Commands used for generating simulated species trees, gene trees, and subgene trees

Command used for species tree generation:

```bash
#!/bin/bash
java -jar sagephy-1.0.0.jar HostTreeGen -min 100 -max 100 -bi 1.0 5.0 2.0
```

Command used for gene tree generation:

```bash
#!/bin/bash
seed=$RANDOM
# Rates for duplication, loss, additive transfer, and replacing transfer are
# 0.3, 0.6, 0.3, and 0.3 respectively.
java -jar sagephy-1.0.0.jar GuestTreeGen -s $seed -rt 0.5 -max 250 \
species.pruned.tree 0.3 0.6 0.6
```

The average numbers of gene duplications, additive transfers, replacing transfers, and losses in the generated gene trees are 5.83, 5.61, 5.94, and 14.12, respectively. We point out that the specific parameters used for simulating gene trees and species trees are not important in the current context since the focus of our study is on the evolution of "subgene" trees within gene trees rather than on the evolution of gene trees within species trees.

Command used for subgene tree generation:

```bash
#!/bin/bash
seed=$RANDOM
# Rates for duplication, loss, and replacing transfer are 0, 0, and 0.4,
# respectively, by default. Replacing transfer rates of 0.2 and 0.6
# were used to generate additional subgene trees.
java -jar sagephy-1.0.0.jar DomainTreeGen -s $seed -rt 1.0 -ig 0 -max 250 \
species.pruned.tree genetree/prunedGeneTree/ 0 0 0.4
```