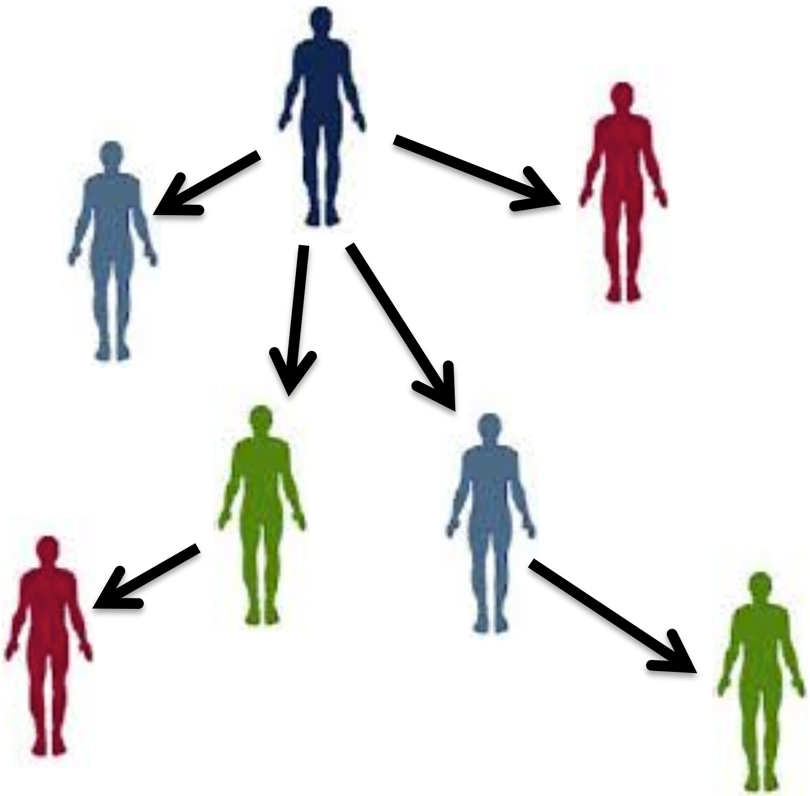
SCOTTI: Inferring transmission with the Structured Coalescent

Nicola De Maio, Chieh-Hsi Wu, Daniel Wilson



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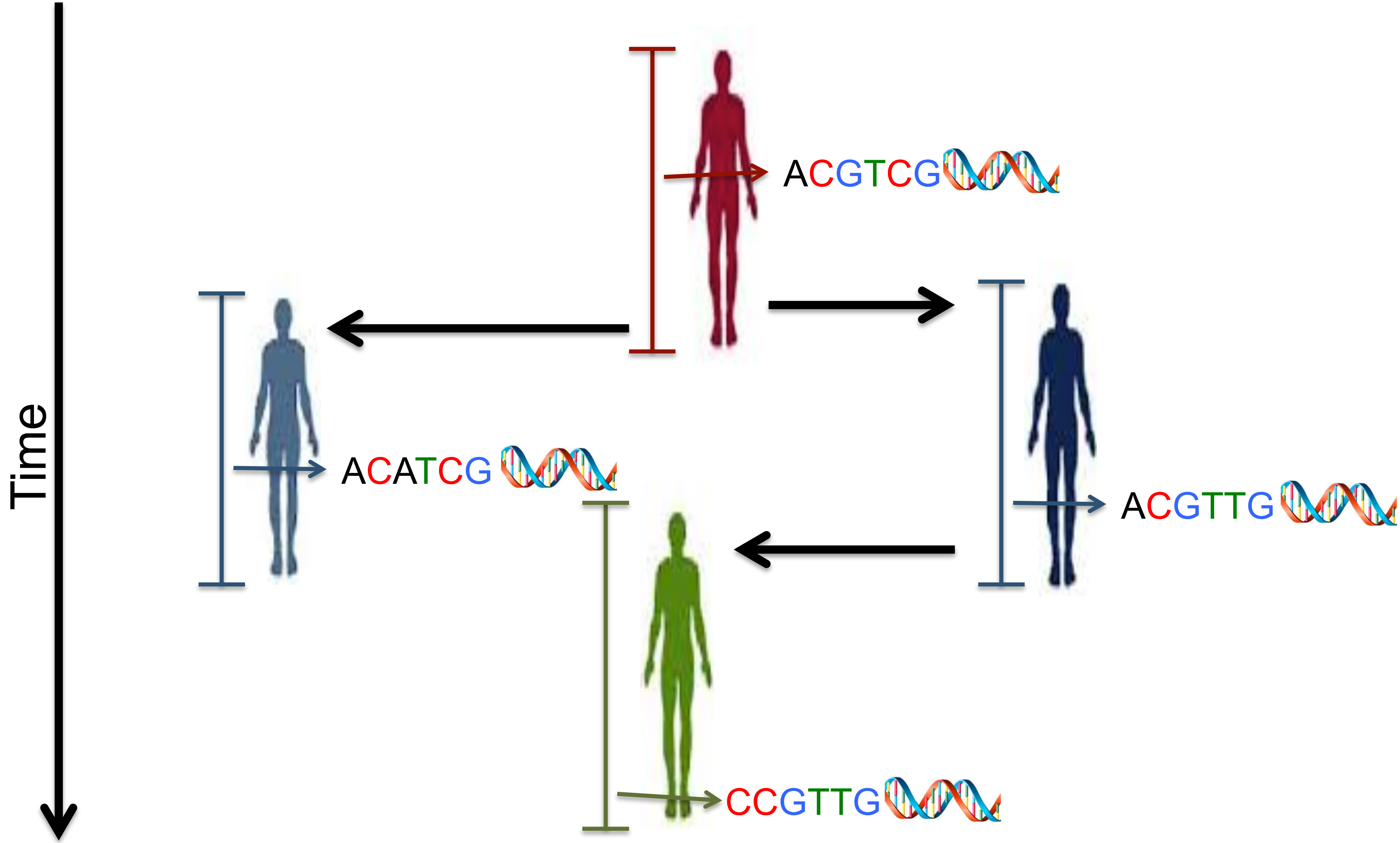
Host information



