

Lecture 12: Introduction to Age Models

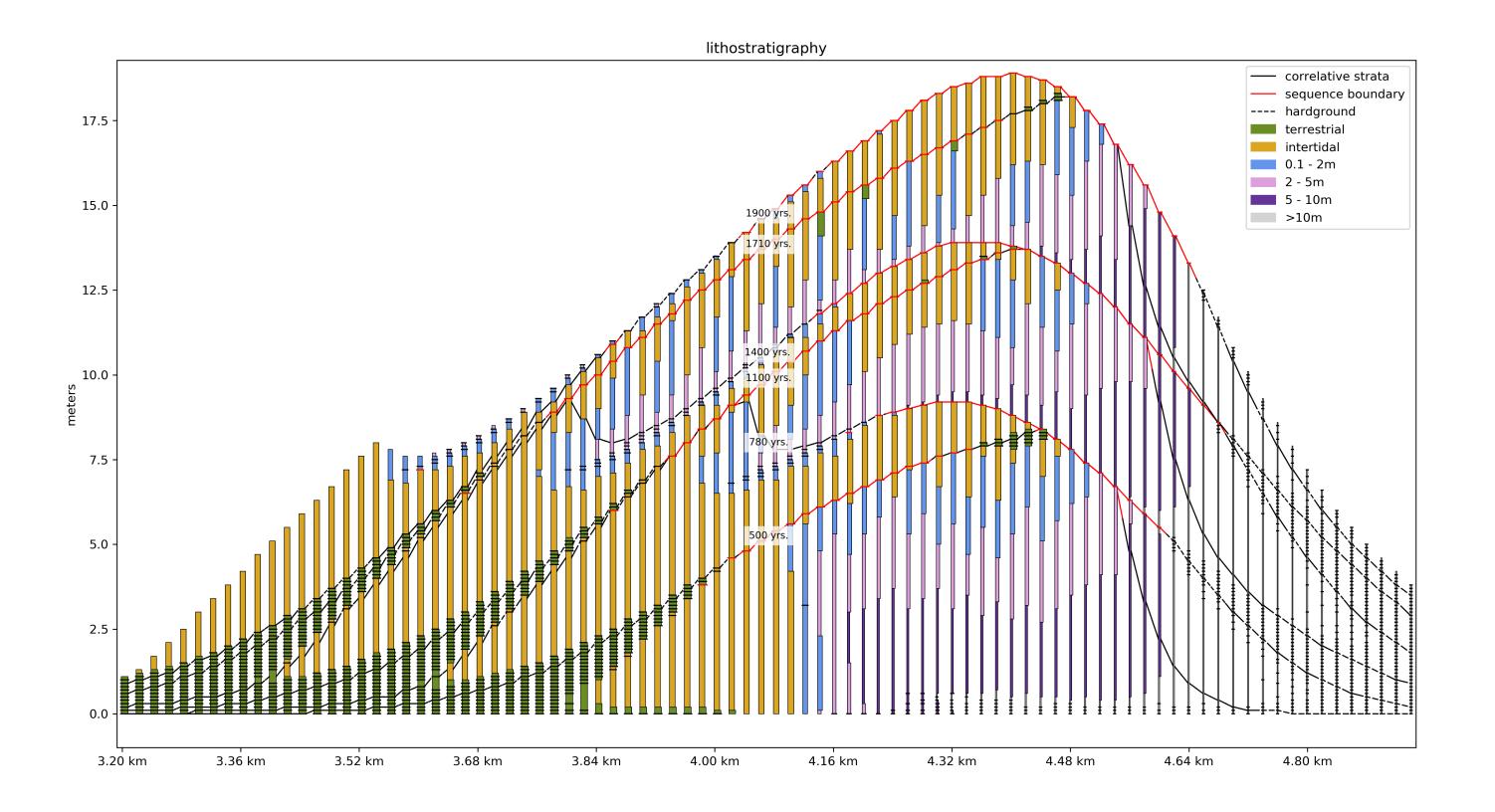
- 1. The importance of knowing time
- 2. Building an age model
 - Markov chain Monte Carlo approaches
 - constant sedimentation rates
 - varying sedimentation rates

We acknowledge and respect the $l \ni k^w \ni \eta \ni n$ peoples on whose traditional territory the university stands and the Songhees, Esquimalt and $W S \land N E \textcircled{E}$ peoples whose historical relationships with the land continue to this day.





