Supplementary information for ‘Two MCMC moves for the multi-species coalescent model’ by Graham Jones: tests on priors for STACEY with three new operators

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1 Introduction

This technical report describes some tests carried out on the BEAST2 package STACEY. Version 2.1.3 of BEAST and 0.3.0 of STACEY were used. The main purpose is to test that three new MCMC operators correctly sample from the prior (that is, the posterior when there is no sequence data). The operators are NodesNudge, FocusedScaler, and CoordinatedPruneRegraft. NodesNudge was described in Jones (2014). FocusedScaler and CoordinatedPruneRegraft are described in ‘Two MCMC moves for the multi-species coalescent model’ (unpublished).

There are two sets of tests. One uses a fixed number (8) of species and samples from the prior on the species tree. The other has an unknown number of species (between 1 and 8). Although there is no sequence data, the assumptions about the number of species constitute some ‘meta-data’. In both sets of tests, there is one gene tree with no data, that is with a sequence “?” at each tip. Throughout the following abbreviations are used for the sets of operators.

B: The usual BEAST2 operators. The only ones changing the species tree are NodeReheight and overall scaling operators.

BF: As B with FocusedScaler added.

BN: As B with NodesNudge added.

BR: As B with CoordinatedPruneRegraft added.

None of the three new operators without NodeReheight result in an irreducible MCMC chain. NodesNudge and FocusedScaler only affect heights, and CoordinatedPruneRegraft only affects topology. Even with all three it is not clear (to me now) if they would produce an irreducible chain: there might be issues at the root. Therefore they are used in combination with NodeReheight. They were given equal weight to NodeReheight in BF, BN, and BR, which was equal to half that used for NodeReheight in B.

2 Species tree prior with fixed delimitation

2.1 Scenario and settings

Here is the config file. The BEAST XML was generated from this using an R script.

```
PROGRAMPARAMETERS
beast.popmean.prior fixed 0.01 0.01
beast.growthrate.prior fixed 100 100
beast.reldeathrate.prior fixed 0 0
beast.relativerates.prior lnorm 0 1
beast.collapseweight.prior fixed 0 0
```

```
beast.collapseheight 0.00001
beastseed 42
beastchainlength 55000000
beastscreen.logevery 100000
beastparams.logevery 20000
beastgtrees.logevery 20000
beastspptree.logevery 20000
treeann.gtrees.burnin 101
treeann.stree.burnin 101
sppdelimanal.burnin 101
sppdelimanal.collapseheight 0.00001
sppdelimanal.simcutoff 1.0
msc.model STACEYD
SCENARIO
nofGNRT 1
1 * 1 1 1e-8
genelength 1
nofspp 1
a                           nindivs 8   hgt 0      tipp 138600 rootp 69300
```

The format of the file was designed for a somewhat different purpose, so several things are ignored or overridden. The XML files should be examined to clarify any doubts.

The population scaling factor (‘beast.popmean.prior’ above) σ is fixed to 0.01. A Yule model for the species tree prior was assumed. To achieve this, the relative death rate μ is set to 0. The growth rate λ was 100. The combination $\lambda = 100$, $\sigma = 0.01$ means that a pair of sequences coalesce in a time equal to the mean branch length. This results in a moderate amount of incomplete lineage sorting.

Since the collapse weight w is fixed at zero, the collapse height is ignored.

The burnin was set to 10% of the run (overriding the values above). There were about 2500 samples.

Note that the species tree in the config file is ignored (it is usually used to simulate sequences). This was the simplest way to produce XML in which there are 8 sequences at the tips of the gene tree, one per species.

2.2 Results

Figure 1 shows how the 4 combinations of operators sample from the possible topologies. The theoretical values can be calculated by using the fact that each of the splits in a tree sampled form the Yule model is distributed uniformly. For example, a clade of size 8 is is equally likely to split 1:7, 2:6, 3:5, 4:4, 5:3, 6:2, 7:1 at the root. The following table shows the calculations.

(*,(*,(*,(*,U))))	(2/7)*(2/6)*(2/5)*(2/4)*(2/3)
(*,(*,(*,(*,B))))	(2/7)*(2/6)*(2/5)*(2/4)*(1/3)
(*,(*,(*,(C,T))))	(2/7)*(2/6)*(2/5)*(2/4)
(*,(*,(C,U)))	(2/7)*(2/6)*(2/5)*(2/3)
(*,(*,(C,B)))	(2/7)*(2/6)*(2/5)*(1/3)
(*,(*,(T,T)))	(2/7)*(2/6)*(1/5)
(*,(C,(*,U)))	(2/7)*(2/6)*(2/4)*(2/3)
(*,(C,(*,B)))	(2/7)*(2/6)*(2/4)*(1/3)
(*,(C,(C,T)))	(2/7)*(2/6)*(2/4)
(*,(T,U))	(2/7)*(2/6)*(2/3)
(*,(T,B))	(2/7)*(2/6)*(1/3)
(C,(*,(*,U)))	(2/7)*(2/5)*(2/4)*(2/3)
(C,(*,(*,B)))	(2/7)*(2/5)*(2/4)*(1/3)
(C,(*,(C,T)))	(2/7)*(2/5)*(2/4)

```
(C,(C,U))          (2/7)*(2/5)*(2/3)
(C,(C,B))          (2/7)*(2/5)*(1/3)
(C,(T,T))          (2/7)*(1/5)
(T,(*,U))          (2/7)*(2/4)*(2/3)
(T,(*,B))          (2/7)*(2/4)*(1/3)
(T,(C,T))          (2/7)*(2/4)
(U,U)              (1/7)*(2/3)*(2/3)
(U,B)              (1/7)*(2/3)*(1/3)*2
(B,B)              (1/7)*(1/3)*(1/3)
```

Figures 2, 3, 4, and 5 show how the 4 combinations of operators sample the speciation heights. The theoretical values come from Gernhard (2008).

