Inferring Ancestor-Descendant Relationships in the Fossil Record

(With Statistics)

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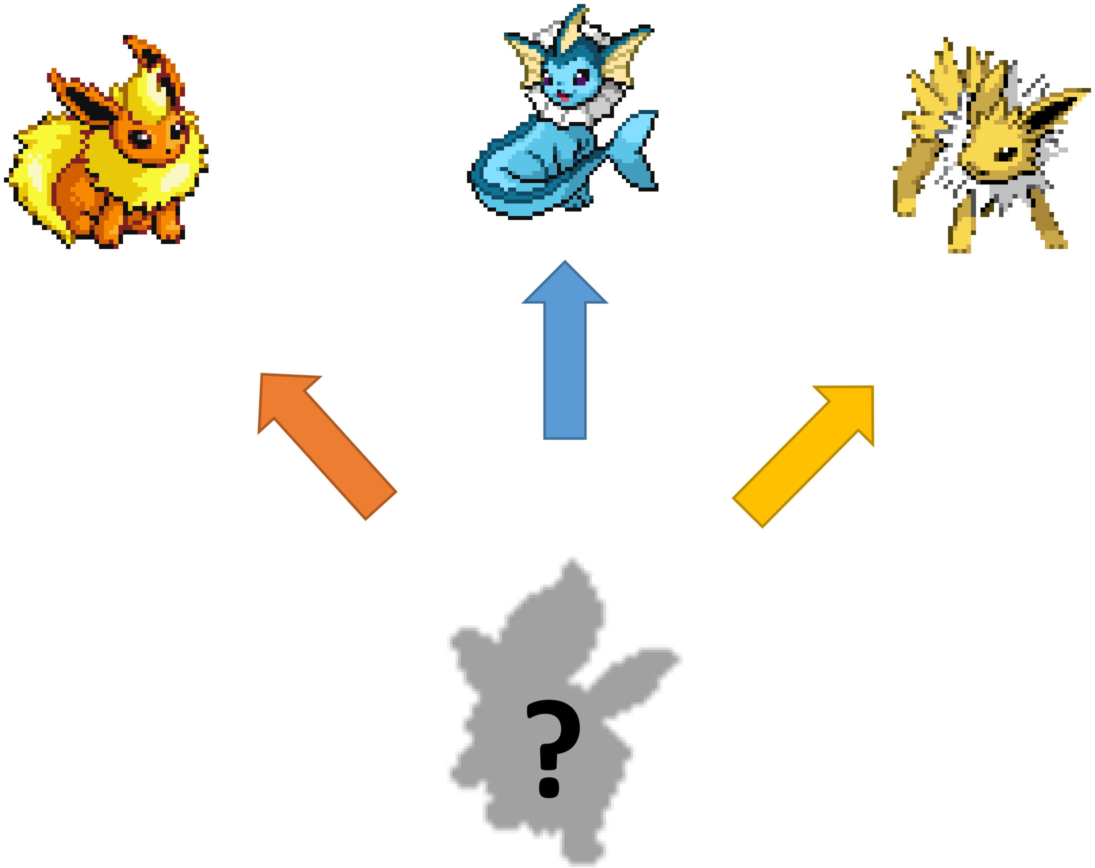
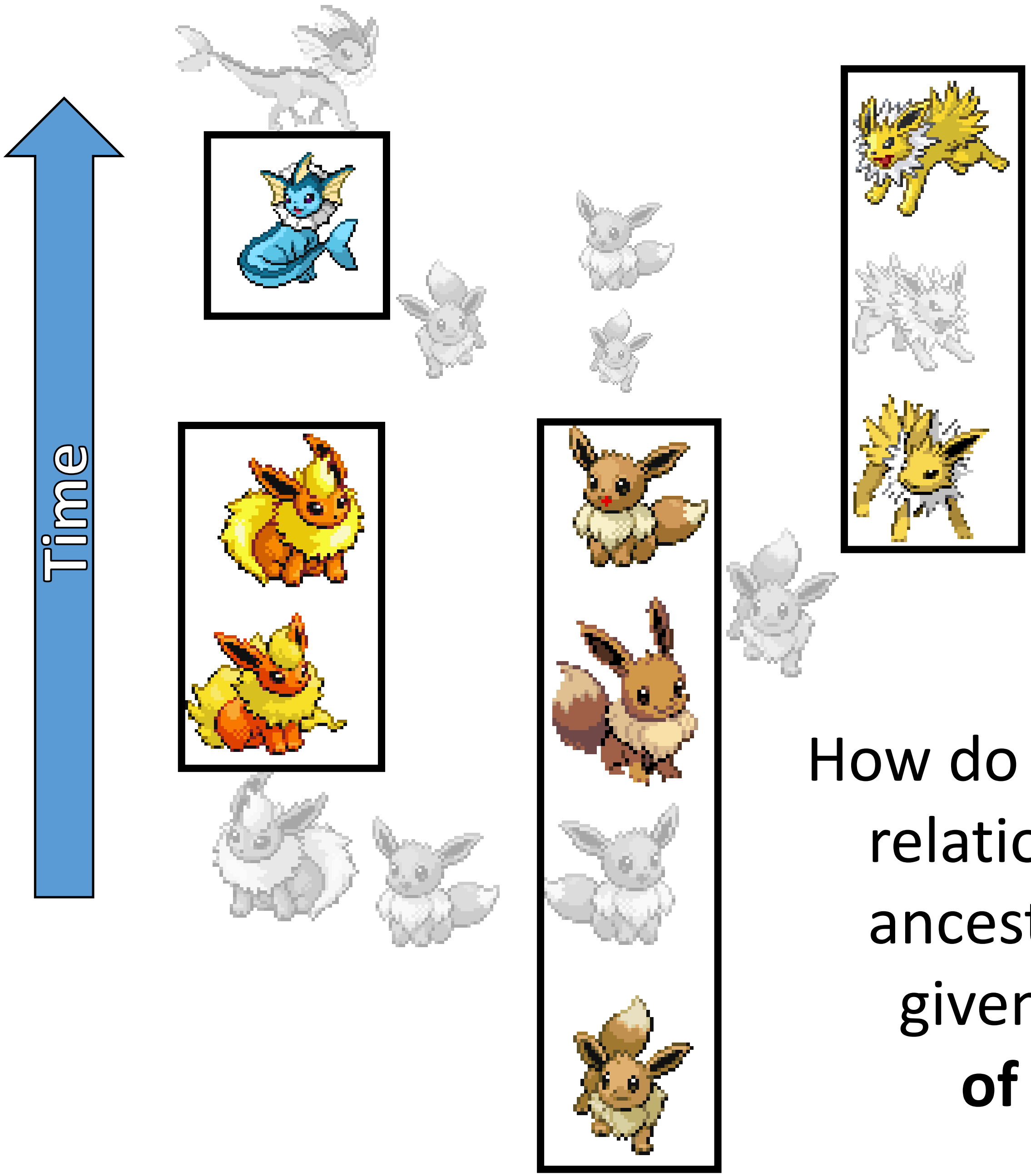
The Question of Ancestors in the Fossil Record

