Recall that we are integrating

$$\int d\bar{z} P(data|\bar{z}, s) P(s) P(\bar{z}|s) \tag{1}$$

where s is the infection ordering, and $\bar{z}$ are the actual infection times. Also note that for any s we can explicitly compute $P(s)$. This is simply the product of the term on the far right of mcmc_calc.pdf (equation 2 below for convenience).

$$P(s_2, \bar{z_2}|s_1.z_1 = 0) = \lambda(1)e^{-\lambda(1)(\bar{z_2}-\bar{z_1})} \times \frac{\lambda(1,2)}{\lambda(1)} \tag{2}$$

(from mcmc_calc.tex) "as in the Gillespie algorithm – the expression on the RHS equals the probability that the first transition among all the nodes that are connected to s_1 occurs at the time $\bar{z_2}$, times the probability that it is node s_2 that makes that transition). "

Also, note that if we knew the infection ordering s we would be able to draw from the distribution of the infection times. To do so we sample the infection time, $\bar{z_2}$ of s_2 from an exponential distribution that is truncated at T. Then we would sample z_3 from $\bar{z_2}$ + an exponential random variable truncated at $T - \bar{z_2}$. Proceeding in this way, we can sample all of the infection times from their true distribution given s.

The implication for the MCMC is that we do not need to accept/reject based on the infection times $\bar{z}$ but instead accept and reject based only on the node ordering s and for each s, we can compute $P(data|z, s)P(z)$ by simple monte carlo. The pseudo code would be as follows:

- Create a set S that contains all allowable node infection orderings of size $M \leq N$.

- likelihoods-given-s $\rightarrow$ []

- **Draw** a starting value $\hat{s}$ from S

- **for** order-sample **in** 1:number of mcmc samples
    - **Draw** $\widetilde{s}$ from S
    - **if** $\frac{P(\widetilde{s})}{P(\hat{s})} > U$
        * $\hat{s} = \widetilde{s}$
    - samples-given-s $\rightarrow$ []
    - **for** time-sample **in** 1: number of samples per ordering
        * **Draw** $\bar{z}$ from $P(\bar{z}|\hat{s})$ by the method above.
        * **append** $P(\text{data } |\bar{z}, \hat{s})$ to samples-given-s
    - **append** mean(samples-given-s) to likelihoods-given-s

- **return** mean(likelihoods-given-s)