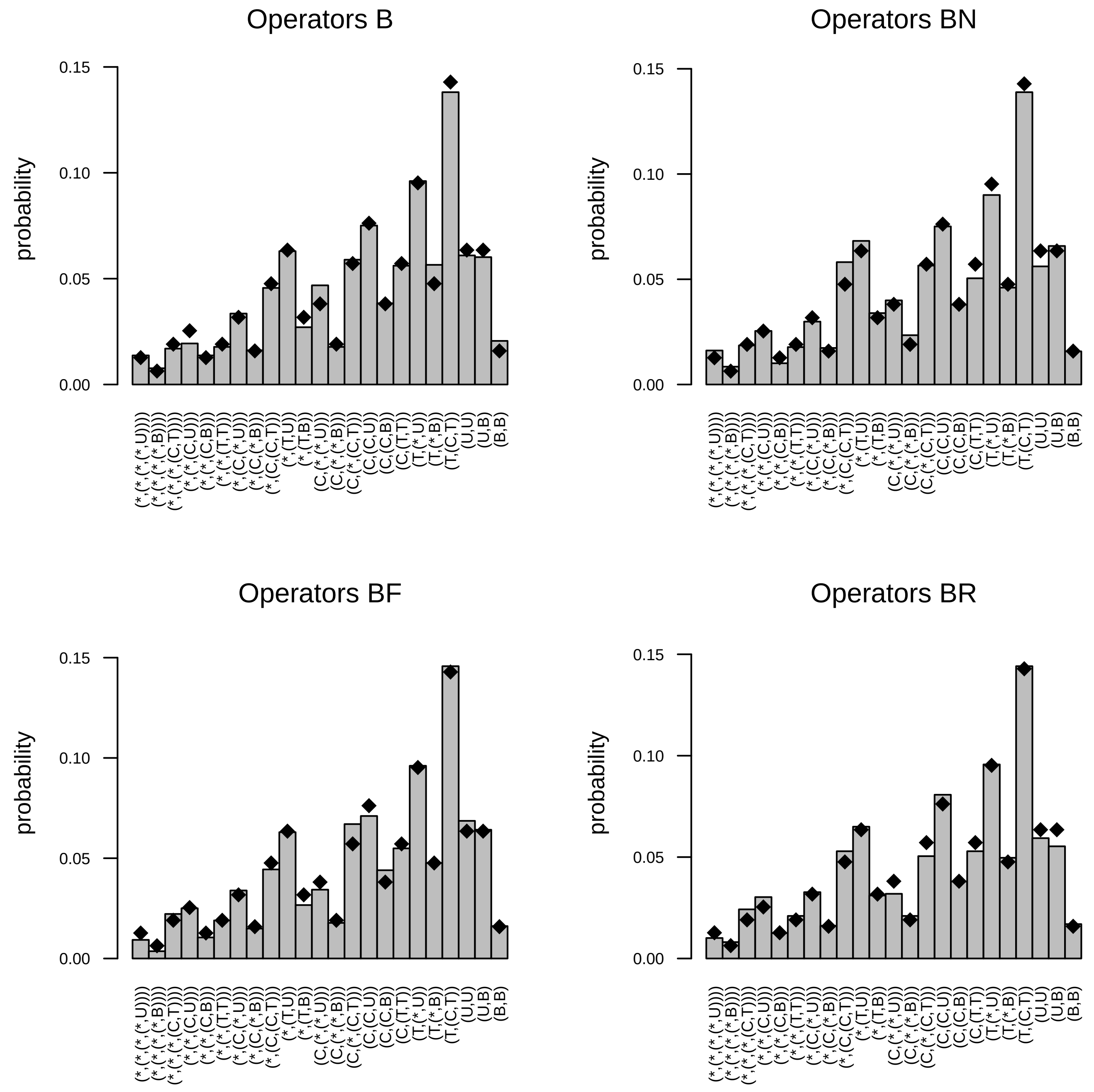


Figure 1: Estimated posterior probabilities for each of the 23 unlabeled rooted topologies with eight tips are shown in grey bars. The theoretical values are shown as diamonds. The x-axis annotations show the topologies in the following format. A tip is shown by *****. A cherry **(*,*)** is denoted as **C**, a 3-tip tree **(*,(*,*))** as **T**, an unbalanced 4-tip tree as **U** and a balanced 4-tip tree as **B**. Otherwise, the Newick format is used. For example **(T,(*,U))** is short for **((*,(*,*)),(*,(*,(*,(*,*)))))**.

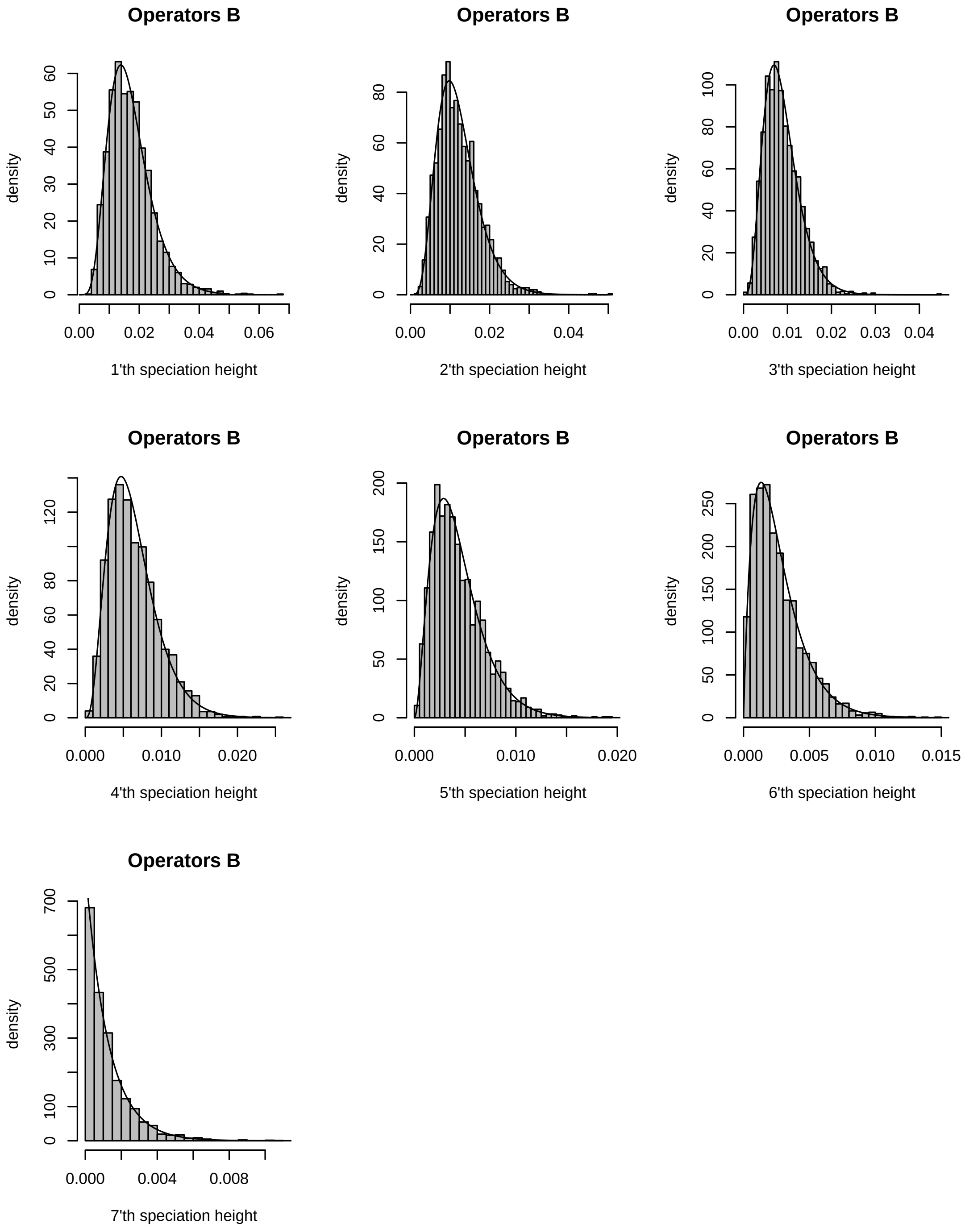


Figure 2: Histograms of the MCMC samples for the successive speciation heights. The theoretical densities are shown as curves.