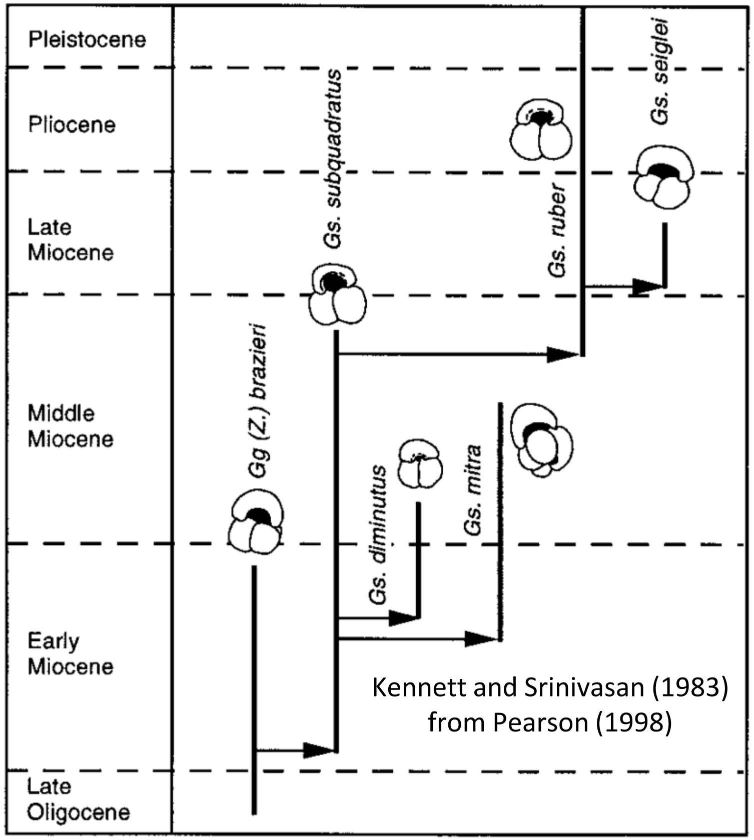


The problem is, very rarely can we read the fossil record as literally as this

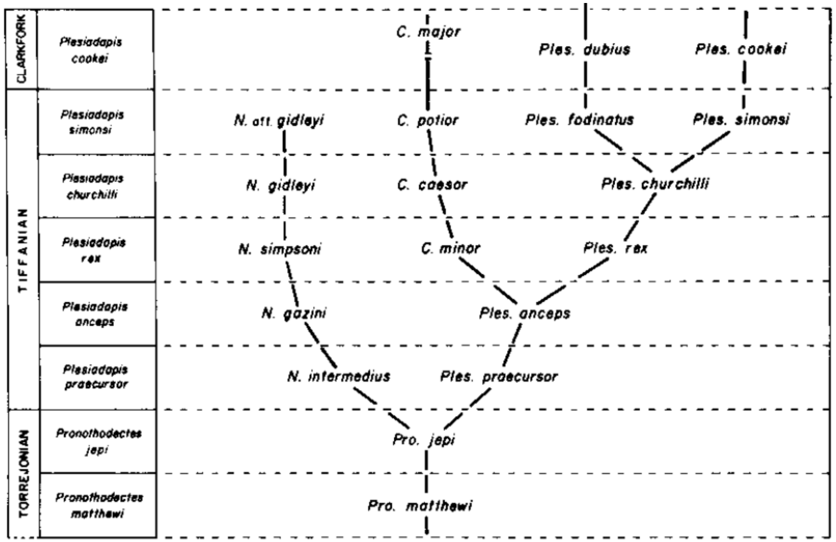


How do we infer the relationships among ancestors & their descendants, given **the incompleteness of the fossil record**?