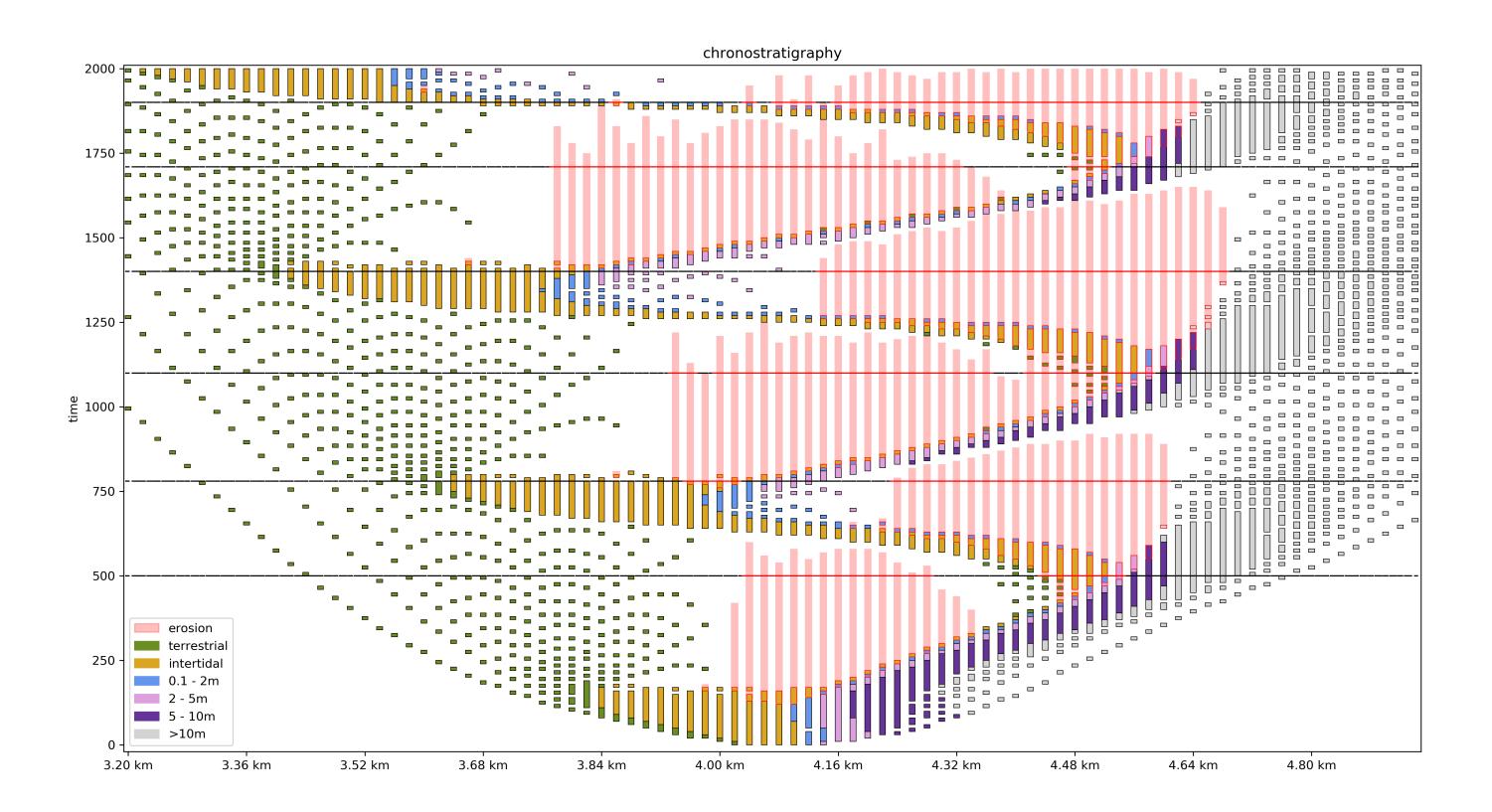
Importance of knowing time







Importance of knowing time







Age models are important: how do we get them?

