

The Past Sure Is Tense: On Interpreting Phylogenetic Divergence Time Estimates

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Abstract.—Divergence time estimation — the calibration of a phylogeny to geological time — is an integral first step in modelling the tempo of biological evolution (traits and lineages). However, despite increasingly sophisticated methods to infer divergence times from molecular genetic sequences, the estimated age of many nodes across the tree of life contrast significantly and consistently with timeframes conveyed by the fossil record. This is perhaps best exemplified by crown angiosperms, where molecular clock (Triassic) estimates predate the oldest (Early Cretaceous) undisputed angiosperm fossils by tens of millions of years or more. While the incompleteness of the fossil record is a common concern, issues of data limitation and model inadequacy are viable (if underexplored) alternative explanations. In this vein, [Beaulieu et al. \(2015\)](#) convincingly demonstrated how methods of divergence time inference can be misled by both (i) extreme state-dependent molecular substitution rate heterogeneity and (ii) biased sampling of representative major lineages. While these (essentially model-violation) results are robust (and probably common in empirical data sets), we note a further alternative: that the configuration of the statistical inference problem alone precluded the reconstruction of the paleontological timeframe for the crown age of angiosperms. We demonstrate, through sampling from the joint prior (formed by combining the tree (diversification) prior with the various calibration densities specified for fossil-calibrated nodes), that with no data present at all, an Early Cretaceous crown angiosperms is rejected (i.e., has essentially zero probability). More worrisome, however, is that for the 24 nodes calibrated by fossils, almost all have indistinguishable marginal prior and posterior age distributions, indicating an absence of relevant information in the data. Given that these calibrated nodes are strategically placed in disparate regions of the tree, they essentially anchor the tree scaffold, and so the posterior inference for the tree as a whole is largely determined by the pseudo-data present in the (often arbitrary) calibration densities. We recommend, as for any Bayesian analysis, that marginal prior and posterior distributions be carefully compared, especially for parameters of direct interest. Finally, we note that the results presented here do not refute the biological modelling concerns identified by [Beaulieu et al. \(2015\)](#). Both sets of issues remain apposite to the goals of accurate divergence time estimation, and only by considering them in tandem can we move forward more confidently. [Angiosperms; divergence time estimation; fossil record; marginal priors; information content; diptych; wild speculation.]

1 “Molecular clocks are not up to the job, but neither is
2 the fossil record.” [Donoghue and Benton \(2007\)](#)

3 Divergence time estimation from molecular genetic
4 sequences is fraught with uncertainty. The errors
5 involved in routine phylogenetic reconstruction
6 (suboptimal alignments, inadequate substitution
7 models, insufficient taxon/gene sampling, real gene
8 tree/species tree conflict, etc.) are compounded by
9 assumptions required to transform a phylogram (in
10 units of expected number of substitutions per site)
11 into a chronogram (in units of geological time): 1) an
12 appropriate model of substitution rate heterogeneity
13 among lineages and across time, and 2) temporal
14 calibrations, generated from the fossil (or biogeographic)
15 record, used to inform and constrain the extent of rate
16 variation.

17 It is therefore not surprising that there are
18 discrepancies between inferred molecular genetic
19 and paleontological timescales. However, while many
20 disagreements are minor and may innocuously be
21 attributed to insufficient sampling (genes, taxa, or
22 fossils), others are so severe and consistent that they
23 cast serious doubt on the appropriateness of molecular
24 clock models, the fossil record, or both. One prominent
25 example concerns placental mammals, where molecular
26 estimates (e.g., [Meredith et al. 2011](#)) of the crown
27 age almost double those from the fossil record (e.g.,
28 [O’Leary et al. 2013](#)), obscuring the role of the K-Pg
29 mass extinction on the evolutionary trajectory of this

group. Another conspicuous example, also spanning the
K-Pg boundary, is crown birds (Neornithes; [Ksepka
et al. 2014](#)), where (re)analyses have repeatedly lead
to incongruous inferred evolutionary timeframes (e.g.,
[Ericson et al. 2006](#) vs. [Brown et al. 2007](#); [Jarvis et al.
2014](#) vs. [Mitchell et al. 2015](#); [Prum et al. 2015](#)).

However, perhaps the best exemplified recalcitrant
node in terms of absolute age is that of crown
angiosperms, where molecular clocks pervasively infer a
Triassic age (e.g., [Bell et al. 2010](#); [Smith et al. 2010](#);
[Zeng et al. 2014](#); [Beaulieu et al. 2015](#); [Foster et al. 2016](#);
see a comprehensive review of estimates in [Magallón
et al. 2015](#)) while the oldest undisputed fossil remains
are restricted to the Early Cretaceous (136 Ma; [Brenner
1996](#)). Moreover, using a model of uniform random
fossilization ([Marshall 2008](#)) applied to 137 fossils lead
[Magallón et al. \(2015\)](#) to infer an upper bound on the
origin of crown angiosperms of just ~140 Ma. The age of
this one node, more than any other, has seriously called
into question the utility of both molecular clock models
and the fossil record.

