First results from simulations

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1 Scenarios

Three scenarios, as shown in Figure 1 were used. Each scenario represents a 'true' MUL-tree. Heights are in expected substitutions per site. All allopolyploidizations occur at 0.01. Population sizes are numbers of gene copies within diploid populations, or numbers of gene copies with the same diploid parent, for allotetraploid populations. If the population size is S, the probability of coalescence between a pair of gene copies is $1/S$ per generation.

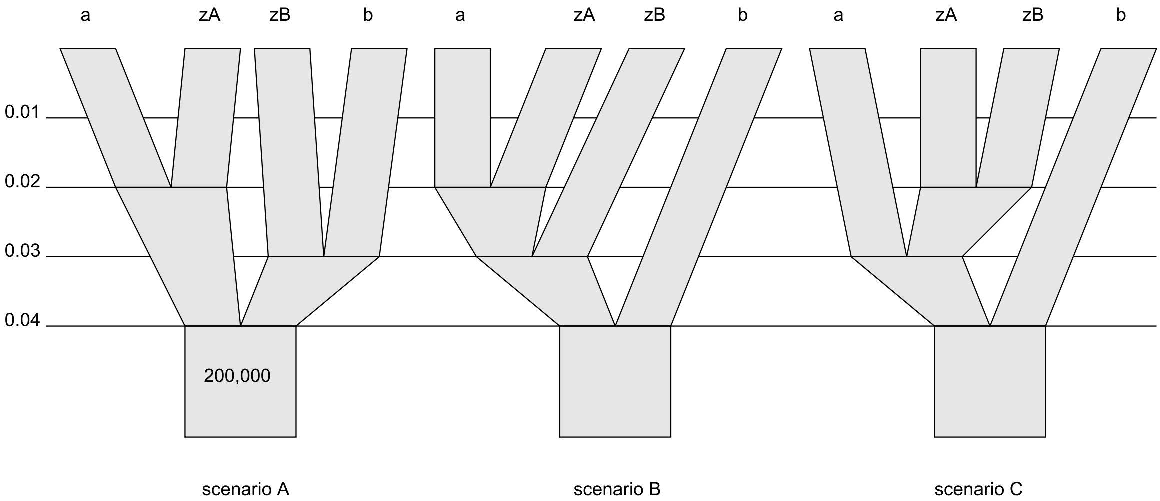

Figure 1: Scenarios

All genes have length 500. Population sizes are 100,000 at tips, and at rootward ends of branches, and 200,000 at tipward ends of internal branches and at the root.

These three scenarios were each tested with the number of genes G equal to 1,3,10, the number of individuals N per species equal to 1,3, and the mutation rates T set to 4e-8 and 8e-8. This is a total of 12 possibilities per scenario.

The T values are in expected substitutions per site per generation. All scenarios have a root height of 0.04. Changing T while keeping this height fixed changes the number of generations the tree represents. T=4e-8 means 0.04/4e-8 = 1e6 or a million generations root to tip. T=8e-8 means 0.04/8e-8 = 5e5 or half a million generations root to tip.

2 Other parts of the model

Strict clock branch rates assumed in simulation and BEAST.

HKY substitution model assumed in simulation and BEAST. In simulations, the Seq-Gen parameters are kappa=3, frequencies .3 A and T, .2 C and G. (Seq-Gen called with `-t3.0 -f0.3,0.2,0.2,0.3`. These are estimated in BEAST.

No site rate heterogeneity assumed within genes in simulation and BEAST.

Genes have the same mutation rate in simulations. Rates are estimated in BEAST.

Priors on population sizes are similar to *BEAST.

An example BEAST XML file is below.

3 Results

For each scenario, and each set of 12 (G, N, T) values, 20 replicates were simulated and run for one million generations in BEAST, a total of 720 BEAST runs. This took about ten hours on one processor per scenario, the bulk of time running BEAST. MUL-trees were sampled every 1000 generations, and the first 200 samples (of 1001) discarded as burn-in. The tables below show the results as number of times the correct topology of the MUL-tree was recovered as the concensus tree.

Scenario A	Generations root to tip	
G, N	1,000,000	500,000
1, 1	16 / 20	12 / 20
1, 3	19 / 20	12 / 20
3, 1	18 / 20	17 / 20
3, 3	20 / 20	15 / 20
10, 1	20 / 20	19 / 20
10, 3	20 / 20	19 / 20

Scenario B	Generations root to tip	
G, N	1,000,000	500,000
1, 1	12 / 20	13 / 20
1, 3	16 / 20	9 / 20
3, 1	19 / 20	18 / 20
3, 3	20 / 20	13 / 20
10, 1	20 / 20	20 / 20
10, 3	18 / 20	17 / 20