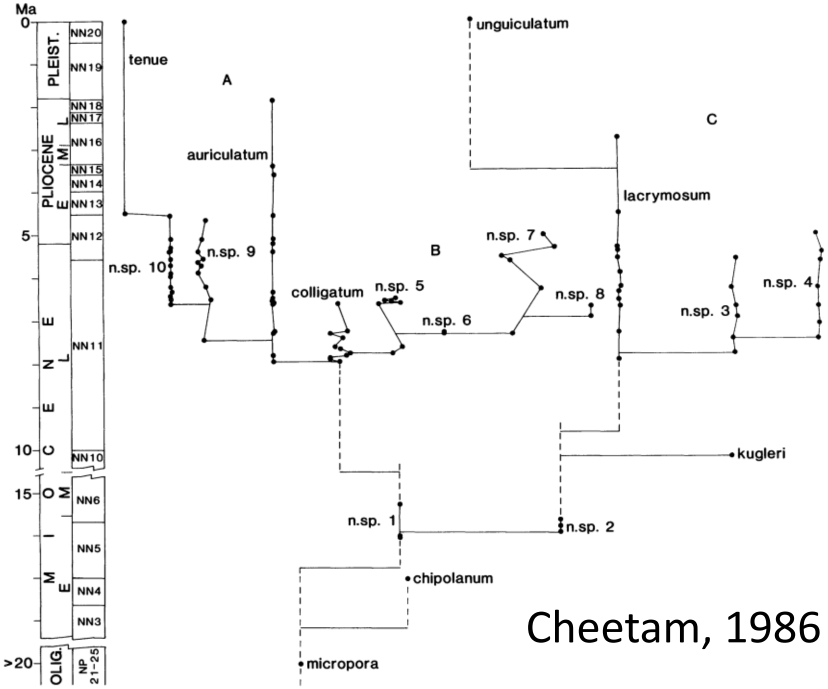
Stratophenetics: Ancestors on Diagrams



Kennett and Srinivasan (1983) from Pearson (1998)



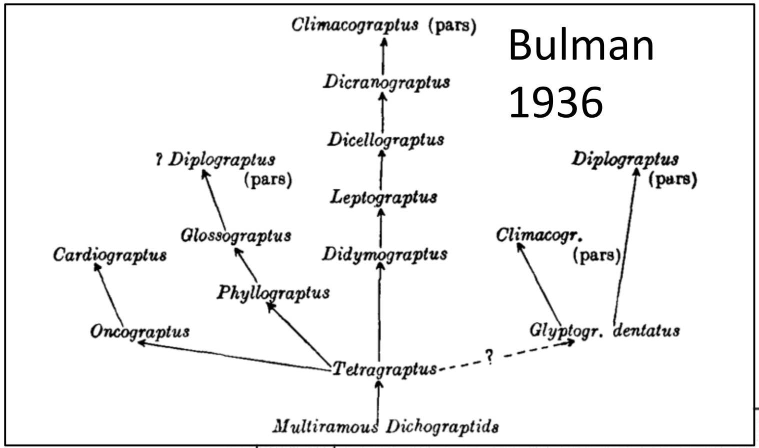
Primate tree from Gingerich (1976)