Time

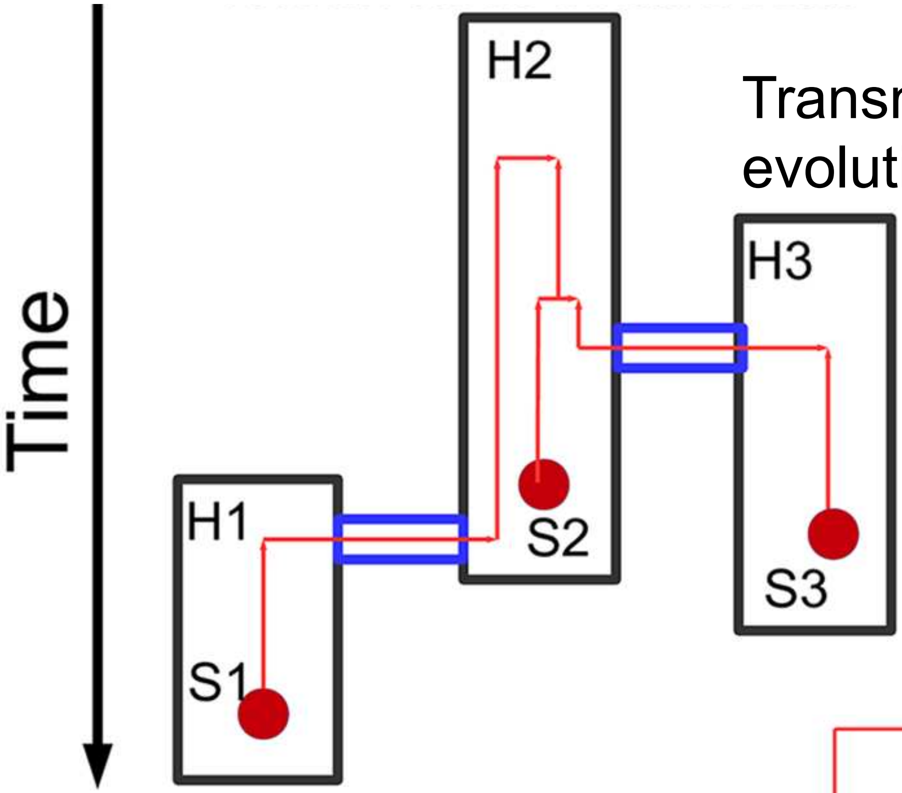
ACGTCG

ACATCG

ACGTTG

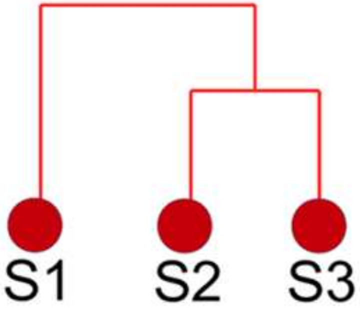
CCGTTG

Complications: within-host coalescent



Transmission and evolution history

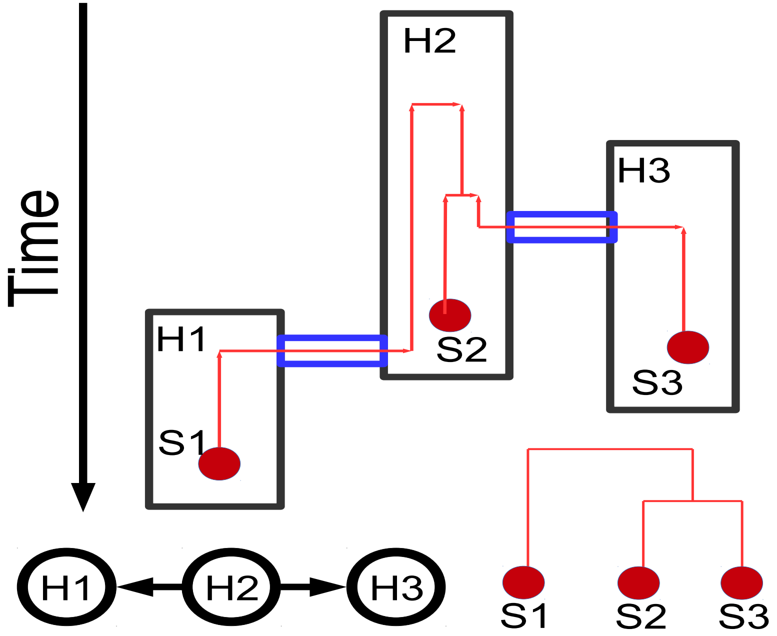
Transmission network



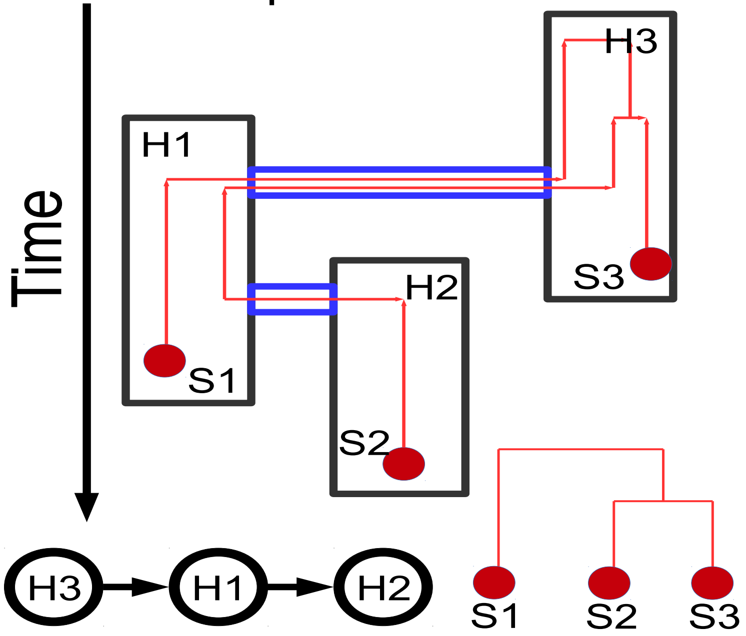
Phylogenetic tree

Complications

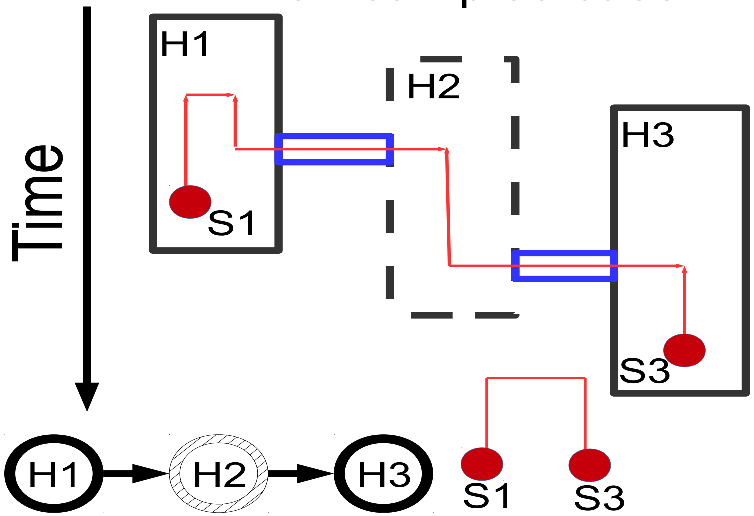
Within-host coalescent



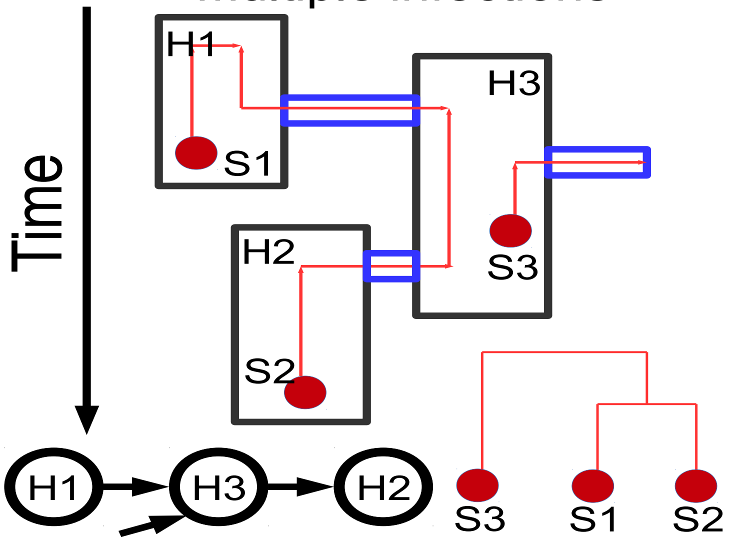