Numerous reasons have been put forth to explain the
disparity of molecular and paleontological timescales. On
the one hand we have concerns with the fossil record.
By their nature, fossils *must* postdate the origin of
taxa, meaning that molecular estimates *should* predate
those from the fossil record. Furthermore, it is clear
that the fossil record is imperfect (more so for some
groups than others), such that in some instances it may
prove impossible to ever have a tight correlation with

molecular clock estimates. However, ‘absence of evidence’ vs. ‘evidence of absence’ is a complex matter, so a more productive avenue to pursue may be that of considering molecular approaches. While it has been speculated that molecular clocks might ‘run fast’ during radiations (thereby misleading clocks into inferring a long period of time has occurred; Benton 1999), this has no empirical support. However, it is known that substitution model mis-specification can mislead divergence time estimation (Phillips 2009; Schenk and Hufford 2010) and ultimately downstream analyses (Revell *et al.*, 2005). Likewise, mis-specification of relaxed clock models may also lead to inaccurate results (Dornburg *et al.* 2012; Worobey *et al.* 2014). Being only semi-identifiable, molecular clock methods require calibration from the fossil record, so appropriate calibration use is critically important (Inoue *et al.* 2010; Sauquet *et al.* 2011; Warnock *et al.* 2012; Magallón *et al.* 2013; Zhu *et al.* 2015). Finally, Beaulieu *et al.* (2015) recently demonstrated through simulation two further ways where molecular clocks might be misled: (i) through extreme state-dependent molecular substitution rate heterogeneity, and (ii) biased sampling of representative major lineages (both of which are essentially instances of model violation). While these are all valid concerns that should always be kept in mind, we explore below a further non-biological possibility that may unknowingly be at play in many data analyses.

DIPTYCH: A METAPHOR FOR DATA ANALYSIS?

A diptych is a device commonly used in western art and literature. It consists of paired, complementary works, in the artistic tradition typically two images joined at a hinge (e.g., Fig. 1). The function of a diptych is to reciprocally illuminate the component images, ideally revealing some more holistic concept. It is this feature that suggests an association with Bayesian data analysis. It is *de rigueur* in any Bayesian analysis to carefully compare paired prior and posterior parameter distributions to gauge how information content (via the likelihood) drives the results, as well as to establish the sensitivity of inferences to prior specifications. A diptych is, we argue, therefore a useful metaphor for describing the process of changes in belief in parameter values from the prior (*before* data have been observed) to the posterior (*after* data have been observed). We note that the phylogenetic systematics community has been generally lax in this respect, despite available Bayesian software packages making such reflections straightforward. We argue that this is especially important in divergence time estimation analyses, as it is generally unappreciated that there are *three* sets of distributions to consider. In addition to the temporal fossil calibration specified by the investigator (the ‘user prior’) and the resulting marginal posterior distribution, there exists an intermediate distribution, the marginal prior (also called the ‘effective’ or ‘joint’ prior by some authors), which is formed by the interaction among user priors and the underlying ‘tree



FIGURE 1. Diptych of Stilicho, ca. 395. Individual images can be viewed on their own, but the work as a whole is only coherent when considering the component pieces together. Photograph from Hayford Pierce and Royal Tyler, “L’art byzantin”, Paris, 1932. Public domain.

prior’ (for nodes not directly calibrated by a fossil; typically a birth-death prior). Here we turn our attention to these distributions to see what, if anything, we can glean about the age of crown angiosperms.

A RE-REANALYSIS OF THE AGE OF ANGIOSPERMS

We reanalyzed the data set provided by Beaulieu *et al.* (2015). The molecular alignment consists of four genes (chloroplast: *atpB*, *psbB*, and *rbcL*; nuclear: 18S) for 124 taxa including 91 angiosperms representing all extant orders (data file provided in the Supplementary Material; see also data from the original paper available on Dryad at <http://dx.doi.org/10.5061/dryad.629sc>). Sampling was originally designed specifically for dating the origin of angiosperms by allowing the placement of 24 (15 angiosperm) fossil calibrations from across landplants. All dating analyses reported here, like those in the original paper, were performed using the uncorrelated lognormal (UCLN) clock model and birth-death tree prior in BEAST v1.8.2 (Drummond *et al.* 2006; Drummond and Rambaut 2007) using the CPU implementation of the BEAGLE v2.1.2 library (Ayes *et al.* 2012).

We regenerated the posterior results of Beaulieu *et al.* (2015) by employing the original lognormal user priors specified in Table 1 and the following analysis settings: 3 replicate analyses of 50 million generations, sampling every 1000 generations. As in the original Beaulieu *et al.* (2015) paper we fixed the tree topology (their Figure 1). These analyses were re-run without any data (i.e.,

TABLE 1. Lognormal fossil calibration parameters as originally defined in [Beaulieu et al. 2015](#).

Name	Mean	St. Dev.	Offset	Clade
Anacostia	1.5	0.5	125.0	Angiosperms
Aquifoliaceae	1.5	0.5	65.0	Angiosperms
Araceae	1.5	0.5	112.0	Angiosperms
Archaeofructus	1.5	0.5	125.0	Angiosperms
Arecales	1.5	0.5	85.5	Angiosperms
Cornales	1.5	0.5	85.8	Angiosperms
Endressinia	1.5	0.5	114.0	Angiosperms
Fagales	1.5	0.5	93.6	Angiosperms
Mauldinia	1.5	0.5	99.6	Angiosperms
Myrtales	1.5	0.5	85.8	Angiosperms
Sapindopsis	1.5	0.5	105.8	Angiosperms
Tricolpites	1.5	0.5	125.0	Angiosperms
Typhaceae	1.5	0.5	40.4	Angiosperms
Virginianthus	1.5	0.5	105.8	Angiosperms
Walkerpollis	1.5	0.5	125.0	Angiosperms
Araucarites	1.5	0.5	213.0	Gymnosperms
Cratonia	1.5	0.5	114.0	Gymnosperms
Emporia	2.0	0.5	299.0	Gymnosperms
Paleotaxus	1.5	0.5	197.0	Gymnosperms
Baragwanathia	2.0	0.5	423.0	Outgroups
Palaeosmunda	1.5	0.5	251.0	Outgroups
Pekinopteris	1.5	0.5	228.0	Outgroups
Rellimia	2.0	0.5	388.0	Outgroups
Stachypteris	1.5	0.5	168.0	Outgroups

Notes: ‘Offset’ denotes the age of the oldest undisputed fossil in Ma. Mean and standard deviation are given in log space. Distributions with a mean of 1.5 have 95% of the prior mass with 10.2 Ma of the fossil age, while those with a mean of 2.0 have 95% of the prior mass with 16.82 Ma of the fossil age.