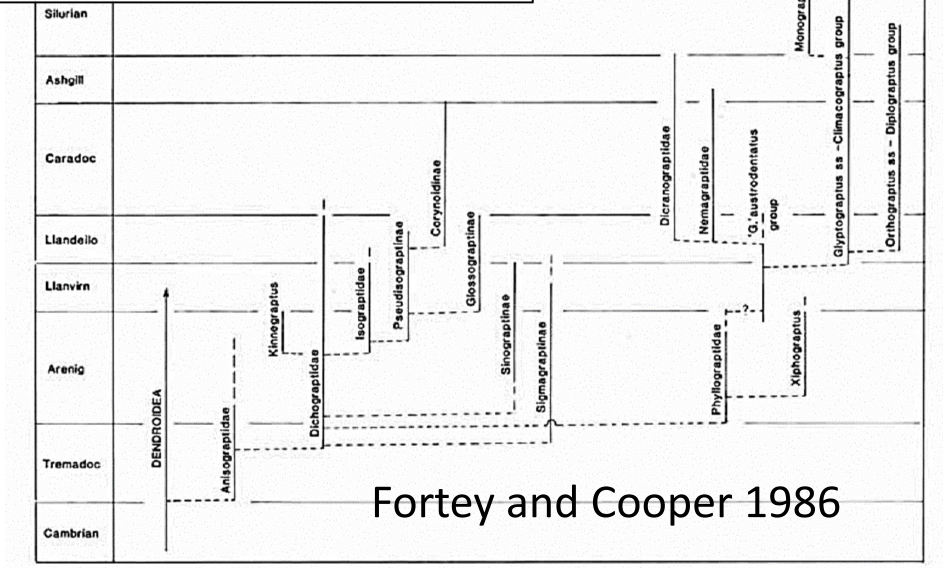
Cheetam, 1986

- Generally qualitative, or based on cluster analyses

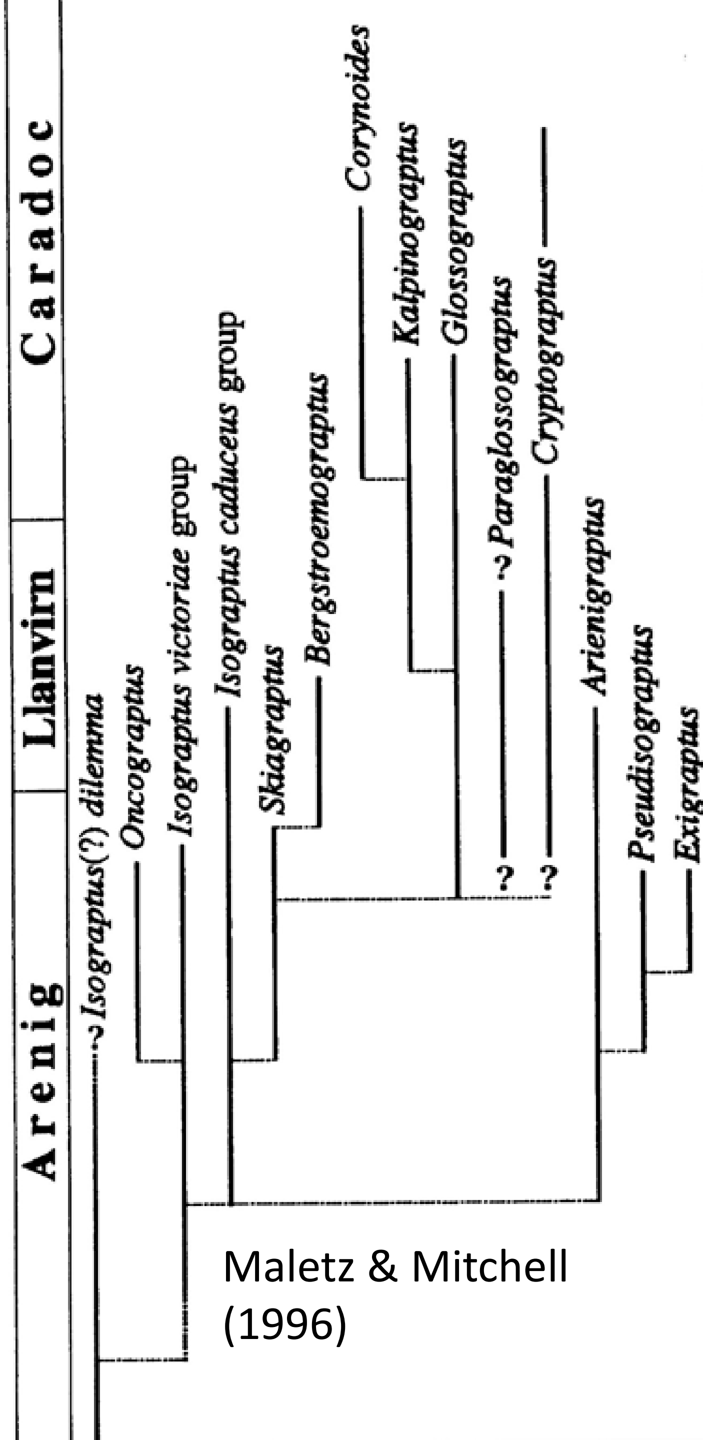
A Very Persistent Idea



Bulman 1936

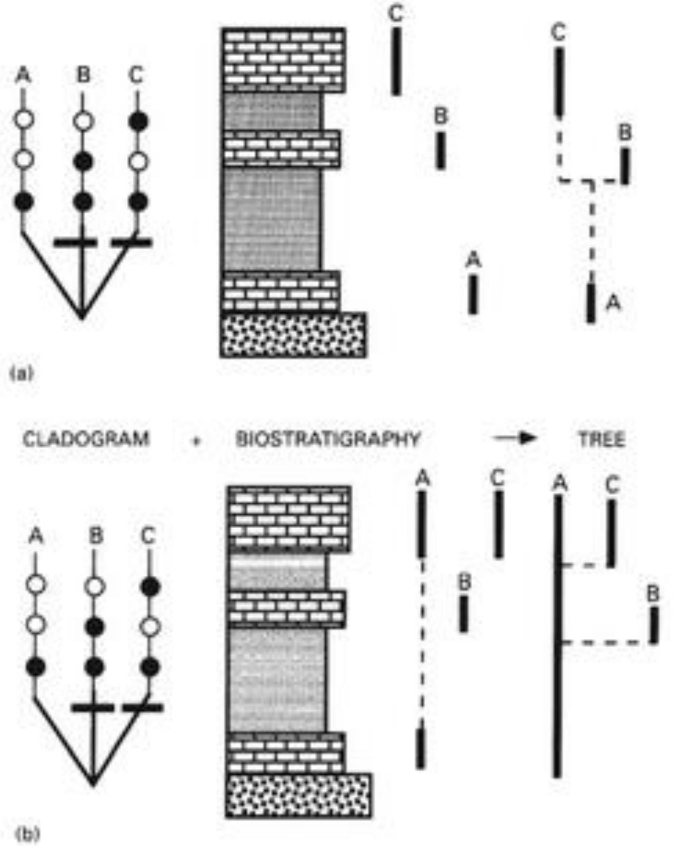


Fortey and Cooper 1986

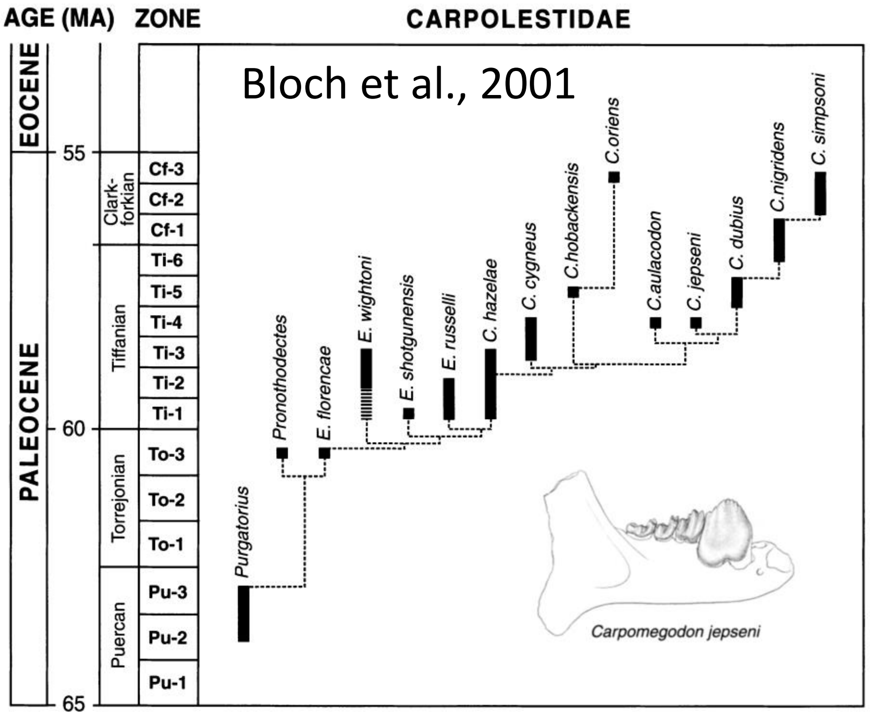


Maletz & Mitchell (1996)

Putative Ancestors and Stratocladistics



