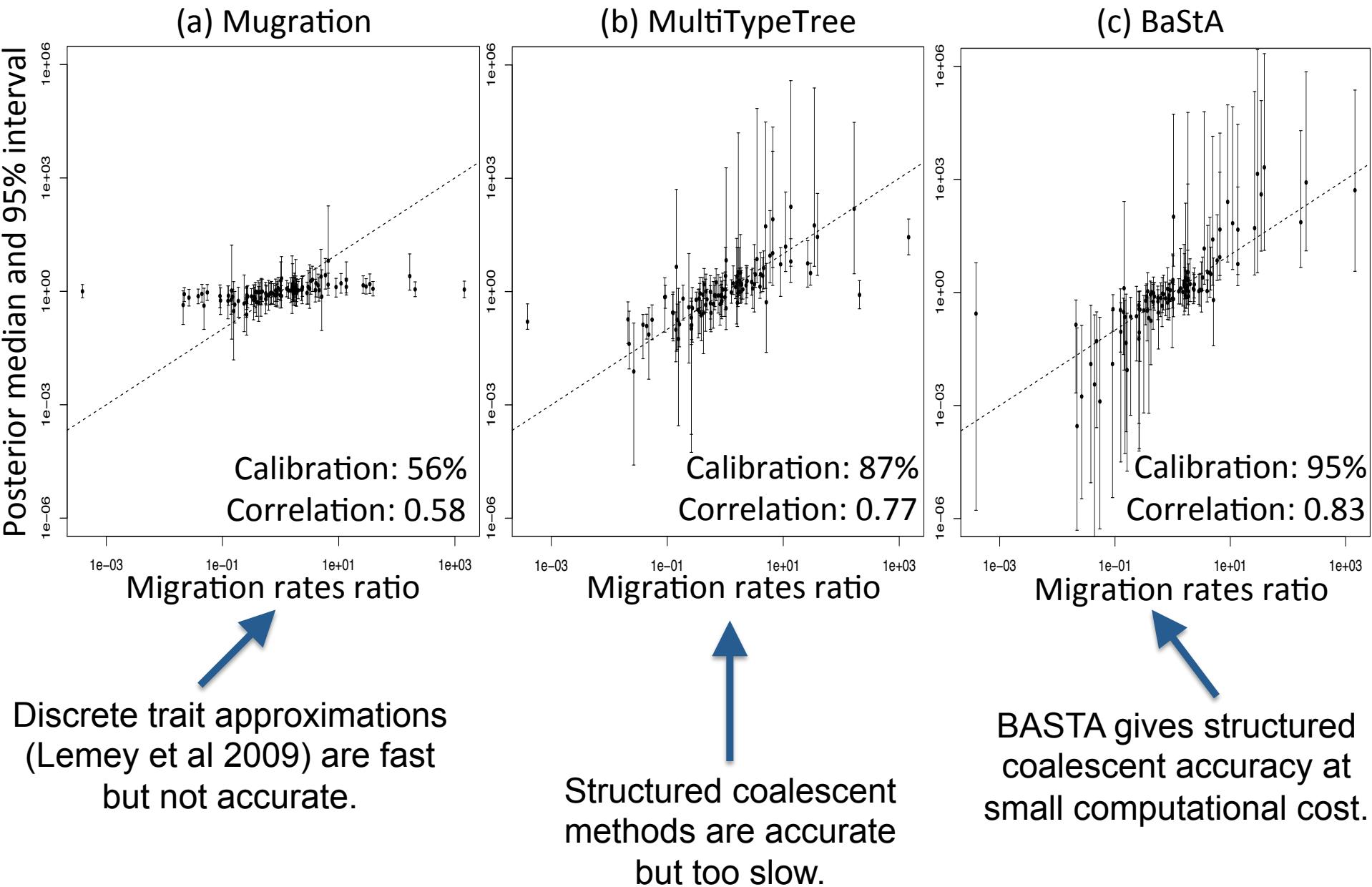
Coalescence events only within demes

Migration moves single lineages between demes.



