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**Algorithm 1** Algorithm of the MCMC sampling

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1: function SCsnvcna( $D, n_{\text{ITER}}, m_h, T, \theta, \sigma$ )
2: Initialize  $G$ , and SNV and cell placements.
3: while Search <  $n_{\text{ITER}}$  do
4:   Sample  $r \sim U(0, 1)$ 
5:   if  $r < \pi$  then
6:     Sample  $\theta' \sim q_\theta(\theta'|\theta), r_\theta \sim U(0, 1)$ 
7:     Calculate acceptance ratio  $R_\theta = \frac{\prod_{i,j=1}^{n,m} P(D_{ij}|\theta', G_{ij})}{\prod_{i,j=1}^{n,m} P(D_{ij}|\theta, G_{ij})} \frac{p(\theta')}{p(\theta)} \frac{q_\theta(\theta|\theta')}{q_\theta(\theta'|\theta)}$ 
8:     if  $R_\theta \geq 1$  then
9:       Accept  $\theta'$ 
10:    else if  $R_\theta < m_h$  then
11:      Accept  $\theta'$  with probability  $\min\{R_\theta, 1\}$ 
12:    end if
13:  else if  $r < \pi + p_\lambda$  then
14:    Sample  $\sigma' \sim q_\sigma(\sigma'|\sigma), r_\sigma \sim U(0, 1)$ 
15:    Calculate acceptance ratio  $R_\sigma = \frac{\prod_{j=1}^m P(M_j^k|\bar{V}_j, \sigma')}{\prod_{j=1}^m P(M_j^k|\bar{V}_j, \sigma)} \frac{p(\sigma')}{p(\sigma)} \frac{q_\sigma(\sigma|\sigma')}{q_\sigma(\sigma'|\sigma)}$ 
16:    if  $R_\sigma \geq 1$  then
17:      Accept  $\sigma'$ 
18:    else if  $r_\sigma < m_h$  then
19:      Accept  $\sigma'$  with probability  $\min\{R_\sigma, 1\}$ 
20:    end if
21:  else
22:    Randomly select and place mutation  $j$  on a new branch  $E_k$ 
23:    if there is  $\geq 1$  copy number loss on the subtree of  $E_k$  overlapping with  $j$ 
24:    then
25:      Randomly sample an edge,  $E_l$ , on which there is such a copy number loss
26:      Make  $j$  lost in the subtree of  $E_l$  with probability 0.5
27:    end if
28:    Place SNV cells on the leaves according to SNV placements.
29:    Calculate acceptance ratio  $R_M = \frac{\prod_{i=1}^n P(M_j^{k'}|\bar{V}_j, \sigma) P(C_i^{y_i'}|M_j^{k'})}{\prod_{i=1}^n P(M_j^k|\bar{V}_j, \sigma) P(C_i^{y_i}|M_j^k)} \frac{q_p(M_j^k|M_j^{k'})}{q_p(M_j^{k'}|M_j^k)}$ 
30:    Sample  $r_M \sim U(0, 1)$ 
31:    if  $R_M \geq 1$  then
32:      Accept branch  $E_k$  for mutation  $j$  along with cell placements and proposed mutation loss
33:    else if  $r_M < m_h$  then
34:      Accept branch  $E_k$  for mutation  $j$  along with cell placements and proposed mutation loss with probability  $\min\{R_M, 1\}$ 
35:    end if
36:    Update  $G$  based on new SNV and cell placements, and mutaiton loss
37:    Update  $\bar{V}$  base on new  $G$ 
38:  end if
39: end while
40: return the tree with highest probability.

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