

Simulation study to test vivax genetic relatedness model

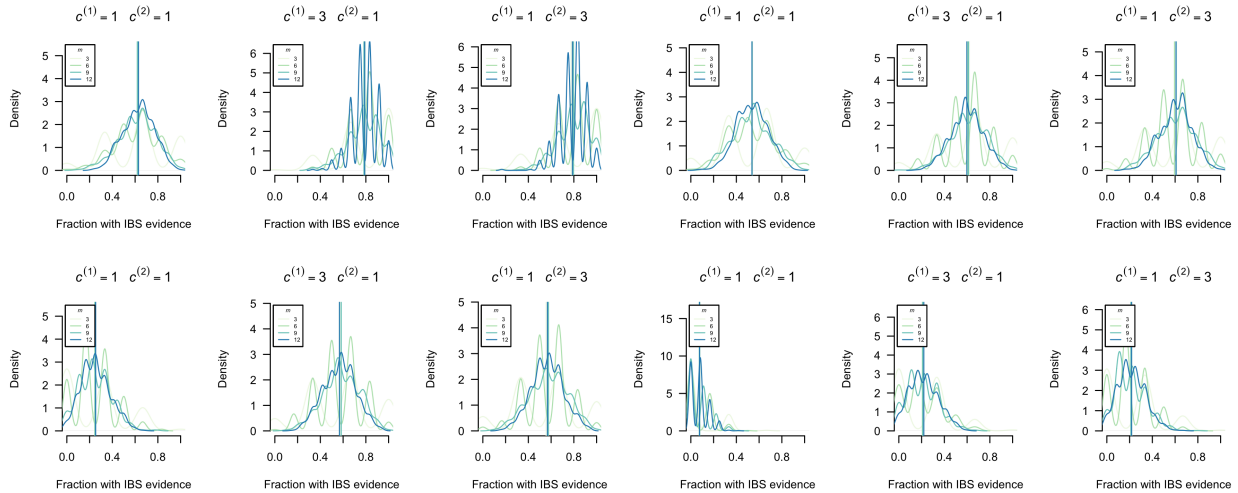
Reviewer's example: "a recurrence with MOI of 3, containing a clone and two unrelated strains, but with overall pairwise relatedness close to 0.5."

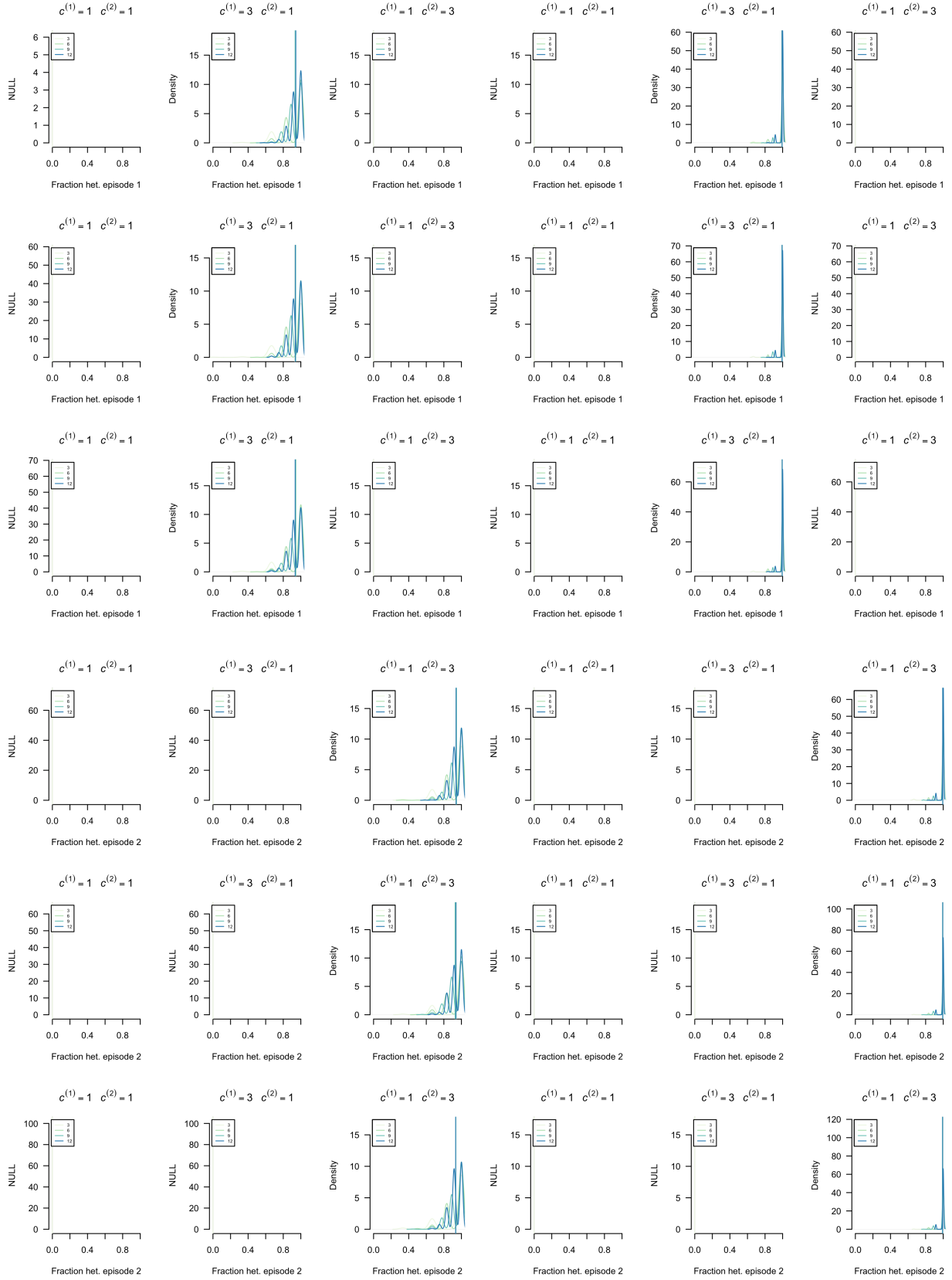
Simulation 1: Effective Complexity of Infection