Incomplete bottleneck



Non-sampled case

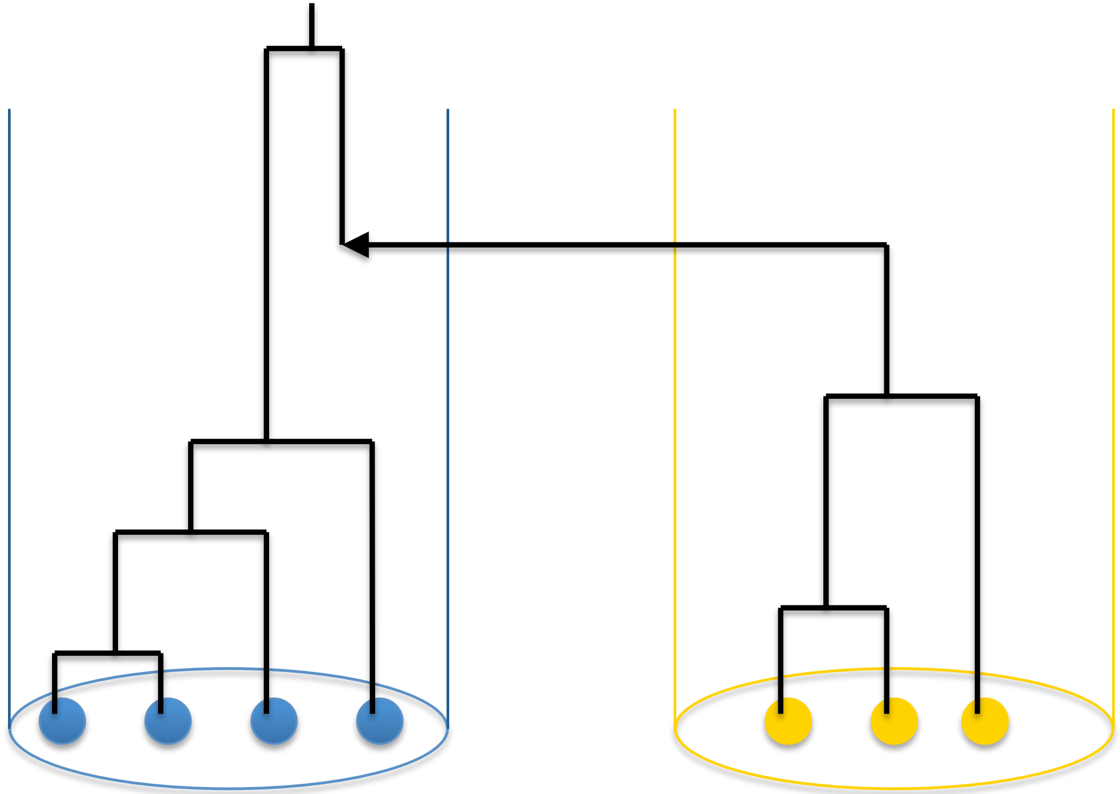


Multiple infections



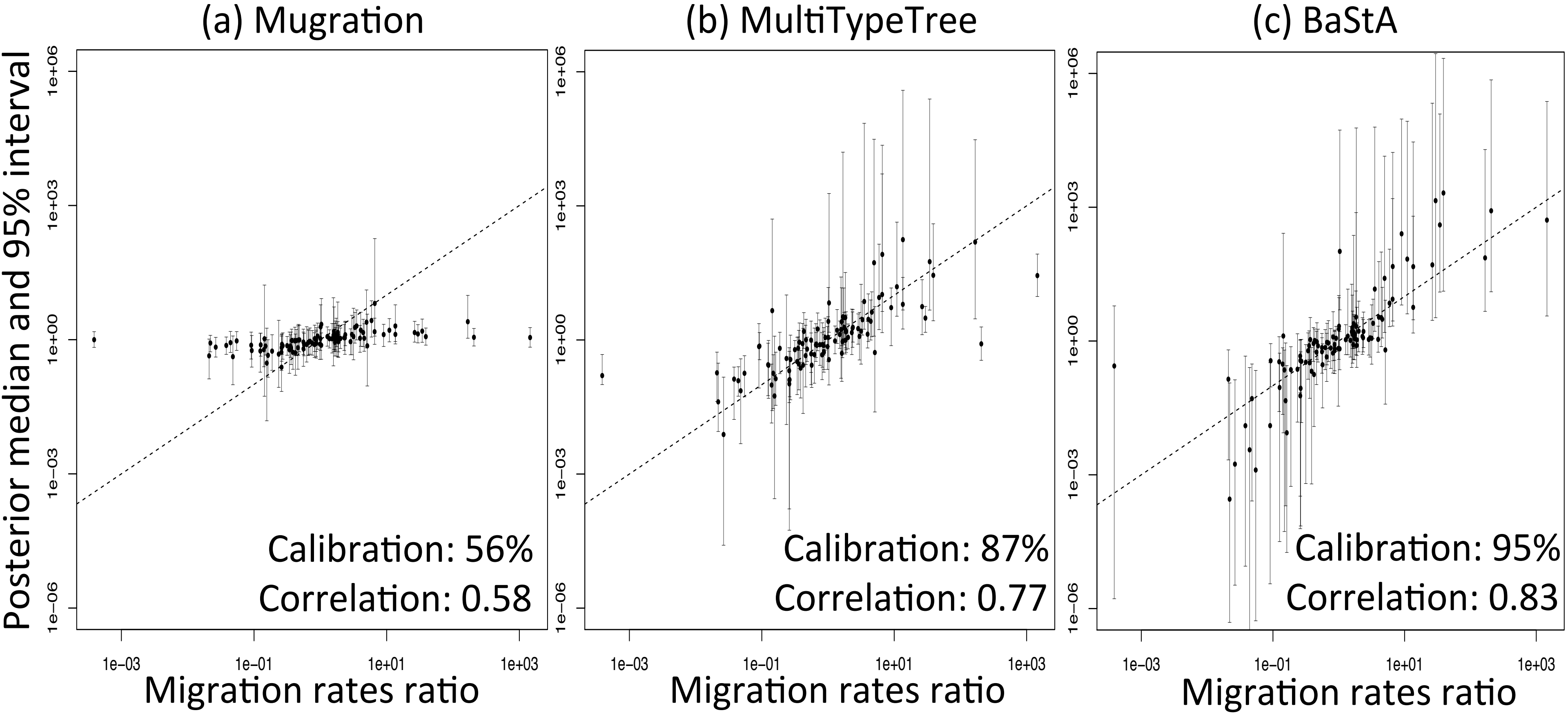
Structured coalescent

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

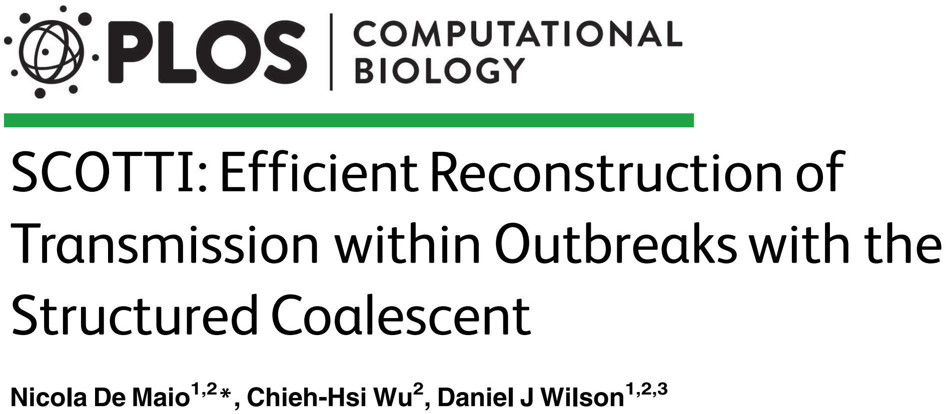


Discrete trait
(Lemey et al 2009)
fast but inaccurate.

Structured coalescent
(Vaughan et al 2014)
accurate but slow.

BASTA
(De Maio et al 2015)
accurate and fast.