Scenario C	Generations root to tip	
G, N	1,000,000	500,000
1, 1	14 / 20	9 / 20
1, 3	15 / 20	12 / 20
3, 1	18 / 20	18 / 20
3, 3	20 / 20	17 / 20
10, 1	20 / 20	20 / 20
10, 3	20 / 20	20 / 20

4 Scenario config files

4.1 Scenario A

```
nofGNRT 6
1 1 20 4e-8 8e-8
1 3 20 4e-8 8e-8
3 1 20 4e-8 8e-8
3 3 20 4e-8 8e-8
10 1 20 4e-8 8e-8
10 3 20 4e-8 8e-8
noftetratrees 1
genelength 500
ditree ntips 2
a height 0 tippop 100000 prevpop 100000
b height 0 tippop 100000 prevpop 100000
(a,b) height 0.04 tippop * prevpop *
tetratree ntips 1
z height 0 tippop 100000 prevpop *
hyb 0.01 100000 join * * foot1 a .02 100000 foot2 b .03 100000
```

4.2 Scenario B

```
nofGNRT 6
1 1 20 4e-8 8e-8
1 3 20 4e-8 8e-8
3 1 20 4e-8 8e-8
3 3 20 4e-8 8e-8
10 1 20 4e-8 8e-8
10 3 20 4e-8 8e-8
noftetratrees 1
genelength 500
ditree ntips 2
a height 0 tippop 100000 prevpop 100000
b height 0 tippop 100000 prevpop 100000
(a,b) height 0.04 tippop * prevpop *
tetratree ntips 1
z height 0 tippop 100000 prevpop *
hyb 0.01 100000 join * * foot1 a .02 100000 foot2 a .03 100000
```

4.3 Scenario C

```
nofGNRT 6
1 1 20 4e-8 8e-8
1 3 20 4e-8 8e-8
3 1 20 4e-8 8e-8
3 3 20 4e-8 8e-8
10 1 20 4e-8 8e-8
10 3 20 4e-8 8e-8
noftetratrees 1
genelength 500
ditree ntips 2
a height 0 tippop 100000 prevpop 100000
b height 0 tippop 100000 prevpop 100000
(a,b) height 0.04 tippop * prevpop *
tetratree ntips 1
z height 0 tippop 100000 prevpop *
hyb 0.01 100000 join 0.02 100000 foot1 a .03 100000 foot2 * * *
```