- Smith (1996): Plesiomorphic, early-appearing taxa



Bloch et al., 2001

- Fisher (1991, 1994): treat time (strat) similar parsimony debt from morph
- Place as ancestors those taxa that reduce stratigraphic debt, offset by additional morphological debt

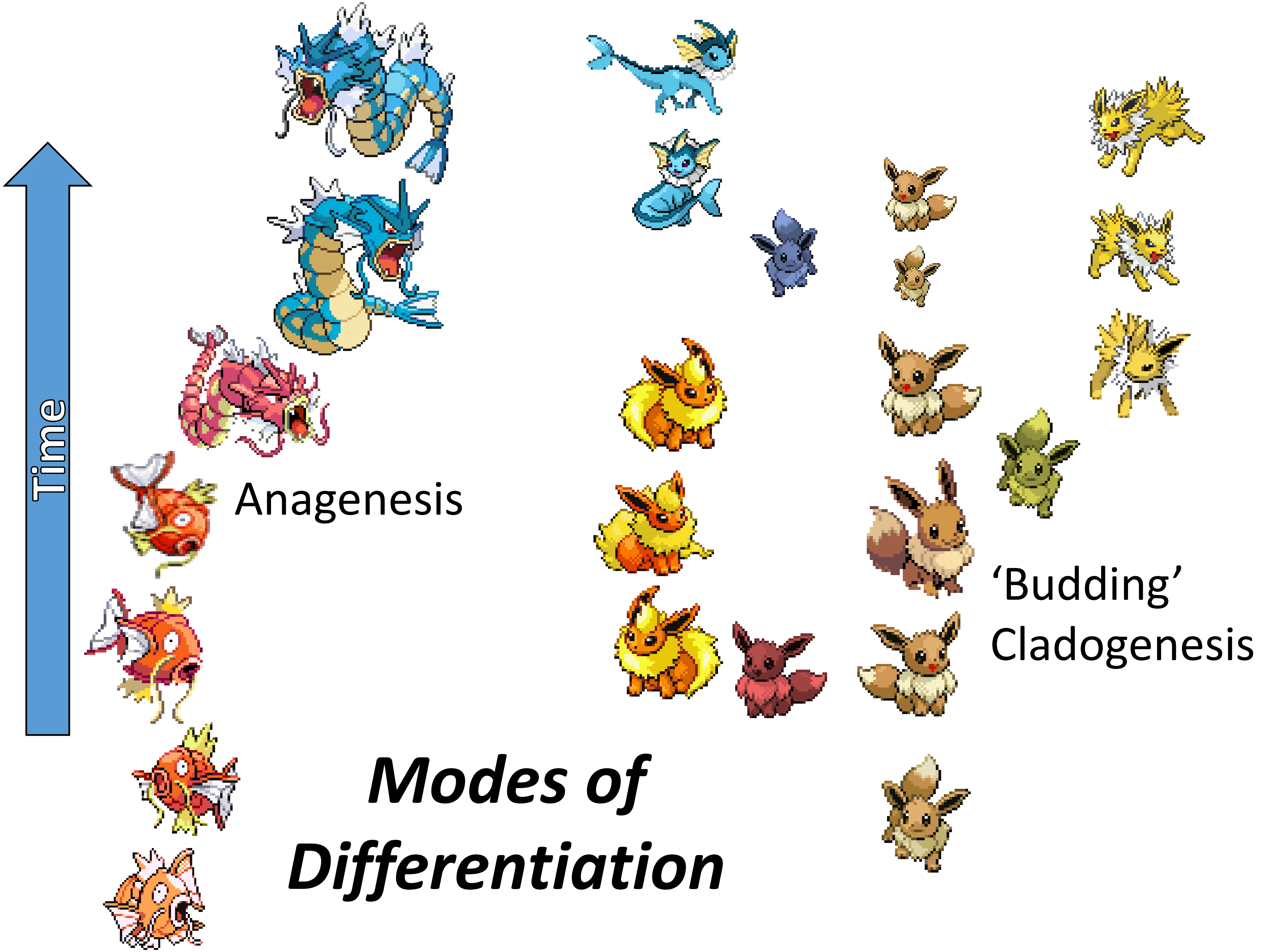
Challenges

- We can’t expect ancestors to always lack autapomorphies (Wagner, 1996)
- Can’t quantify probabilistic support for specific ancestor-descendant pairs
  - Equating morph and strat ‘debt’ is messy
- Inferring ancestors a subset of determining when divergences occurred for fossil lineages
  - Timing of divergences requires formal model of incompleteness in the fossil record: reflecting origination, extinction & sampling
  - Eg. Fossilized birth-death (FBD) model
    (Stadler, 2010; Heath et al., 2014)