SCOTTI

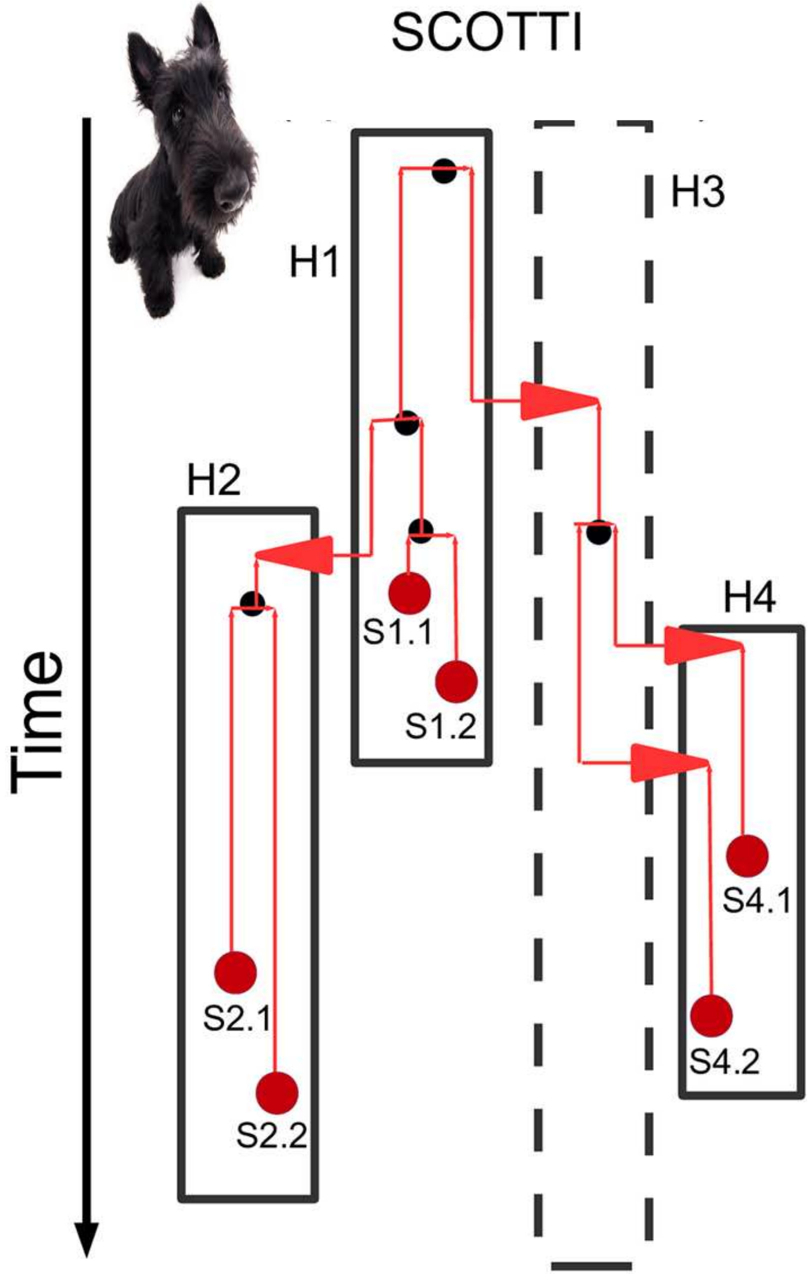


PLOS | COMPUTATIONAL BIOLOGY

SCOTTI: Efficient Reconstruction of Transmission within Outbreaks with the Structured Coalescent

Nicola De Maio[1,2]*, Chieh-Hsi Wu[2], Daniel J Wilson[1,2,3]

- Hosts (demes) have same population size.
- Hosts have limited lifespan.
- No bottlenecks at transmission.
- Lineages do not migrate together at transmission.



Simulated model

Extension of:

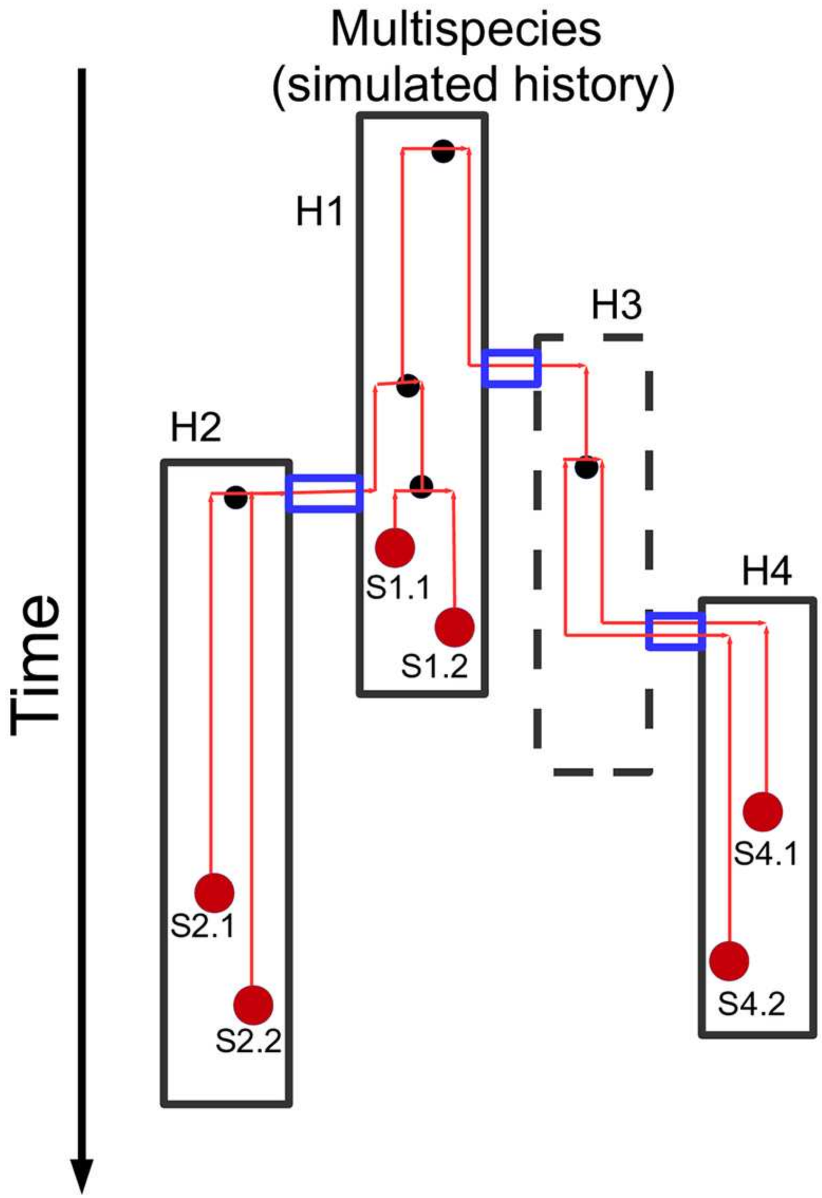
Didelot et al 2014 MBE.

Hall et al 2015
PLOS Comput Biol.

- Bottlenecks at transmission.

- Lineages migrate together at transmission.

- Only one transmission per host.



Benchmark model

Jombart et al 2014 PLOS Comput Biol

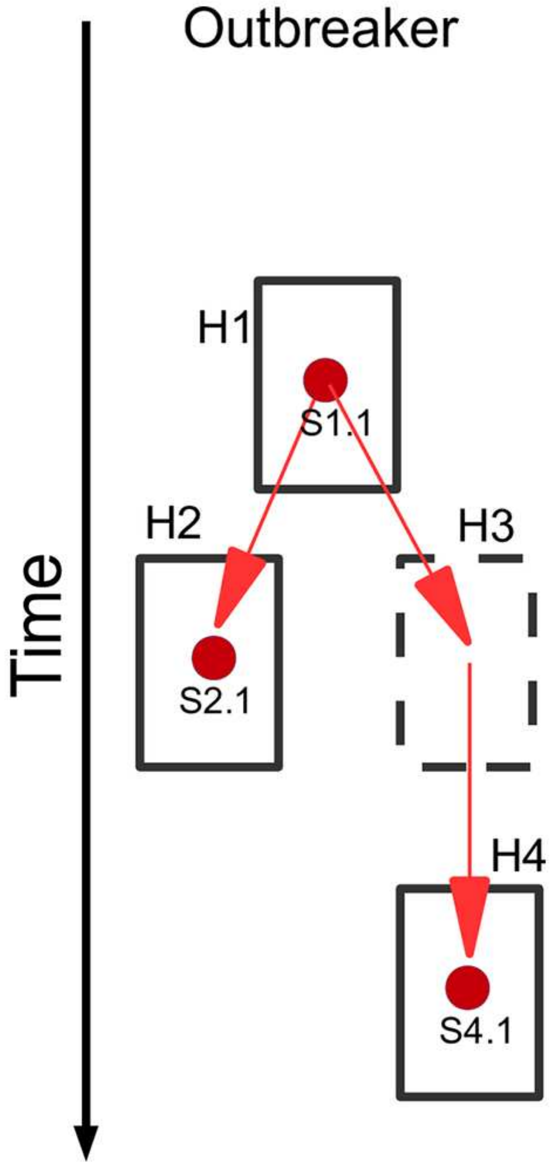
- No within-host population.

- No within-host evolution.

- Mutations accumulate at transmission.