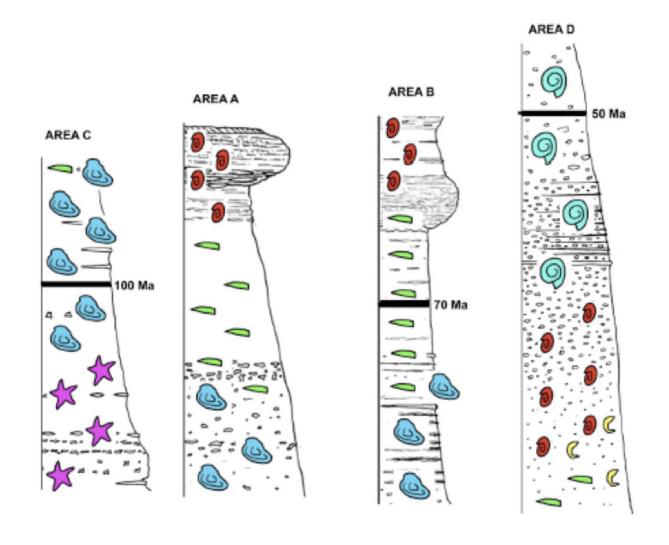
- 1. Cyclostratigraphy
- 2. Biostratigraphy
- 3. Absolute ages
 - U-Pb (volcanics), Ar-Ar (volcanics), Re-Os (sediments)
- 4. Signal matching
 - magnetostratigraphy
 - chemostratigraphy
- 5. Relative ages
 - Amino Acid Racemization





Biostratigraphy

• based on the unique, sequential, nonrepeating appearance of fossils through time



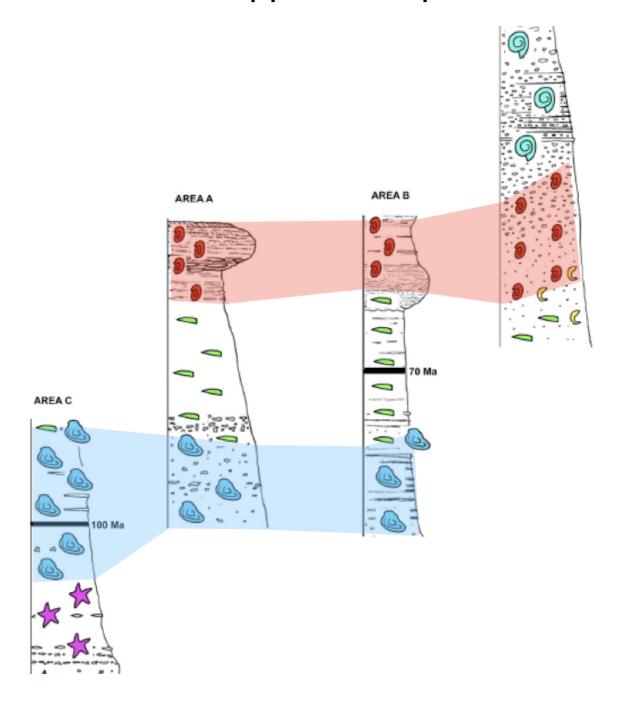
http://www.labspaces.net/pictures/blog/4d497dd38d7031296661971_blog.jpg