The posterior results of [Magallón et al. \(2015\)](#) were regenerated by running 3 replicate analyses of 100 million generations, sampling every 5000 generations. These analyses included the uniform calibration prior (139.5–136 Ma) on the age of crown angiosperms. To assess the influence of this single prior, 4 replicate analyses of 50 million generations were performed without the prior. Finally, as above, analyses sampling from the marginal prior (i.e., without any data) were performed for both sets of fossil calibrations (each with 4 replicates of 50 million generations).

Prior to summarization, the MCMC log files from each set of replicated analyses were concatenated while removing a conservative 10% sample burnin using the `pxlog` program from the `phyx` package ([Brown et al. 2017](#)). All results were processed in R v3.3.2 ([R Core Team, 2016](#)) and were visualized using `ggplot2` v2.2.1 ([Wickham, 2009](#)) and code adapted from `phyloch` v1.5-3 ([Heibl, 2008](#)).

THE INACCESSIBILITY OF AN EARLY CRETACEOUS CROWN ANGIOSPERMS

As in the original [Beaulieu et al. \(2015\)](#) paper we were unable to recover a posterior age estimate for crown angiosperms that corresponded with the prevailing paleontological timeframe, even when employing overly precise exponential fossil calibration user priors. However, when considering the diptych interpretation by examining the joint marginal prior, it is clear that we need not invoke modelling complications (e.g., due to biased lineage sampling or structured excessive rate heterogeneity) to explain the results. Rather, when running the analysis without any data, we see that an Early Cretaceous crown angiosperms is precluded based on the configuration of the statistical problem alone (Fig. 2). From the trace plots (Fig. 3) we see that the parameter regarding the age of crown angiosperms departs immediately from ~140 Ma to >200 Ma. In no instance did the MCMC samplers ever return to a ‘young’ age of angiosperms. The minimum post-burnin value for the prior and posterior analyses for the original lognormal calibration priors were 185.9 Ma and 192.0 Ma, respectively (181.1 Ma and 176.0 Ma for the exponential calibration priors). We note that these findings do not have to do with any peculiarity of the [Beaulieu et al. \(2015\)](#) data set as the results generated from the [Magallón et al. \(2015\)](#) data set without the uniform prior on crown angiosperms confirms the findings (minimum post-burnin ages for the prior and posterior analyses are 226.1 Ma and 197.2 Ma, respectively). In fact, the [Magallón et al. \(2015\)](#) data set, containing far more data (genes, taxa, and fossils) generated the oldest mean posterior estimate (249.7 Ma vs. 233.0 Ma for the original [Beaulieu et al. \(2015\)](#) priors vs. 213.3 Ma for the same data set using exponential calibration priors).

While rejecting an Early Cretaceous origin based on the marginal prior alone, both data sets *do* seem to

sampling from the marginal prior). Because these latter analyses were not as computationally demanding, as well as to perform a thorough exploration of parameter space, analyses were run in duplicate for 1 billion generations each, sampling every 10 thousand generations. Finally, we replicated all analyses but replaced the lognormal user prior calibrations from Table 1 with ‘extreme exponential’ distributions with a mean of 1.0 (offset by fossil ages); such distributions lend the utmost credence to the fossil record, as 95% of the prior masses lie within 3 Ma of the relevant fossil ages. Importantly, all analyses (posterior and prior-only) were initialized with chronograms wherein crown angiosperms originated ~140 Ma (i.e., consistent with the prescription of [Magallón et al. 2015](#)).

We focus here on the data (taxon, gene, and fossil sampling) and settings (model and priors) of [Beaulieu et al. \(2015\)](#) because it is representative of a standard dating analysis. However, to demonstrate that our own results are not restricted to this particular data set, we also reanalyze the data set of [Magallón et al. \(2015\)](#), albeit to a more limited degree because computational requirements. This data set consists of 5 genes (chloroplast: *atpB*, *rbcL* and *matK*; nuclear: 18S and 26S) for 799 taxa (792 angiosperms) and 121 fossil calibrations (note that the original analysis included 137 fossil calibrations, but 16 non-essential calibrations were subsequently found to be missing from the file shared by the original authors). All analyses employed the UCLN model as above and a fixed tree topology (their Figure 3).