We want to assess recurrence state inference as a function of the number of markers typed, adding extra noisy parasites into an infections with $\text{COI} > 1$. Outline of simulation is as follows: for each "job",

- Simulate data for N individuals, with M markers for two episodes, the second including a clonal, sibling or stranger parasite.
- Summarise the simulated data with a series of plots.
- Compute resulting recurrence state estimates (this is currently done in a separate file)
- Plot resulting recurrence state estimates as a function m

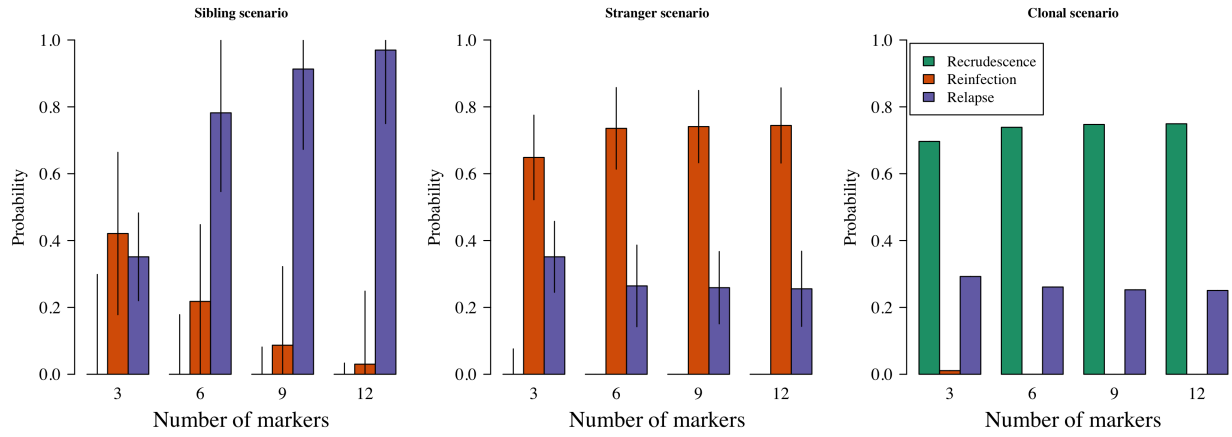
Note that when we previously specified a cut off for the number of heterolallelic calls ($K_{\text{poly_markers}} < M$), we were unwittingly amplifying evidence for relapse because when $M \leq K_{\text{poly_markers}}$ the noisy parasite will be a stranger in relation to the other parasites in the same infection; when $K_{\text{poly_markers}} \approx 0.5 \cdot M$ the noisy parasite will be more like a sibling of the other parasites in the same infection; when $K_{\text{poly_markers}} \ll M$, the noisy parasite will approach a clone of the other parasites in the same infection, but will be considered a sibling under the model.