Biostratigraphy

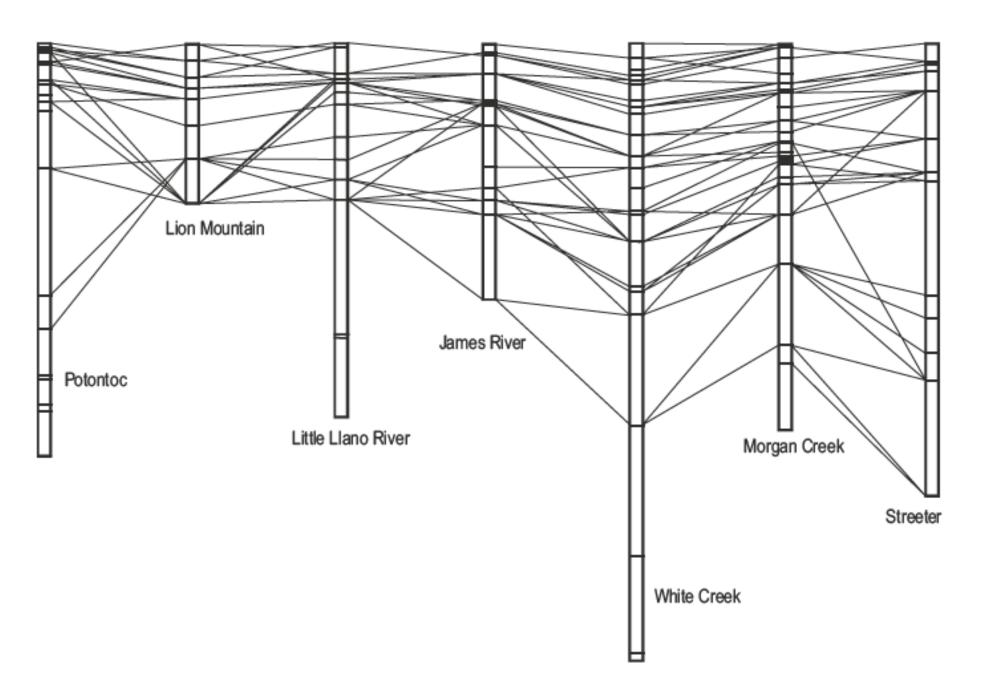
- based on the unique, sequential, nonrepeating appearance of fossils through time
- observations are: first appearance and last appearance per section







- what is wrong with this picture?
- fence diagram (correlation) of the observed FADs and LAD between 7 sections that preserve 62 taxa of the Cambrian Riley Formation of Texas (data from Palmer, 1954; Shaw, 1964).
- lines are meant to represent time lines, so equal time