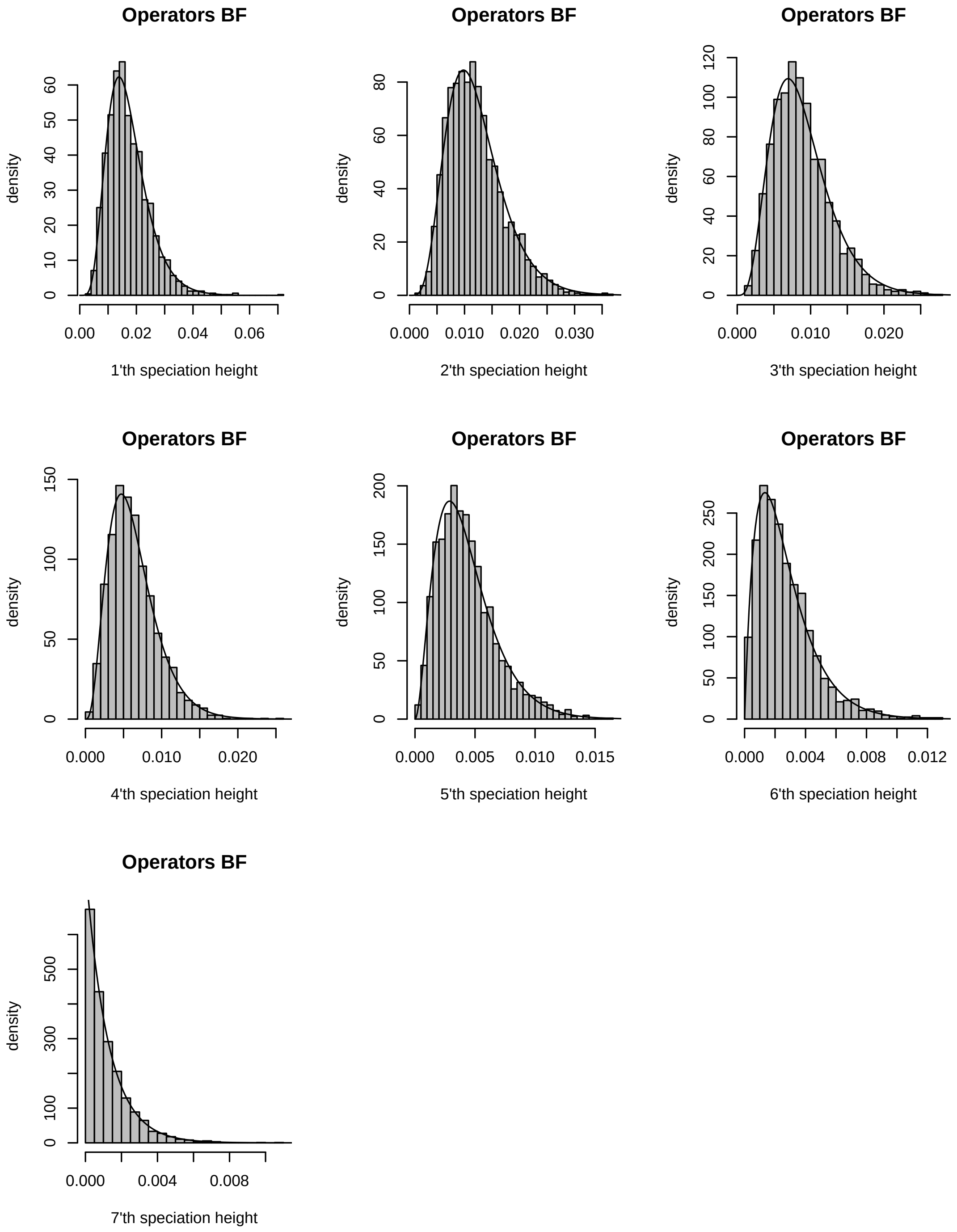


Figure 3: Histograms of the MCMC samples for the successive speciation heights. The theoretical densities are shown as curves.

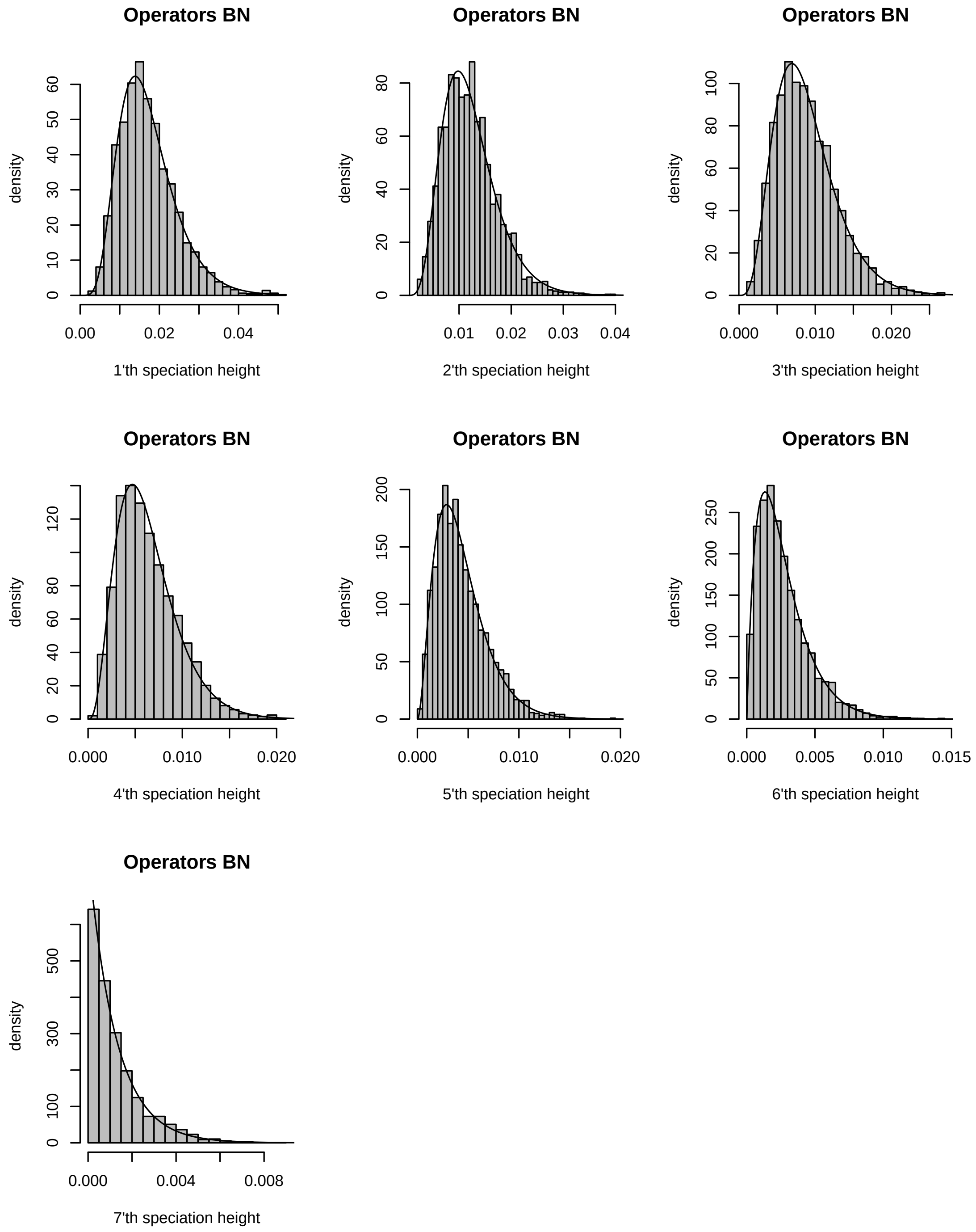


Figure 4: Histograms of the MCMC samples for the successive speciation heights. The theoretical densities are shown as curves.

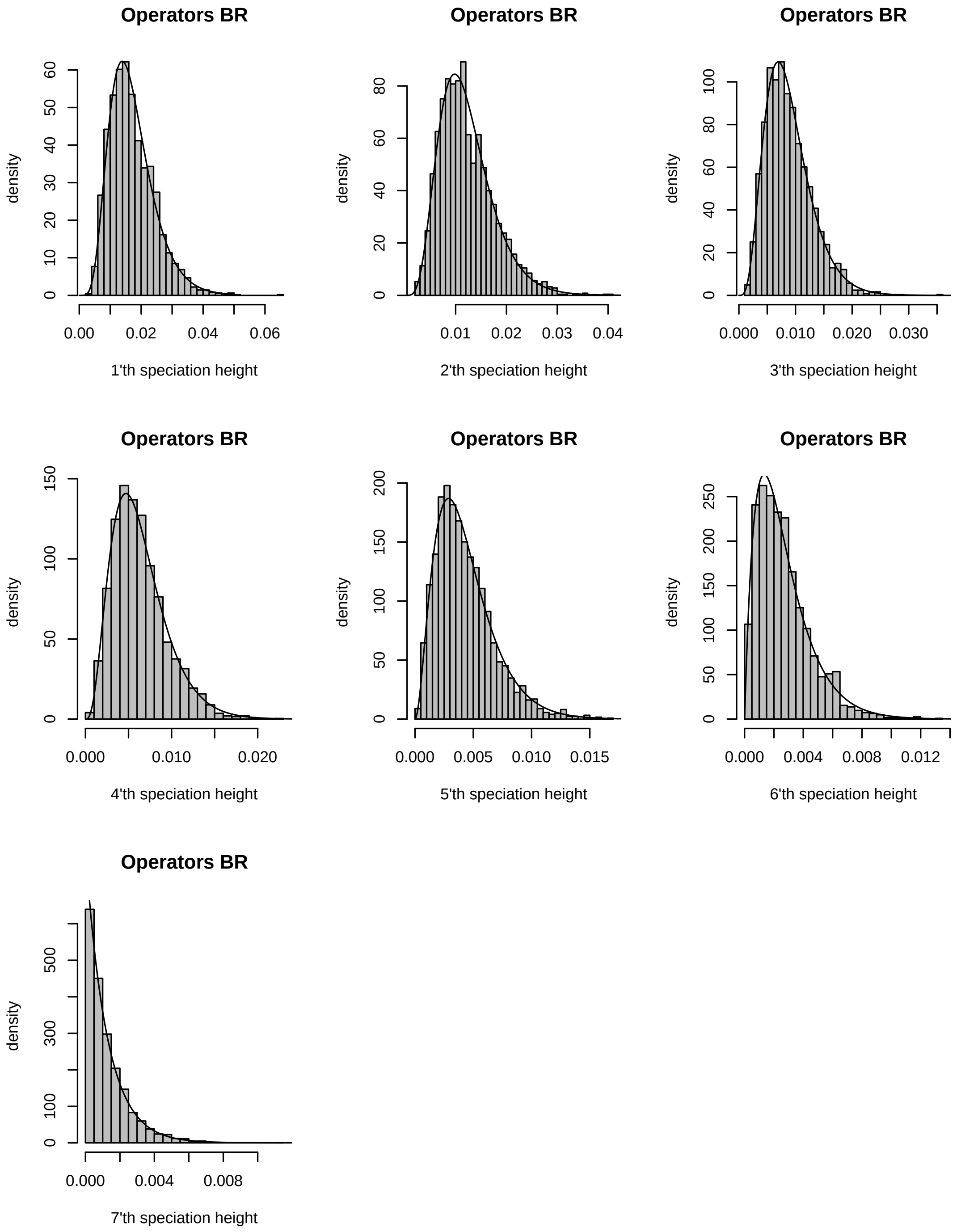


Figure 5: Histograms of the MCMC samples for the successive speciation heights. The theoretical densities are shown as curves.