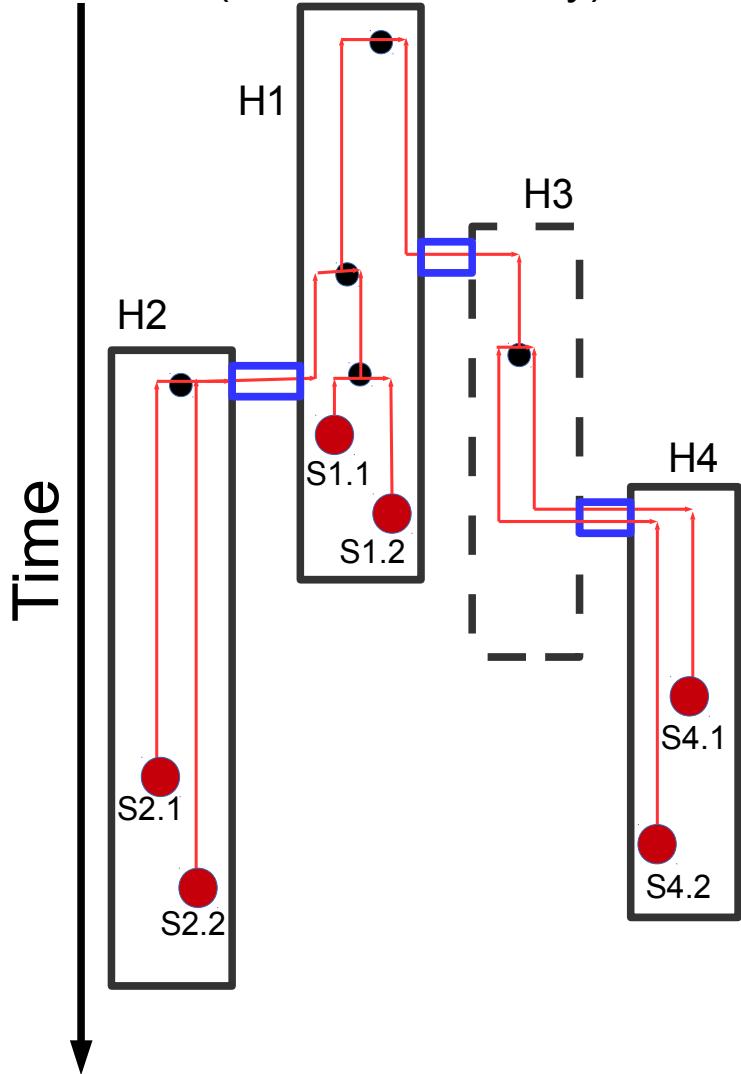
We use a recent efficient approximation to the structured coalescent: BASTA (De Maio et al 2015 PLOS Genetics).