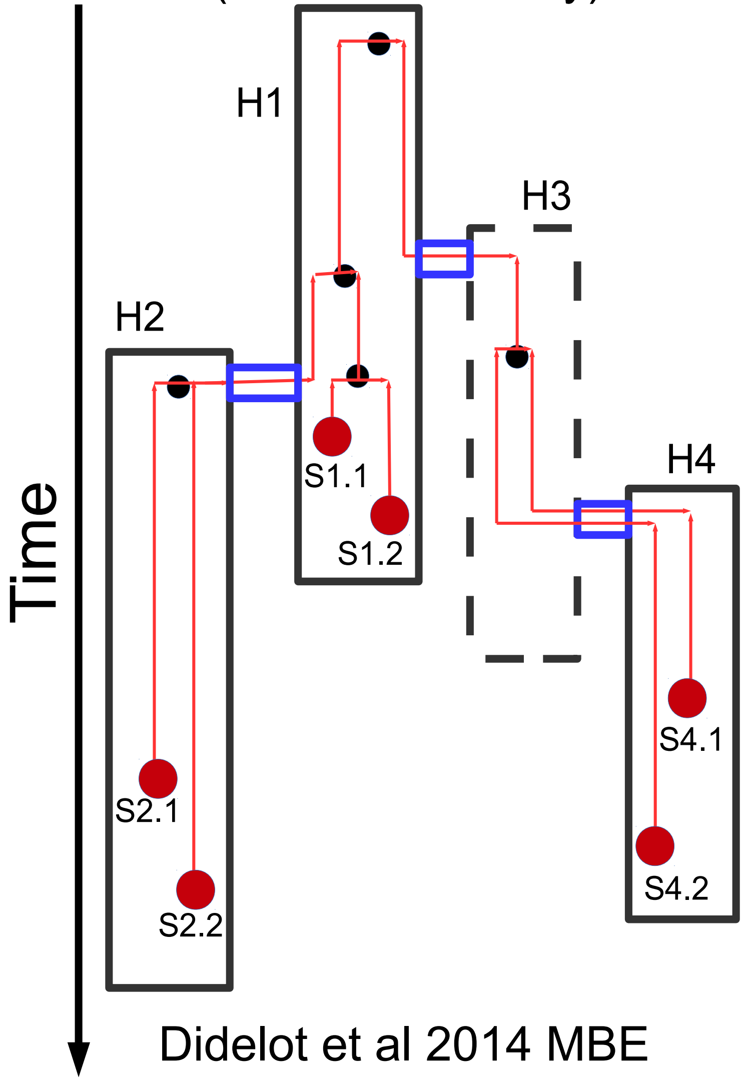
- Only one sample per host.

- Generations of same lengths.



Models used

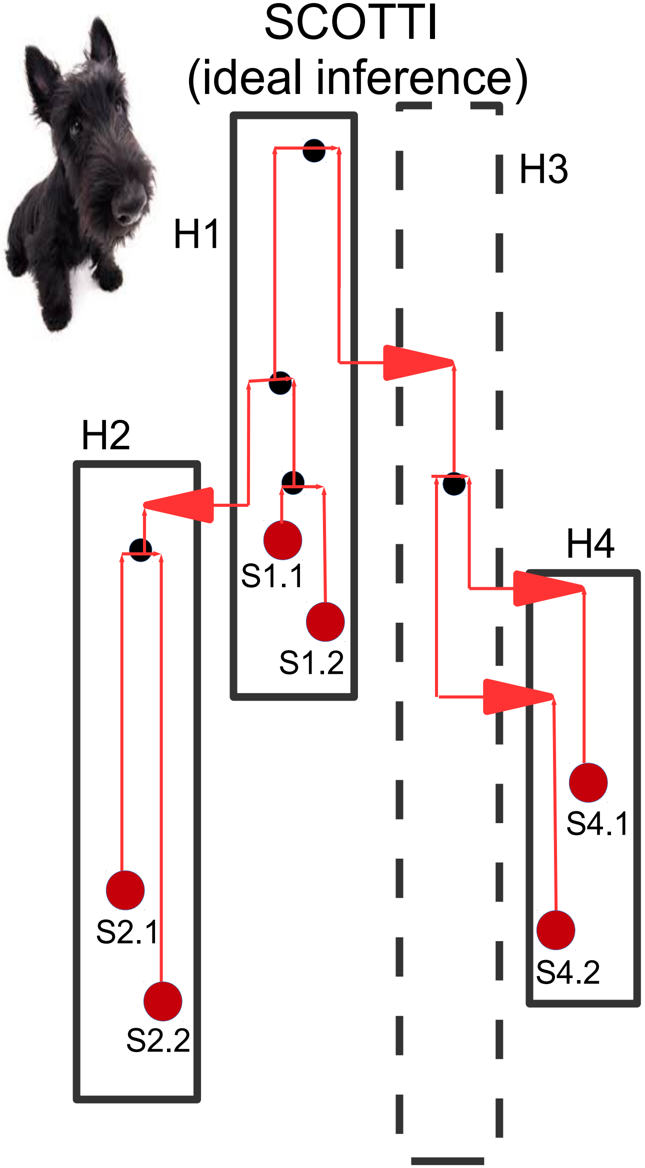
Multispecies
(simulated history)



Didelot et al 2014 MBE

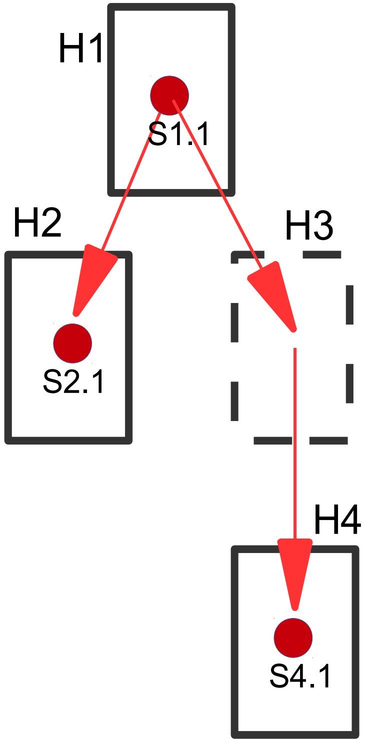
Hall et al 2015 PLOS Comput Biol

SCOTTI
(ideal inference)



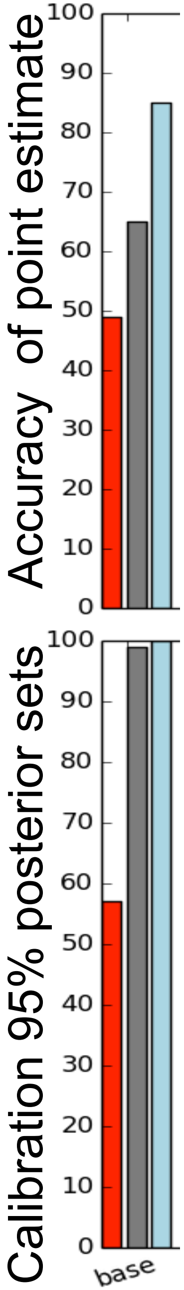
De Maio et al 2016
PLOS Comput Biol

Outbreaker
(ideal inference)