5 Example BEAST XML file

File `A3BXg3n3t80r1.xml` (scenario A, 3 genes, 3 individuals, mutation rate 8e-8). Sequences are truncated.

```
<?xml version="1.0" standalone="yes"?>
<!--  Simulated data for allopolyploids made by seqgen and R code  -->
<beast>
<!--  Taxa. Each taxon is a sequence (labelled A,B,...) from  -->
<!--  an individual (01,02,03,...) in a species (a,b,c...).  -->
<taxa id="taxa">
<taxon id="01aA"/>
<taxon id="01bA"/>
<taxon id="01zA"/>
<taxon id="01zB"/>
<taxon id="02aA"/>
<taxon id="02bA"/>
<taxon id="02zA"/>
<taxon id="02zB"/>
<taxon id="03aA"/>
<taxon id="03bA"/>
<taxon id="03zA"/>
<taxon id="03zB"/>
</taxa>
<!--  Simulated alignment for gene 1 of 3 genes.  -->
<alignment id="alignment1" dataType="nucleotide">
<sequence>
<taxon idref="03aA" />
ATTTAGCTGCCCTGTAAAAACCACCAGAATAGGTATATATATATGTATAATCTCGTGGCCGGATTATTACTTAGTGATTCTTAA
```

```
</sequence>
<sequence>
<taxon idref="01aA" />
ATTTAGCTGCCCTGTAAAAACCACCAGCATAGGTATATATATATGTATAATCTCGTGGCCGGATTATTACTTAGTGATTCTTAA
</sequence>
<sequence>
<taxon idref="02aA" />
ATTTAGCTGCCCTGTAAAAACCACCAGAATAGGTATATATATATGTATAATCTCGTGGCCGGATTATTACTTAGTGATTCTTAA
</sequence>
<sequence>
<taxon idref="02zA" />
ATTTAGCTGCCCTGTAAAAACCACCAGAATAGGTATATATGTATATATAATCTCATGGTCGGATTACTACTTAGTGATTCTTAA
</sequence>
<sequence>
<taxon idref="03zA" />
ATTTAGCTGCCCTGTAAAAACCACCAGAATAGGTATATATGTATATATAATCTCATGGTCGGATTATTACTTAGTGATTCTTAA
</sequence>
<sequence>
<taxon idref="01zA" />
ATTTAGCTGCCCTGTAAAAACCACCAGAATAGGTATATATGTATATATAATCTCATGGTCGGATTATTACTTAGTGATTCTTAA
</sequence>
<sequence>
<taxon idref="01bA" />
ATTTAGCTGCCCTGTAAAAACCACCAGGATAGGTATATATGTATGTATAATCTTATGGCCGGATTATTATCTAGTGATTATTAT
</sequence>
<sequence>
<taxon idref="02bA" />
ATTTAGCTGCCCTGTAAAAACCACCAGGATAGGTATATATGTATGTATAATCTTATGGCCGGATTATTATCTAGTGATTATTAT
</sequence>
<sequence>
<taxon idref="03bA" />
ATTTAGCTGCCCTGTAGAAACCTCCAGAATAGGTATATATGTATGTATAATCTTATGGCCGGATTATTATCTAGTGATTATTAT
</sequence>
<sequence>
<taxon idref="03zB" />
ATTTAGCTGCCCTGTAAAAACCACCAGAATAGGTATATATGTATGTCTAATATCATGGTCGGATTACTATCCGGTGATTTTTAA
</sequence>
<sequence>
<taxon idref="02zB" />
ATTTAGCTGCCCTGTAAAAACCACCAGAATAGGTATATATGTATGTCTAATATCATGGTCGGATTACTATCCAGTGATTTTTAA
</sequence>
<sequence>
<taxon idref="01zB" />
ATTTAGCTGCCCTGTAAAAACCACCAGAATAGGTATATATGTATGTCTAATATCATGGTCGGATTACTATCCAGTGATTTTTAA
</sequence>
</alignment>
<!--  Simulated alignment for gene 2 of 3 genes.  -->
<alignment id="alignment2" dataType="nucleotide">
<sequence>
<taxon idref="02zB" />
GTTATTCTAAAGAATATGGCTCCTTAAACAATACAAAAAGACCTTGAAGTTTGTCCGGACCGATATCCCCTTGGAAATTCTAT
</sequence>
```

```
<sequence>
<taxon idref="01zB" />
GTTATTCCAAAGAATATGGCTCCTTAAACAATACAAAAAGATCTTGAATTTTGTCTGGACCGATATCCCCTTGGAAATTCTATG
</sequence>
<sequence>
<taxon idref="03zB" />
GTTATTCCAAAGAATATGGCTCCTTAAACAATACAAAAAGATCTTGAATTTTGTCTGGACCGATATCCCCTTGGAAATTCTATGG
</sequence>
<sequence>
<taxon idref="02bA" />
GTTCTTCTAAAGAATATGGCTCCTTAAACAATACAAAAAGATCTTGAAGTTTGTCTGAACCGATATCCCCTTGGAAATTCTATGG
</sequence>
<sequence>
<taxon idref="01bA" />
GTTCTTCTAAAGAATATGGCTCCTTAAACAATACAAAAAGATCTTGAAGTTTGTCTGAACCGATATCCCCTTGGAAATTCTATGG
</sequence>
<sequence>
<taxon idref="03bA" />
GTTCTTCTAAAGAATATGGCTCCTTAAACAATACAAAAAGATCTTGAAGTTTGTCTGAACCGATATCCCCTTGGAAACTCTATGG
</sequence>
<sequence>
<taxon idref="02zA" />
GTTATTCTAAAGAATATGGCCCCTTAAACAATACAAAAAGACCTTGAAGCTTATCTGGACCGATATCCCCTTGGAAGTTCTATGG
</sequence>
<sequence>
<taxon idref="03zA" />
GTTATTCTAAAGAATATGGCCCCTTAAACAATACAAAAAGACCTTGAAGCTTATCTGGACCGATATCCCCTTGGAAGCTCTATGG
</sequence>
<sequence>
<taxon idref="01zA" />
GTTATTCTAAAGAATATGGCCCCTTAGACAATACAAAAAGACCTTGAAGCTTATCTGGACCGATATCCCCTTGGAAGCTCTATGA
</sequence>
<sequence>
<taxon idref="03aA" />