Phylogeography with BASTA

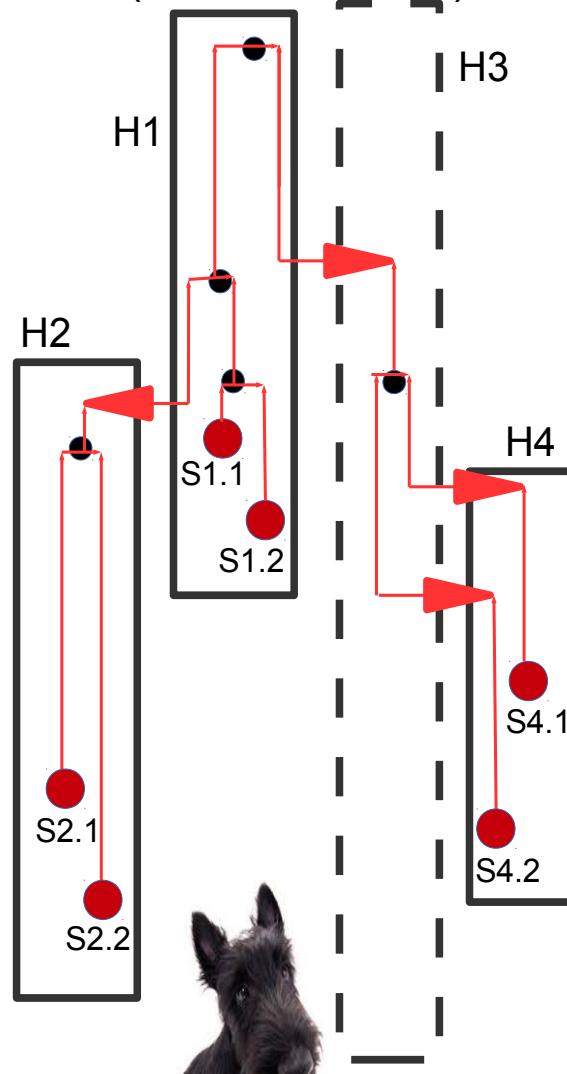


Models used

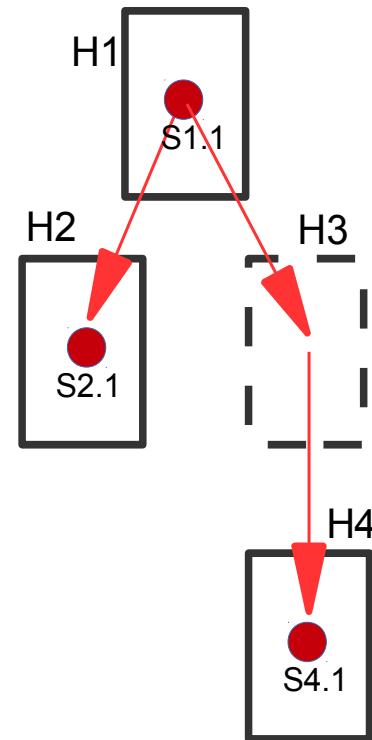
Multispecies
(simulated history)



