Table 3. Conditions for neutral coalescent simulation under alternative demographic models

Model	No. of demes (sampling among demes)	Parameters of population size change, migration, and divergence among demes
Two-epoch	1 (100)	$\tau=0.02$, $\upsilon=0.1$
	`ms 100 300 -t 108 -eN 0.01 0.1`	
Bottleneck	1 (100)	$\tau_1=0.2$, $\upsilon_1=1$; $\tau_2=0.1$, $\upsilon_2=0.1$; $\upsilon_3=0.5$
	`ms 100 300 -t 40 -eN 0.1 0.1 -eN 0.15 0.5`	
Island	10 (30 30 30 10 0 0 0 0 0 0)	$M_{ij}=5.0$ for all i, j, $i \neq j$, equal population sizes
	`ms 100 300 -t 2.35 -I 10 30 30 30 10 0 0 0 0 0 0 5.0`	
Complex	4 (30 30 30 10)	deme 1: $\tau_1=0.1$, $\upsilon_1=1$; $\upsilon_2=0.1$ deme 2: $\tau_3=0.1$, $\upsilon_3=1$; $\tau_4=0.1$, $\upsilon_4=0.1$; $\tau_5=0.8$, $\upsilon_5=0.5$ deme 3: $\tau_6=0.1$, $\upsilon_6=1$; $\tau_7=0.1$, $\upsilon_7=0.1$; $\tau_8=0.8$, $\upsilon_8=0.5$ deme 4: $\tau_9=0.02$, $\upsilon_9=1$; $\tau_{10}=0.004$, $\upsilon_{10}=0.05$; $\tau_{11}=0$ $M_{ij}=5.0$ for current populations i, j, $i \neq j$; for past populations, M_{ij} scaled by past population sizes
	`ms 100 300 -t 22 -I 4 30 30 30 10 5.0 -en 0.05 3 0.1 -en 0.1 3 0.5 -en 0.05 2 0.1 -en 0.1 2 0.5 -en 0.05 1 0.1 -en 0.01 4 0.05 -ej 0.012 4 3 -ej 0.5 2 1 -ej 0.5 3 1`	

For each model we simulated 2,000 data sets, each composed of 100 loci sequenced at 300 unlinked genes, with complete linkage within genes, known ancestral states for each SNP, and a mutation rates selected to produce, on average, ~37,000 SNPs, which were randomly divided into putatively neutral (97.5% of SNPs) and potentially selected (2.5% of SNPs) categories. Times are scaled $2N_1$ generations, where N_1 is the current size of the first deme. For each historical population size N_i, we define $\upsilon_i=N_i/N_1$. The MS command line input for each iteration of each model is also shown (note that MS scales time in $4N_1$ generations so all times are divided by 2).