Question 1

What was your final average standard deviation of split frequencies?
>   0.001041

Which of the moves were tree rearrangements? What were the acceptance rates for these moves?
>   There are three types of tree rearrangement moves:
>>   Nearest neighbor interchange (NNI)
>>   Subtree pruning and regrafting (SPR)
>>   Tree bisection and reconnection (TBR)
>   The highlighting parts are tree rearrangement moves and their acceptance rates.

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Acceptance rates for the moves in the "cold" chain of run 1:
  With prob.   (last 100)   chain accepted proposals by move
    39.5 %      ( 48 %)       Dirichlet(Revmat)
    58.2 %      ( 59 %)       Slider(Revmat)
    17.0 %      ( 20 %)       Dirichlet(Pi)
    27.0 %      ( 23 %)       Slider(Pi)
    30.6 %      ( 24 %)       Multiplier(Alpha)
    67.9 %      ( 69 %)       Slider(Pinvar)
     0.2 %      (  0 %)       ExtSPR(Tau,V)
     0.0 %      (  0 %)       ExtTBR(Tau,V)
     0.3 %      (  0 %)       NNI(Tau,V)
     0.9 %      (  1 %)       ParsSPR(Tau,V)
    36.8 %      ( 36 %)       Multiplier(V)
    24.4 %      ( 20 %)       Nodeslider(V)
    15.8 %      ( 13 %)       TLMultiplier(V)

Acceptance rates for the moves in the "cold" chain of run 2:
  With prob.   (last 100)   chain accepted proposals by move
    29.2 %      ( 25 %)       Dirichlet(Revmat)
    56.1 %      ( 53 %)       Slider(Revmat)
    16.2 %      ( 22 %)       Dirichlet(Pi)
    29.3 %      ( 29 %)       Slider(Pi)
    39.8 %      ( 37 %)       Multiplier(Alpha)
    65.6 %      ( 78 %)       Slider(Pinvar)
     0.4 %      (  0 %)       ExtSPR(Tau,V)
     0.2 %      (  0 %)       ExtTBR(Tau,V)
     0.4 %      (  0 %)       NNI(Tau,V)
     0.4 %      (  0 %)       ParsSPR(Tau,V)
    37.4 %      ( 36 %)       Multiplier(V)
    25.4 %      ( 25 %)       Nodeslider(V)
    13.9 %      (  9 %)       TLMultiplier(V)
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Question 2

By double-clicking on the Burn-In value in the Trace Files: panel modify the burn-in to a reasonable amount. How does this affect the ESS values?

  As we have more burn-in samples, most of the ESS values drop because we have less and less samples.

By repeating step 1 and 2 above, load the file primates.nex.run2.p from the second MrBayes run (remember MrBayes ran two parallel runs). Set an appropriate burn-in for the second run, and then click on Combined to view the samples from both MCMC runs combined. How does this affect ESS values?

  The combined ESS values are roughly the sum of the ESS values for run 1 and run 2. By combining the two runs, we can have an overall higher ESS value.

You now have both ESS and ASDSF values (ASDSF values from Question 1). Do they agree on whether or not convergence has been reached?

  Run 1 burn-in: 7000 ESS value: 26.085
  Run 2 burn-in: 5000 ESS value: 35.6784
  Combined - ESS value: 68.6287
  - - ASDSF: 0.001041 (from Question 1)

  The ESS values are all smaller than 200. In addition, the trace of the combined data does not look like a perfect "furry caterpillar". Consequently, according to the ESS values and the trace figure, it does not totally converge.
  On the other hand, we expect ASDSF to be as close to zero as we can since this value represent the difference of the result of run 1 and run 2. If this value is zero, it means the run 1 and run 2 results do converge to some certain states. In our case, the ASDSF is very close to zero. Thus, it looks like it should agree that the convergence has been reached.

Send me a screen shot of your entire Tracer window with combined runs showing.
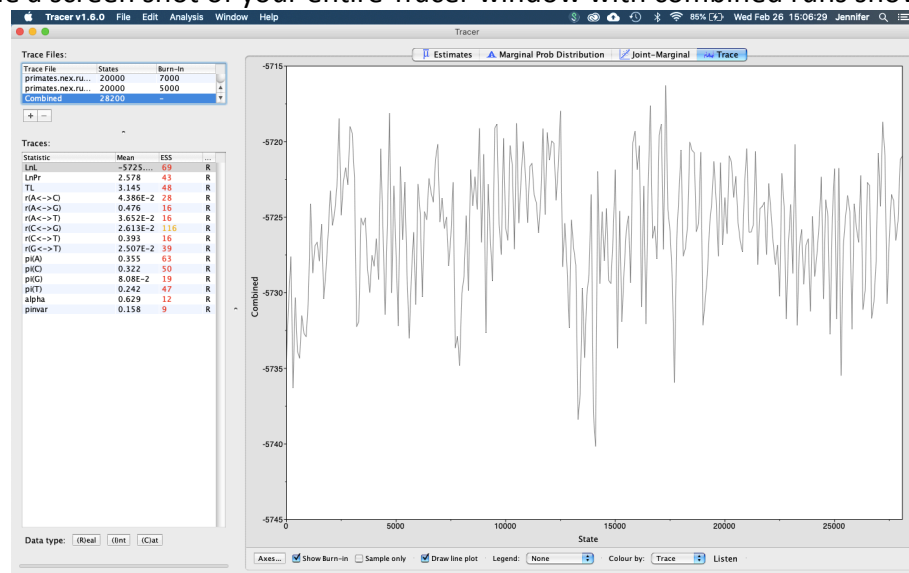
Question 3

It should run pretty fast. Once it is complete, open the .log file in Tracer. How do the ESS values look? Should the MCMC be run longer?

>The ESS value is 138.4601. It's larger than the original values we have. Yet, the ESS value is still smaller than 200. Consequently, I think the MCMC should be run longer in order to get an adequate ESS value.

What is the estimated mean age of the ingroup's most recent common ancestor?

>The estimated mean age of the ingroup's most recent common ancestor is **35.119** million years.

Question 4

Open the summary tree in FigTree. Figure out how to add the 95% HPD node age ranges as node bars to the tree. Also add the posterior probabilities on the nodes of the tree. Send me a screen shot.