3 Species delimitation

3.1 Scenario and settings

Here is the config file.

```
PROGRAMPARAMETERS
beast.popmean.prior fixed 0.01 0.01
beast.growthrate.prior fixed 100 100
beast.reldeathrate.prior fixed 0 0
beast.relativerates.prior lnorm 0 1
beast.collapseweight.prior beta 1 1
beast.collapseheight 0.00001
beastseed 42
beastchainlength 110000000
beastscreen.logevery 100000
beastparams.logevery 10000
beastgtrees.logevery 10000
beastspptree.logevery 10000
treeann.gtrees.burnin 1001
treeann.stree.burnin 1001
sppdelimanal.burnin 1001
sppdelimanal.collapseheight 0.00001
sppdelimanal.simcutoff 1.0
msc.model STACEYD
SCENARIO
nofGNRT 1
1 * 1 1 1e-8
genelength 1
nofspp 1
a                           nindivs 8  hgt 0      tipp 138600 rootp 138600
```

In this case w is given a uniform prior on [0,1], resulting in a flat prior on the number of species between 1 and 8.

The population scaling factor 'popmean' σ is fixed to 0.01. A Yule model for the species tree prior was assumed. To achieve this, the relative death rate μ is set to 0. The growth rate λ was 100. The combination $\lambda = 100$, $\sigma = 0.01$ means that a pair of sequences coalesce in a time equal to the mean branch length.

The burnin was set to 10% of the run (overriding the values above). There were about 10000 samples.

The collapse height ϵ was set to 1e-5. This is about 1/1000 of the expected branch lengths of 0.01.

3.2 Results

Figure 6 shows estimated and theoretical values for the 22 partitions of the number 8. Each partition of 8 represents one or more clusterings of 8 objects. There are a total of 4140 clusterings of 8 objects, and these can be grouped into 22 sets corresponding to the partitions of 8. For example suppose the 8 objects are a, b, c, d, e, f, g, h. One clustering is $\{\{a, b, c\}, \{d\}, \{e, f, g, h\}\}$, which corresponds to the partition 4+3+1 of 8. There are 280 clusterings with the shape 4+3+1, and whenever one of these are visited during the MCMC, it counts towards the posterior probability of this partition of 8. The following table shows the list of partitions and their probabilities given the number of clusters N. These values are calculated using the supplementary information of Jones et al. (2014). The assumption of a uniform prior on the number of clusters means that $P(N = i) = 1/8$ for $1 \leq i \leq 8$ so the theoretical values shown in the Figure are 1/8 of the numbers in the table.

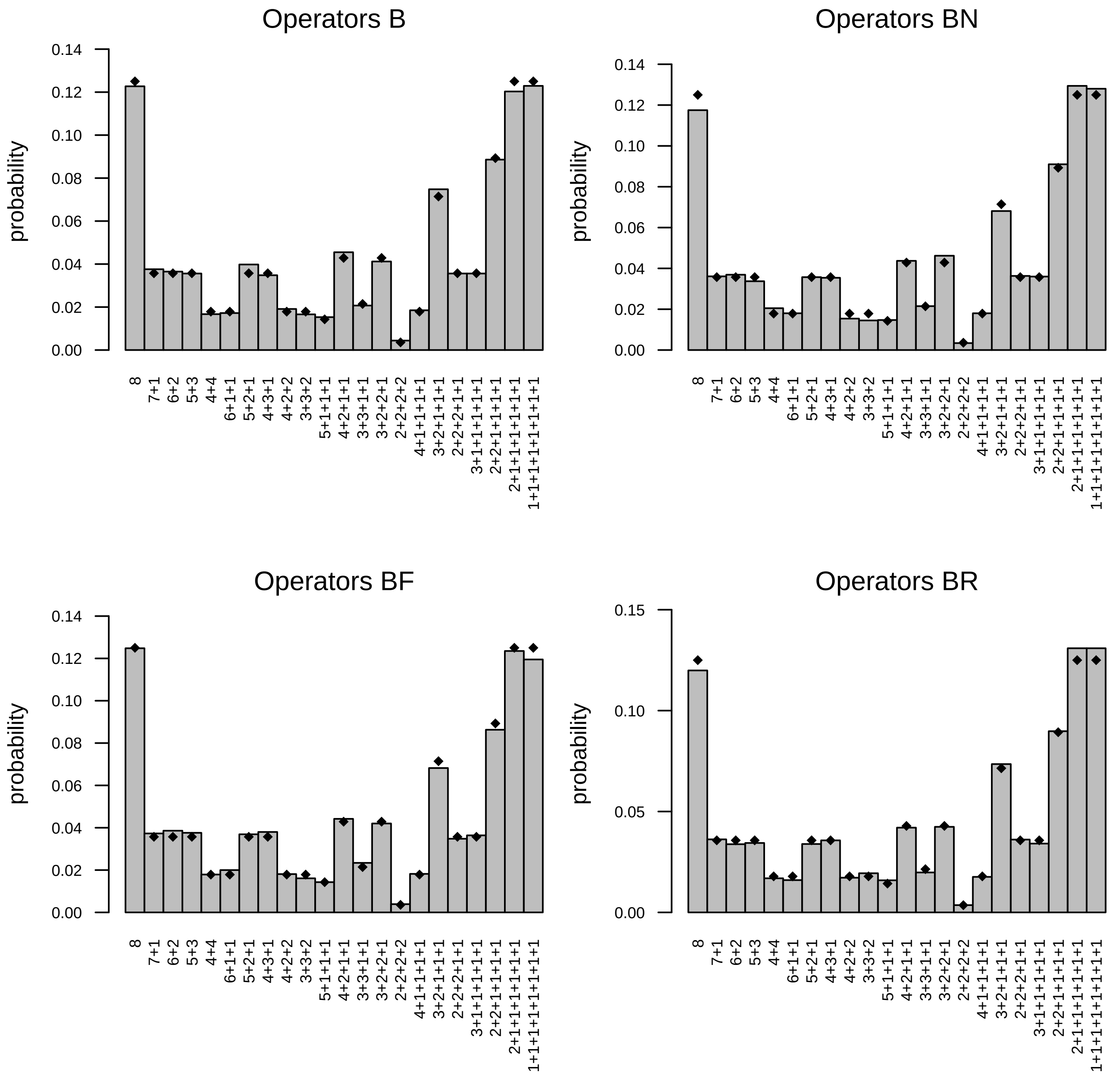
```
partition of 8   P(shape|N)
```

```
8                 35/35

7+1               10/35
6+2               10/35
5+3               10/35
4+4                5/35

6+1+1              5/35
5+2+1             10/35
4+3+1             10/35
4+2+2              5/35
3+3+2              5/35

5+1+1+1            4/35
4+2+1+1           12/35
3+3+1+1            6/35
3+2+2+1           12/35
2+2+2+2            1/35

4+1+1+1+1          5/35
3+2+1+1+1         20/35
2+2+2+1+1         10/35

3+1+1+1+1+1       10/35
2+2+1+1+1+1       25/35

2+1+1+1+1+1+1     35/35

1+1+1+1+1+1+1+1   35/35
```

Figures 7, 8, 9, and 10, show how the 4 combinations of operators sample some parameters and other values. The likelihood is extremely close to zero as expected. The posteriors for w and the number of clusters are close to uniform, as they should be.