Jombart et al 2014
PLOS Comput Biol

Simulations

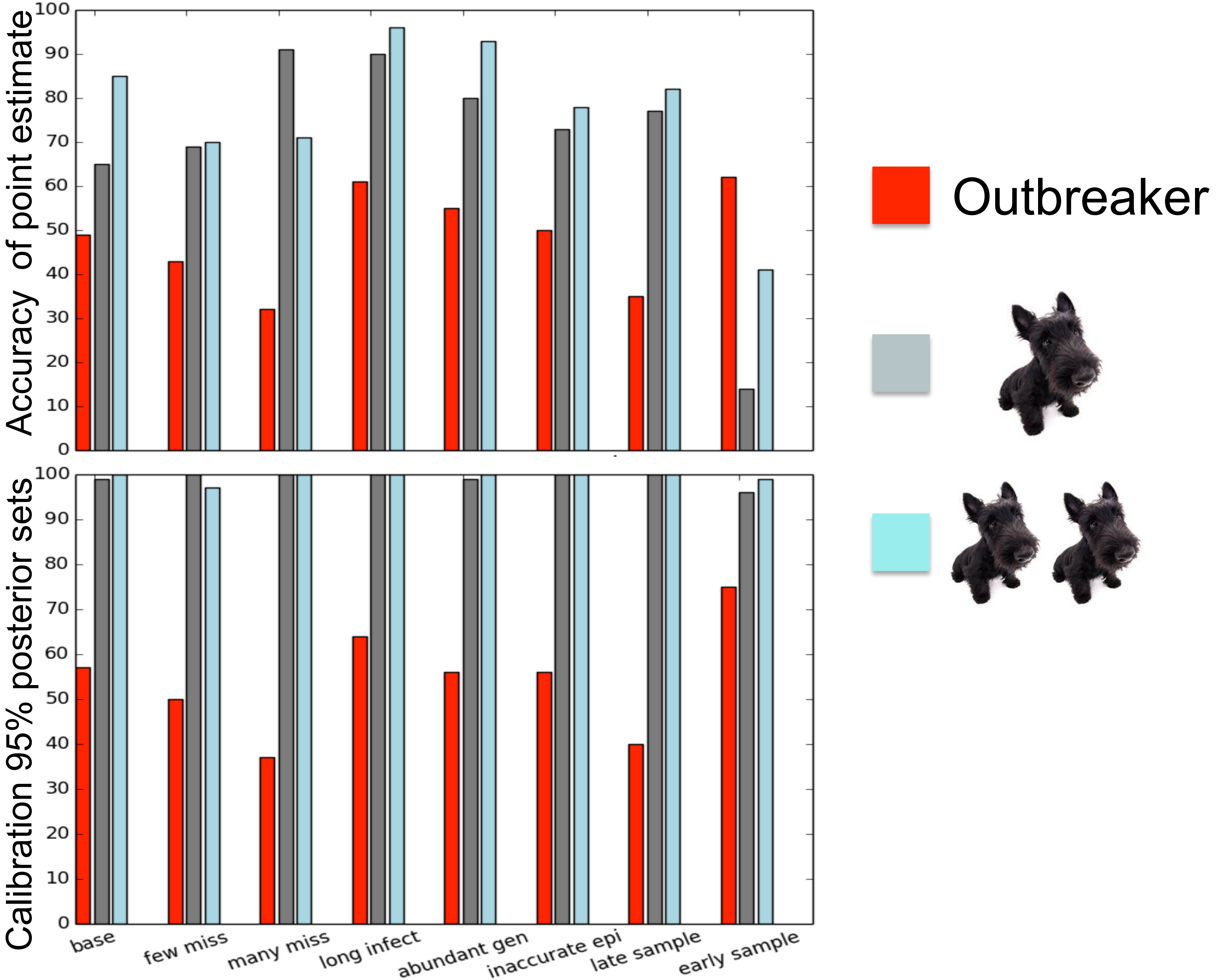


🟥 Outbreaker

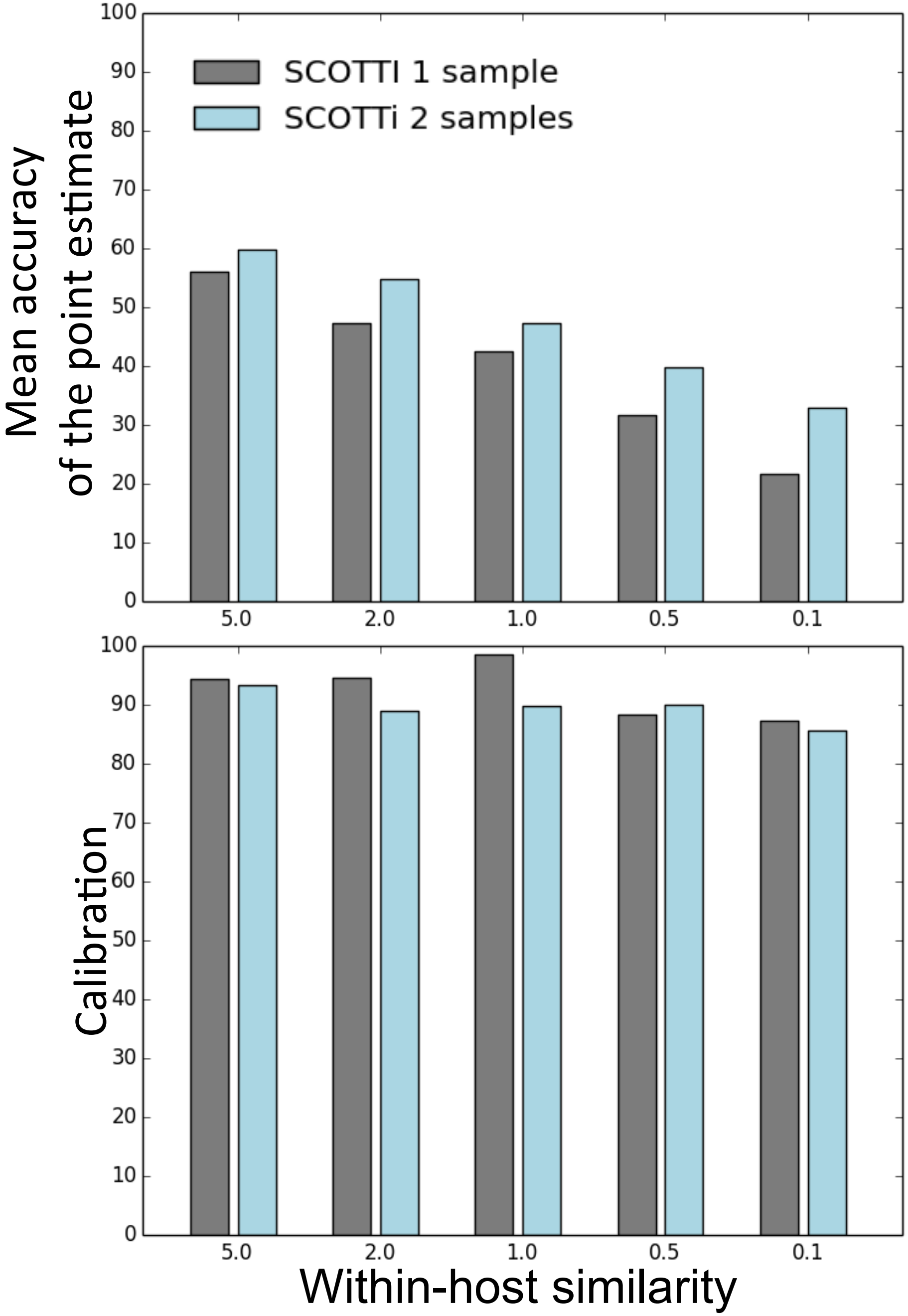
⬜ 

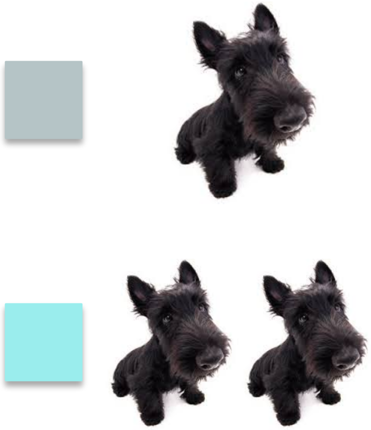
🟦 

Simulations

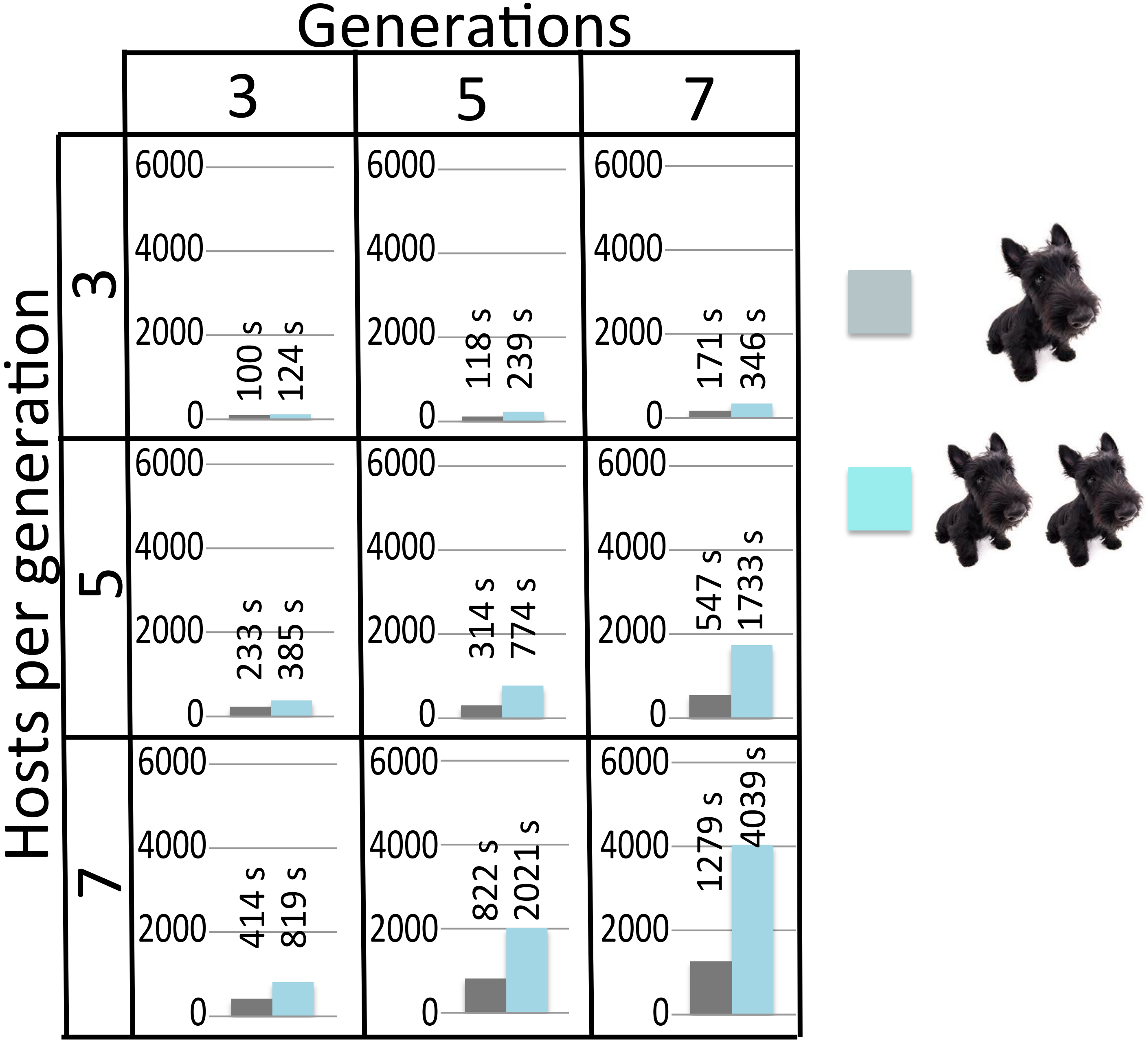


Simulations





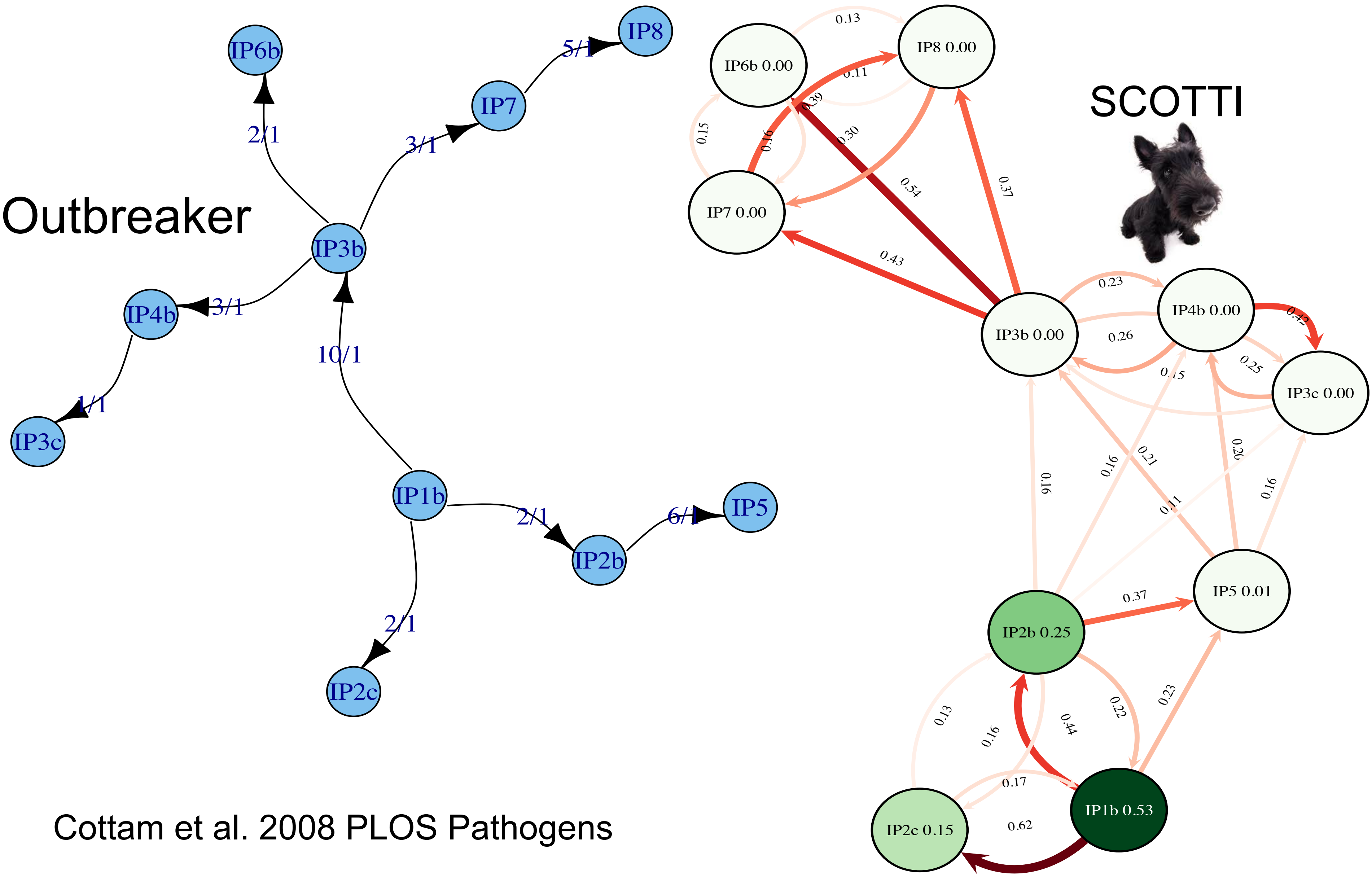
Simulations – Running time



