

DMLE+

Burn-in: Iterations:

Iteration = 4801 Log Likelihood = -1283.6 Mutation Location = -0.0415358 Mutation Age = 70.4

Acceptance Rates: Tree = 0.36576 Location = 0.76338 Ancestral Node Alleles = 0.15288

Internal Node Alleles = 0.18160 Allele Frequency = 0.61800

SqR =

Adjustment Window

Current values of:	Adjust to:	Current values of Acceptance Rates:
tree = 2.0000	tree = <input type="text" value="2.0000"/>	tree = 0.36576
recdist = 0.0050	recdist = <input type="text" value="0.0050"/>	location = 0.76338
ancestral = 0.5000	ancestral = <input type="text" value="0.5000"/>	ancestral node alleles = 0.15288
internal states = 0.5000	internal states = <input type="text" value="0.5000"/>	internal node alleles = 0.18160
alleles = 0.0500	alleles = <input type="text" value="0.0500"/>	allele frequency = 0.61800


```

0
Use fixed random seed?:(0 = no (=random), negative integer = yes (=fixed), and is the seed):
-39
# Chromosomes (N):
140
# Loci per chromosome (L):
5
Numbers of haplotypes in the normal(base) pop.:
?? 1 1 1 1 7

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