

Burn-in:  Iterations: 

Iteration = 3301      Log Likelihood = -1329.9      Mutation Location = -0.0491949      Mutation Age = 67.4

Acceptance Rates:    Tree = 0.39170      Location = 0.76553      Ancestral Node Alleles = 0.15510

Internal Node Alleles = 0.18242      Allele Frequency = 0.61527

SqR =

Status:

Current input file: genseq1.txt

N.B. - Please quit and reload DMLE+ after a complete run. Click inside the text box below and press the up and down arrows to browse file (Page Up and Page Down buttons do not work). Modifying the contents of the window below will have no effect on calculation values.

```
Data as genotypes? (0 = No, 1 = Yes)
1
Genetic model: (0 = Dominant, 1 = Recessive)
1
Read old file?: (0 = no, 1 = yes):
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
```

Load

