
Algorithm 1 Algorithm of the MCMC sampling

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1: function SCsncna( $D, n_{\text{ITER}}, m_h, T, \theta, \sigma$ )
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  $j$ 
        then
24:          Randomly sample an edge,  $E_l$ , on which there is such a copy number
          loss
25:          Make  $j$  lost in the subtree of  $E_l$  with probability 0.5
26:        end if
27:        Place SNV cells on the leaves according to SNV placements.
28:        Calculate acceptance ratio  $R_M = \frac{\prod_{i=1}^n P(M_j^{k'}|\bar{V}_j, \sigma) P(C_i^{y_i'}|M_j^{k'})}{\prod_{i=1}^n P(M_j^k|\bar{V}_j, \sigma) P(C_i^{y_i}|M_j^k)} \frac{q_p(M_j^k|M_j^{k'})}{q_p(M_j^{k'}|M_j^k)}$ 
29:        Sample  $r_M \sim U(0, 1)$ 
30:        if  $R_M \geq 1$  then
31:          Accept branch  $E_k$  for mutation  $j$  along with cell placements and pro-
            posed mutation loss
32:        else if  $r_M < m_h$  then
33:          Accept branch  $E_k$  for mutation  $j$  along with cell placements and pro-
            posed mutation loss with probability  $\min\{R_M, 1\}$ 
34:        end if
35:        Update  $G$  based on new SNV and cell placements, and mutation loss
36:        Update  $\bar{V}$  base on new  $G$ 
37:      end if
38:    end while
39: return the tree with highest probability.
  
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