In the BirthDeathCollapseModel graph, which shows the contribution this makes to the posterior, distinct peaks can be seen which appear to represent the different numbers of clusters (although some peaks are merged).

As well as the figures, the summary output from CODA (Plummer et al., 2006) is shown.


Operators B

Operators BN

Operators BF

Operators BR

Figure 6: Estimated posterior probabilities for the 22 partitions of the integer 8 are shown in grey bars. The theoretical values are shown as diamonds. See text for further explanation.

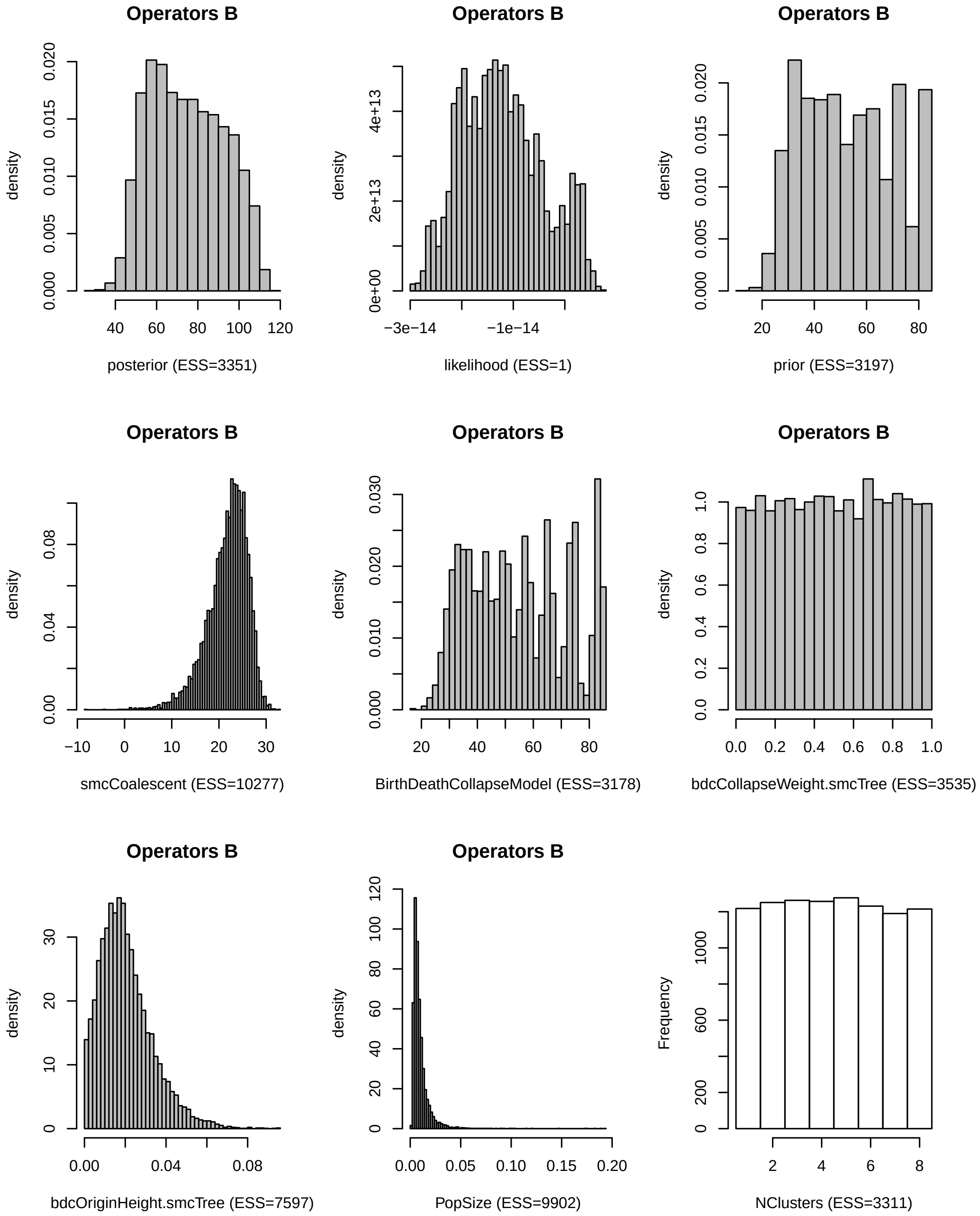


Figure 7: Histograms for various quantities and other qunatities.

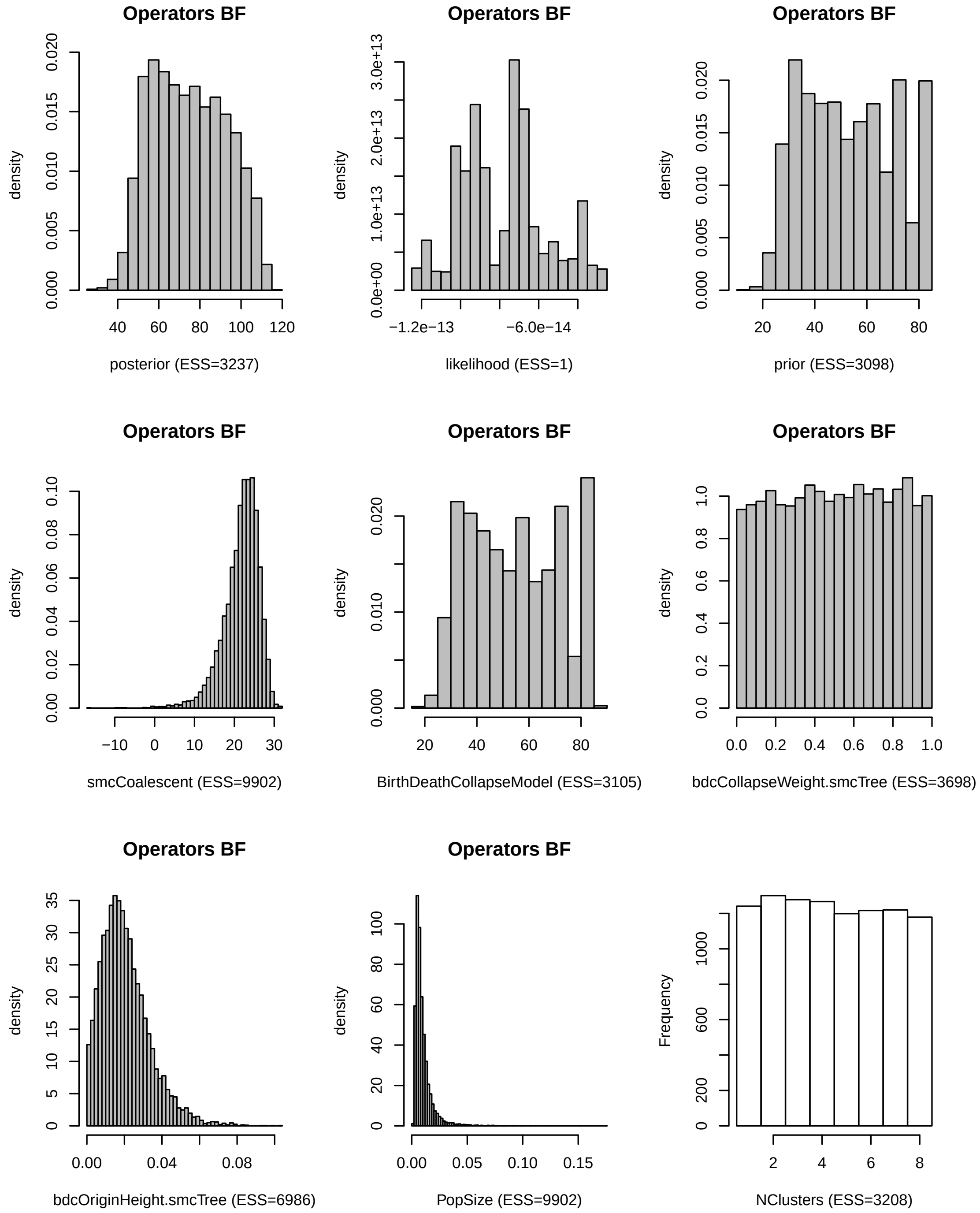


Figure 8: xxxxxx.