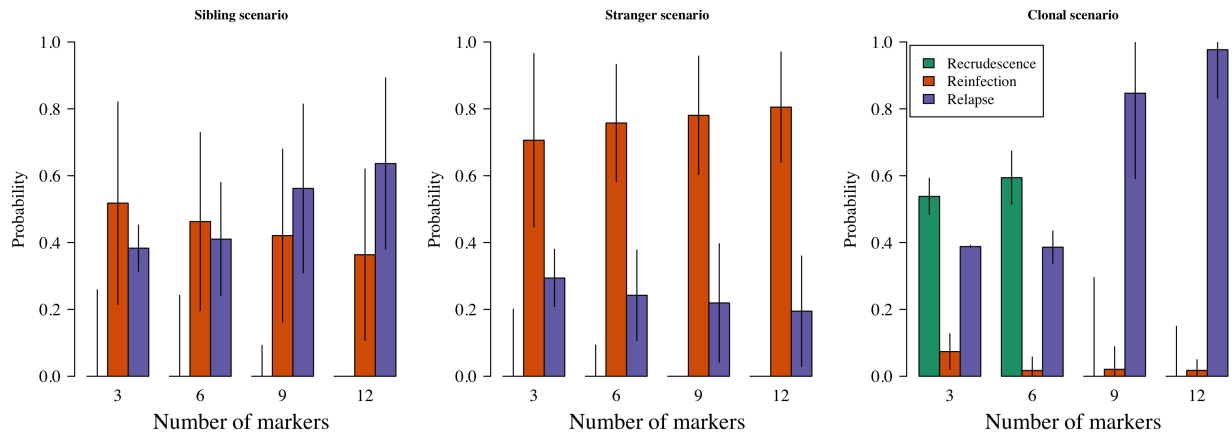


Plot results

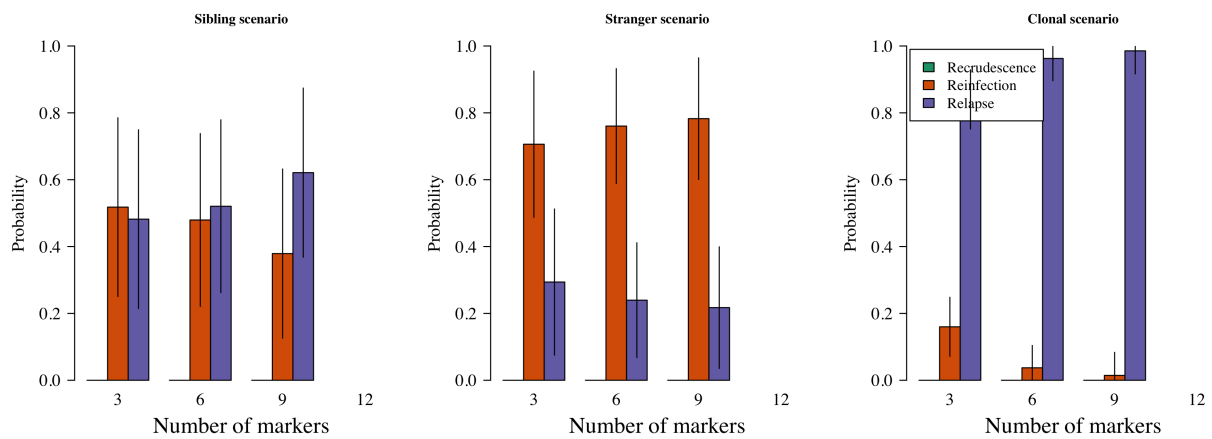
Marker cardinality: 4
COI of first and second infection: 1 and 1, respectively



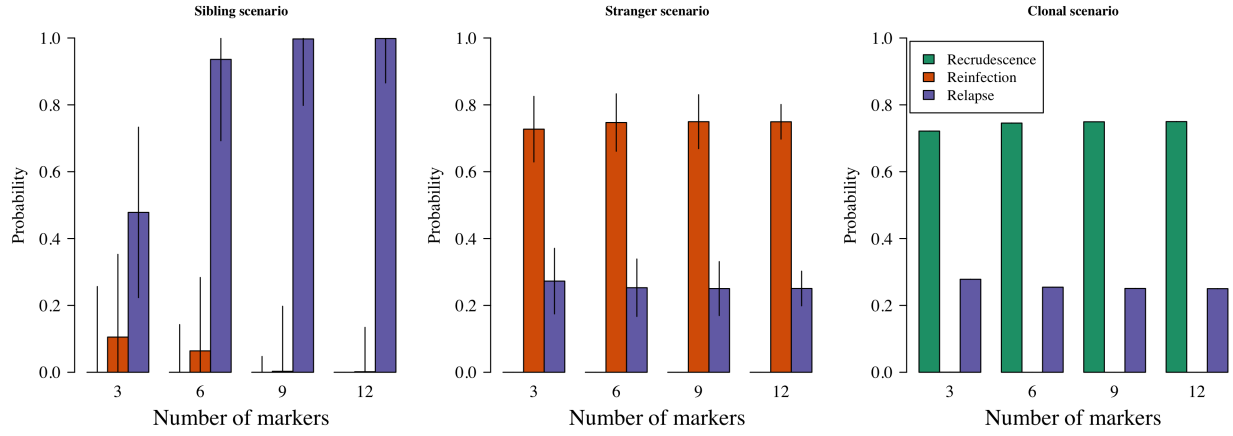
Marker cardinality: 4
COI of first and second infection: 3 and 1, respectively