GTTATTCTAAAGAATATGGCCCCTTAAACAATACGAAAAGACCTTGAAGCTTATTTGAACCGATATCCCCTTGGAAATTCTATGG
</sequence>
<sequence>
<taxon idref="02aA" />
GTTATTCTAAAGAATATGGCCCCTTAAACAATACAAAAAGACCTTGAAGCTTATTTGAACCGATATCCCCTTGGAAATTCTATGG
</sequence>
<sequence>
<taxon idref="01aA" />
GTTATTCTAAAGAATATGGCCCCTTAAACAATACAAAAAGACCTTGAAGCTTATTTGAACCGATATCCCCTTGGAAATTCTATGG
</sequence>
</alignment>
<!--  Simulated alignment for gene 3 of 3 genes.  -->
<alignment id="alignment3" dataType="nucleotide">
<sequence>
<taxon idref="03bA" />
GGTGTTGCTCTCCTGTTCATGTCTTATGTAATGATACTAGAACTTCGTAGGCCGGTTTTAAATACCATTTAACAGACTTAACCTGG
</sequence>
<sequence>
```

```
<taxon idref="02bA" />
GGTGTTGCTCTCCTGTTCATGTCTTATGTAATGATACTAGAACTTCGTAGGCCGGTTTTAAATACCATTTAACAGACTTAACCTGG
</sequence>
<sequence>
<taxon idref="01bA" />
GCTGTTGCTTTCCTGTTCATGTCTTATGTAATGATACTAGAACTTCGTAGGCTGGTTTTAAATACCATTTAACAGACTTAACCTGG
</sequence>
<sequence>
<taxon idref="01zB" />
AGTGTTGCTTTCCTGTTCATGTCTTATGTAATGATACTAGAACTTCGTAGCCCGGTCTTAAATACCATTTAACAGACTTAACCTGG
</sequence>
<sequence>
<taxon idref="02zB" />
AGTGTTGCTTTCCTGTTCATGTCTTATGTAATGATACTAGAACTTCGTAGCCCGGTCTTAAATACCATTTAACAGACTTAACCTGG
</sequence>
<sequence>
<taxon idref="03zB" />
AGTGTTGCTTTCCTGTTCATGTCGTATGTAATGATACTAGAACTTCGTAGCCCGGTCTTAAATACCATTTAACAGACTTAACCTAGC
</sequence>
<sequence>
<taxon idref="03aA" />
AGTGTTGTTTTCCTGTTCATGTCTTTTATAGTGATACTAGAACTTCGCAGTCCTATTTTGAATTCCATTTCACAGACTTACCCTGGC
</sequence>
<sequence>
<taxon idref="01aA" />
AGTGTTGTTTTCCTGTTCATGTCTTTTATAGTGATACTAGAACTTCGCAGTCCTATTTTGAATTCCATTTCACAGACTTACCCTGGC
</sequence>
<sequence>
<taxon idref="02aA" />
AGTGTTGTTTTCCTGTTCATGTCTTTTATAGTGATACTAGAACTTCGCAGTCCTATTTTGAATTCCATTTCACAGACTTACCCTGGC
</sequence>
<sequence>
<taxon idref="02zA" />
AGTGTTGTTTTCCTGTTCATGTCTTTTATAGTGATACTAGAACTTCGCAGCCCTATTTTGAATATCATTTCACAGACTTAACCTGG
</sequence>
<sequence>
<taxon idref="03zA" />
AGTGTTGTTTTCCTGTTCATGTCTTTTATAGTGATACTAGAACTTCGCAGCCCTATTTTGAATACCATTTCACAGACTTAACCTGG
</sequence>
<sequence>
<taxon idref="01zA" />
AGTGTTGTTTTCCTGTTCATGTCTTTTATAGTGATACTAGAACTTCGCAGCCCTATTTTGAATACCATTTCACAGACTTAACCTGG
</sequence>
</alignment>
<!--  Patterns  -->
 <patterns id="1.patterns" from="1" >
 <alignment idref="alignment1" />
 </patterns>
 <patterns id="2.patterns" from="1" >
 <alignment idref="alignment2" />
 </patterns>
 <patterns id="3.patterns" from="1" >
```

```
 <alignment idref="alignment3" />
 </patterns>
<!--  Constant size population parameter used to generate starting trees.  -->
 <constantSize id="constant" units="substitutions" >
 <populationSize>
 <parameter id="constant.popSize" value="0.016" lower="0" upper="Infinity" />
 </populationSize>
 </constantSize>
<!--  Randomly generated starting trees for genes.  -->
 <coalescentTree  id="1.startingTree" rootHeight="0.2" >
 <taxa idref="taxa" />
 <constantSize idref="constant" />
 </coalescentTree>
 <coalescentTree  id="2.startingTree" rootHeight="0.2" >
 <taxa idref="taxa" />
 <constantSize idref="constant" />
 </coalescentTree>
 <coalescentTree  id="3.startingTree" rootHeight="0.2" >
 <taxa idref="taxa" />
 <constantSize idref="constant" />
 </coalescentTree>
<!--  Tree models for gene trees.  -->
 <treeModel id="1.treeModel" >
 <coalescentTree idref="1.startingTree" />
 <rootHeight>
 <parameter id="1.treeModel.rootHeight" />
 </rootHeight>
 <nodeHeights internalNodes="true" >
 <parameter id="1.treeModel.internalNodeHeights" />
 </nodeHeights>
 <nodeHeights internalNodes="true" rootNode="true" >
 <parameter id="1.treeModel.allInternalNodeHeights" />
 </nodeHeights>
 </treeModel>
 <treeModel id="2.treeModel" >
 <coalescentTree idref="2.startingTree" />
 <rootHeight>
 <parameter id="2.treeModel.rootHeight" />
 </rootHeight>
 <nodeHeights internalNodes="true" >
