

<sup>1</sup> DateLife: leveraging databases and analytical tools to reveal the dated Tree of Life

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17

## Abstract

18 Achieving a high-quality reconstruction of a phylogenetic tree with branch lengths  
19 proportional to absolute time (chronogram) is a difficult and time-consuming task. But the  
20 increased availability of fossil and molecular data, and time-efficient analytical techniques  
21 has resulted in many recent publications of large chronograms for a large number and wide  
22 diversity of organisms. Knowledge of the evolutionary time frame of organisms is key for  
23 research in the natural sciences. It also represent valuable information for education, science  
24 communication, and policy decisions. When chronograms are shared in public, open  
25 databases this wealth of expertly-curated and peer-reviewed data on evolutionary timeframe  
26 is exposed in a programmatic and reusable way, as intensive and localized efforts have  
27 improved data sharing practices, as well as incentivized open science in biology. Here we  
28 present DateLife, a service implemented as an R package and an R Shiny website application  
29 available at [www.datelife.org](http://www.datelife.org), that provides functionalities for efficient and easy finding,  
30 summary, reuse, and reanalysis of expert, peer-reviewed, public data on time frame of  
31 evolution. The main DateLife workflow constructs a chronogram for any given combination  
32 of taxon names by searching a local chronogram database constructed and curated from the  
33 Open Tree of Life Phylesystem phylogenetic database, which incorporates phylogenetic data  
34 from the TreeBASE database as well. We implement and test methods for summarizing time  
35 data from multiple source chronograms using supertree and congruification algorithms, and  
36 using age data extracted from source chronograms as secondary calibration points to add  
37 branch lengths proportional to absolute time to a tree topology. DateLife will be useful to  
38 increase awareness of the existing variation in alternative hypothesis of evolutionary time for  
39 the same organisms, and can foster exploration of the effect of alternative evolutionary  
40 timing hypotheses on the results of downstream analyses, providing a framework for a more  
41 informed interpretation of evolutionary results.

42

*Keywords:* Tree; Phylogeny; Scaling; Dating; Ages; Divergence times; Open Science;

<sup>43</sup> Congruification; Supertree; Calibrations; Secondary calibrations

<sup>44</sup> Word count: 4823

45 DateLife: leveraging databases and analytical tools to reveal the dated Tree of Life

46 **Introduction**

47 Chronograms –phylogenies with branch lengths proportional to time– provide key data  
48 on evolutionary time frame for the study of natural processes in many areas of biological  
49 research, such as developmental biology (Delsuc et al., 2018; Laubichler & Maienschein,  
50 2009), conservation biology (Felsenstein, 1985; C. Webb, 2000), historical biogeography  
51 (Posadas, Crisci, & Katinas, 2006), and species diversification (Magallon & Sanderson, 2001;  
52 Morlon, 2014).

53 Building a chronogram is not an easy task. It requires obtaining and curating data to  
54 construct a phylogeny, selecting and placing appropriate calibrations on the phylogeny using  
55 independent age data points from the fossil record or other dated events, and inferring the  
56 full dated tree; it also generally requires specialized biological training, taxonomic domain  
57 knowledge, and a non-negligible amount of research time, computational resources and  
58 funding.

59 Here we present the DateLife project which has the main goal of capturing age data  
60 from published chronograms, and making these data readily accessible to the community for  
61 reuse and reanalysis. DateLife’s core software application is available as an R package  
62 (Sanchez-Reyes et al., 2022), and as an online Rshiny interactive website at [www.datelife.org](http://www.datelife.org).  
63 It features key elements for scientific reproducibility, such as a versioned, open and fully  
64 public source database (McTavish et al., 2015), data stored and available in a computer  
65 readable format (Vos et al., 2012), automated and programmatic ways of accessing the data  
66 (Stoltzfus et al., 2013) and methods to summarize and compare the data.

67 **Description**

68 DateLife’s core software application consists of the R package `datelife`. Its latest  
69 stable version – v0.6.2, is available from the CRAN repository (Sanchez-Reyes et al., 2022),

70 and relies on functionalities from various biological R packages: ape (Paradis, Claude, &  
71 Strimmer, 2004), bold (Chamberlain et al., 2019), geiger (Pennell et al., 2014), paleotree  
72 (Bapst, 2012), phyloch (Heibl, 2008), phylocomr (Ooms & Chamberlain, 2018), phytools  
73 (Revell, 2012), rotl (Michonneau, Brown, & Winter, 2016), and taxize (Chamberlain & Szöcs,  
74 2013; Chamberlain et al., 2019). Figure 1 provides a graphical summary of the three main  
75 steps of the DateLife algorithm: creating a search query, searching a database, and  
76 summarizing results from the search.

## 77 Creating a search query

78 DateLife starts by processing an input consisting of at least two taxon names, which  
79 can be provided as a comma separated character string or as tip labels on a tree. If the input  
80 is a tree, it can be provided as a classic newick character string (Archie et al., 1986), or as a  
81 “phylo” R object (Paradis et al., 2004). The input tree is not required to have branch lengths,  
82 and its topology is used in the summary steps described in the next section.