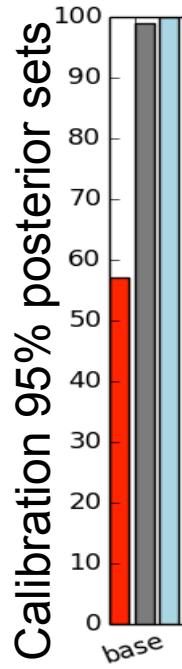
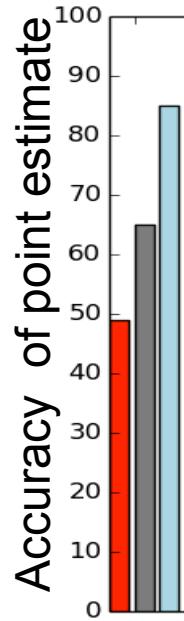
SCOTTI
(ideal inference)



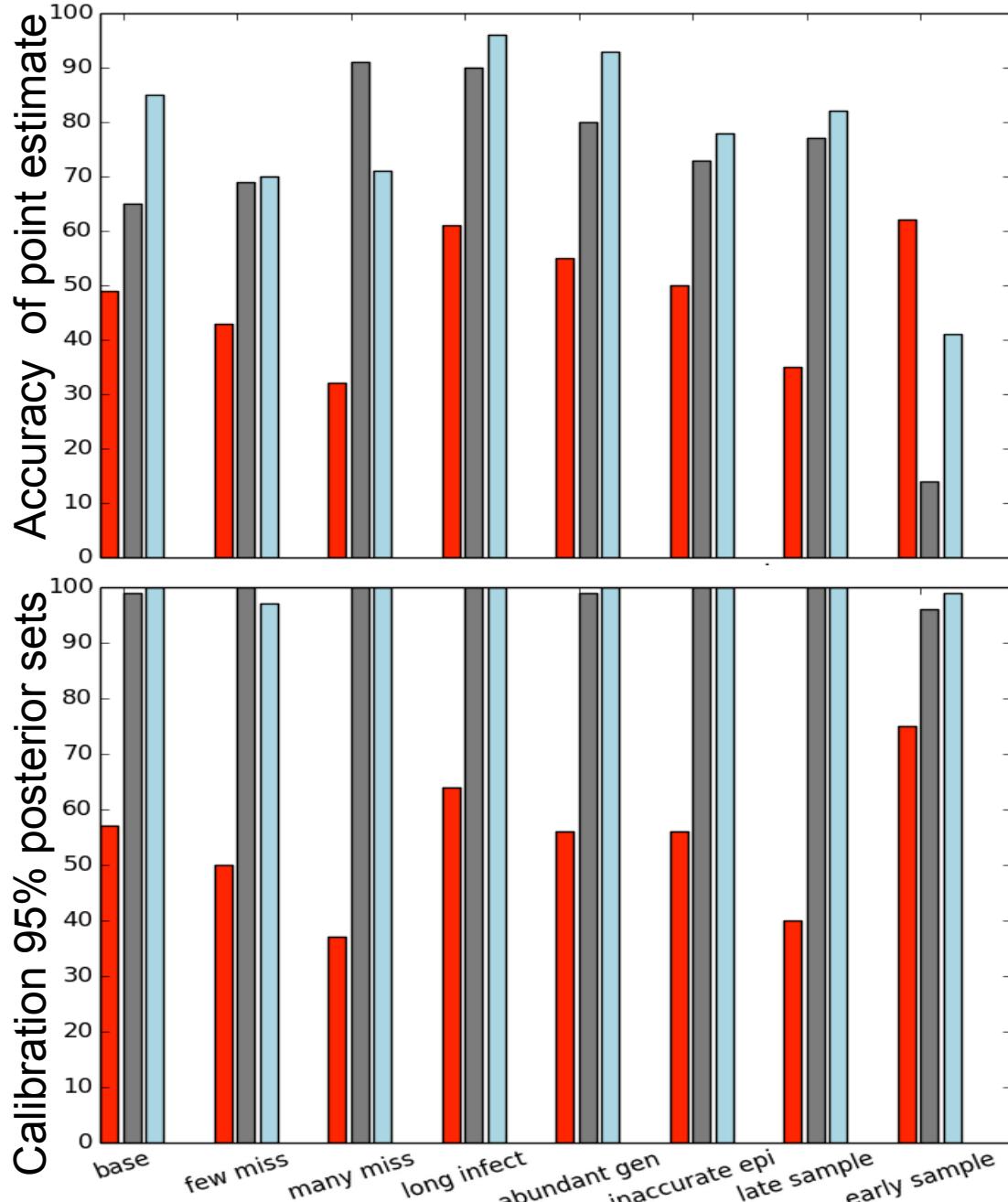
Outbreaker
(ideal inference)