 <parameter id="2.treeModel.internalNodeHeights" />
 </nodeHeights>
 <nodeHeights internalNodes="true" rootNode="true" >
 <parameter id="2.treeModel.allInternalNodeHeights" />
 </nodeHeights>
 </treeModel>
 <treeModel id="3.treeModel" >
 <coalescentTree idref="3.startingTree" />
 <rootHeight>
 <parameter id="3.treeModel.rootHeight" />
 </rootHeight>
 <nodeHeights internalNodes="true" >
```

```
 <parameter id="3.treeModel.internalNodeHeights" />
 </nodeHeights>
 <nodeHeights internalNodes="true" rootNode="true" >
 <parameter id="3.treeModel.allInternalNodeHeights" />
 </nodeHeights>
 </treeModel>
<!--  Branch models for gene trees.  -->
 <strictClockBranchRates id="1.branchRates" >
 <rate>
 <parameter id="1.clock.rate" value="1" lower="0" upper="Infinity" />
 </rate>
 </strictClockBranchRates>
 <strictClockBranchRates id="2.branchRates" >
 <rate>
 <parameter id="2.clock.rate" value="1" lower="0" upper="Infinity" />
 </rate>
 </strictClockBranchRates>
 <strictClockBranchRates id="3.branchRates" >
 <rate>
 <parameter id="3.clock.rate" value="1" lower="0" upper="Infinity" />
 </rate>
 </strictClockBranchRates>
<!--  HKY substitution models for gene trees.  -->
 <HKYModel id="1.hky" >
 <frequencies>
 <frequencyModel dataType="nucleotide" >
 <frequencies>
 <parameter id="1.frequencies" value="0.25 0.25 0.25 0.25" />
 </frequencies>
 </frequencyModel>
 </frequencies>
 <kappa>
 <parameter id="1.kappa" value="2" lower="0" upper="Infinity" />
 </kappa>
 </HKYModel>
 <HKYModel id="2.hky" >
 <frequencies>
 <frequencyModel dataType="nucleotide" >
 <frequencies>
 <parameter id="2.frequencies" value="0.25 0.25 0.25 0.25" />
 </frequencies>
 </frequencyModel>
 </frequencies>
 <kappa>
 <parameter id="2.kappa" value="2" lower="0" upper="Infinity" />
 </kappa>
 </HKYModel>
 <HKYModel id="3.hky" >
 <frequencies>
 <frequencyModel dataType="nucleotide" >
 <frequencies>
 <parameter id="3.frequencies" value="0.25 0.25 0.25 0.25" />
```

```
 </frequencies>
 </frequencyModel>
 </frequencies>
 <kappa>
 <parameter id="3.kappa" value="2" lower="0" upper="Infinity" />
 </kappa>
 </HKYModel>
<!--  Site models for gene trees.  -->
 <siteModel id="1.siteModel" >
 <substitutionModel>
 <HKYModel idref="1.hky" />
 </substitutionModel>
 </siteModel>
 <siteModel id="2.siteModel" >
 <substitutionModel>
 <HKYModel idref="2.hky" />
 </substitutionModel>
 </siteModel>
 <siteModel id="3.siteModel" >
 <substitutionModel>
 <HKYModel idref="3.hky" />
 </substitutionModel>
 </siteModel>
<!--  Likelihoods for gene trees.  -->
 <treeLikelihood id="1.treeLikelihood" useAmbiguities="false" >
 <patterns idref="1.patterns" />
 <treeModel idref="1.treeModel" />
 <siteModel idref="1.siteModel" />
 <strictClockBranchRates idref="1.branchRates" />
 </treeLikelihood>
 <treeLikelihood id="2.treeLikelihood" useAmbiguities="false" >
 <patterns idref="2.patterns" />
 <treeModel idref="2.treeModel" />
 <siteModel idref="2.siteModel" />
 <strictClockBranchRates idref="2.branchRates" />
 </treeLikelihood>
 <treeLikelihood id="3.treeLikelihood" useAmbiguities="false" >
 <patterns idref="3.patterns" />
 <treeModel idref="3.treeModel" />
 <siteModel idref="3.siteModel" />
 <strictClockBranchRates idref="3.branchRates" />
 </treeLikelihood>
<!--  Species network model.  -->
<!--  Assignments of sequences to individuals and individuals to species.  -->
 <alloppSpecies id="alloppSpecies" minGeneNodeHeight="0.2" >
 <apsp id="a" ploidylevel="2" >
 <individual id="01a" >
 <taxon idref="01aA" />
 </individual>
 <individual id="02a" >
 <taxon idref="02aA" />
 </individual>
```

```
 <individual id="03a" >
 <taxon idref="03aA" />
 </individual>
 </apsp>
 <apsp id="z" ploidylevel="4" >
 <individual id="01z" >
 <taxon idref="01zA" />
