Model Adequacy

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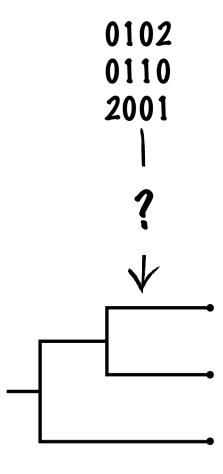




Model selection vs. Model adequacy

Take a bunch of different models and test which is the *best*

Gives the **relative** fit



Assess whether a model is capturing the evolutionary dynamics that generated the data

Gives the **absolute** fit

Model Adequacy

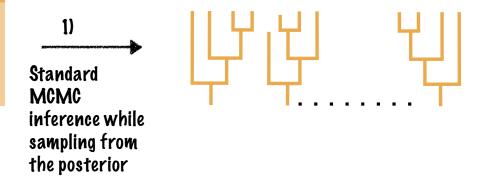
We know that none of our models are really true. Can we be sure that the chosen model captures the salient features of the evolutionary process and provides reliable inferences

Could the model and priors plausibly have given rise to the data

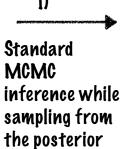
Allows us to ask whether **any** of our models are doing a good job describing the evolutionary processes that produced our data

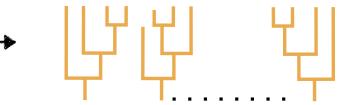
taxa 1 0 1 0 1 2 1 taxa 2 1 2 1 0 1 0 1 taxa 3 0 0 1 0 0 1 taxa 4 1 1 0 1 0 1

taxa 1 0 1 0 1 2 1 taxa 2 1 2 1 0 1 0 1 taxa 3 0 0 1 0 0 1 taxa 4 1 1 0 1 0 1



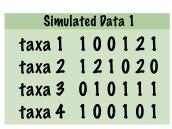
taxa 1 0 1 0 1 2 1 taxa 2 1 2 1 0 1 0 1 taxa 3 0 0 1 0 0 1 taxa 4 1 1 0 1 0 1





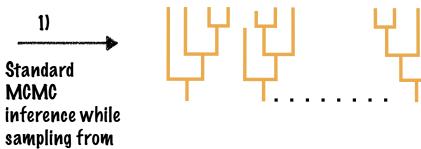
Using the information sampled in 1) generate new data sets

2)

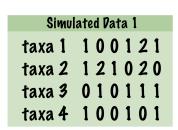


Simulated Pata 2		
taxa 1	110121	
taxa 2	111010	
taxa 3	011101	
taxa 4	120101	

Empirical Data taxa 1 0 1 0 1 2 1 taxa 2 1 2 1 0 1 0 taxa 3 001001 taxa 4 1 1 0 1 0 1







Simulated Data 2		
taxa 1	110121	
taxa 2	111010	
taxa 3	011101	
taxa 4	120101	

Simulated Data n taxa 1 1 1 0 1 2 1 taxa 2 1 1 1 0 1 0 taxa 3 0 1 1 1 0 1 taxa 4 1 2 0 1 0 1

Carry out the same inference as in step 1) using the new simulated data sets

generate new

data sets



the posterior

Empirical Data

taxa 1 0 1 0 1 2 1 taxa 2 1 2 1 0 1 0 taxa 3 0 0 1 0 0 1 taxa 4 1 1 0 1 0 1

Standard
MCMC
inference while
sampling from
the posterior

dard 1C

Compare simulated to empirical (the more similar the

better!)

4)

Using the

Carry out the same inference as in step 1) using the new simulated data sets

taxa 2 1

Using the information sampled in 1) generate new data sets

Simulated Pata 1

taxa 1 100121 taxa 2 121020 taxa 3 010111 taxa 4 100101

Simulated Pata n

taxa 1 1 1 0 1 2 1 taxa 2 1 1 1 0 1 0 taxa 3 0 1 1 1 0 1 taxa 4 1 2 0 1 0 1

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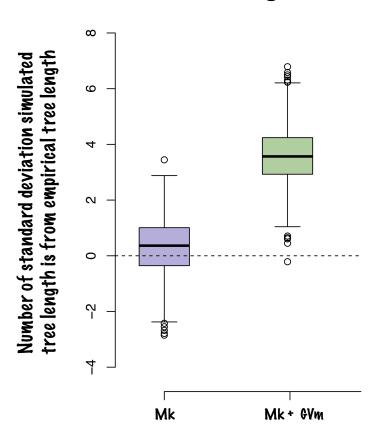
How can we compare trees and morphological matrices?