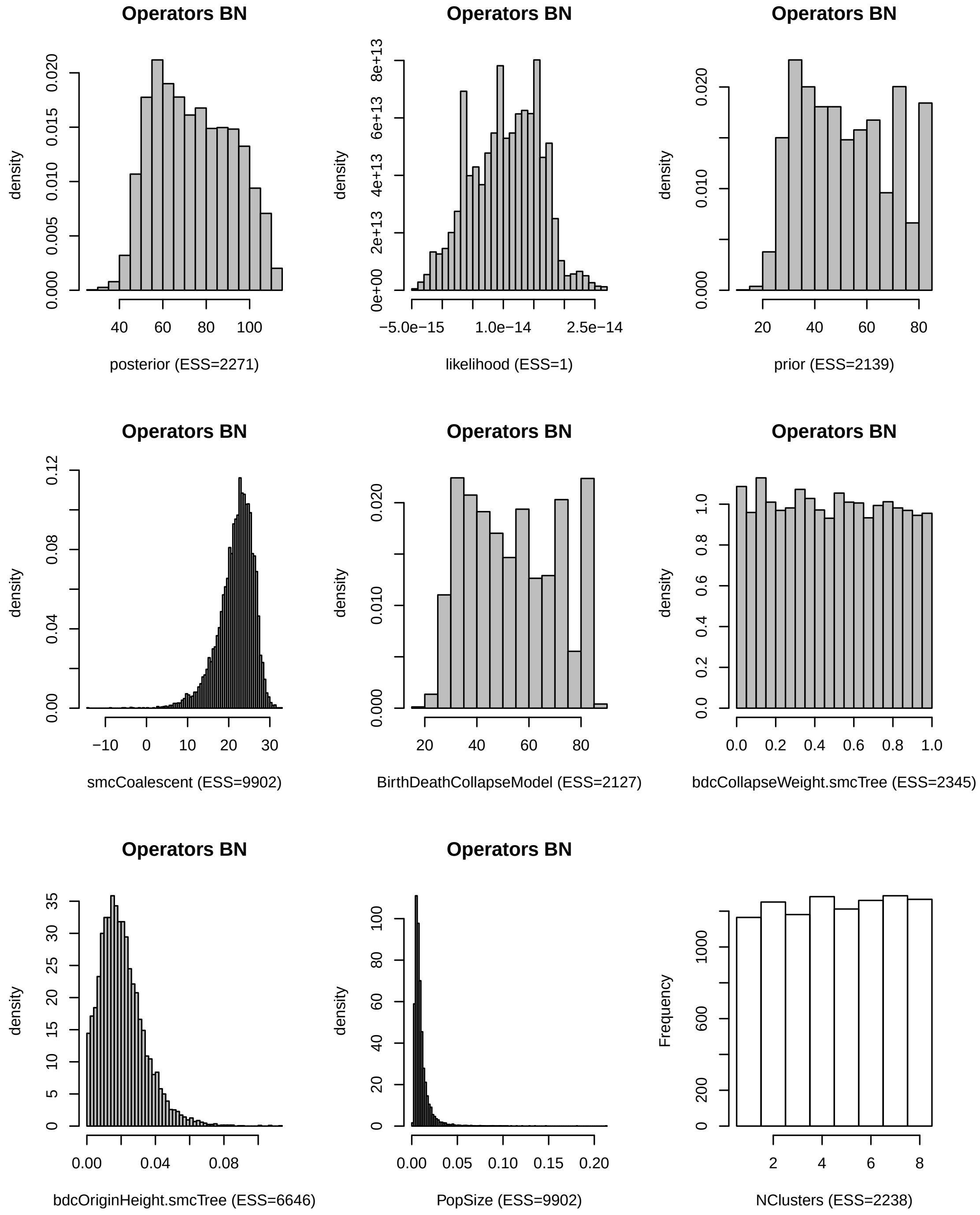


Figure 9: xxxxxx.

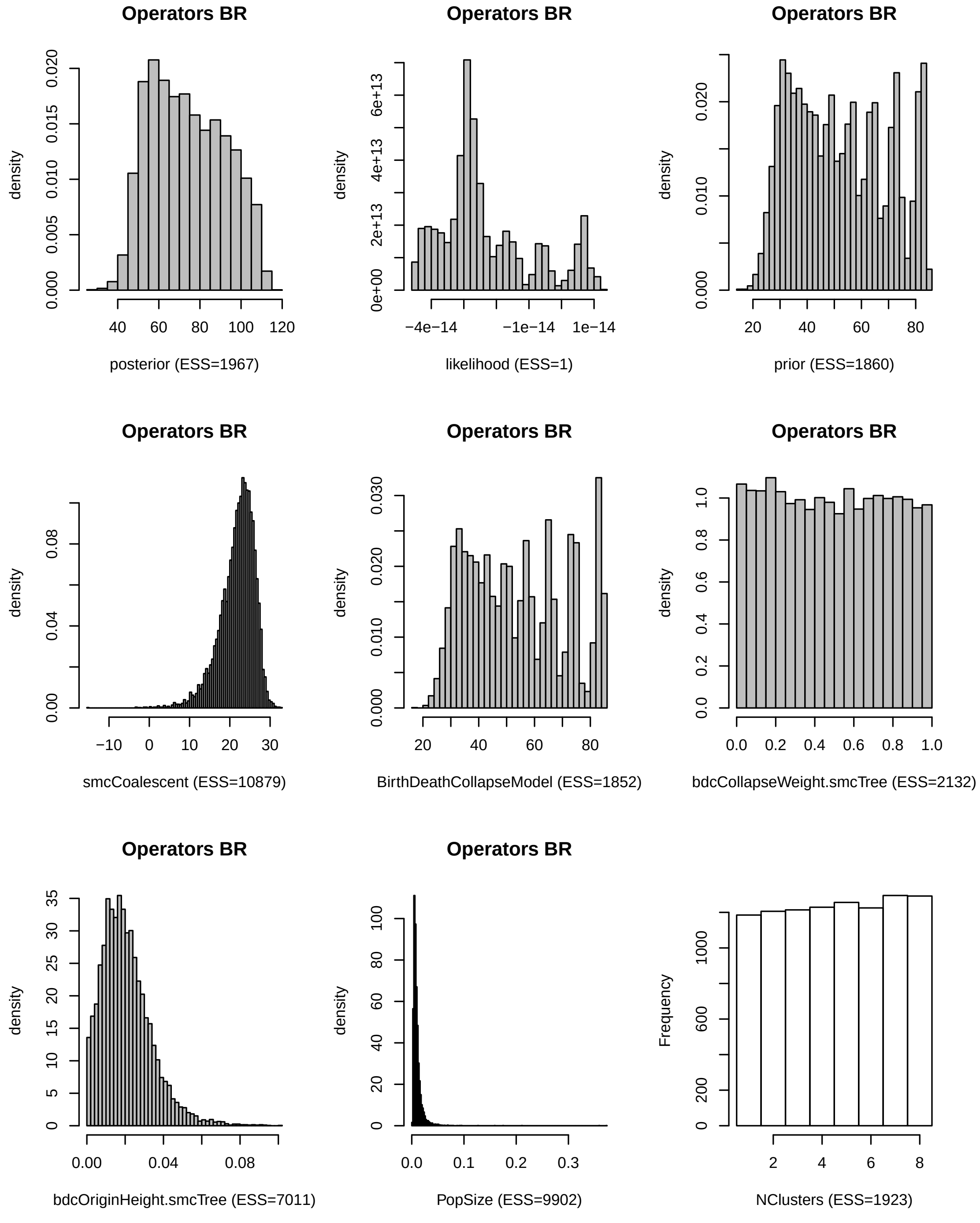


Figure 10: xxxxxx.

