Once a cell tree, T, has been built, individual cell genotypes can be inferred from the phylogeny directly. This will give our final estimate for genotype probabilities.

$$P(g_{ij} \mid D_i, T) = (1 - P(\sigma = 0)) \sum_{e \in E} [P(g_{ij} \mid e, T, D_i) P(e \mid T, D_i)] + P(\sigma = 0) P(g_{ij} \mid \sigma = 0)$$

where E is the set of all edges in the rooted tree. To begin with, we compute the probabilities for all descendents of each node having the same genotype: $\pi_0(e), \pi_1(e)$ and $\pi_2(e)$ being the probability that all descendents of e are homozygous reference, heterozygous and homozygous alternate respectively. These values are taken to be

$$\pi_g(e) = \prod_{\{j \succ e\}} P(g_j = g)$$

where $\{j \succ e\}$ is the set of all indices of cells below e. We also compute a fouth value, $\pi_m(e)$ defined as the probability that all descendents of e have genotype 1 or 2. These four values can be computed recursively in $O(m)$ time by multiplying the corresponding values from the two branches directy beneath each branch. Assuming the site contains a mutation and no loss of heterozygosity, the probability that the mutation occured on branch e is given by:

$$P(e \mid T, D_i) = \frac{\pi_m(e)\pi_0(s_e)}{\sum_{e' \in E} \pi_m(e')\pi_0(s_{e'})}$$

where s_e is the sibling edge to e: the other edge that descends immediately from the same node as e.