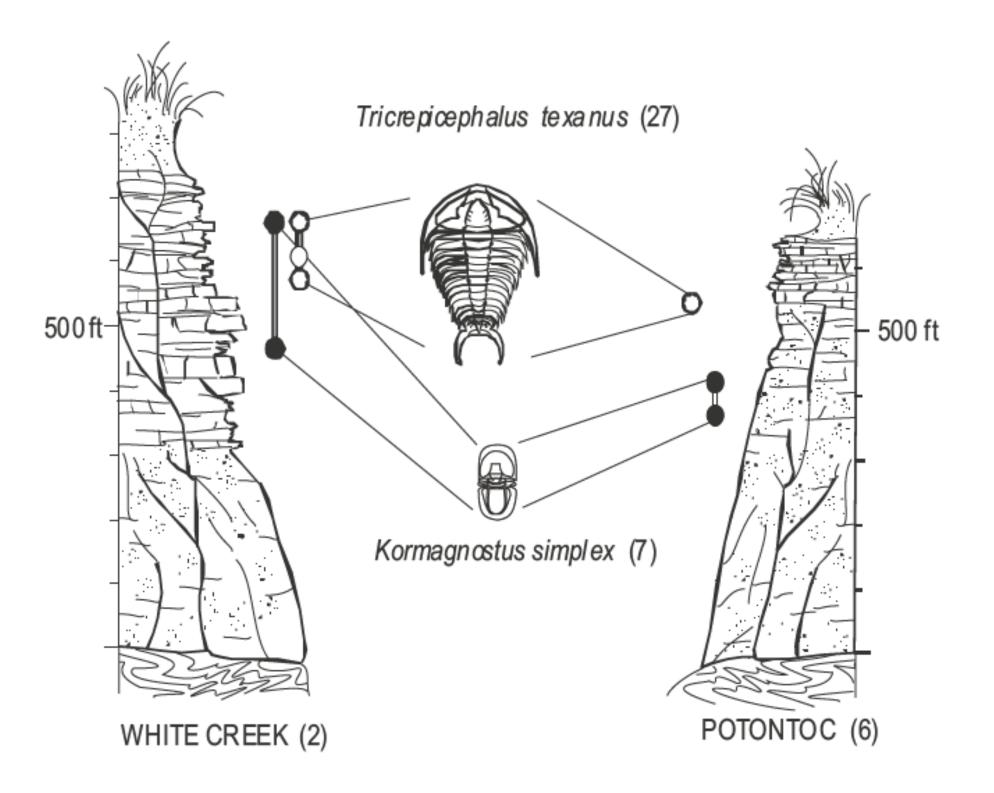






Contradictory ranges

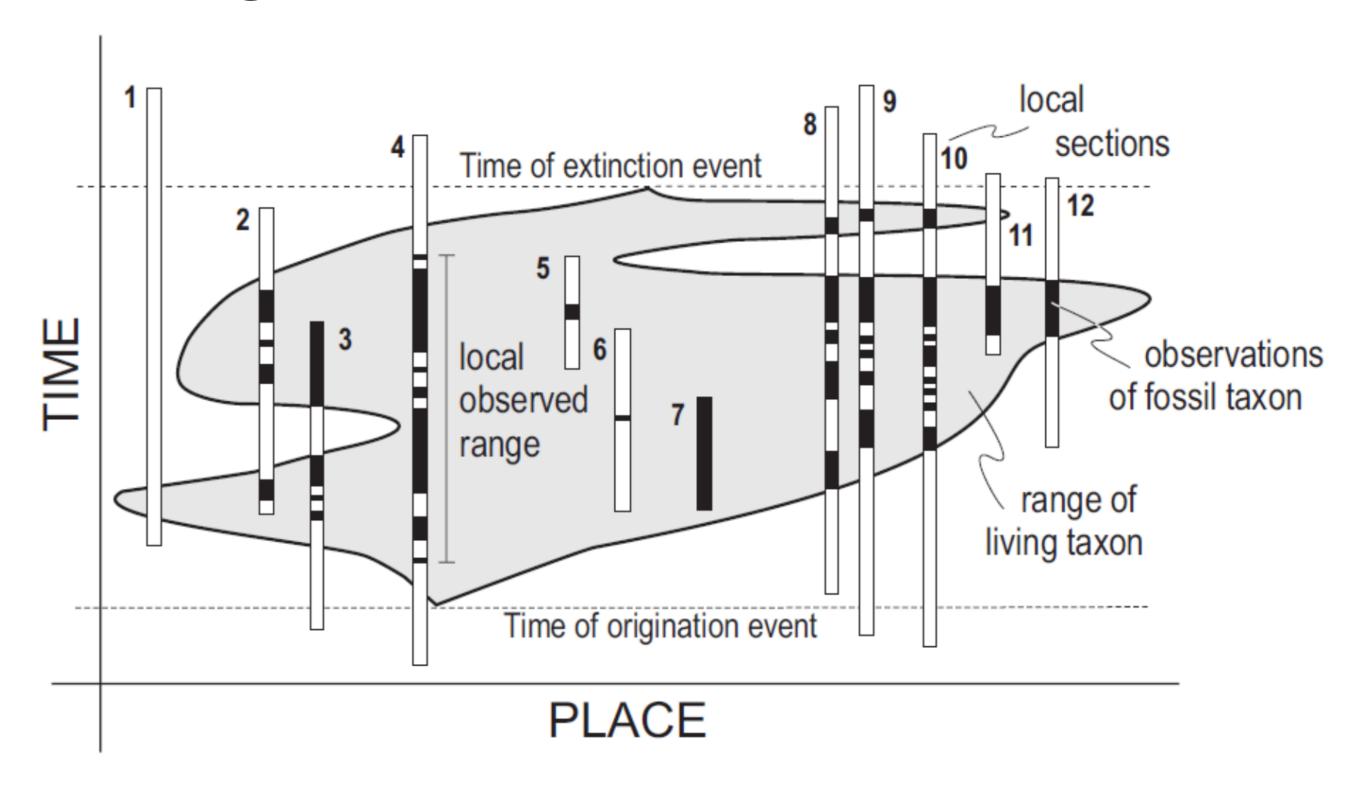
what could be causing this?