 <taxon idref="01zB" />
 </individual>
 <individual id="02z" >
 <taxon idref="02zA" />
 <taxon idref="02zB" />
 </individual>
 <individual id="03z" >
 <taxon idref="03zA" />
 <taxon idref="03zB" />
 </individual>
 </apsp>
 <apsp id="b" ploidylevel="2" >
 <individual id="01b" >
 <taxon idref="01bA" />
 </individual>
 <individual id="02b" >
 <taxon idref="02bA" />
 </individual>
 <individual id="03b" >
 <taxon idref="03bA" />
 </individual>
 </apsp>
 <geneTrees id="geneTrees" >
 <treeModel idref="1.treeModel" />
 <treeModel idref="2.treeModel" />
 <treeModel idref="3.treeModel" />
 </geneTrees>
 </alloppSpecies>
<!--  Species network, like species tree in *BEAST  -->
 <alloppSpeciesNetwork id="apspnetwork" oneHybridization="true" >
 <alloppSpecies idref="alloppSpecies" />
 <sppSplitPopulations value="0.2" >
 <parameter id="apspnetwork.splitPopSize" />
 </sppSplitPopulations>
 </alloppSpeciesNetwork>
<!--  Prior model for species network (Yule-like model, one parameter)  -->
 <alloppNetworkPriorModel id="one.rate" units="substitutions" >
 <eventRate>
 <parameter id="apspnetwork.prior.eventRate" value="100" lower="0" upper="Infinity" />
 </eventRate>
 </alloppNetworkPriorModel>
<!--  Prior probability for species network  -->
 <apspNetworkPrior id="apspnetwork.prior" >
 <model>
 <alloppNetworkPriorModel idref="one.rate" />
```

```
 </model>
 <apspNetwork>
 <alloppSpeciesNetwork idref="apspnetwork" />
 </apspNetwork>
 </apspNetworkPrior>
<!--  Coalescent for species network: probability that gene trees fit  -->
<!--  into the network.  -->
 <apspCoalescent id="apsp.coalescent" >
 <alloppSpecies idref="alloppSpecies" />
 <alloppSpeciesNetwork idref="apspnetwork" />
 </apspCoalescent>
<!--  Prior for population parameter (vector theta = N*mu)  -->
 <mixedDistributionLikelihood id="species.popSize" >
 <distribution0>
 <gammaDistributionModel>
 <shape>
 2
 </shape>
 <scale>
 <parameter id="species.popMean" value="0.2" lower="0" upper="Infinity" />
 </scale>
 </gammaDistributionModel>
 </distribution0>
 <distribution1>
 <gammaDistributionModel>
 <shape>
 4
 </shape>
 <scale>
 <parameter idref="species.popMean" />
 </scale>
 </gammaDistributionModel>
 </distribution1>
 <data>
 <parameter idref="apspnetwork.splitPopSize" />
 </data>
 <indicators>
 <parameter value=" 1 1 1 0 0 0 0 0" />
 </indicators>
 </mixedDistributionLikelihood>
<!--  Operators for gene trees.  -->
 <operators id="operators" >
 <scaleOperator scaleFactor="0.75" weight="1" >
 <parameter idref="1.kappa" />
 </scaleOperator>
 <scaleOperator scaleFactor="0.75" weight="1" >
 <parameter idref="2.kappa" />
 </scaleOperator>
 <scaleOperator scaleFactor="0.75" weight="1" >
 <parameter idref="3.kappa" />
 </scaleOperator>
 <deltaExchange delta="0.01" weight="1" >
```

```
<parameter idref="1.frequencies" />
</deltaExchange>
<deltaExchange delta="0.01" weight="1" >
<parameter idref="2.frequencies" />
</deltaExchange>
<deltaExchange delta="0.01" weight="1" >
<parameter idref="3.frequencies" />
</deltaExchange>
<scaleOperator scaleFactor="0.75" weight="1" >
<parameter idref="2.clock.rate" />
</scaleOperator>
<scaleOperator scaleFactor="0.75" weight="1" >
<parameter idref="3.clock.rate" />
</scaleOperator>
<subtreeSlide size="0.002" gaussian="true" weight="15" >
<treeModel idref="1.treeModel" />
</subtreeSlide>
<subtreeSlide size="0.002" gaussian="true" weight="15" >
<treeModel idref="2.treeModel" />
</subtreeSlide>
<subtreeSlide size="0.002" gaussian="true" weight="15" >
<treeModel idref="3.treeModel" />
</subtreeSlide>
<narrowExchange weight="15" >
<treeModel idref="1.treeModel" />
</narrowExchange>
<narrowExchange weight="15" >
<treeModel idref="2.treeModel" />
</narrowExchange>