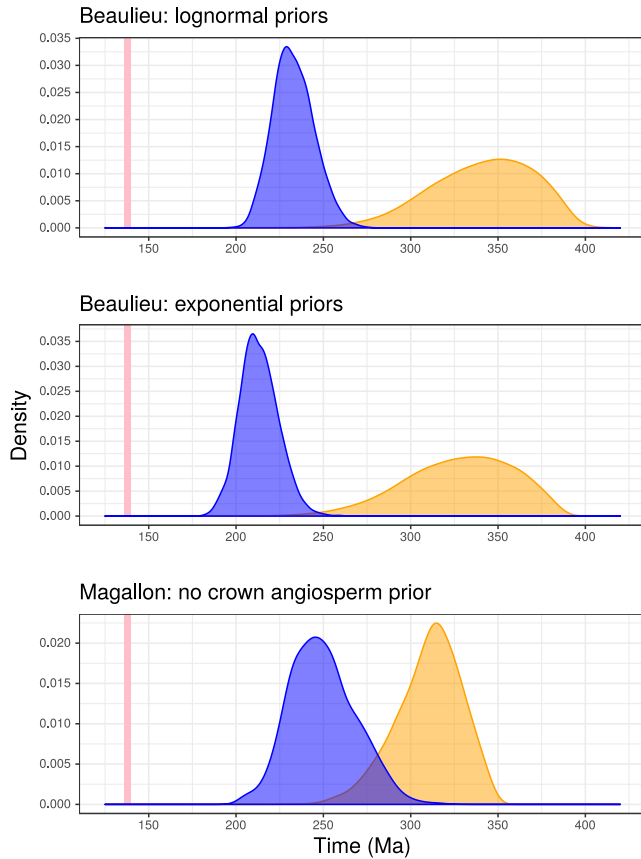


FIGURE 2. Diptychs comparing marginal prior (orange) and posterior (blue) distributions for the age of crown angiosperms. The top panel displays results using the original lognormal fossil calibration priors with the [Beaulieu et al. \(2015\)](#) data set, while the middle panel uses the exponential priors for the same data set. The bottom panel displays results for the [Magallón et al. \(2015\)](#) data set. Note that none of the analyses include a user prior for this node. For reference the uniform prior (139.5–136 Ma; pink) used by [Magallón et al. \(2015\)](#), reflecting the paleontological estimate, is shown.

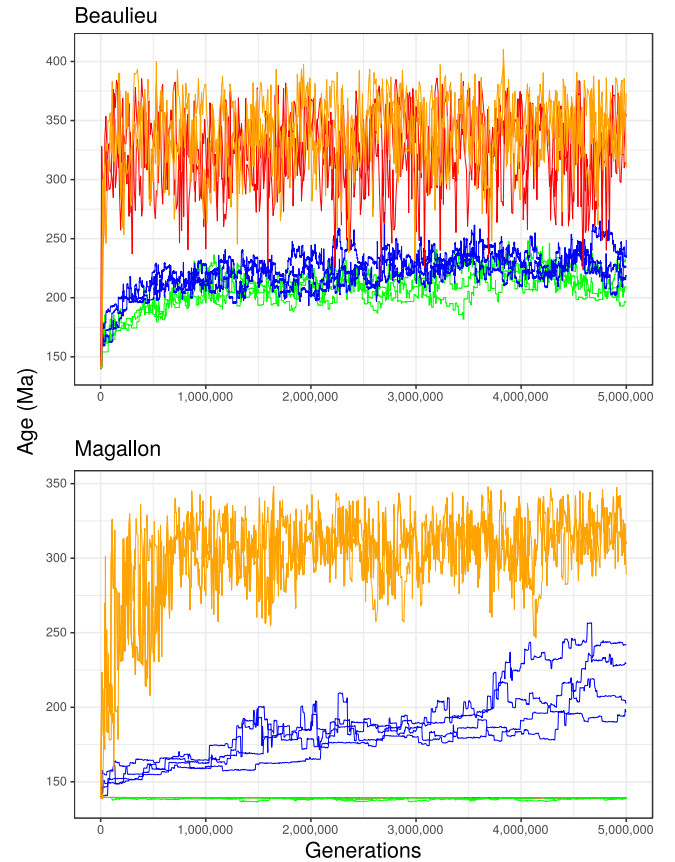


FIGURE 3. Traces of the age of the crown angiosperm node across replicate analyses (burnin phase only) for [Beaulieu et al. \(2015\)](#) (top) and [Magallón et al. \(2015\)](#) (bottom) data sets. Top: prior (lognormal priors), orange ($n = 2$); posterior (lognormal priors), blue ($n = 3$); prior (exponential priors), red ($n = 2$); posterior (exponential priors), green ($n = 3$). Bottom: prior (no angiosperm constraint), orange ($n = 4$); posterior (no angiosperm constraint), blue ($n = 4$); prior (all constraints), green ($n = 4$); posterior (all constraints), red ($n = 3$); note that this is mostly obscured by the green prior trace). All analyses were initialized with the age of crown angiosperms set at ~ 140 Ma.

PRIORS AND POSTERIOR: A DIPTYCH IN THREE PARTS

Above we introduced ‘diptych’ as a useful metaphor for interpreting Bayesian analytical results. The paired nature of a diptych mirrors the before (prior) and after (posterior) reflection on what has been learned about probable parameter values.

The metaphor is slightly more complicated for some parameters involved in divergence time analyses. Nodes not explicitly calibrated by fossil data (henceforth, ‘uncalibrated’ nodes) still require an age prior, which is provided by a ‘tree prior’, typically a birth-death, Yule, or coalescent prior. Such nodes thus have marginal prior and posterior distributions, and are conducive to the diptych metaphor. For those nodes that *are* directly calibrated using fossil information, the interpretation of the results of inference are more complicated. These nodes have a ‘user prior’, a distribution constructed in some way using information from the fossil record.

contain signal relevant to the age of crown angiosperms, as the marginal posterior estimates are shifted significantly younger than the marginal prior (Fig. 2). This raises the question: if true, what kind/amount of data would be required to recover an Early Cretaceous age for crown angiosperms? Ultimately this comes down to quantifying phylogenetic ‘information content’. Intriguing possibilities to addressing this sort of question therefore lie in Shannon information theory ([Shannon 1948](#)), a field which the systematics community has largely ignored. Recently [Lewis et al. \(2016\)](#) made substantial strides forward by applying this theory (in the discrete case) towards assessing the information content of prior and posterior tree topology distributions. Applications to the continuous case, however, are much more difficult, and no theory (let alone software) currently exists to address the present problem (Paul Lewis, personal communication).

