Lab 10:

Introduction to RevBayes:
Phylogenetic Analysis Using Graphical Models
and Markov chain Monte Carlo
By Will Freyman

1 Before you begin

In a few of the upcoming labs we'll use a Linux virtual machine that has RevBayes and other software pre-installed. The virtual machine will work on Mac OSX, Linux, and Windows computers. I'm providing this virtual machine because compiling RevBayes from source can be tricky (it's still experimental software), but I encourage you to try installing on your own machine if you are interested. Learning to compile and install scientific software is an important bioinformatics skill.

Please do these steps before coming to lab. The download is too large to do during lab.

1. Download and install VirtualBox:
   `https://www.virtualbox.org/`
   This is the "virtual box" within which we'll install our Linux environment. Be sure to download and install both the **VirtualBox** application as well as the **VirtualBox Extension Pack**.

2. Download the Ubuntu virtual machine:
   `http://ib.berkeley.edu/courses/ib200/`
   This is a .ova file which is basically a disk image of the Linux distribution Ubuntu with RevBayes and other phylogenetic software pre-installed.

3. Start the virtual machine:
   Start up **VirtualBox**, and then double click on the downloaded .ova file. This will load the virtual machine. Accept all the default settings. Now within the **VirtualBox Manager** window, double click on the Ubuntu machine to boot it up. You'll be asked for a password, which is **ib200**.

4. Navigating the virtual machine:
   Most of our work will be done in a terminal window which will appear once you login. You can also access the web through the Firefox web browser by clicking on the icon on the left of the screen. If you have not used Linux before, please take time to explore the operating system.

2 Introduction to Graphical Models

A graphical model is a probabilistic model represented by a graph where each node in the graph is a variable, and the edges of the graph represent the dependency structure between variables. Graphical models are commonly used in machine learning and statistics, and

nearly all probabilistic models can be considered special cases of graphical models. The graphical model framework provides a precise representation of complex, parameter rich models that allows them to be constructed and utilized effectively.

There are a number of programming languages that specialize in describing graphical models such as Stan, JAGS, and BUGS. However, in phylogenetics

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execute primates.nex
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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.

Please email me the following:

1. The answers to questions 1-4.

2. Screenshots for questions 2 and 4.

References