Algorithm 1: Coancestry estimation: a simple case with haploid individuals and without missing data

Data: For each locus, the sequences of nucleotides that vary between individuals

Result: Estimated coancestry matrix

Init: Initialize the coancestry matrix $\mathbf{C}$, so that $\mathbf{C}_{ij}=0$ for all i and j

```
1  foreach RAD locus do
2  |    foreach individual i // a recipient
3  |    do
4  |    |    foreach individual j ≠ i // potential donors
5  |    |    do
6  |    |    |    Dij = number of SNPs between i and j;
7  |    |    end
8  |    |    Mi = minj≠i(Dij); // The minimum of Dij for all j≠i
9  |    |    NMi = countj≠i(Dij==Mi); // Count the number of 'donors'
10 |    |    foreach individual j ≠ i do
11 |    |    |    if (Dij == Mi) // If individuals i and j are closest, j is a 'donor'
12 |    |    |    then
13 |    |    |    |    // Assign an equal proportion of coancestry to each donor
14 |    |    |    |    Cij = Cij + 1/NMi
15 |    |    |    end
16 |    |    end
17 |    end
18 end
```