

Supplementary Material

1. Simulations

All simulated datasets were generated with indelible using the following configuration:

```
[TYPE] NUCLEOTIDE 1 // nucleotide simulation using algorithm from method 1

[MODEL] simple_model
[submodel] GTR 0.2 0.4 0.6 0.8 1.2 // GTR: a=0.2, b=0.4, c=0.6, d=0.8, e=1.2, f=1
[statefreq] 0.20 0.25 0.25 0.30 // pi_T, pi_C, pi_A, pi_G
[indelmodel] NB 0.5 1
[inserttrate] 0.001
[deleterate] 0.001

[TREE] random_tree
[unrooted] 1500 2.4 1.1 0.2566 0.34 // ntaxa birth death sample mut
[seed] 2381242

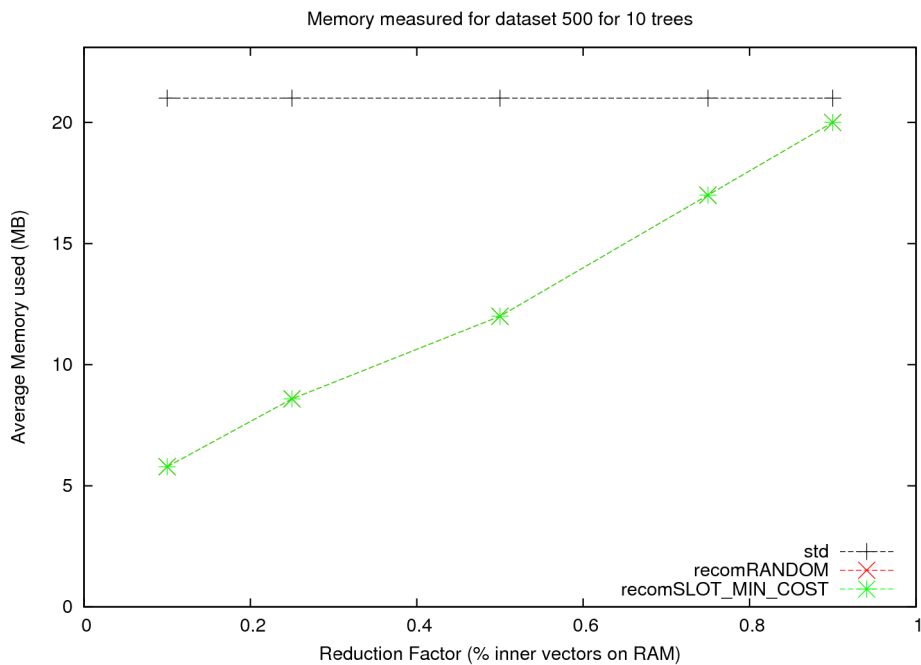
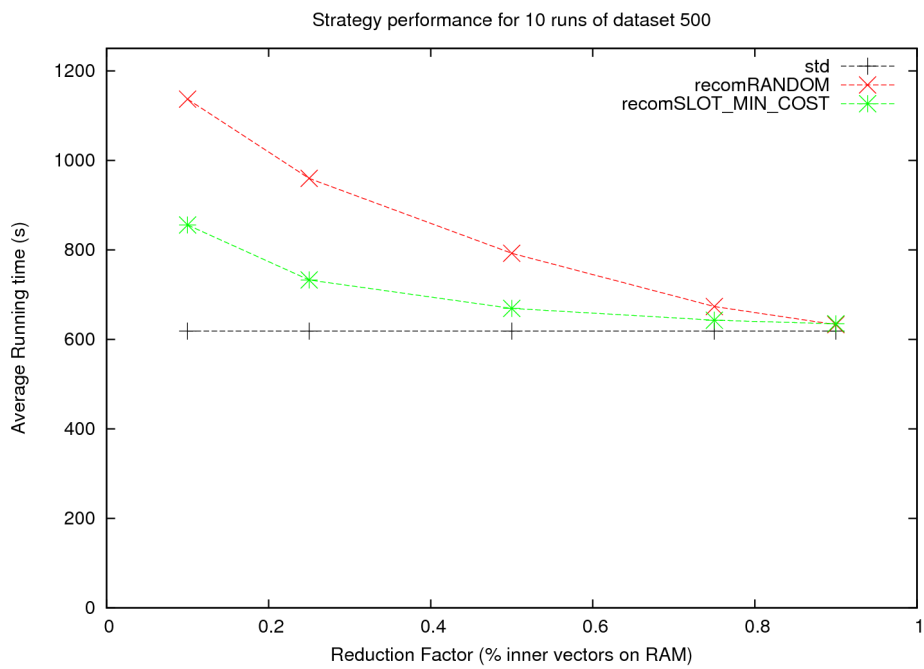
[PARTITIONS] simulated_gene
[random_tree simple_model 400] // #base pairs

[EVOLVE] simulated_gene 1 simulated_alignment
```