<narrowExchange weight="15" >
<treeModel idref="3.treeModel" />
</narrowExchange>
<wideExchange weight="3" >
<treeModel idref="1.treeModel" />
</wideExchange>
<wideExchange weight="3" >
<treeModel idref="2.treeModel" />
</wideExchange>
<wideExchange weight="3" >
<treeModel idref="3.treeModel" />
</wideExchange>
<wilsonBalding weight="3" >
<treeModel idref="1.treeModel" />
</wilsonBalding>
<wilsonBalding weight="3" >
<treeModel idref="2.treeModel" />
</wilsonBalding>
<wilsonBalding weight="3" >
<treeModel idref="3.treeModel" />
</wilsonBalding>
<scaleOperator scaleFactor="0.75" weight="3" >
<parameter idref="1.treeModel.rootHeight" />
```

```
 </scaleOperator>
 <scaleOperator scaleFactor="0.75" weight="3" >
 <parameter idref="2.treeModel.rootHeight" />
 </scaleOperator>
 <scaleOperator scaleFactor="0.75" weight="3" >
 <parameter idref="3.treeModel.rootHeight" />
 </scaleOperator>
 <uniformOperator weight="30" >
 <parameter idref="1.treeModel.internalNodeHeights" />
 </uniformOperator>
 <uniformOperator weight="30" >
 <parameter idref="2.treeModel.internalNodeHeights" />
 </uniformOperator>
 <uniformOperator weight="30" >
 <parameter idref="3.treeModel.internalNodeHeights" />
 </uniformOperator>
 <upDownOperator scaleFactor="0.75" weight="30" >
 <up>
 </up>
 <down>
 <parameter idref="1.treeModel.allInternalNodeHeights" />
 </down>
 </upDownOperator>
 <upDownOperator scaleFactor="0.75" weight="30" >
 <up>
 <parameter idref="2.clock.rate" />
 </up>
 <down>
 <parameter idref="2.treeModel.allInternalNodeHeights" />
 </down>
 </upDownOperator>
 <upDownOperator scaleFactor="0.75" weight="30" >
 <up>
 <parameter idref="3.clock.rate" />
 </up>
 <down>
 <parameter idref="3.treeModel.allInternalNodeHeights" />
 </down>
 </upDownOperator>
<!--  Operator for both network and gene trees,stretches/squeezes everything.  -->
 <upDownOperator scaleFactor="0.75" weight="30" >
 <up>
 <parameter idref="2.clock.rate" />
 <parameter idref="3.clock.rate" />
 <parameter idref="apspnetwork.prior.eventRate" />
 </up>
 <down>
 <alloppSpeciesNetwork idref="apspnetwork" />
 <parameter idref="species.popMean" />
 <parameter idref="apspnetwork.splitPopSize" />
 <parameter idref="1.treeModel.allInternalNodeHeights" />
 <parameter idref="2.treeModel.allInternalNodeHeights" />
```

```
 <parameter idref="3.treeModel.allInternalNodeHeights" />
 </down>
 </upDownOperator>
<!--  Operators for network.  -->
 <scaleOperator scaleFactor="0.9" weight="5" >
 <parameter idref="species.popMean" />
 </scaleOperator>
 <scaleOperator scaleFactor="0.5" weight="30" >
 <parameter idref="apspnetwork.splitPopSize" />
 </scaleOperator>
 <scaleOperator scaleFactor="0.5" weight="30" >
 <parameter idref="apspnetwork.prior.eventRate" />
 </scaleOperator>
 <networkNodeReHeight weight="30" >
 <alloppSpecies idref="alloppSpecies" />
 <alloppSpeciesNetwork idref="apspnetwork" />
 </networkNodeReHeight>
 <sequenceReassignment weight="30" >
 <alloppSpecies idref="alloppSpecies" />
 <alloppSpeciesNetwork idref="apspnetwork" />
 </sequenceReassignment>
 <moveLegs weight="30" >
 <alloppSpecies idref="alloppSpecies" />
 <alloppSpeciesNetwork idref="apspnetwork" />
 </moveLegs>
 </operators>
 <mcmc id="mcmc" chainLength="1000000" autoOptimize="true" >
 <posterior id="posterior" >
 <prior id="prior" >
 <apspCoalescent idref="apsp.coalescent" />
 <mixedDistributionLikelihood idref="species.popSize" />
 <apspNetworkPrior idref="apspnetwork.prior" />
 <logNormalPrior mean="1" stdev="1.25" offset="0" meanInRealSpace="false" >
 <parameter idref="1.kappa" />
 </logNormalPrior>
 <logNormalPrior mean="1" stdev="1.25" offset="0" meanInRealSpace="false" >
 <parameter idref="2.kappa" />
 </logNormalPrior>
