# File S1 Conditional posterior densities of the dnIGE model parameters

Using the joint posterior distribution of the dnIGE model parameters, it can be found that the conditional posterior distributions of the variances are

$$\sigma^2_{S,g}|\cdot \sim \text{IG}\left(S/2 + \alpha_{S,g}, \frac{\boldsymbol{a}_g^\top \boldsymbol{a}_g}{2} + \nu_{S,g}\right), \quad (1)$$

$$\sigma^2_{S,f}|\cdot \sim \text{IG}\left(S/2 + \alpha_{S,f}, \frac{\boldsymbol{a}_f^\top \boldsymbol{a}_f}{2} + \nu_{S,f}\right), \quad (2)$$

$$\sigma^2_{E,g}|\cdot \sim \text{IG}\left((N - n_0)/2 + \alpha_{E,g}, \frac{\boldsymbol{e}_g^\top \boldsymbol{e}_g}{2} + \nu_{E,g}\right), \quad (3)$$

and

$$\sigma^2_{E,f}|\cdot \sim \text{IG}\left(I_f/2 + \alpha_{E,f}, \frac{\boldsymbol{e}_f^\top \boldsymbol{e}_f}{2} + \nu_{E,f}\right). \quad (4)$$

Therefore samples from the conditional posteriors of the variances can be obtained by applying the Gibbs sampling algorithm. This algorithm can also be used to sample from the conditional posterior distribution of $\beta$, which is a gamma distribution such that

$$\beta|\cdot \sim \text{Gamma}\left(a + I - n_0, b + \sum_{j:h_j=1} g_j \sum_{k:p_k=p_j} (\tau_j - \tau_k) f_k l_k(\tau_j)\right). \quad (5)$$

In the conditional posterior of the susceptibility additive genetic effect of each sire $i$, the log-likelihood was evaluated only for the offspring of $i$ which are not index cases. These animals are represented by the set $l_{g,i} = \{j : h_j = 1 \cap s(j) = i\}$. Hence, the log-conditional posterior of $a_{g,i}$, $i = 1, \ldots, S$, is,

$$\begin{aligned}\log(p(\boldsymbol{a}_{g,i}|\cdot)) &\propto \log(L(\boldsymbol{\theta})p(\boldsymbol{a}_g|\sigma^2_{A,g})) \\ &\propto \sum_{\substack{j:j\in l_{g,i}\\ \tau_j\le T}} a_{g,s(j)} - \beta \sum_{\substack{j:j\in l_{g,i}\\ \tau_j\le T}} \mathrm{e}^{a_{g,s(j)}+e_{g,j}} \sum_{k:p_k=p_j} (\tau_j-\tau_k) l_k(\tau_j) \mathrm{e}^{a_{f,s(k)}+e_{f,k}} \\ &- \beta \sum_{\substack{j:j\in l_{g,i}\\ \tau_j> T}} \mathrm{e}^{a_{g,s(j)}+e_{g,j}} \sum_{k:p_k=p_j} (T-\tau_k) l_k(\tau_j) \mathrm{e}^{a_{f,s(k)}+e_{f,k}} - \frac{a^2_{g,i}}{2\sigma^2_{S,g}}.\end{aligned} \tag{6}$$

Additionally, in the conditional posterior of the infectivity additive genetic effect of each sire $i$, the log-likelihood is evaluated for each animal $j$ that has a group mate who is an offspring of sire $i$ and infected before $j$. These animals are represented by the set