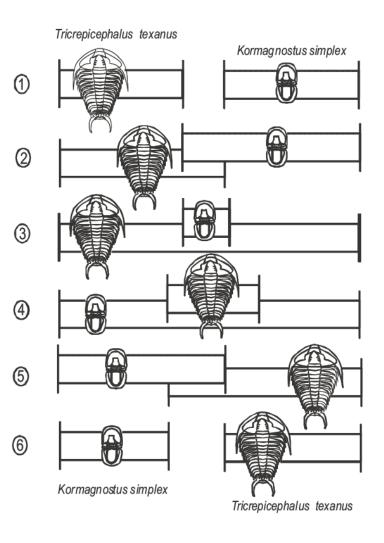
Contradictory ranges







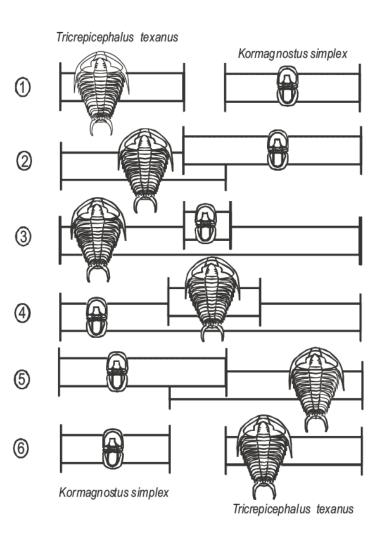
• ranges of original data need modification to be consistent everywhere (time goes left to right)







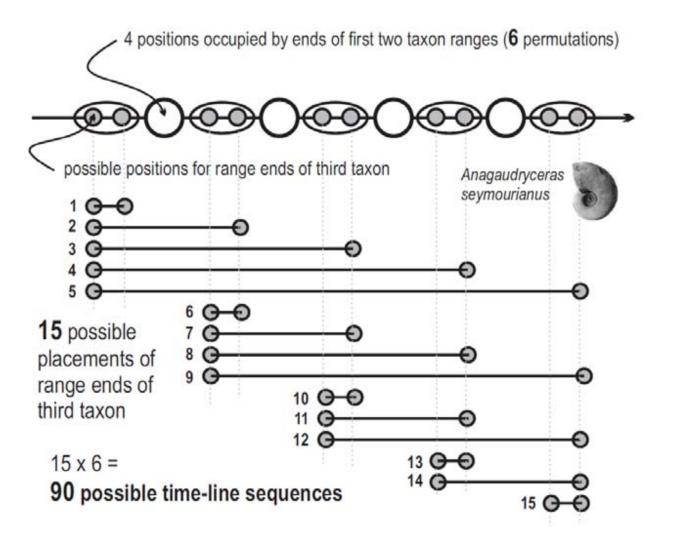
• can we rule any out? working out the possibilities not so hard with just two taxa..