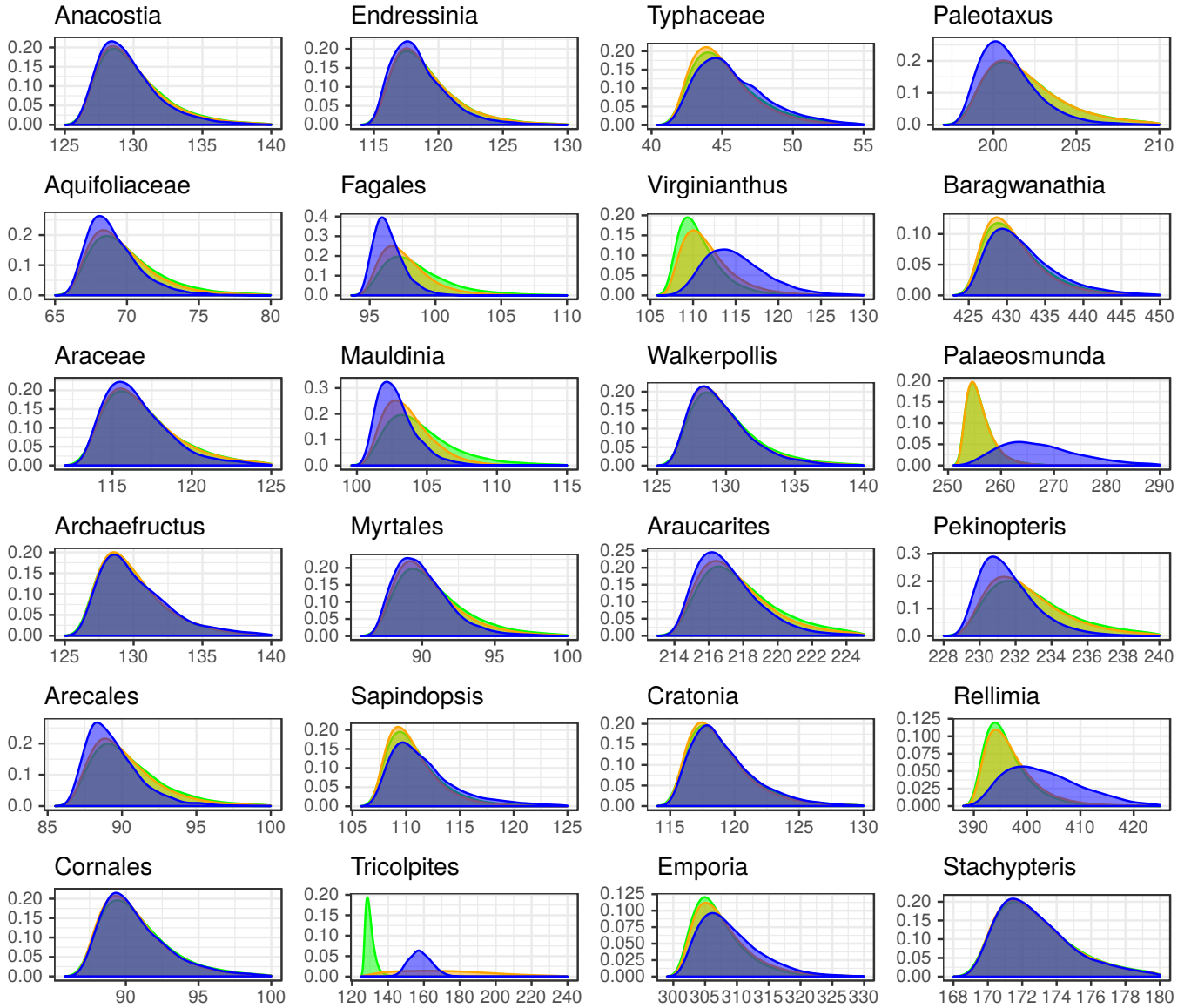


FIGURE 4. Densities for fossil-calibrated nodes from Beaulieu *et al.* 2015 (see Table 1); green indicates the user-specified lognormal prior, orange indicates the marginal prior, and blue indicates the marginal posterior. It is clear, for the majority of calibrated nodes, that (from the nearly complete overlap of prior and posterior distributions) the data contain little information for the parameters of interest.

1 However, these nodes are also involved in the tree
 2 prior. The resulting ‘marginal prior’ is a multiplicative
 3 combination of the user and tree priors, and may
 4 also be influenced by interactions with adjacent user-
 5 calibrated nodes (e.g., ancestor and descendant nodes
 6 which have overlapping user priors). The resulting
 7 marginal prior thus does not necessarily reflect the
 8 original user prior. This is, in our judgement, *far*
 9 *too rarely assessed*. Finally, these nodes have marginal
 10 posterior distributions. However, unlike the uncalibrated
 11 nodes (which involve only two distributions, and thus
 12 a simple interpretation), calibrated nodes involve three
 13 distributions (two priors and one posterior), which
 14 complicates interpretation. [We prefer to continue with

the diptych metaphor for these nodes, rather than the
 obvious ‘trptych’, as the focus lies still on the change
 in belief on parameter values before (prior) and after
 (posterior) observing the data, even if the prior involves
 two components.] The difference between the marginal
 prior and marginal posterior, like the uncalibrated
 nodes, reflects information in the data (that is, the
 likelihood). However, the difference between the user and
 marginal priors, if present, may be better described as
 demonstrating the influence of ‘pseudo-data’ present in
 the various user priors.