$$l_{f,i} = \{j : \tau_j > \min\{\tau_k : p_k = p_j \cap s(k) = i\}\}$$

Hence the log-conditional posterior of $a_{f,i}$, $i = 1, \ldots, S$ is,

$$\begin{aligned}\log(p(\boldsymbol{a}_{f,i}|\cdot)) &\propto \log(L(\boldsymbol{\theta})p(\boldsymbol{a}_f|\sigma^2_{A,f})) \\ &\propto \sum_{\substack{j:j\in l_{f,i}\\ \tau_j\le T}} \log\left[\sum_{k:p_k=p_j} l_k(\tau_j)\mathrm{e}^{a_{f,s(k)}+e_{f,k}}\right] \\ &- \beta \sum_{\substack{j:j\in l_{f,i}\\ \tau_j\le T}} \mathrm{e}^{a_{g,s(j)}+e_{g,j}} \sum_{k:p_k=p_j} (\tau_j-\tau_k) l_k(\tau_j) \mathrm{e}^{a_{f,s(k)}+e_{f,k}} \\ &- \beta \sum_{\substack{j:j\in l_{f,i}\\ \tau_j> T}} \mathrm{e}^{a_{g,s(j)}+e_{g,j}} \sum_{k:p_k=p_j} (T-\tau_k) l_k(\tau_j) \mathrm{e}^{a_{f,s(k)}+e_{f,k}} - \frac{a^2_{f,i}}{2\sigma^2_{S,f}}.\end{aligned} \tag{7}$$

Since equations (6) and (7) do not have standard forms, samples from the conditional posterior distributions of infectivity and susceptibility sire effects were obtained through the MH algorithm.This MCMC method was also applied to sample from the conditional distributions of the environmental effects. As these effects are assumed independent, the log-conditional posterior of the susceptibility environmental effect of each animal $j$ *which* *is not an index case* is

$$\begin{aligned}
\log(p(e_{g,j}|\cdot)) &\propto \log(L(\boldsymbol{\theta})p(e_{g,j}|\sigma^2_{E,g})) \\
&\propto \left[e_{g,j} - \mathrm{e}^{a_{g,s(j)}+e_{g,j}}\beta \sum_{k:p_k=p_j} (\tau_j - \tau_k) l_k(\tau_j) \mathrm{e}^{a_{f,s(k)}+e_{f,k}}\right]\delta_j \\
&- \left[\mathrm{e}^{a_{g,s(j)}+e_{g,j}}\beta \sum_{k:p_k=p_j} (T - \tau_k) l_k(\tau_j) \mathrm{e}^{a_{f,s(k)}+e_{f,k}}\right](1-\delta_j) \\
&- \frac{e^2_{g,j}}{2\sigma^2_{E,g}}.
\end{aligned} \tag{8}$$

where $\delta_j = 1$ if animal $j$ was observed as infected during the observation period and $\delta_j = 0$ otherwise.

In the conditional posterior of the infectivity environmental effect of each infected animal $j$, the log-likelihood is evaluated for its group mates who were infected after $j$, as individuals can only express infectivity after getting infected and if there are remaining susceptibles in their groups after infection. Hence, the log-conditional posterior of the enviromental effect of animal $j$, $j = 1, \ldots, I$ is

$$\begin{aligned}
&\log(p(e_{f,j}|\cdot)) \propto \log(L(\boldsymbol{\theta})p(e_{f,j}|\sigma^2_{E,f})) \propto \\
&\sum_{\substack{i:p_i=p_j \\ \tau_i \geq \tau_j}} \left\{ \log\left[\sum_{k:p_k=p_i} l_k(\tau_i)\mathrm{e}^{a_{f,s(k)}+e_{f,k}}\right] - \beta \mathrm{e}^{a_{g,s(i)}+e_{g,i}} \sum_{k:p_k=p_i} (\tau_i - \tau_k) l_k(\tau_i) \mathrm{e}^{a_{f,s(k)}+e_{f,k}} \right\}\delta_i \\
&- \beta \sum_{\substack{i:p_i=p_j \\ \tau_i > T}} \left\{ \mathrm{e}^{a_{g,s(i)}+e_{g,i}} \sum_{k:p_k=p_i} (T - \tau_k) l_k(\tau_i) \mathrm{e}^{a_{f,s(k)}+e_{f,k}} \right\}(1-\delta_i) - \frac{e^2_{f,j}}{2\sigma^2_{E,f}}.
\end{aligned} \tag{9}$$