

HOMEWORK ASSIGNMENT 12

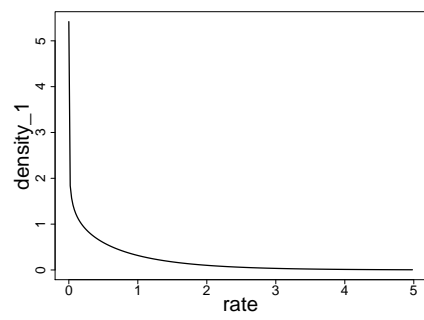
1. Watch at least the first 32 minutes of the video

[Phyloseminar #60 Andrew Roger](#)

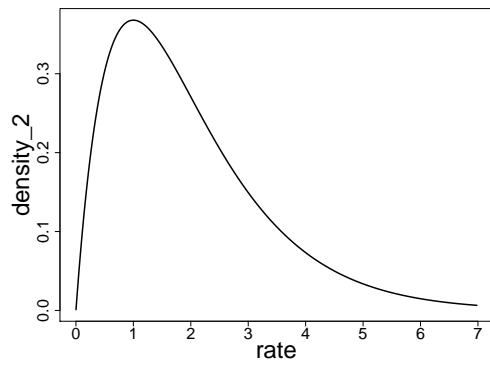
on protein modeling. This is an *excellent* exposition of the pitfalls and benefits of the assumptions of probabilistic models in phylogenetic inference. Then answer the following questions:

- (a) In your own words, explain the meaning of *heterotachy*. Looking at the class notes, how does the covarion model begin to incorporate heterotachy into a phylogenetic model?
  - (b) Give two examples of things that you liked in the video. Briefly explain why these ideas or exposition appealed to you.
2. Do **two** Maximum Likelihood searches on the primate data. (In truth, you will do more than two, but only two will be reported with your HW assignment.) You have a free hand here to some extent, but I would like to see you pick two different models for the analysis: one “simple” model and one “more complex” model. The choice is yours. In addition, make a NJ tree on the data.  
  
In your writeup, compare the trees and discuss any differences in topology and branch lengths you see. Please keep your writeup brief and include only pertinent details (E.g., I used the \_\_\_\_\_ model with \_\_\_\_\_ parameters estimated. I did an exhaustive/heuristic search, etc.)
  3. Repeat the last problem on the HPV dataset.
  4. Please refer to the figures on the next pages. In the figures, you see two  $\Gamma$ -density functions and an arbitrary density from which rates in a rates-across-sites model might be drawn at random. Briefly give a plausible value of the shape parameter  $\alpha$  for the two  $\Gamma$  distributions and explain in words what the choices of density says about the speed ups or slow downs you expect to see in data.

(a)



(b)



(c)