We now turn our attention to the fossil-calibrated
 nodes. Ideally we would find that the user and marginal
 priors are identical (that is, that the marginal priors

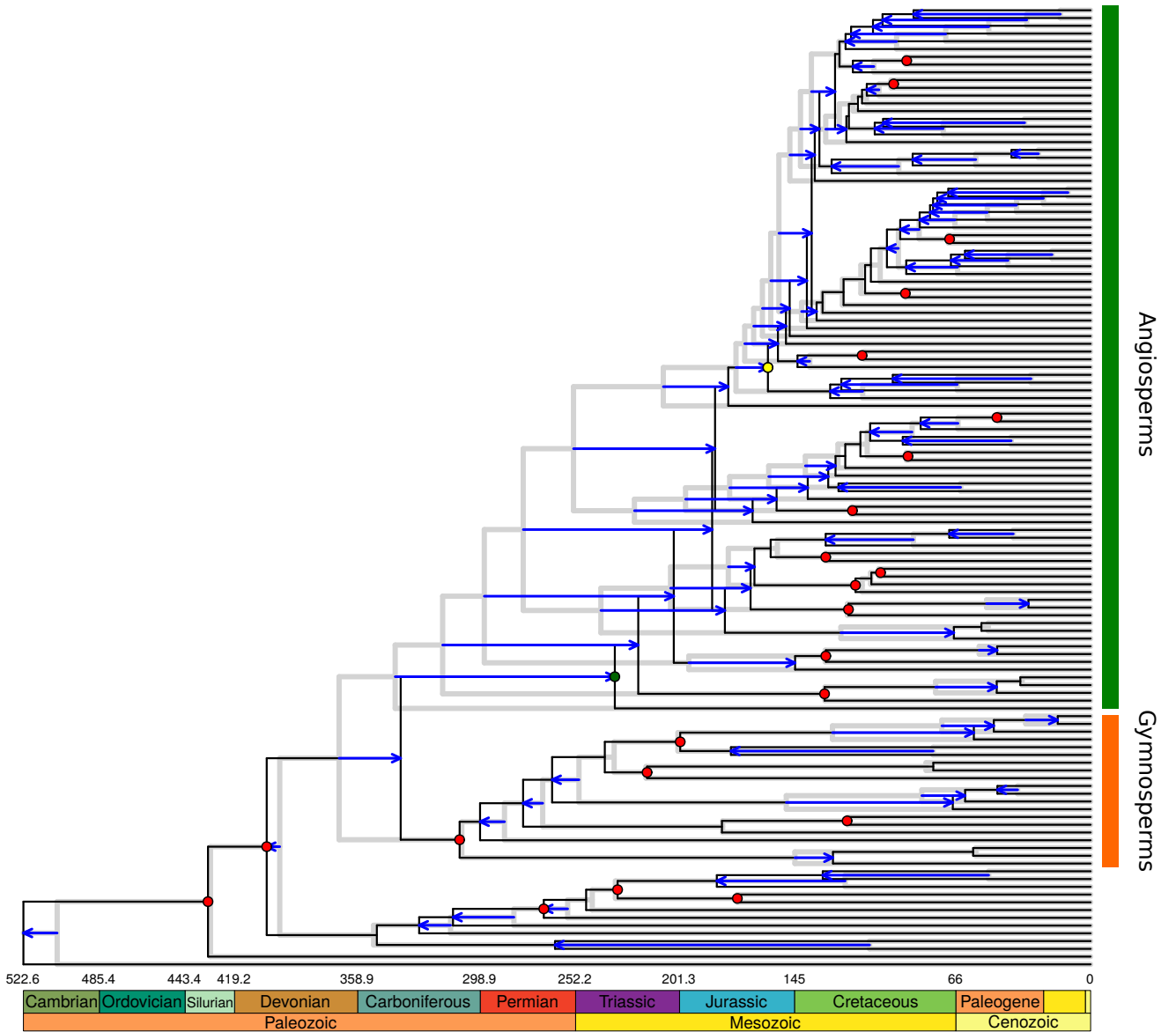


FIGURE 5. Mean prior (grey) and posterior (black) age estimates using the original lognormal calibration priors for the [Beaulieu et al. \(2015\)](#) data set. Blue arrows indicate shifts in age estimates from the prior to the posterior (nodes without arrows have shifted less than 5 Ma from prior to posterior). Nodes that are calibrated by fossil prior distributions are indicated with red circles, except the Tricolpites node which is indicated with a yellow circle. Finally, the (uncalibrated) crown angiosperm node is indicated in green.

1 reflect the intentions of the researcher), and the marginal
 2 priors and posteriors to differ (indicating information
 3 present in the data relevant to the parameter of interest).
 4 We plot in Fig. 4 the three sets of distributions for the
 5 24 fossil-calibrated nodes for the [Beaulieu et al. 2015](#)
 6 data set. In general, user and marginal priors match quite
 7 closely. However, there is a stark exception involving the
 8 Tricolpites constraint: while the user prior specifies that
 9 95% of the prior mass should lie between 135.2–125 Ma,
 10 the marginal prior has a 95% highest posterior density
 11 (HPD) range of 226.1–128.7 Ma. The marginal posterior

of this node age has a 95% HPD range of 170.7–146.6 Ma,
 which already surpasses the angiosperm paleontological
 estimate of ~140 Ma despite being well nested within the
 clade. We note that Tricolpites is the oldest constraint
 within angiosperms used by [Beaulieu et al. 2015](#) (see
 Table 1 and Fig. 5). However, it is clear that it is not
 this particular calibration which is forcing angiosperms
 to be ‘too old’. Reanalysis without this specific constraint
 yielded even older posterior estimates for both this node
 (95% HPD: 181.2–154.3 Ma) and crown angiosperms
 (mean 241.0 Ma vs. 233.0 Ma with the constraint; data

not shown). We cannot currently identify the cause of the disruption of the Tricolpites user prior.

