Parameters Used For Running COLONY

Parameters for Testing Simulation A (10K SNPs)

'filename' !Dataset name
'filename' !Output file name
50 ! Number of offspring in the sample
10000 ! Number of loci
1234 ! Seed for random number generator
1 ! 0/1=Not updating/updating allele frequency
2 ! 2/1=Dioecious/Monoecious species
0 ! 0/1=No inbreeding/inbreeding
0 ! 0/1=Diploid species/HaploDiploid species
0 0 ! 0/1=Polygamy/Monogamy for males & females
0 ! 0/1=Clone inference =No/Yes
0 ! 0/1=Full sibship size scaling =No/Yes
0 ! 0,1,2,3=No,weak,medium,strong sibship size prior; mean paternal & meteral sibship size
0 ! 0/1=Unknown/Known population allele frequency
1 ! Number of runs
2 ! Length of run
0 ! 0/1=Monitor method by Iterate#/Time in second
100000 ! Monitor interval in Iterate# / in seconds
0 ! non-Windows version
1 ! 0/1 pairwise/Fulllikelihood
2 ! 1/2/3=low/medium/high Precision for Fulllikelihood
m@ !Marker names
0@ !Marker types, 0/1 = codominant/dominant
0@ !Allelic dropout rate
0.01@ !false allele rate
0 0 !prob. of dad/mum included in the candidates
0 0 !numbers of candiadte males & females
0 0 !#known fater-offspring dyads, paternity exclusion threshold
0 0 !#known moter-offspring dyads, maternity exclusion threshold
0 !#known paternal sibship with unknown fathers
0 !#known maternal sibship with unknown mothers
0 !#known paternity exclusions
0 !#known maternity exclusions
0 !#known paternal sibship exclusions
0 !#known maternal sibship exclusions

Parameters for Testing Simulation B (20 Microsatellites)

The parameters were the same as they were for Simulation A, except the number of loci was set to 20 and the allele dropout rate was set to 0.05.