

INPUT: a genotype G_i partitioned into m segments $\{(g_1, g'_1), \dots, (g_m, g'_m)\}$ and a threshold f .

Let L and L' denote two lists of quadruplets.

Make a “root” quadruplet q_R as in algorithm 1.

Put q_R in L .

For j from 2 to m

For each “parent” quadruplet $q_p = \{h_p, \alpha_p, h'_p, \alpha'_p\}$ of L do

Compute $\Pr(h_p, h'_p \mid H_{-i}^{(t)}, \rho)$ by expression (2) and (1).

If $\Pr(h_p, h'_p \mid H_{-i}^{(t)}, \rho) > f$ then

Make 2 “children” quadruplets q_{C1} and q_{C2} from q_p as in algorithm 1.

Put q_{C1} and q_{C2} in L' .

Delete L .

$L = L'$.

OUTPUT:

For each “leaf” quadruplet $q_L = \{h_L, \alpha_L, h'_L, \alpha'_L\}$ of L do

Put (h_L, h'_L) in S_i .

Compute $\Pr(h_L, h'_L \mid H_{-i}^{(t)}, \rho)$ from α_L and α'_L by expression (3) and (1).