Finally, we consider differences between the marginal prior and posterior distributions of age estimates for these same fossil-calibrated nodes. As discussed above, shifts in these paired distributions (i.e., following the diptych metaphor) would indicate the presence/degree of relevant phylogenetic ‘information’ (although theory has not yet been worked out on how to quantify this). However, from Fig. 4 we note that, for the most part, these distributions are nearly indistinguishable. This pattern is even more clear in Fig. 5 where, while uncalibrated nodes show significant shifts between prior and posterior analyses, calibrated nodes show no movement. This lack of updating in belief from prior to posterior for the calibrated nodes suggests two non-mutually exclusive interpretations: (i) that the UCLN model, through allowing independent molecular substitution rates on all edges, may be overfitting the data, essentially allowing all calibrations to be mutually consistent (we do not expect, for example, that all of our calibration densities are equally ‘good’ - that is, that some constraints should conflict); (ii) that the data set considered here lacks relevant phylogenetic ‘information’, or at least insufficient information to overrule the pseudo-data present in the fossil calibration densities.

The finding of equivalent prior and posterior distributions may come as a surprise to some users, as unbounded (e.g., lognormal) temporal priors are typically used to ‘let the data speak for themselves’. Certainly, divergence time inference is only semi-identifiable (dos Reis and Yang 2013), so we do expect some level of association. It is the *degree* of association that is worrying. We are unaware of any other type of Bayesian analysis in evolutionary biology where identical prior and posterior distributions would not cause concern. The present results go a long way to explaining why divergence time estimation shows such a strong sensitivity to the fossil calibrations used (Inoue *et al.* 2010; Sauquet *et al.* 2011; Warnock *et al.* 2012). The interpretation of fossil calibrations contributing pseudo-data (rather than, say, fossils setting simple minimum age constraints as they have been traditionally) suggests that we might benefit from rethinking lessons that have been learned in the early days of phylogenetic divergence time estimation. We briefly consider one now.

ARE MORE FOSSILS REALLY BETTER IN NODE DATING ANALYSES?

There is an adage in the divergence time estimation literature that as many fossils as possible should be used to calibrate nodes (Benton and Donoghue 2007). This makes sense, as of course we would like to include as much information as possible into a reconstruction. However, this advice largely came about when dating methods (e.g., *r8s*, Sanderson 2003; *multidivtime*, Thorne and Kishino 2002) employed constraints (e.g., boolean minimum ages for the age of the fossil) rather

than probabilistic distributions. As long as fossils were correctly placed within the phylogeny, the inclusion of more fossils should not produce misleading results. For instance, fossils that are ‘too young’ (that is, do not closely approximate in age the node they are calibrating) are either simply uninformative, or appropriately represent limitations of the fossil record. As an extreme example, a chicken bone found in a back alley gutter is a valid (if imprecise) minimum age constraint for *Gallus gallus* (recently estimated at 2.9 Ma; Stein *et al.* 2015).

However, from the results reported above (Figs. 4,5) we find several concerns with including as many fossils as possible in a probabilistic node-dating analysis. [We note that these concerns do not apply to the fossilized birth-death model (Heath *et al.* 2014) or tip-dating (Ronquist *et al.* 2012) approaches to divergence time estimation, which do not involve such calibrations.] First, as with the Tricolpites example above, calibrations can interact with each other and the tree prior in unpredictable ways to produce marginal priors that do not represent the originally intended user priors. While this is a recognized (though under-appreciated) issue, the available solutions work only for a small number of calibrations (Heled and Drummond 2012; Heled and Drummond 2015). Second, given that the marginal prior and posterior calibrated node ages are often indistinguishable (suggesting little relevant phylogenetic information content), it is worrisome that the act of employing temporal calibration priors can directly determine the resulting posterior patterns of rate heterogeneity across a tree. It is not inconceivable, for example, that the parametric use of the best available fossils from an incomplete fossil record could turn a clock-like data set unclock-like, needlessly increasing the model complexity (and therefore uncertainty) involved.

Our final concern with unrestrained parametric calibration use is the form of the calibrations themselves. A flexible assortment of distribution families are available (Ho and Phillips 2009; see also discussion in Brown and van Tuinen 2011), allowing essentially any prior belief to be employed. In addition, researchers can make use of the fossil calibration database (Ksepka *et al.* 2015), and prescribed ‘best practices’ (Parham *et al.* 2012) can help avoid naive errors when dealing with the fossil record. Nevertheless, the vast majority of user calibration priors employed in the literature are wholly idiosyncratic and arbitrary (we include ourselves here). This is not necessarily a result of molecular phylogeneticists lacking the appropriate paleontological expertise (and isn’t that what collaboration is for?), but rather a property of data involved.

While methods exist to generate a distribution from a set of fossils (Marshall 2008; Nowak *et al.* 2013; Claramunt and Cracraft 2015), these require well sampled data. Scant data is an entirely different problem. How does one fit a distribution to a single (exceptionally old, and therefore exceptionally informative) fossil? Minimum bounds are simple (the age of the oldest

fossil), but as [Parham *et al.* \(2012\)](#) note, there exists no standard protocol for formulating maximum ages (let alone the shape of the distribution spanning the upper and lower bounds). Indeed, the process of constructing temporal priors is so nebulous that [Lee and Skinner \(2011\)](#) likened it to “educated guesswork”. However, it is not the arbitrariness of the calibrations *per se* that is of concern, but rather that they act as a strong source of pseudo-data. Taken to a hyperbolic extreme, if calibration priors were applied to every node in a tree, then the results above would suggest that there would be no use in running the analysis at all. In other types of Bayesian analysis we expect that an increase in data can overrule poorly constructed priors and converge on an answer. It is presently unclear whether this is true when performing node-dating using the UCLN model, and if so, how much data (or ‘information’, whatever that turns out to be) would be required. Certainly it is known that the uncertainty in divergence time estimates cannot be reduced arbitrarily, even with infinite amounts of data ([Rannala and Yang 2007](#); [Yang and Rannala 2006](#); [dos Reis and Yang 2013](#)), but it is unclear how data can override the pseudo-data present in the node calibration priors.

