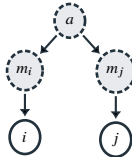


Observed Pairwise DataTesting-time difference: t_{ij} Consensus genetic distance: g_{ij} **LATENT TRANSMISSION SCENARIOS (S_M)****Ancestor-Descendant $H_{AD}(m)$** Direct transmission $i \rightarrow j$, $m = 0$ **Common Ancestor $H_{CA}(m_i, m_j)$** Co-primary infection $(m_i, m_j) = (0, 0)$ **Natural-history Model**Gamma stages ($E/P/I$)Incubation period: $\tau_{\text{inc}} = y_E + y_P$ Generation time: $\tau_{\text{gen}} = \tau_{\text{inc}} + y_{\text{toit}}$ Testing delay: x_{test} Clock rate: $\lambda = \nu L/365$ (strict or relaxed)**MC Temporal Draws**AD: $T_s = \sum_{r=0}^m \tau_{\text{gen},r} + \tau_{\text{obs},j} - \tau_{\text{obs},i}$ CA: $T_s = \sum_{s=1}^{m_j+1} \tau_{\text{gen},s}^{(j)} - \sum_{r=1}^{m_i+1} \tau_{\text{gen},r}^{(i)} + \tau_{\text{obs},j} - \tau_{\text{obs},i}$ *Signed difference for temporal ordering***Temporal Compatibility**

$$C_{T,s} = 1 - 2|\Pr(T_s \leq t_{ij}) - 0.5|$$

**MC Genetic Draws**AD: $B_s = \sum \tau_{\text{gen}} + \tau_{\text{inc},j} + \tau_{\text{obs},j} - \tau_{\text{obs},i}$ CA: $B_s = \sum \tau_{\text{gen}} + \sum \tau_{\text{gen}}^{(j)} + \tau_{\text{obs},i} + \tau_{\text{obs},j}$ Deterministic: $G_s = \lambda B_s$ or stochastic: $G_s \sim \text{Poisson}(\lambda B_s)$ **Genetic Compatibility**

$$C_{G,s} = 1 - 2|\Pr(G_s \leq g_{ij}) - 0.5|$$

**Aggregated Compatibility Score**Scenario: $C_s(i, j) = C_{T,s} \cdot C_{G,s}$ Target Set: $C_{S_*}(i, j) = \sum_{s \in S_*} C_s(i, j)$