New Methods

- Bayesian sampled-ancestor tip-dating
    - Infer dated phylogenies from character and stratigraphic data simultaneously, under models of morph change & and FBD model (Heath et al., 2014)
    - Taxa are instantaneous points but can be placed as sampled-ancestors (Gavryushkina et al., 2014)
- cal3 (Bapst, 2013)
    - Take an existing undated cladogram, sample potential divergence dates for nodes under a three-rate model of incompleteness
    - Treat taxa as persistent morphotaxa, allowing for you to categorize ancestor-descendant relationships based on the overlap of their stratigraphic durations

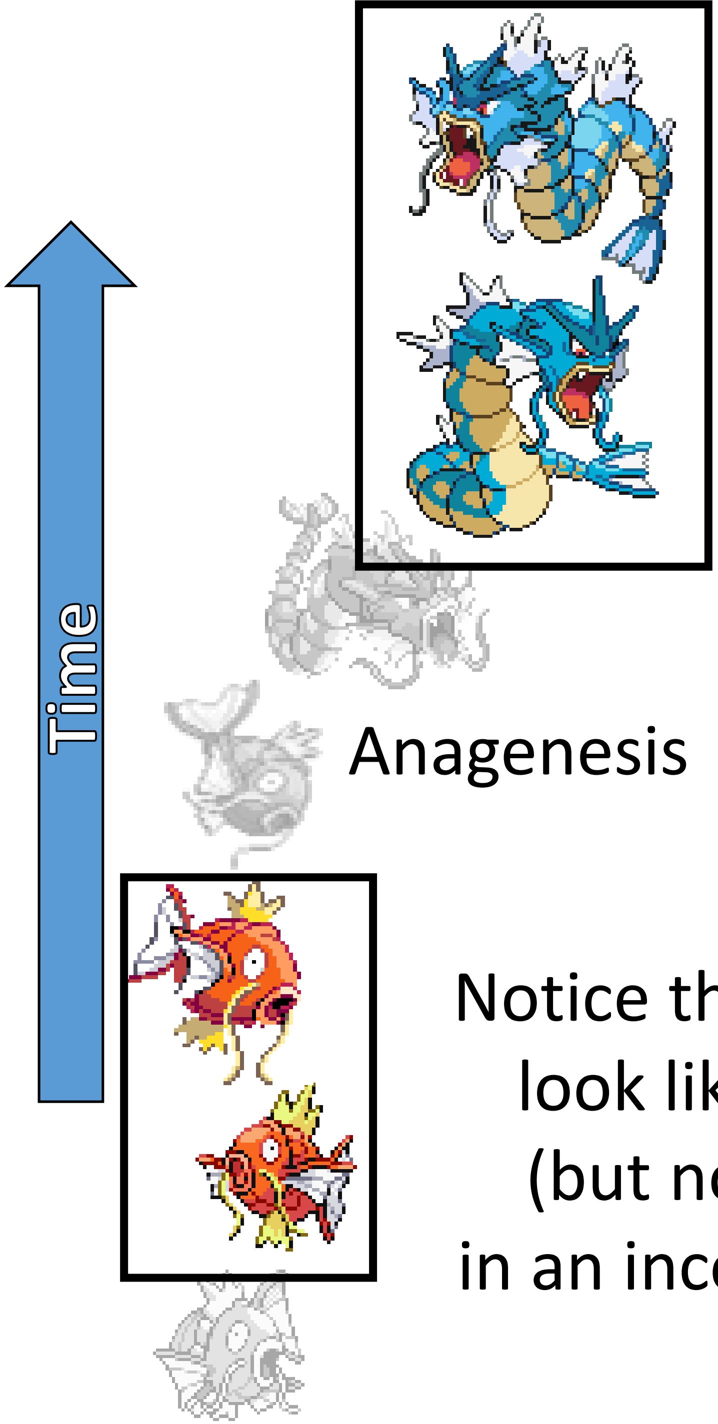
Modes of Differentiation



Time

Anagenesis

'Budding' Cladogenesis



Anagenesis

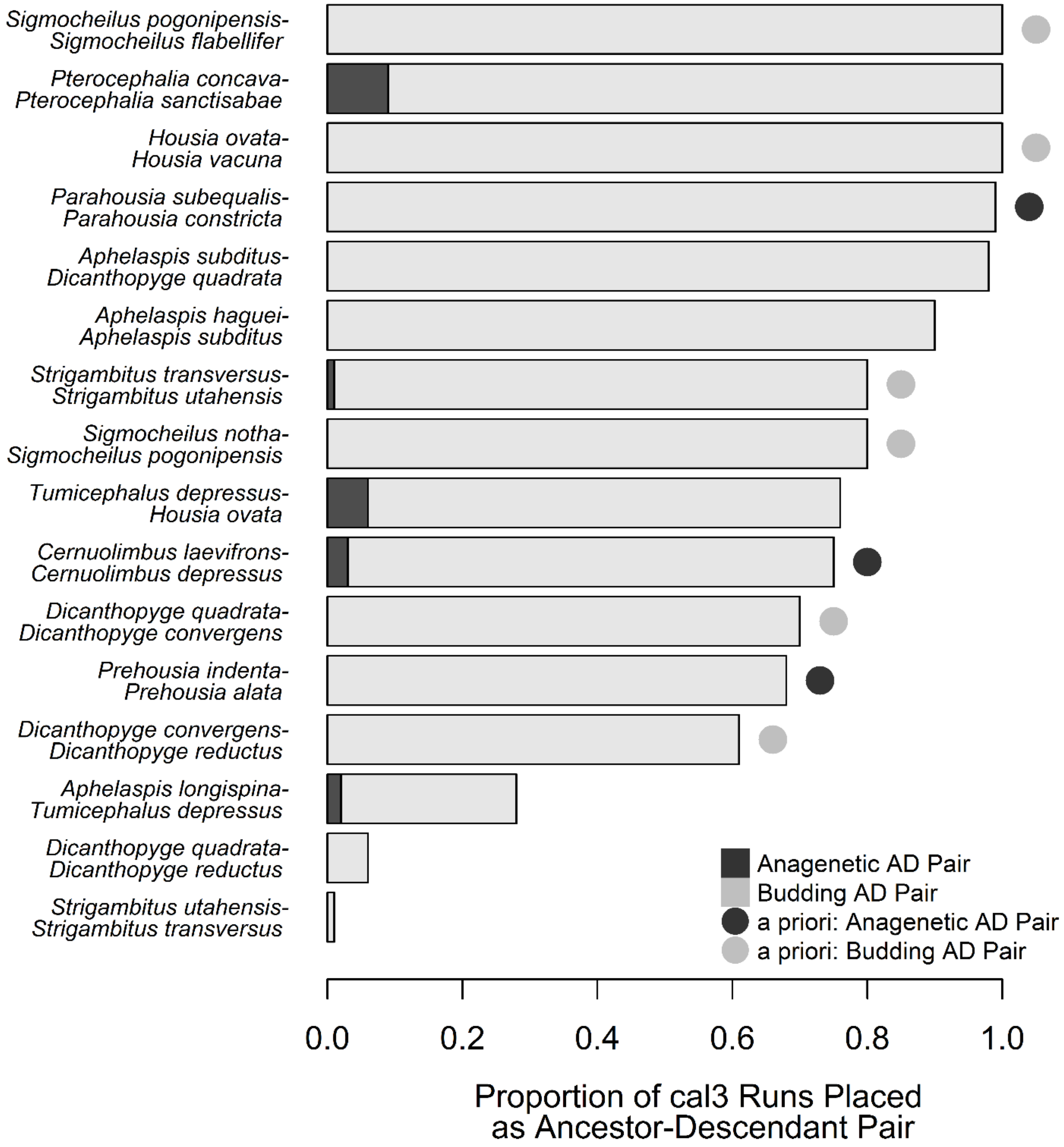
‘Budding’

Notice that budding can
look like anagenesis
(but not *vice versa*)
in an incomplete record

Case 1:
Cambrian pterocephaliid trilobites

- Hopkins (2011) did a cladistic analysis and reviewed a number of (qualitative) ancestor-descendant pairs previously suggested for this group
- Does cal3 find support for those pairs, and does it match the mode inferred by previous authors?
  - Apply cal3 to the single maximum-parsimony topology & 100 CONOP solutions from Hopkins (2011)
  - Obtained 100 dated phylogenies, quantified support for a given AD pair as the proportion of trees

Bapst & Hopkins, now in press at Paleobiology!