 <logNormalPrior mean="1" stdev="1.25" offset="0" meanInRealSpace="false" >
 <parameter idref="3.kappa" />
 </logNormalPrior>
 <oneOnXPrior>
 <parameter idref="species.popMean" />
 </oneOnXPrior>
 <oneOnXPrior>
 <parameter idref="apspnetwork.prior.eventRate" />
 </oneOnXPrior>
 <gammaPrior shape="0.1" scale="10" offset="0" >
 <parameter idref="2.clock.rate" />
 </gammaPrior>
 <gammaPrior shape="0.1" scale="10" offset="0" >
 <parameter idref="3.clock.rate" />
```

```
 </gammaPrior>
 </prior>
 <likelihood id="likelihood" >
 <treeLikelihood idref="1.treeLikelihood" />
 <treeLikelihood idref="2.treeLikelihood" />
 <treeLikelihood idref="3.treeLikelihood" />
 </likelihood>
 </posterior>
 <operators idref="operators" />
<!--  Log to screen.  -->
 <log id="screenLog" logEvery="1000" >
 <column label="Posterior" dp="4" width="12" >
 <posterior idref="posterior" />
 </column>
 <column label="Prior" dp="4" width="12" >
 <prior idref="prior" />
 </column>
 <column label="Likelihood" dp="4" width="12" >
 <likelihood idref="likelihood" />
 </column>
 <column label="PopMean" sf="6" width="12" >
 <parameter idref="species.popMean" />
 </column>
 </log>
<!--  Main log to file.  -->
 <log id="fileLog" logEvery="1000" fileName=
  "C:/AAA/Programming/Goteborg/simulation_di_tets_multigene/scenarioA/Ag3n3t80/A4LOGg3n3t80r1.txt" >
 <posterior idref="posterior" />
 <prior idref="prior" />
 <likelihood idref="likelihood" />
 <alloppSpecies idref="alloppSpecies" />
 <apspCoalescent idref="apsp.coalescent" />
 <mixedDistributionLikelihood idref="species.popSize" />
 <apspNetworkPrior idref="apspnetwork.prior" />
 <parameter idref="species.popMean" />
 <parameter idref="apspnetwork.splitPopSize" />
 <parameter idref="apspnetwork.prior.eventRate" />
 <parameter idref="1.treeModel.rootHeight" />
 <parameter idref="2.treeModel.rootHeight" />
 <parameter idref="3.treeModel.rootHeight" />
 <parameter idref="1.kappa" />
 <parameter idref="2.kappa" />
 <parameter idref="3.kappa" />
 <parameter idref="1.frequencies" />
 <parameter idref="2.frequencies" />
 <parameter idref="3.frequencies" />
 <parameter idref="1.clock.rate" />
 <parameter idref="2.clock.rate" />
 <parameter idref="3.clock.rate" />
 <treeLikelihood idref="1.treeLikelihood" />
 <treeLikelihood idref="2.treeLikelihood" />
 <treeLikelihood idref="3.treeLikelihood" />
```

```
 </log>
<!--  Gene tree log files.  -->
 <logTree id="1.treeFileLog" logEvery="1000" fileName=
  "C:/AAA/Programming/Goteborg/simulation_di_tets_multigene/scenarioA/Ag3n3t80/A4GTSg3n3t80r1-1.txt"
  sortTranslationTable="true" nexusFormat="true" >
 <treeModel idref="1.treeModel" />
 </logTree>
 <logTree id="2.treeFileLog" logEvery="1000" fileName=
  "C:/AAA/Programming/Goteborg/simulation_di_tets_multigene/scenarioA/Ag3n3t80/A4GTSg3n3t80r1-2.txt"
  sortTranslationTable="true" nexusFormat="true" >
 <treeModel idref="2.treeModel" />
 </logTree>
 <logTree id="3.treeFileLog" logEvery="1000" fileName=
  "C:/AAA/Programming/Goteborg/simulation_di_tets_multigene/scenarioA/Ag3n3t80/A4GTSg3n3t80r1-3.txt"
  sortTranslationTable="true" nexusFormat="true" >
 <treeModel idref="3.treeModel" />
 </logTree>
<!--  MUL-tree log file.  -->
 <logTree id="multreeFileLog" logEvery="1000" fileName=
  "C:/AAA/Programming/Goteborg/simulation_di_tets_multigene/scenarioA/Ag3n3t80/A4MTSg3n3t80r1.txt"
  sortTranslationTable="true" nexusFormat="true" >
 <alloppSpeciesNetwork idref="apspnetwork" />
 </logTree>
<!--  Debugging and tuning log.  -->
 <log id="alloppDBUGTUNE" logEvery="10000" fileName=
  "C:/AAA/Programming/Goteborg/simulation_di_tets_multigene/scenarioA/Ag3n3t80/A9DBUGTUNEg3n3t80r1.txt" >
 <alloppSpeciesNetwork idref="apspnetwork" />
 </log>
 </mcmc>
</beast>
```