Operators B

```
Iterations = 1:9902,
Thinning interval = 1
Number of chains = 1
Sample size per chain = 9902
1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:
                                   Mean        SD  Naive SE Time-series SE
Sample                        6.049e+07 2.859e+07 2.873e+05      2.334e+07
posterior                     7.477e+01 1.778e+01 1.787e-01      3.072e-01
likelihood                   -1.212e-14 7.872e-15 7.911e-17      0.000e+00
prior                         5.299e+01 1.748e+01 1.757e-01      3.092e-01
smcCoalescent                 2.178e+01 4.266e+00 4.287e-02      4.208e-02
popPriorScale                 1.000e-02 0.000e+00 0.000e+00      0.000e+00
BirthDeathCollapseModel       5.463e+01 1.744e+01 1.752e-01      3.093e-01
bdcGrowthRate.smcTree         1.000e+02 0.000e+00 0.000e+00      0.000e+00
bdcRelativeDeathRate.smcTree  0.000e+00 0.000e+00 0.000e+00      0.000e+00
bdcCollapseWeight.smcTree     5.028e-01 2.877e-01 2.892e-03      4.839e-03
bdcOriginHeight.smcTree       2.037e-02 1.278e-02 1.284e-04      1.466e-04
NClusters                     4.480e+00 2.276e+00 2.288e-02      3.956e-02
PopSize                       9.924e-03 9.457e-03 9.503e-05      9.503e-05
genetreeLhood.1              -1.212e-14 7.872e-15 7.911e-17      0.000e+00
clockRate.1                   1.000e+00 0.000e+00 0.000e+00      0.000e+00
kappa.1                       2.175e+00 3.964e+00 3.984e-02      4.615e-02
frequencies.11                2.487e-01 1.930e-01 1.940e-03      2.314e-03
frequencies.12                2.531e-01 1.954e-01 1.964e-03      2.352e-03
frequencies.13                2.522e-01 1.948e-01 1.958e-03      2.333e-03
frequencies.14                2.461e-01 1.942e-01 1.952e-03      2.354e-03

2. Quantiles for each variable:
                                   2.5%        25%        50%        75%     97.5%
Sample                        1.347e+07  3.574e+07  6.049e+07  8.525e+07 1.075e+08
posterior                     4.618e+01  5.978e+01  7.374e+01  8.923e+01 1.075e+02
likelihood                   -2.576e-14 -1.821e-14 -1.277e-14 -6.883e-15 3.331e-15
prior                         2.580e+01  3.762e+01  5.164e+01  6.718e+01 8.307e+01
smcCoalescent                 1.172e+01  1.949e+01  2.249e+01  2.481e+01 2.808e+01
popPriorScale                 1.000e-02  1.000e-02  1.000e-02  1.000e-02 1.000e-02
BirthDeathCollapseModel       2.779e+01  3.913e+01  5.331e+01  6.942e+01 8.421e+01
bdcGrowthRate.smcTree         1.000e+02  1.000e+02  1.000e+02  1.000e+02 1.000e+02
bdcRelativeDeathRate.smcTree  0.000e+00  0.000e+00  0.000e+00  0.000e+00 0.000e+00
bdcCollapseWeight.smcTree     2.473e-02  2.532e-01  5.021e-01  7.518e-01 9.745e-01
bdcOriginHeight.smcTree       1.810e-03  1.111e-02  1.829e-02  2.713e-02 5.116e-02
NClusters                     1.000e+00  3.000e+00  4.000e+00  6.000e+00 8.000e+00
PopSize                       2.802e-03  5.040e-03  7.421e-03  1.146e-02 3.202e-02
genetreeLhood.1              -2.576e-14 -1.821e-14 -1.277e-14 -6.883e-15 3.331e-15
clockRate.1                   1.000e+00  1.000e+00  1.000e+00  1.000e+00 1.000e+00
kappa.1                       8.527e-02  4.250e-01  1.014e+00  2.298e+00 1.191e+01
frequencies.11                8.426e-03  9.136e-02  2.042e-01  3.675e-01 7.044e-01
frequencies.12                1.038e-02  9.339e-02  2.075e-01  3.753e-01 7.178e-01
frequencies.13                8.560e-03  9.262e-02  2.064e-01  3.733e-01 7.090e-01
frequencies.14                6.870e-03  8.802e-02  2.030e-01  3.675e-01 7.006e-01
```

```
Operators BF
Iterations = 1:9902
Thinning interval = 1
Number of chains = 1
Sample size per chain = 9902

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:
                                   Mean        SD  Naive SE Time-series SE
Sample                        6.049e+07 2.859e+07 2.873e+05      2.334e+07
posterior                     7.490e+01 1.797e+01 1.806e-01      3.158e-01
likelihood                   -7.795e-14 2.220e-14 2.231e-16      0.000e+00
prior                         5.318e+01 1.758e+01 1.767e-01      3.159e-01
smcCoalescent                 2.173e+01 4.438e+00 4.460e-02      4.460e-02
popPriorScale                 1.000e-02 0.000e+00 0.000e+00      0.000e+00
BirthDeathCollapseModel       5.485e+01 1.752e+01 1.760e-01      3.143e-01
bdcGrowthRate.smcTree         1.000e+02 0.000e+00 0.000e+00      0.000e+00
bdcRelativeDeathRate.smcTree  0.000e+00 0.000e+00 0.000e+00      0.000e+00
bdcCollapseWeight.smcTree     5.046e-01 2.871e-01 2.885e-03      4.721e-03
bdcOriginHeight.smcTree       2.059e-02 1.286e-02 1.293e-04      1.539e-04
NClusters                     4.445e+00 2.283e+00 2.294e-02      4.031e-02
PopSize                       9.939e-03 8.714e-03 8.757e-05      8.757e-05
genetreeLhood.1              -7.795e-14 2.220e-14 2.231e-16      0.000e+00
clockRate.1                   1.000e+00 0.000e+00 0.000e+00      0.000e+00
kappa.1                       2.259e+00 4.347e+00 4.368e-02      4.982e-02
frequencies.11                2.495e-01 1.936e-01 1.945e-03      2.533e-03
frequencies.12                2.514e-01 1.917e-01 1.926e-03      2.537e-03
frequencies.13                2.508e-01 1.940e-01 1.949e-03      2.525e-03
frequencies.14                2.483e-01 1.928e-01 1.938e-03      2.559e-03

2. Quantiles for each variable:
                                   2.5%        25%        50%        75%      97.5%
Sample                        1.347e+07  3.574e+07  6.049e+07  8.525e+07  1.075e+08
posterior                     4.567e+01  5.972e+01  7.402e+01  8.949e+01  1.079e+02
likelihood                   -1.179e-13 -9.481e-14 -7.527e-14 -6.684e-14 -3.453e-14
prior                         2.569e+01  3.758e+01  5.214e+01  6.815e+01  8.316e+01
smcCoalescent                 1.124e+01  1.944e+01  2.243e+01  2.481e+01  2.825e+01
popPriorScale                 1.000e-02  1.000e-02  1.000e-02  1.000e-02  1.000e-02
BirthDeathCollapseModel       2.790e+01  3.922e+01  5.422e+01  7.063e+01  8.424e+01
bdcGrowthRate.smcTree         1.000e+02  1.000e+02  1.000e+02  1.000e+02  1.000e+02
bdcRelativeDeathRate.smcTree  0.000e+00  0.000e+00  0.000e+00  0.000e+00  0.000e+00
bdcCollapseWeight.smcTree     2.668e-02  2.571e-01  5.084e-01  7.529e-01  9.755e-01
bdcOriginHeight.smcTree       1.990e-03  1.134e-02  1.851e-02  2.747e-02  5.200e-02
NClusters                     1.000e+00  2.000e+00  4.000e+00  6.000e+00  8.000e+00
PopSize                       2.769e-03  5.130e-03  7.486e-03  1.164e-02  3.221e-02
genetreeLhood.1              -1.179e-13 -9.481e-14 -7.527e-14 -6.684e-14 -3.453e-14
clockRate.1                   1.000e+00  1.000e+00  1.000e+00  1.000e+00  1.000e+00
kappa.1                       8.565e-02  4.326e-01  1.014e+00  2.406e+00  1.203e+01
frequencies.11                7.723e-03  9.145e-02  2.082e-01  3.681e-01  7.092e-01
frequencies.12                7.584e-03  9.299e-02  2.089e-01  3.748e-01  6.884e-01
frequencies.13                8.579e-03  9.234e-02  2.070e-01  3.741e-01  7.061e-01
