BADTRIP
Reconstructing Transmission from Within-Host SNPs
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Inferring transmission

Aim: reconstruct the chain of transmissions within an outbreak

Important to understand how to stop transmission.
Within-host diversity

Within-host pathogen is not genetically uniform. We use genetic variants to aid transmission inference.
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PoMo model with sequencing errors and bottlenecks.

Sequencing:
H1: 23 A, 0 C, 0 G, 1 T
H2: 3 A, 0 C, 4 G, 0 T

Time
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Time

$H_1$

$H_1_i \rightarrow l_{H_1} = \emptyset \rightarrow t_{H_1} \rightarrow H_1_i$

$G_{S1,1} = 4,0,0,0$

$H_1_r \rightarrow t_{S1} \rightarrow t_{H_2} \rightarrow H_2_i$

$H_2$

$l_{H_2} = H_1 \rightarrow H_2_i$

$H_2_r \rightarrow t_{H_2} \rightarrow H_2_i$

$H_3$

$l_{H_3} = H_2 \rightarrow H_3_i$

$H_3_r \rightarrow t_{H_3} \rightarrow H_3_i$

$G_{S2,1} = 4,0,40,1$

$t_{S2}$

$G_{S3,1} = 0,0,3,0$

$t_{S3}$
Simulations

Combining epidemiological data and between and within-host genetic diversity increases accuracy.
Summary

• Within-host pathogen diversity aids transmission reconstruction, in particular combined with epidemiological data.

• An explicit probabilistic model of pathogen population evolution increases power and robustness.

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