

## S1 Algorithmic description of the Bayesian inference procedure

Algorithm S1 summarises the Markov chain Monte Carlo scheme used to jointly sample model parameters and individual-level hidden infection states. The tuning of this algorithm is described in the main text. The initial state probabilities correspond to the parameters  $\delta_{S0}^1, \delta_{I0}^1, \delta_{ID0}^1, \delta_{D0}^1, \delta_{S1}^1, \delta_{I1}^1, \delta_{ID1}^1, \delta_{D1}^1, \delta_{S0}^2, \delta_{I0}^2, \delta_{ID0}^2, \delta_{D0}^2, \delta_{S1}^2, \delta_{I1}^2, \delta_{ID1}^2$ , and  $\delta_{D1}^2$ . The diagnostic sensitivities and specificities correspond to the parameters  $\phi_{PCR}, \psi_{PCR}, \phi_{ADT}, \psi_{ADT}, \phi_{CEX}$ , and  $\psi_{CEX}$ . For the mean duration parameters  $\mu_I, \mu_{ID0}, \mu_{ID1}, \mu_{D0}$ , and  $\mu_{D1}$ , which are distributed according to a translated negative binomial distribution, we re-parametrise to the probability parameters of the negative binomial distributions, here denoted as  $\zeta_I, \zeta_{ID0}, \zeta_{ID1}, \zeta_{D0}$ , and  $\zeta_{D1}$ . These are related according to

$$\mu = 1 + \frac{2(1 - \zeta)}{\zeta},$$

where 2 is the size parameter of the negative binomial distribution. When updates are undertaken using random-walk Metropolis proposals, this is shortened to RWM.

The hidden infection states are updated using the individual forward-filter backward-sampler algorithm (IFFBS) [1]. Semi-Markov dynamics arising from negative binomial durations are handled by proposing trajectories from an equivalent Markov model and applying a Metropolis–Hastings correction, ensuring that posterior samples are drawn exactly from the semi-Markov target distribution. The full technical details of this portion of the algorithm can be found in [1].

## References

1. Touloupou P, Finkenstädt B, Spencer SEF. Scalable Bayesian inference for coupled hidden Markov and semi-Markov models. *Journal of Computational and Graphical Statistics*. 2019;29(2):238-49. doi:10.1080/10618600.2019.1654880.



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**Algorithm S1** Bayesian inference for the individual-level trachoma model

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1: Input: Diagnostic data, household structure, ages, prior distributions
2: Output: Posterior samples of parameters and hidden infection states

3: Initialise model parameters
4: Initialise hidden infection states
5: for  $m = 1$  to  $M$  do ▷ MCMC iterations
6:   // Update model parameters given hidden states
7:   Update unknown ages using independence Metropolis proposals
8:   Update initial state probabilities via Gibbs sampling
9:   Update diagnostic sensitivities and specificities via Gibbs sampling
10:  Update historic infection rate parameter  $\gamma^1$  using a RWM proposal
11:  Update historic infection rate parameter  $\gamma^2$  using a RWM proposal
12:  Update transmission parameters  $\beta_1^1, \beta_2^1, \beta_3^1$  using RWM proposals in
    a single block
13:  Update transmission parameters  $\beta_1^2, \beta_2^2, \beta_3^2$  using RWM proposals in
    a single block
14:  Update probability parameter  $\zeta_I$  using a RWM proposal
15:  Update probability parameter  $\zeta_{ID0}$  using a RWM proposal
16:  Update probability parameter  $\zeta_{ID1}$  using a RWM proposal
17:  Update probability parameter  $\zeta_{D0}$  using a RWM proposal
18:  Update probability parameter  $\zeta_{D1}$  using a RWM proposal
19:  Update reinfection parameter  $\rho$  using a RWM proposal
20:  Update length-biasing reinfection probability parameter  $\alpha^1$  using a
    RWM proposal
21:  Update length-biasing reinfection probability parameter  $\alpha^2$  using a
    RWM proposal
22:   // Update hidden states given model parameters (IFFBS)
23:   for each individual  $i = 1, \dots, N$  do
24:     Construct a Markovian proposal model for the hidden states, re-
        placing semi-Markov durations with geometric durations
25:     Run modified forward filtering algorithm, conditioning on the
        hidden states of other individuals
26:     Sample hidden states via backward sampling
27:     Accept or reject hidden states using MH correction
28:   end for
29:   Store posterior samples
30: end for
31: return posterior samples
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