frequencies.14                8.344e-03  8.986e-02  2.059e-01  3.661e-01  7.104e-01
```

```
Operators BN
Iterations = 1:9902
Thinning interval = 1
Number of chains = 1
Sample size per chain = 9902

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:
                                Mean        SD  Naive SE Time-series SE
Sample                     6.049e+07 2.859e+07 2.873e+05      2.334e+07
posterior                  7.417e+01 1.790e+01 1.799e-01      3.756e-01
likelihood                 1.043e-14 5.625e-15 5.653e-17      0.000e+00
prior                      5.242e+01 1.759e+01 1.768e-01      3.804e-01
smcCoalescent              2.174e+01 4.304e+00 4.325e-02      4.325e-02
popPriorScale              1.000e-02 0.000e+00 0.000e+00      0.000e+00
BirthDeathCollapseModel    5.405e+01 1.752e+01 1.760e-01      3.798e-01
bdcGrowthRate.smcTree      1.000e+02 0.000e+00 0.000e+00      0.000e+00
bdcRelativeDeathRate.smcTree 0.000e+00 0.000e+00 0.000e+00      0.000e+00
bdcCollapseWeight.smcTree  4.928e-01 2.890e-01 2.905e-03      5.969e-03
bdcOriginHeight.smcTree    2.069e-02 1.296e-02 1.302e-04      1.589e-04
NClusters                  4.553e+00 2.286e+00 2.297e-02      4.831e-02
PopSize                    1.005e-02 9.450e-03 9.497e-05      9.497e-05
genetreeLhood.1            1.043e-14 5.625e-15 5.653e-17      0.000e+00
clockRate.1                1.000e+00 0.000e+00 0.000e+00      0.000e+00
kappa.1                    2.127e+00 3.797e+00 3.816e-02      4.309e-02
frequencies.11             2.507e-01 1.926e-01 1.936e-03      2.730e-03
frequencies.12             2.493e-01 1.940e-01 1.950e-03      2.672e-03
frequencies.13             2.516e-01 1.956e-01 1.966e-03      2.723e-03
frequencies.14             2.484e-01 1.935e-01 1.945e-03      2.687e-03

2. Quantiles for each variable:
                                 2.5%       25%       50%       75%     97.5%
Sample                      1.347e+07 3.574e+07 6.049e+07 8.525e+07 1.075e+08
posterior                   4.549e+01 5.907e+01 7.283e+01 8.880e+01 1.074e+02
likelihood                 -7.772e-16 6.217e-15 1.066e-14 1.488e-14 2.053e-14
prior                       2.554e+01 3.689e+01 5.051e+01 6.664e+01 8.302e+01
smcCoalescent               1.118e+01 1.951e+01 2.246e+01 2.477e+01 2.813e+01
popPriorScale               1.000e-02 1.000e-02 1.000e-02 1.000e-02 1.000e-02
BirthDeathCollapseModel     2.758e+01 3.839e+01 5.207e+01 6.819e+01 8.417e+01
bdcGrowthRate.smcTree       1.000e+02 1.000e+02 1.000e+02 1.000e+02 1.000e+02
bdcRelativeDeathRate.smcTree  0.000e+00 0.000e+00 0.000e+00 0.000e+00 0.000e+00
bdcCollapseWeight.smcTree   2.431e-02 2.438e-01 4.923e-01 7.430e-01 9.772e-01
bdcOriginHeight.smcTree     1.794e-03 1.135e-02 1.870e-02 2.771e-02 5.168e-02
NClusters                   1.000e+00 3.000e+00 5.000e+00 7.000e+00 8.000e+00
PopSize                     2.761e-03 5.167e-03 7.548e-03 1.148e-02 3.292e-02
genetreeLhood.1            -7.772e-16 6.217e-15 1.066e-14 1.488e-14 2.053e-14
clockRate.1                 1.000e+00 1.000e+00 1.000e+00 1.000e+00 1.000e+00
kappa.1                     9.058e-02 4.219e-01 9.943e-01 2.291e+00 1.128e+01
frequencies.11              7.595e-03 9.251e-02 2.106e-01 3.704e-01 7.021e-01
frequencies.12              8.317e-03 9.390e-02 2.019e-01 3.675e-01 7.141e-01
frequencies.13              7.119e-03 8.712e-02 2.096e-01 3.761e-01 7.023e-01
frequencies.14              8.212e-03 8.997e-02 2.038e-01 3.644e-01 7.076e-01
```

```
Operators BR
Iterations = 1:9902
Thinning interval = 1
Number of chains = 1
Sample size per chain = 9902

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:
                                   Mean        SD  Naive SE Time-series SE
Sample                        6.049e+07 2.859e+07 2.873e+05      2.334e+07
posterior                     7.418e+01 1.796e+01 1.805e-01      4.049e-01
likelihood                   -2.324e-14 1.426e-14 1.433e-16      0.000e+00
prior                         5.235e+01 1.758e+01 1.767e-01      4.077e-01
smcCoalescent                 2.182e+01 4.300e+00 4.321e-02      4.122e-02
popPriorScale                 1.000e-02 0.000e+00 0.000e+00      0.000e+00
BirthDeathCollapseModel       5.399e+01 1.753e+01 1.762e-01      4.073e-01
bdcGrowthRate.smcTree         1.000e+02 0.000e+00 0.000e+00      0.000e+00
bdcRelativeDeathRate.smcTree  0.000e+00 0.000e+00 0.000e+00      0.000e+00
bdcCollapseWeight.smcTree     4.938e-01 2.904e-01 2.919e-03      6.290e-03
bdcOriginHeight.smcTree       2.073e-02 1.299e-02 1.305e-04      1.551e-04
NClusters                     4.563e+00 2.293e+00 2.304e-02      5.228e-02
PopSize                       1.009e-02 1.019e-02 1.024e-04      1.024e-04
genetreeLhood.1              -2.324e-14 1.426e-14 1.433e-16      0.000e+00
clockRate.1                   1.000e+00 0.000e+00 0.000e+00      0.000e+00
kappa.1                       2.155e+00 3.944e+00 3.964e-02      4.372e-02
frequencies.11                2.500e-01 1.982e-01 1.992e-03      3.100e-03
frequencies.12                2.502e-01 1.963e-01 1.972e-03      2.950e-03
frequencies.13                2.451e-01 1.914e-01 1.924e-03      2.944e-03
frequencies.14                2.547e-01 1.957e-01 1.966e-03      2.996e-03

2. Quantiles for each variable:
                                   2.5%        25%        50%        75%     97.5%
Sample                        1.347e+07  3.574e+07  6.049e+07  8.525e+07 1.075e+08
posterior                     4.576e+01  5.888e+01  7.259e+01  8.867e+01 1.075e+02
likelihood                   -4.374e-14 -3.175e-14 -2.753e-14 -1.621e-14 7.994e-15
prior                         2.556e+01  3.694e+01  5.049e+01  6.638e+01 8.306e+01
smcCoalescent                 1.163e+01  1.953e+01  2.253e+01  2.484e+01 2.808e+01
popPriorScale                 1.000e-02  1.000e-02  1.000e-02  1.000e-02 1.000e-02
BirthDeathCollapseModel       2.760e+01  3.839e+01  5.187e+01  6.774e+01 8.418e+01
bdcGrowthRate.smcTree         1.000e+02  1.000e+02  1.000e+02  1.000e+02 1.000e+02
bdcRelativeDeathRate.smcTree  0.000e+00  0.000e+00  0.000e+00  0.000e+00 0.000e+00
bdcCollapseWeight.smcTree     2.294e-02  2.378e-01  4.911e-01  7.457e-01 9.760e-01
bdcOriginHeight.smcTree       1.848e-03  1.137e-02  1.873e-02  2.766e-02 5.194e-02
NClusters                     1.000e+00  3.000e+00  5.000e+00  7.000e+00 8.000e+00
PopSize                       2.754e-03  5.250e-03  7.568e-03  1.161e-02 3.243e-02
genetreeLhood.1              -4.374e-14 -3.175e-14 -2.753e-14 -1.621e-14 7.994e-15
clockRate.1                   1.000e+00  1.000e+00  1.000e+00  1.000e+00 1.000e+00
kappa.1                       8.585e-02  4.274e-01  1.002e+00  2.380e+00 1.102e+01
frequencies.11                6.720e-03  8.663e-02  2.014e-01  3.716e-01 7.216e-01
frequencies.12                8.700e-03  8.757e-02  2.050e-01  3.711e-01 7.184e-01
frequencies.13                8.252e-03  8.709e-02  1.979e-01  3.666e-01 6.932e-01
frequencies.14                7.734e-03  9.338e-02  2.108e-01  3.772e-01 7.095e-01
```

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