The probability of a gene on branch e going extinct is:

$$E_e = p_e^L + p_e^S E_f E_g + p_e^D E_e E_e + \left(\frac{1}{|S|} \sum_h p_h^T E_h \right) E_e, \tag{1}$$

where $|S|$ is the number of branches of S including the stem branch leading to the root, the sum goes over all of these, and f and g are descendants of e, if these do not exist the corresponding terms must be dropped. The event probabilities are derived from DTL "rates" according to:

$$\begin{aligned} p_e^S =& 1/(1+\delta_e+\tau_e+\lambda_e), \\ p_e^D =& \delta_e/(1+\delta_e+\tau_e+\lambda_e), \\ p_e^T =& \tau_e/(1+\delta_e+\tau_e+\lambda_e), \\ p_e^L =& \lambda_e/(1+\delta_e+\tau_e+\lambda_e). \end{aligned} \tag{2}$$

The same term $\bar{E}^T = 1/|S| \sum_h p_h^T E_h$ is present for all e, hence more compactly

$$E_e = p_e^L + p_e^S E_f E_g + p_e^L E_e^2 + \bar{E}^T E_e. \tag{3}$$

The equation has the problem of depending on itself (E_e) and the global average $\bar{E}^T$ – we already know E_f and E_g by the time we get to branch e. What I do aside of the usual initial conditions is first set all E_e and $\bar{E}^T$ to zero and run a initial round of calculation from the leaf toward the root during which I also calculate a first estimate of $\bar{E}^T$. Using these values I then repat this to converge toward fix point values for the E_e.

The probability of gene tree branch u on branch e of S is:

$$\begin{aligned} P_{e,u} =& p_e^S \left(P_{g,v} P_{f,w} + P_{g,w} P_{f,v} + E_f P_{g,u} + P_{f,u} E_g\right) \\ &+ p_e^D \left(P_{e,v} P_{e,w} + 2 P_{e,u} E_e\right) \\ &+ \left(\frac{1}{|S|} \sum_h p_h^T P_{h,w} \right) P_{e,v} + \left(\frac{1}{|S|} \sum_h p_h^T P_{h,v} \right) P_{e,w} \\ &+ \left(\frac{1}{|S|} \sum_h p_h^T E_h \right) P_{e,u} + \left(\frac{1}{|S|} \sum_h p_h^T P_{u,h} \right) E_e \end{aligned} \tag{4}$$

Here the recurring terms are $\bar{P}_u^T = 1/|S| \sum_h p_h^T P_{u,h}$, using which we have more compactly

$$\begin{aligned}
P_{e,u} =& p_e^S \left(P_{g,v} P_{f,w} + P_{g,w} P_{f,v} + E_f P_{g,u} + P_{f,u} E_g \right) \\
&+ p_e^D \left(P_{e,v} P_{e,w} + 2 P_{e,u} E_e \right) \\
&+ \bar{P}_w^T P_{e,v} + \bar{P}_v^T P_{e,w} \\
&+ \bar{E}^T P_{e,u} + \bar{P}_u^T E_e, \qquad (5)
\end{aligned}$$

f and g are descendants of e, v and w are descendants of u, if any of these do not exist the corresponding terms must be dropped. The equation again has the problem of depending on itself ($P_{e,u}$) and the global average $\bar{P}_u^T$ – we already know $\bar{P}_v^T$, $\bar{P}_w^T$, $P_{v,*}$ and $P_{w,*}$, as well as all the $P_{*,g}$ and $P_{*,f}$ that we need by the time we get to branch e of S and u of G. What I do aside of the usual initial conditions is first set all $P_{e,u}$ and the $\bar{P}_u^T$ to zero and run a initial round of calculation from the leaf of both S toward the root and using double recursion along G, during which I also calculate a first estimate of $\bar{P}_u^T$. Using these values I then repat this to converge toward fix point values for the $P_{e,u}$.

Incorporating amalgamation is straightforward. Reconciliations can be obtained by stochastic traceback along $P_{e,u}$ such that the $\bar{P}_u^T$ terms are also expanded to decide where a transfer goes.