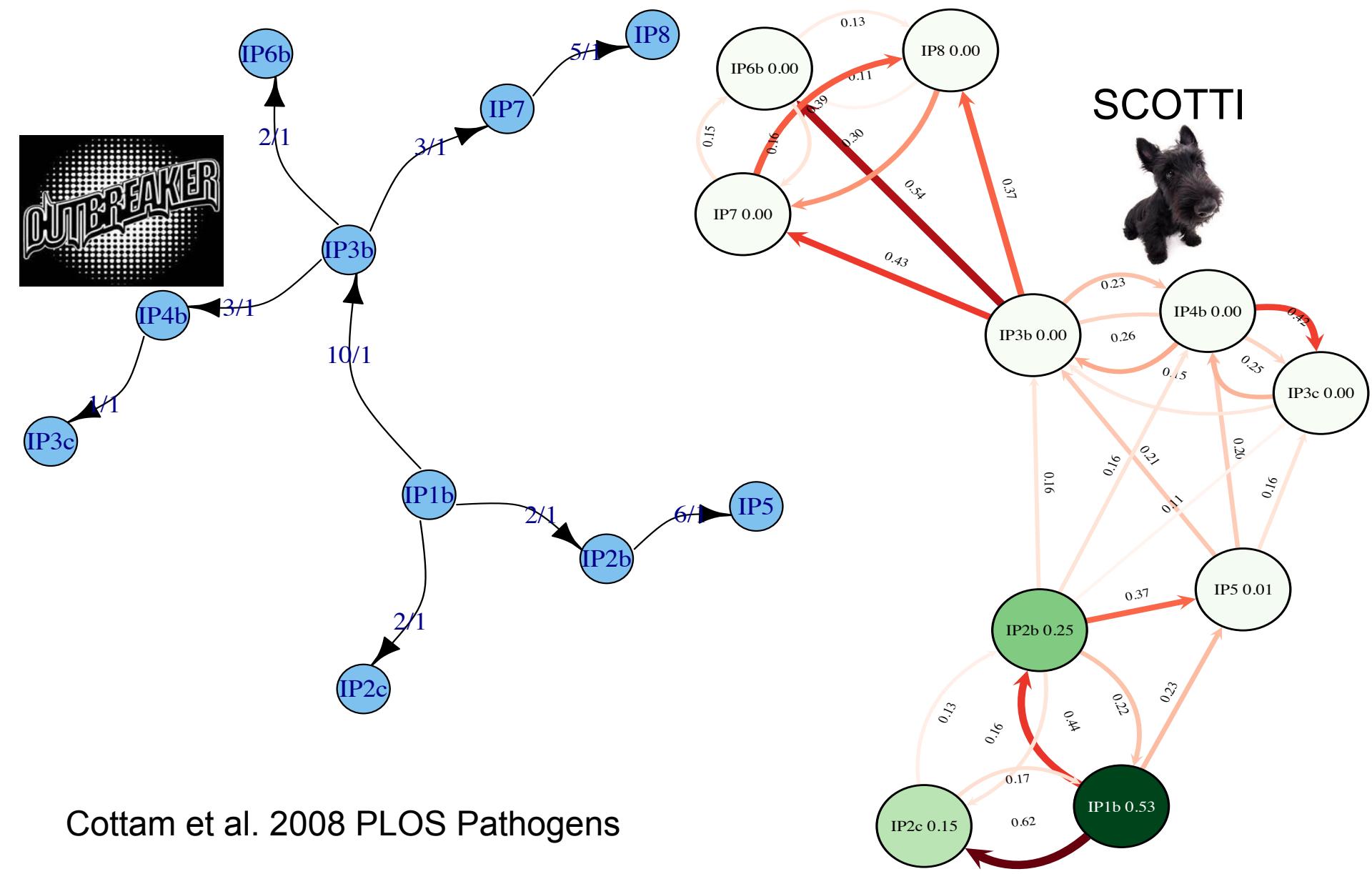
Simulations



Simulations



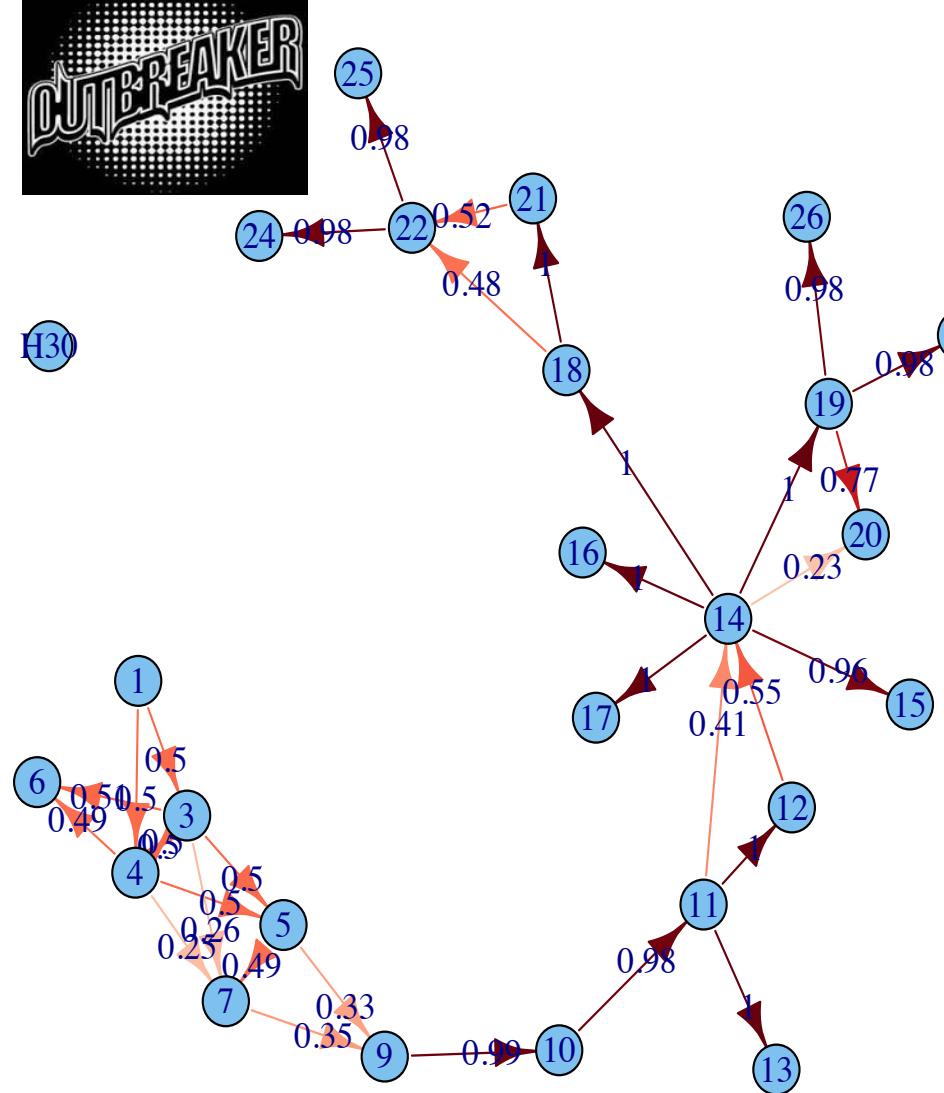
FMDV data



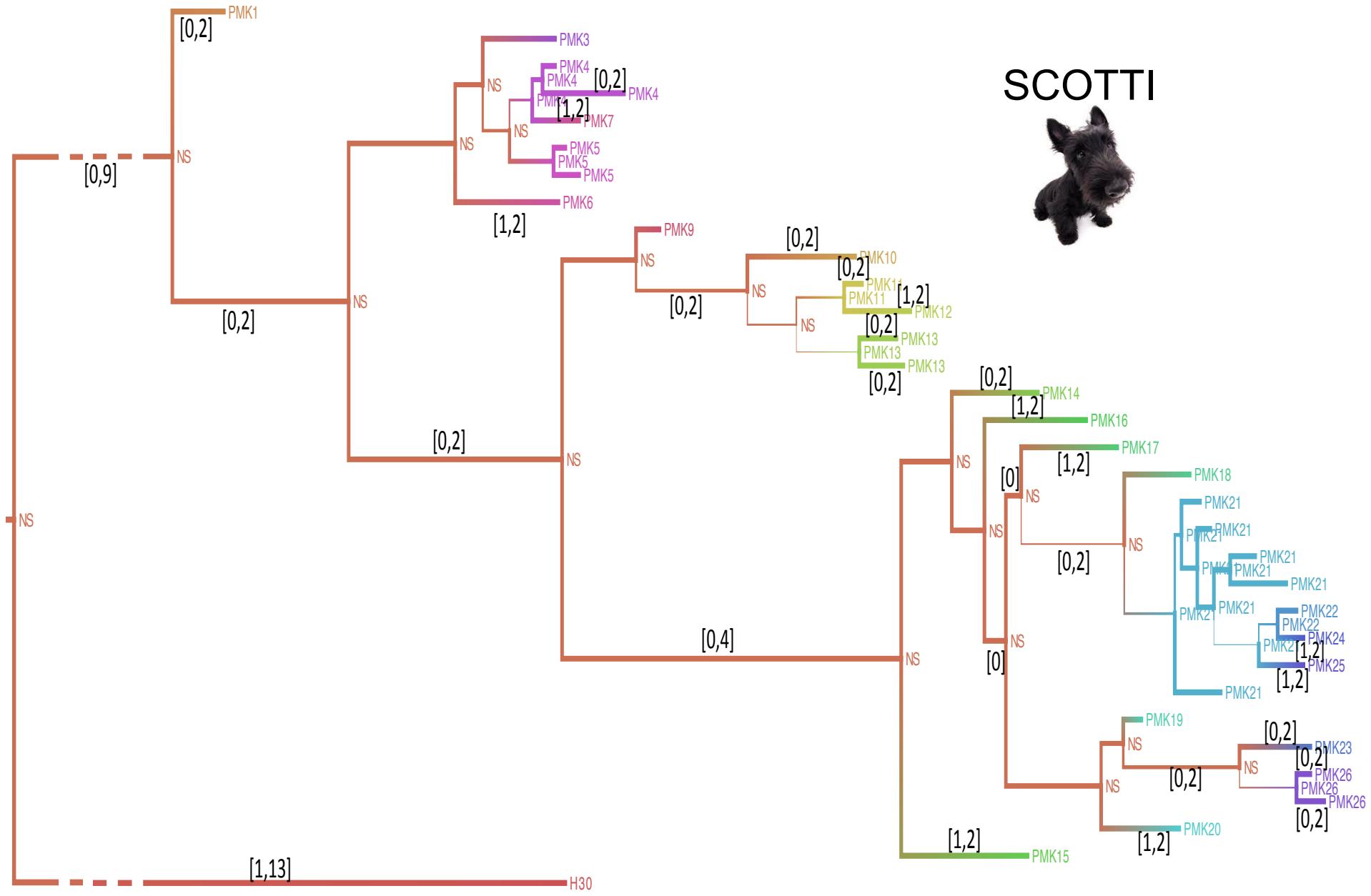
K. pneumoniae data



H30



K. pneumoniae data



Summary SCOTTI

Different models result in different transmission reconstructions.

New inference of transmission in BEAST2:
SCOTTI.

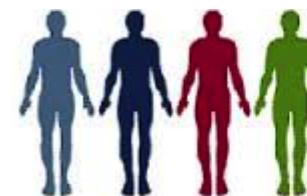
Future work: inclusion of transmission bottlenecks, host population structure, and epidemiological models.

Thanks for listening!

Daniel J Wilson

Chieh-Hsi Wu

Crook group



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