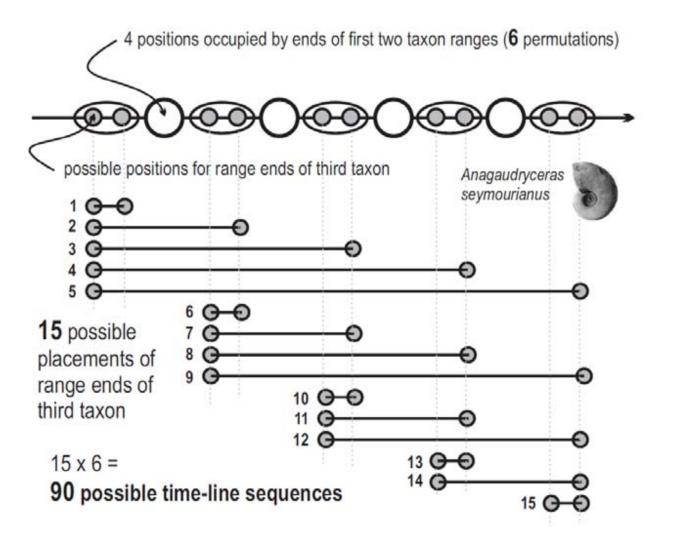


• can we rule any out? working out the possibilities not so hard with just two taxa.. 90 options with 3,





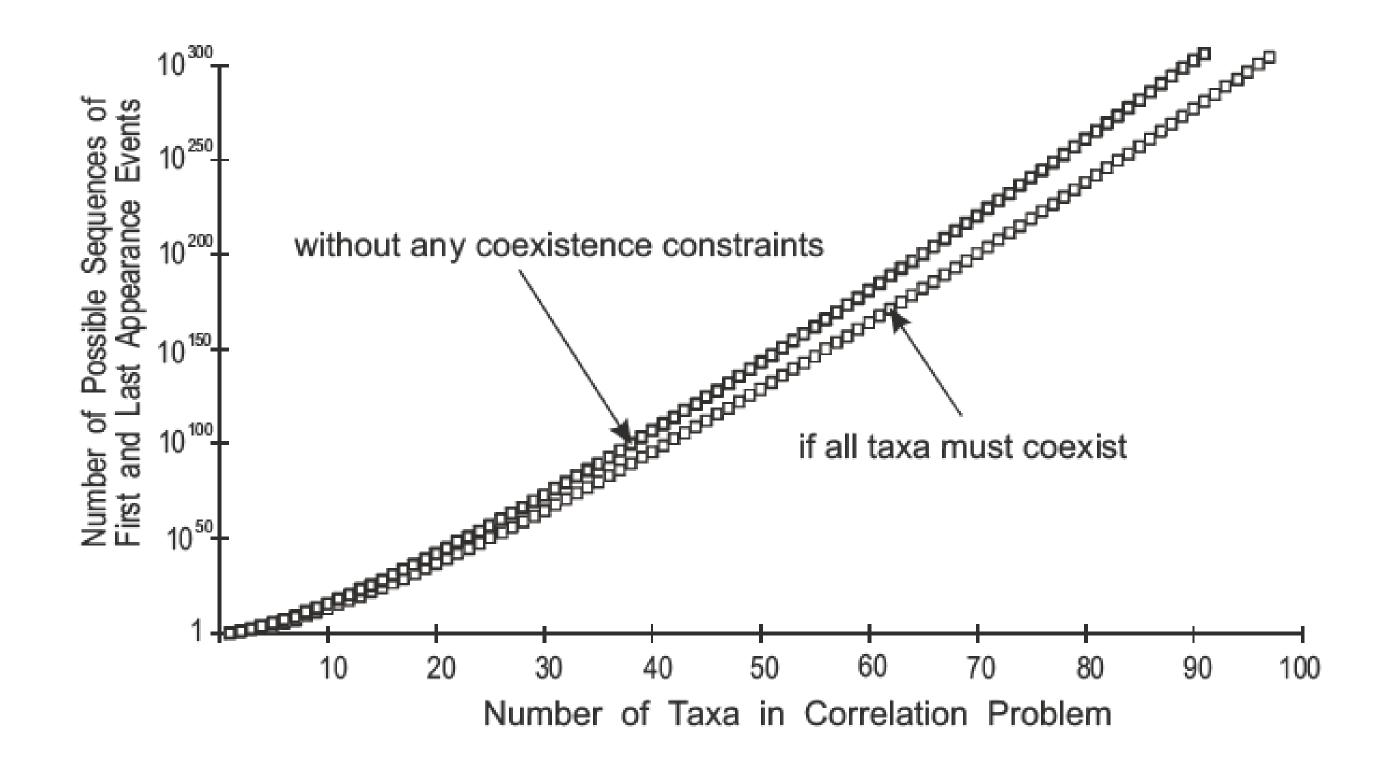
• can we rule any out? working out the possibilities not so hard with just two taxa.. 90 options with 3,