FMDV data

Outbreaker

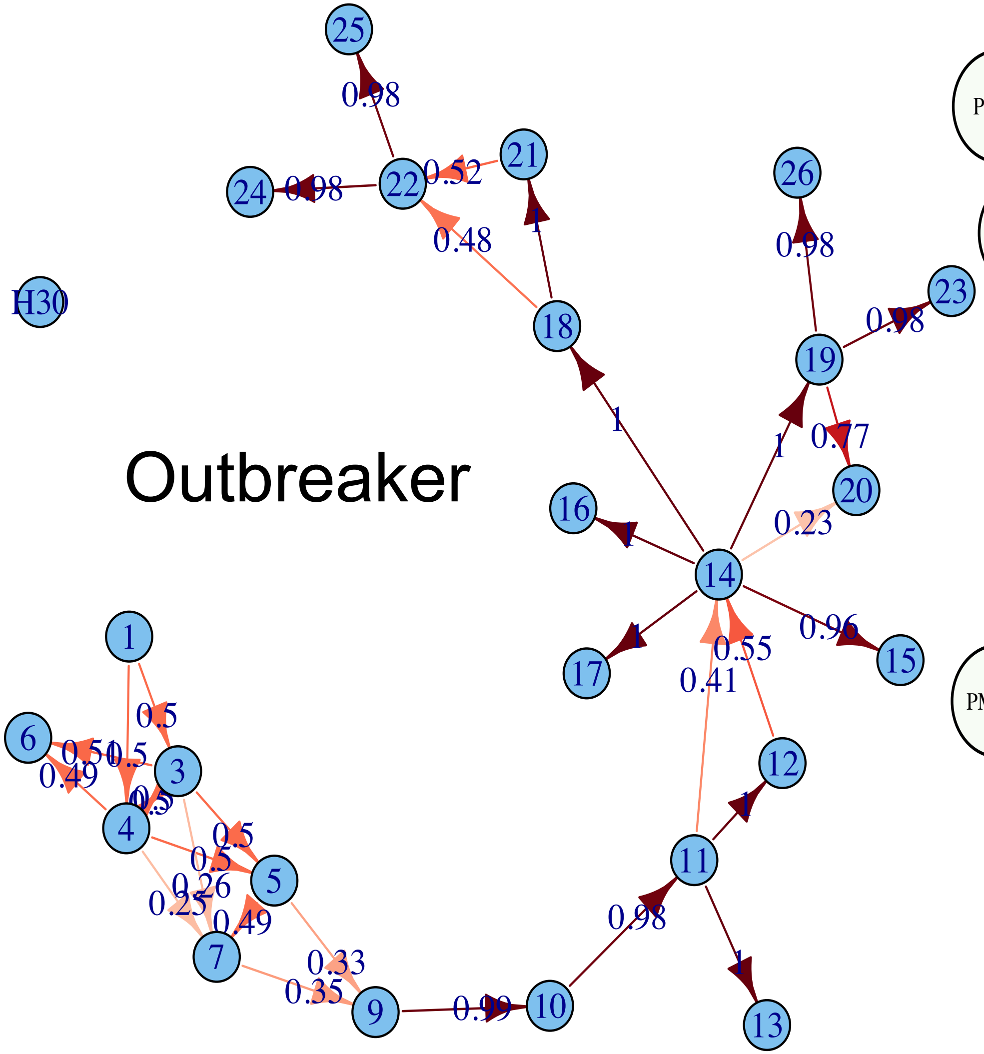
SCOTTI



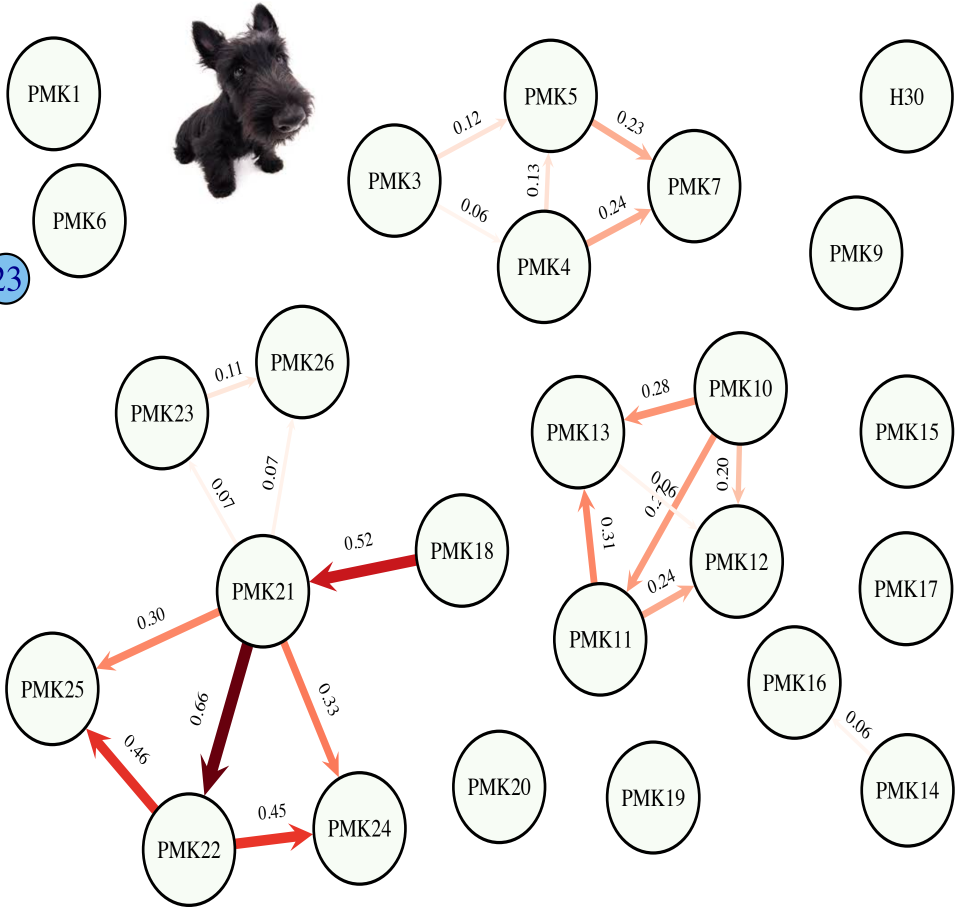
Cottam et al. 2008 PLOS Pathogens

K. Pneumoniae data

Outbreaker

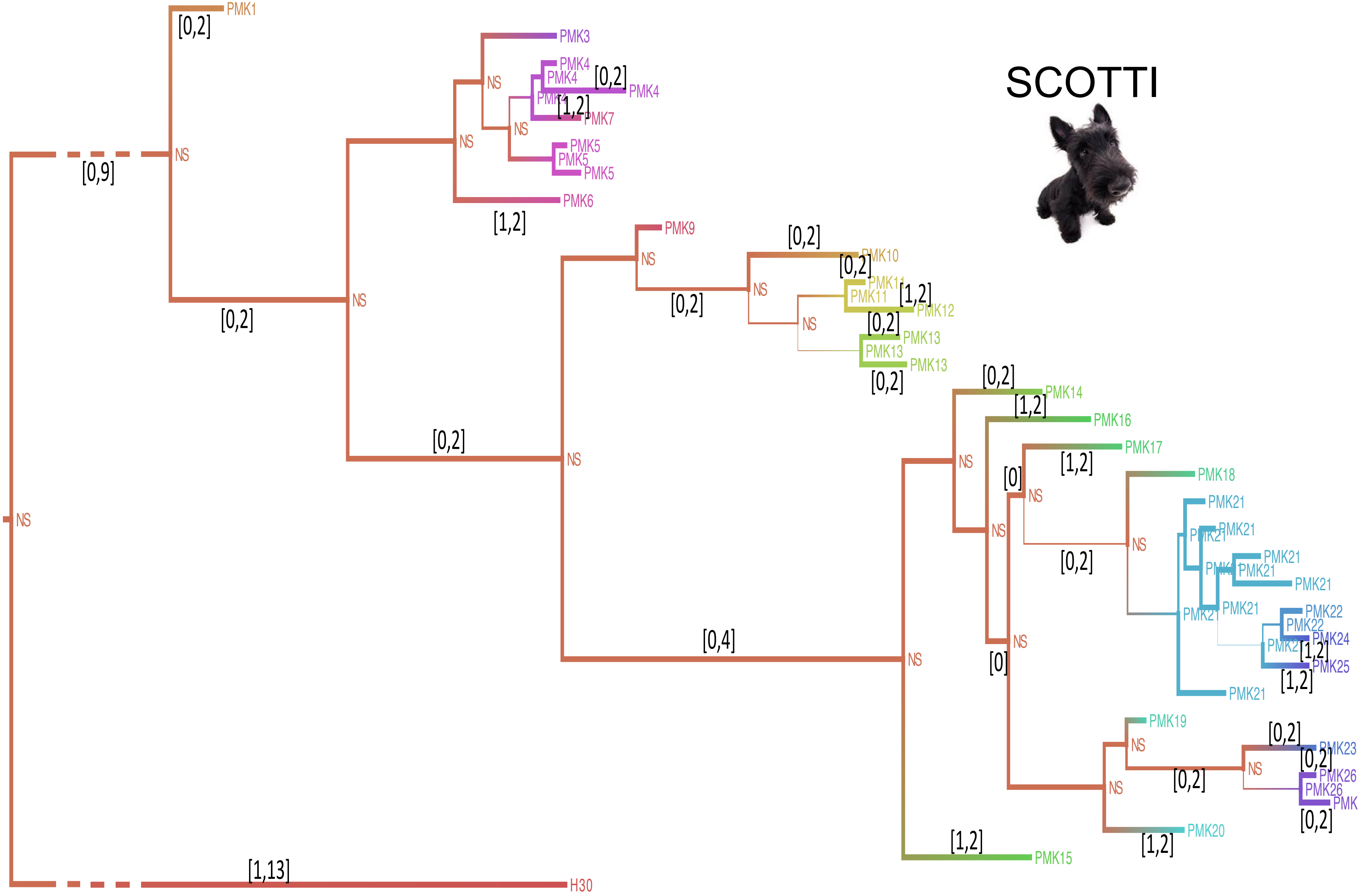


SCOTTI



Stoesser et al. 2014
Antimicrobial agents and chemotherapy

K. Pneumoniae data



SCOTTI

Summary SCOTTI

Different models result in different inferences.

New inference of transmission in BEAST2: SCOTTI.

Future work: transmission bottlenecks, introductions, epidemiological models.

Thanks for listening!

Daniel J Wilson

Chieh-Hsi Wu

Crook group (NDM Microbiology)

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