- Each pair is a stacked barplot
- Dots indicate putative pairs

- Evidence for all *a priori* AD pairs, & a few extra

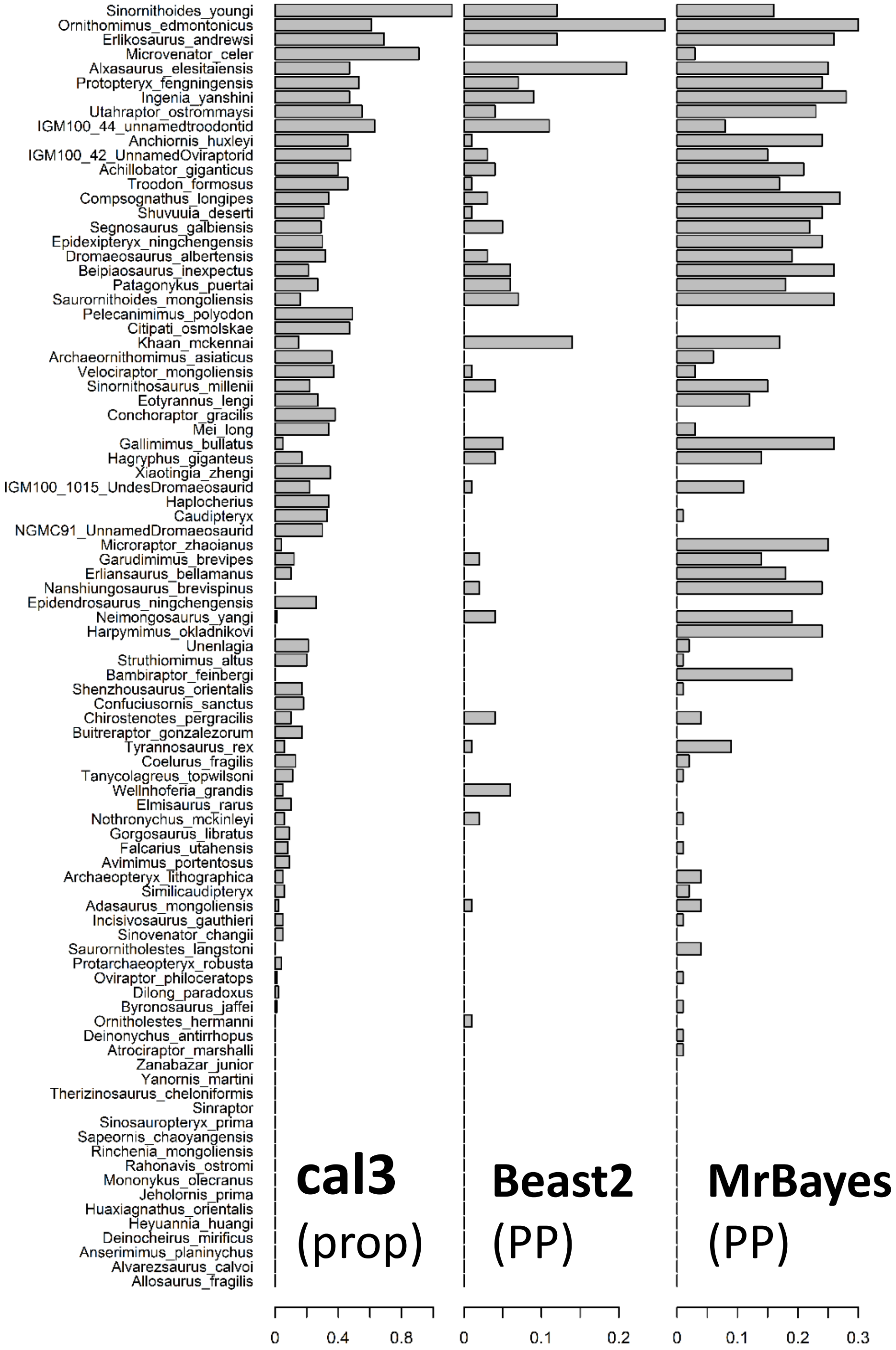
- cal3 finds very little support for anagenesis
    - Given biases, perhaps entirely budding?

Case 2: Mesozoic Theropods

- Take character matrix from Xu et al. 2011 and ages from PaleobioDB and do SA tip-dating with both MrBayes and BEAST2
  - Taxa treated as only occurring at FAD
- Compare to cal3 applied to a sample of most parsimonious topologies
  - Taxa treated as their entire stratigraphic range

- How similar across these methods is the support for single taxa to be sampled ancestors? (not pairs)

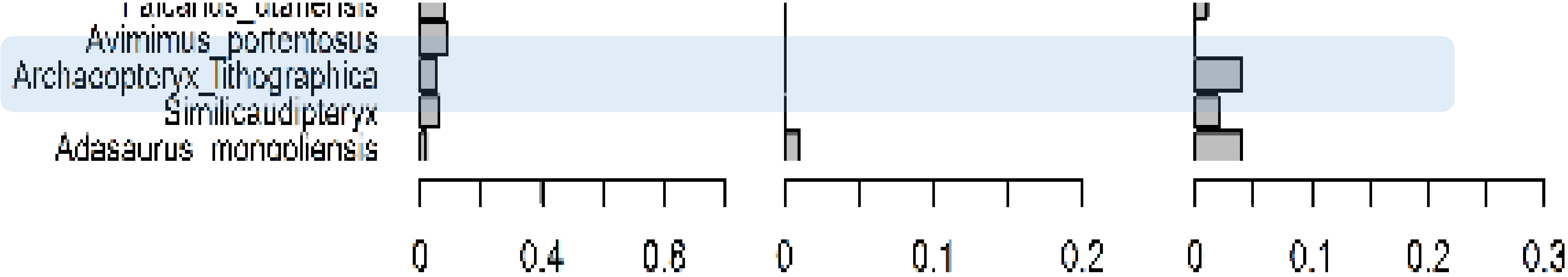
Bapst, Wright, Matzke & Lloyd, 2016; Biology Letters



- Significant rank-order pair-wise correlations of ancestral placement between methods
  - Strongest between MrBayes and BEAST2
- Considerable differences despite similar model
- Median # of ancestors per tree for tip-dating = **1-2**
- With cal3 (using entire taxon durations) = **17**
  - Always ***budding***

Bapst, Wright, Matzke & Lloyd, 2016

Whither the Ancestral Bird?



- *Archaeopteryx* rarely placed as a sampled ancestor
- Never placed as ancestor on lineage leading to extant birds, but rather as a sampled ancestor to its sister taxon / possible synonym *Wellnhoferia*

Bapst, Wright, Matzke & Lloyd, 2016

A New Era of Ancestors on Trees

- In the pterocephaliid trilobites, cal3 finds support for ancestor-descendant pairs long supported by experts
- Different tip-dating software and cal3 infer similar taxa as ancestors in Mesozoic theropods, but some differences particularly in overall frequency
- Strong evidence for budding cladogenesis under cal3, while anagenesis rare or non-existent in both datasets
- Need to expand tip-dating methods to account for persistent chronospecies, particularly we need to adapt morph models for static morphotaxa

Thanks for listening! Questions?