Number of possible sequences

- requires constrained optimization (CONOP9; Sadler and Cooper, 2008)
- number of atoms in universe = 10^{82}

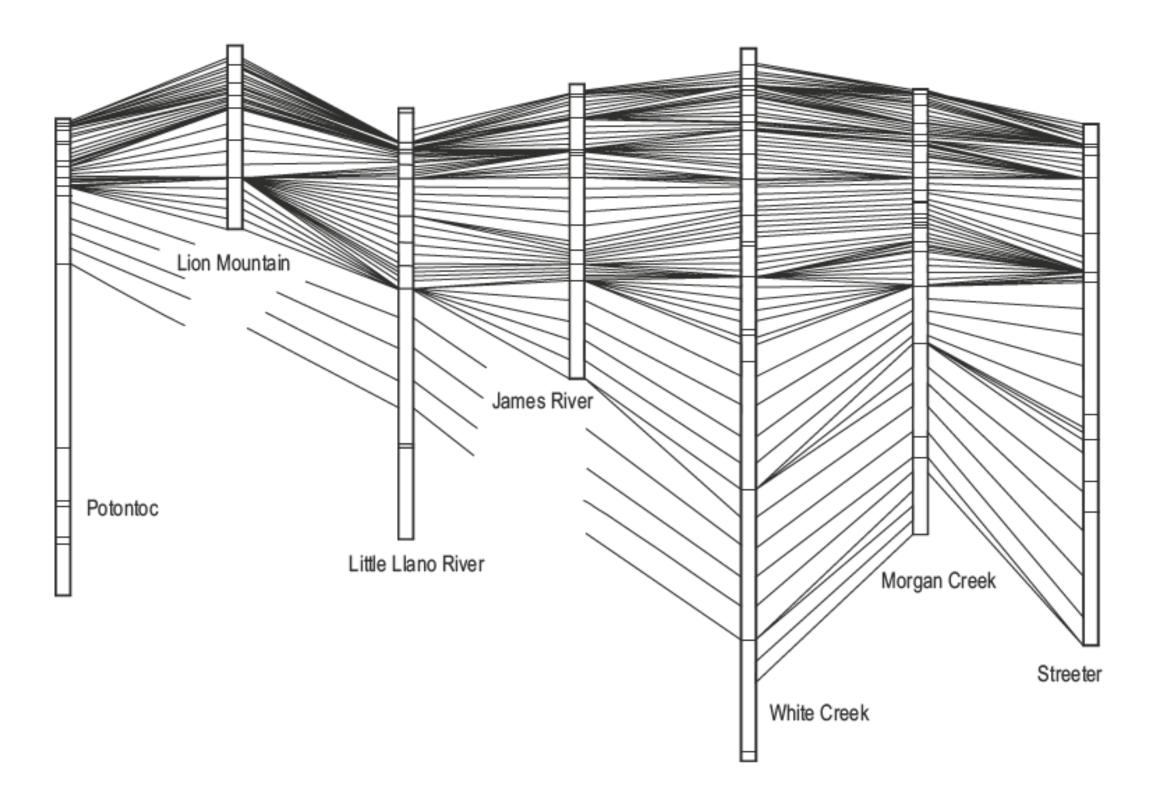






Best-fit solution

• what are some features of this that look familiar to our model outputs?





Building an age model





Building an age model