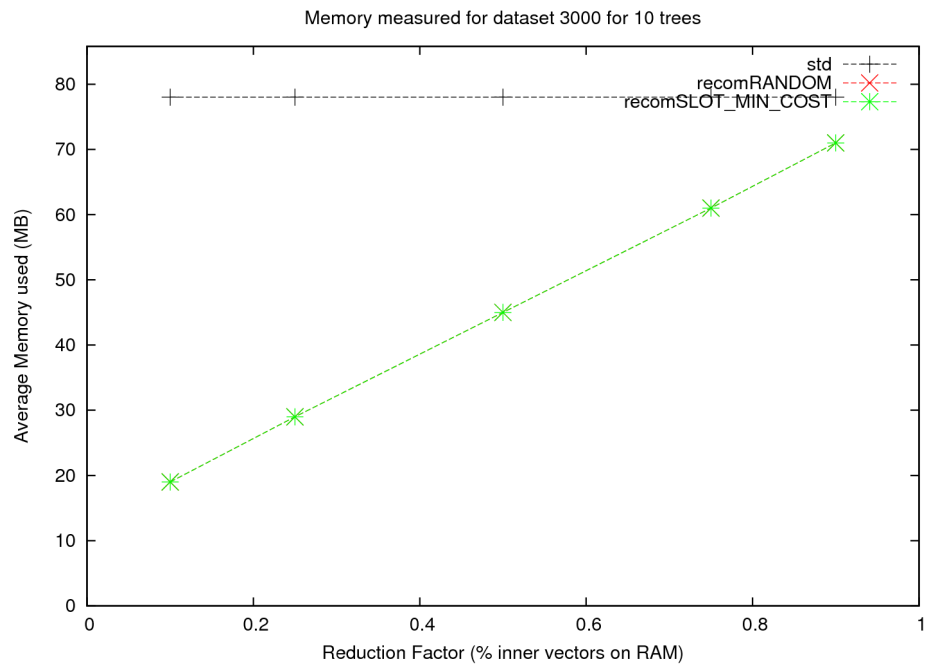
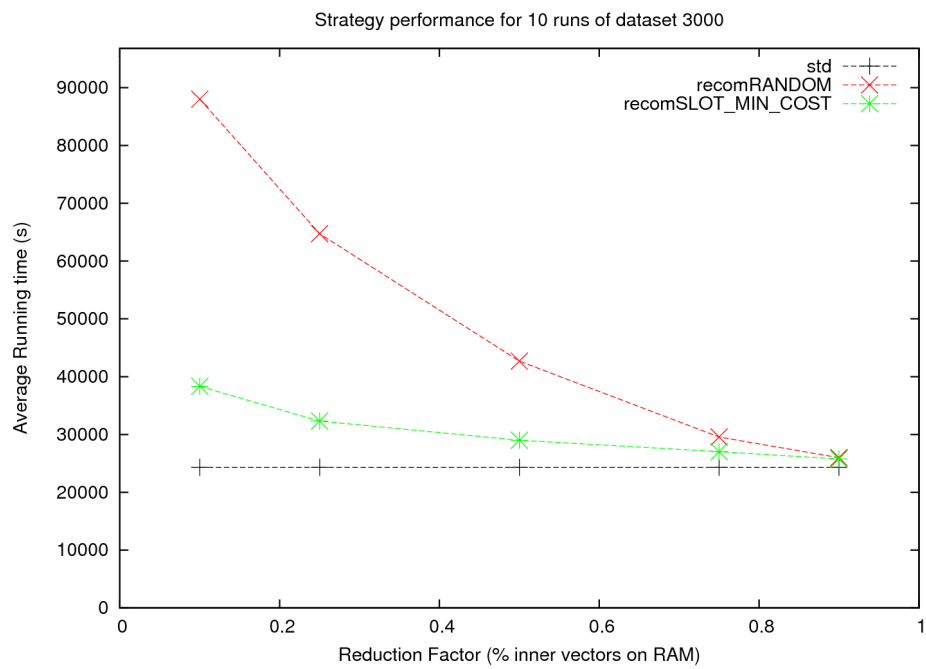
For further details on the configuration file of indelible can be found in:
<http://abacus.gene.ucl.ac.uk/software/indelible/tutorial/>

2. Evaluation of replacement strategies

1. Biological dataset of 500 species, 10 runs with different starting trees



2. Simulated dataset of 3000 species, 10 runs with different starting trees



3. Simulated dataset of 5000 species, 10 runs with different starting trees