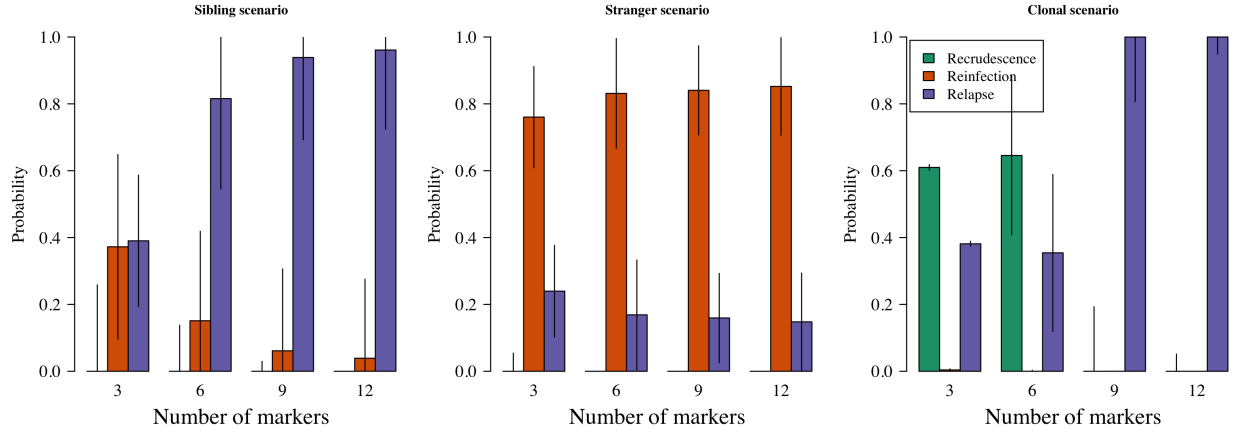
Marker cardinality: 4
COI of first and second infection: 1 and 3, respectively



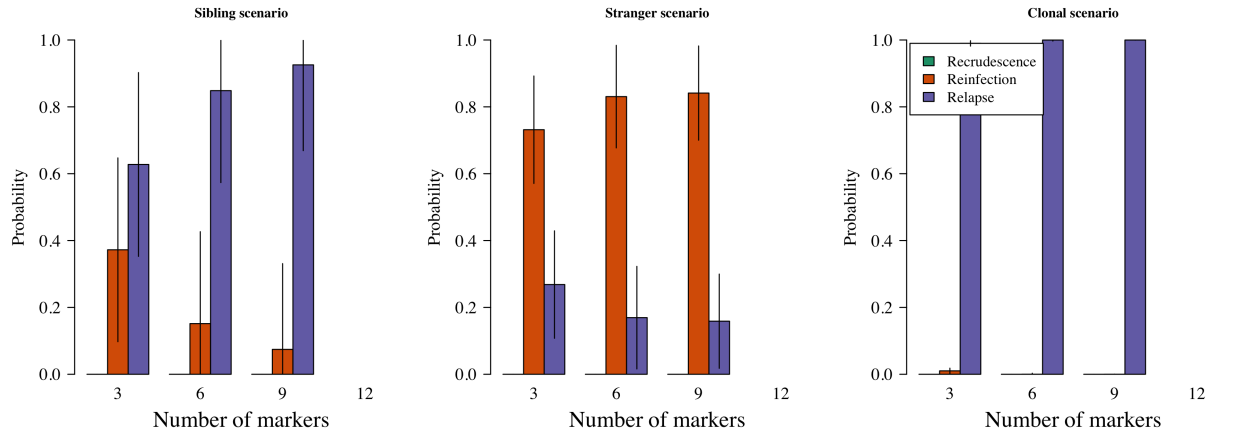
Marker cardinality: 13
COI of first and second infection: 1 and 1, respectively



Marker cardinality: 13
COI of first and second infection: 3 and 1, respectively



Marker cardinality: 13
COI of first and second infection: 1 and 3, respectively



1.379 sec elapsed