Need to get test statistics that compare the difference

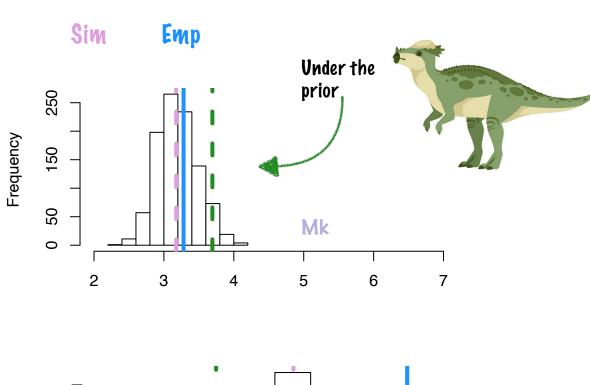
More work has been done for molecular data – easier to compare

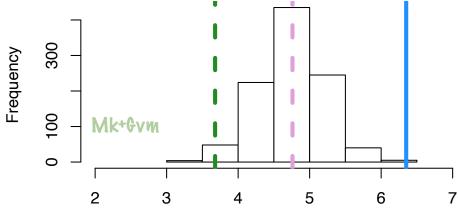
To compare simulations to empirical data we use effect sizes.

Tree Length

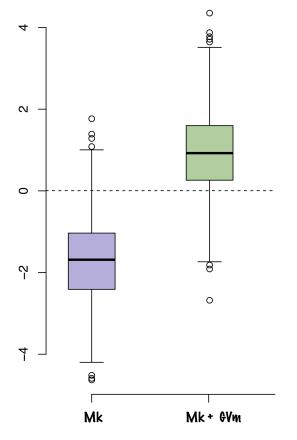


over estimated using the more complex model



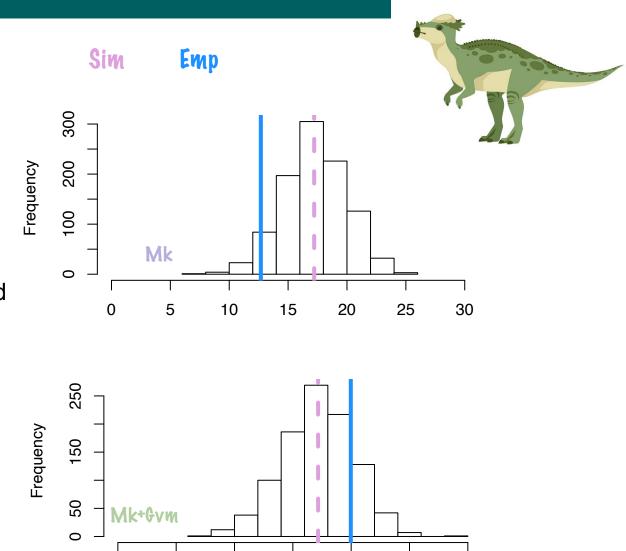


Robinson Foulds



Number of standard deviation simulated RF is from empirical RF

Both models produced similar RF results



10

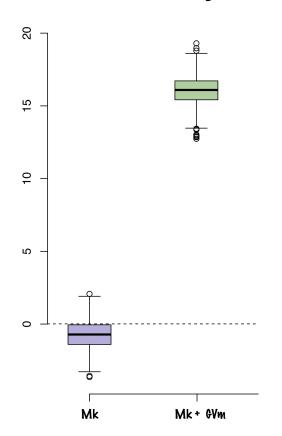
15

20

25

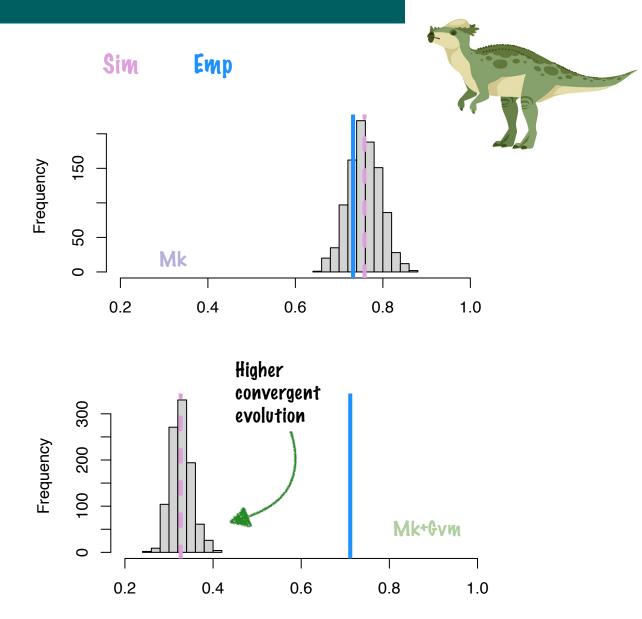
30

Consistency Index



Number of standard deviation simulated Cl is from empirical Cl

The more complex **over** estimated convergent evolution



More test statistics

Tree length
Robinson Foulds
Consistency Index
Retention Index
Hamming distances
Multiple distance metrics

Exercise 3

Check if either of the two models you chose for exercise 1 fit your data using a model adequacy approach