

1 ← 1,2,3 for number of codons to be analysed; set to 4 if require 3 codon *dhfr*

genotype omitting 'impossible' clones

9 ← level of precision required for ML estimate

3 ← level of precision required for CI estimation

8 ← maximum number of clones in any sample

n ← (must be y or n) whether 'minority' genotypes will be missed in typing

0.3 ← the detection limit if minority genotypes are missed e.g. 0.3 means genotypes present at frequency less than 30% will be missed...

n ← (must be y or n) whether MOI is known for each sample

1 ← distribution type to be used if MOI is unknown

y ← (must be y or n) whether to check hillclimbing always converges on the same ML 'peak'

n ← (must be y or n) whether to check programme accuracy by simulating datasets and checking 95% of estimates fall within the 95% CI

H ← (must be H or L in uppercase) If a dataset is simulated should it be for a High or Low transmission setting?

100 ← required size of dataset for simulations to check programme accuracy

500 ← number of replicates used to check hillclimbing or programme accuracy

0 ← a redundant parameter, set to zero. [This allows later programme versions to acquire additional information without making previous input files incompatible]

0 ← a redundant parameter, set to zero.

0 ← a redundant parameter, set to zero.

0 ← a redundant parameter, set to zero

0 ← a redundant parameter, set to zero.