WHERE TO GO FROM HERE?

The results presented here highlight several issues that should be considered as the field moves forward. In regard to angiosperms, is the amount of temporal ‘information’ present in empirical data (or, on the other hand, the adequacy of current relaxed clock models) insufficient to reconstruct such recalcitrant nodes as the age of crown angiosperms? If this is the case, the only way forward, given the methods of inference, may be to apply user priors that are *intended* to constitute pseudo-data. However, this fact needs to be more widely recognized. In some respects this is a defensible position as, if fossil calibrations are constructed with significant information about the fossil record, estimations will be constrained to existing fossil information. In this vein, the results of [Magallón *et al.* \(2015\)](#), which estimate nested angiosperm divergence times within a strict paleontologically-imposed age of the ancestral crown node, are reasonable in the context of the data available ([Sanderson, 2015](#)). Nevertheless, it should be clear when the molecular data, in this context, do not significantly alter the posterior distribution. If this is indeed the way forward, then care should be taken to assess both the validity of the fossils being used ([Sanders and Lee 2007](#); [Brown and Sorhannus 2010](#)) and the form of the calibration priors ([Inoue *et al.* 2010](#); [Brown and Sorhannus 2010](#); [Sauquet *et al.* 2011](#); [Warnock *et al.* 2012](#); [Foster *et al.* 2016](#)). In addition, we strongly advocate the regular use of the diptych approach to data analysis by habitually comparing prior and posterior distributions: it is imperative to understand which parameters in our models are informed by the data present, and which simply recapitulate the prior. When

hypothesis testing it is even more critically important to determine whether a hypothesis is rejected by the data or, as with the crown angiosperm age results above, are effectively precluded by the joint prior.

However, new methods of divergence time inference are emerging that largely bypass the concerns associated with node-dating ([Heath and Moore, 2014](#)). The fossilized birth-death model of [Heath *et al.* \(2014\)](#) incorporates extant and extinct (i.e., sampled fossils) lineages as evolving according to the same underlying diversification model. Alternatively, when morphological data are available for both extinct and extant taxa, divergence times can be estimated using the tip-dating approach of [Ronquist *et al.* \(2012\)](#). Both of these methods can take advantage of an arbitrary number of fossils within a lineage (rather than being reduced to a single distribution as in node-dating) and incorporate fossil temporal information directly without extrapolation. The excitement surrounding these methods might lead us to think it not unreasonable to suppose that in the near future node-dating will be regarded as a useful tool that was ultimately replaced by methods that more directly make use of the available data. However, both of these methods are relatively new, and it is unclear whether they will overthrow node-dating results for the most recalcitrant nodes (i.e., placental mammals, crown birds, crown angiosperms, etc.). These methods also raise new questions in regard to model adequacy, implied and explicit assumptions regarding both diversification and morphology models, and data availability and quality for extinct and extant lineages. Furthermore, the resulting divergence time estimates from these new methods may not differ as much as expected. For example, [Eguchi and Tamura \(2016\)](#) employed the fossilized birth-death model and found monocots arose 174.26–134.14 Ma, which does not conflict strongly with previous node-dating results. It thus appears far too premature to consider the tempo of angiosperm diversification solved.

FINAL THOUGHTS ON THE AGE OF ANGIOSPERMS

Finally, we note that the results presented above do not refute the concerns identified and demonstrated through simulation by [Beaulieu *et al.* \(2015\)](#) regarding violations of biological modelling. While among-lineage molecular substitution rate heterogeneity is regarded as ubiquitous, clade- and trait-specific correlations of rate variation explored by [Beaulieu *et al.* \(2015\)](#) are becoming increasingly recognized as important biological patterns of molecular evolution ([Smith *et al.* 2010](#); [Dornburg *et al.* 2012](#); [Lartillot and Delsuc 2012](#); [Worobey *et al.* 2014](#)). Such processes must be correctly modelled if our divergence time estimates are to be accurate. In this vein, we note that the fit ([Lepage *et al.*, 2007](#)) and adequacy ([Duchêne *et al.*, 2015](#)) of alternative clock models are far too rarely assessed. In addition, the artefacts of lineage sampling identified by [Beaulieu *et al.* \(2015\)](#) casts doubt on the suitability of a homogeneous

birth-death model as a prior on node ages. This doubt is especially manifested with respect to dating the evolution of angiosperms, where it is known *a priori* that lineages exhibit an incredible breadth of diversification rates (Tank *et al.*, 2015), not to mention that the extant angiosperm diversity dwarfs other embryophyte clades. We thus regard our results above as complementary to those of Beaulieu *et al.* (2015), and only with both in mind can we confidently move forward.

SUPPLEMENTARY MATERIAL

Data available from the Dryad Data Repository: <http://dx.doi.org/10.5061/dryad.XXXX>.

FUNDING

J.W.B. and S.A.S. were both supported by the NSF AVATOL Grant 1207915.

ACKNOWLEDGEMENTS

We thank Jeremy Beaulieu and Brian O'Meara for sharing their thoughts on these issues, and Susana Magallón for graciously sharing her BEAST xml input file. We would also like to thank the following for helpful discussions: Ben Redelings, Joseph Walker, Ning Wang, Greg Stull, Aaron King, Michael Landis, Alex Taylor, Paul Lewis, and members of the Smith laboratory. J.W.B. thanks Don Van Vliet for help with the title, Emo Philips for help with broader dissemination, Mark Kozelek for encouragement, and Linda Slote for tracking down an obscure Testudines reference (that was unfortunately dropped from an earlier version of this paper).

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