83 DateLife accepts scientific names that can belong to any inclusive taxonomic group  
84 (e.g., genus, family, tribe, etc.) or a binomial species name. Subspecies and variants are  
85 ignored. If an input taxon name belongs to an inclusive taxonomic group, the algorithm has  
86 two alternative behaviors defined by the “get species from taxon” flag. If the flag is active,  
87 DateLife retrieves all species names within the inclusive taxonomic group (following a  
88 taxonomy of choice; current options are Open Tree of Life, NCBI, GBIF, or IRMNG  
89 taxonomies) and adds them to the input string. If the flag is inactive, DateLife excludes any  
90 taxon names above the species level from the search query.

91 DateLife processes input scientific names using a Taxonomic Name Resolution Service  
92 (TNRS), which increases the probability of correctly finding the queried taxon names in the  
93 chronogram database. TNRS detects, corrects and standardizes name misspellings and typos,  
94 variant spellings and authorities, and nomenclatural synonyms to a single taxonomic

95 standard (Boyle et al., 2013). DateLife implements TNRS using OpenTree's unified  
96 taxonomy as standard (Open Tree Of Life et al., 2016; Rees & Cranston, 2017), storing  
97 OpenTree's Taxonomy identification numbers for further processing.

98 The processed input taxon names are saved as an R object of a newly defined class,  
99 `datelifeQuery`, that is used in the following steps. This object contains the standardized  
100 names, the corresponding OpenTree taxonomic id numbers, and the topology of the input  
101 tree if any was provided.

## 102 Searching a chronogram database

103 At the time of writing of this manuscript , DateLife's chronogram database latest  
104 version consist of 253 chronograms published in 187 different studies. It is curated from  
105 OpenTree's phylogenetic database, the Phylesystem, which constitutes an open source of  
106 expert and peer-reviewed phylogenetic knowledge with rich metadata (McTavish et al., 2015),  
107 which allows automatic and reproducible assembly of our chronogram database. Datelife's  
108 chronogram database is navigable as an R data object within the `datelife` R package.

109 A unique feature of OpenTree's Phylesystem is that the community can add new  
110 published, state-of-the-art chronograms any time through their curator application  
111 (<https://tree.opentreeoflife.org/curator>). As chronograms are added to Phylesystem, they are  
112 incorporated into an updated `datelife`'s database that is assigned a new version number,  
113 followed by a package release on CRAN. `datelife`'s chronogram database is updated as new  
114 chronogram data is added to Phylesystem, at a minimum of once a month and a maximum  
115 of every 6 months. Users can also upload and curate new chronograms to OpenTree  
116 themselves. Then, trigger an update of their local `datelife` database to incorporate the new  
117 chronograms and have them available for their current analysis.

118 A DateLife search is implemented by matching processed taxon names provided by the  
119 user to tip labels in the chronogram database. Chronograms with at least two matching

120 taxon names on their tip labels are identified and pruned down to preserve only the matched  
121 taxa. These matching pruned chronograms are referred to as source chronograms. Total  
122 distance (in units of millions of years) between taxon pairs within each source chronogram  
123 are stored as a patristic distance matrix (Figure 1). The matrix format speeds up extraction  
124 of pairwise taxon ages of any queried taxa, as opposed to searching the ancestor node of a  
125 pair of taxa in a “phylo” object or newick string. Finally, the patristic matrices are  
126 associated to the study citation where the original chronogram was published, and stored as  
127 an R object of the newly defined class `datelifeResult`.

128 **Summarizing search results**

129 Summary information is extracted from the `datelifeResult` object to inform  
130 decisions for subsequent steps in the analysis workflow. Basic summary information available  
131 to the user is:

- 132 1. The matching pruned chronograms as newick strings or “phylo” objects.
- 133 2. The ages of the root of all source chronograms. These ages can correspond to the age  
134 of the most recent common ancestor (mrca) of the user’s group of interest if the source  
135 chronograms have all taxa belonging to the group. If not, the root corresponds to the  
136 mrca of a subgroup within the group of interest.
- 137 3. Study citations where original chronograms were published.
- 138 4. A report of input taxon names matches across source chronograms.
- 139 5. The source chronogram(s) with the most input taxon names.
- 140 6. Various single summary chronograms resulting from summarizing age data, generated  
141 using the methodology described next.

142 ***Choosing a topology.***— DateLife requires a tree topology to summarize age data  
143 upon. We recommend that users provide a tree topology as input from the literature, or one  
144 of their own making. If no topology is provided, DateLife automatically obtains one from the

<sup>145</sup> OpenTree synthetic tree (Open Tree Of Life et al., 2019). These are known as “induced”  
<sup>146</sup> OpenTree subtrees, which do not necessarily correspond to a monophyletic group.  
<sup>147</sup> Alternatively, DateLife can combine topologies from source chronograms using a supertree  
<sup>148</sup> approach. To combine topologies from source chronograms into a single summary (or  
<sup>149</sup> supertree) topology, the DateLife algorithm starts by identifying the source chronograms  
<sup>150</sup> that form a grove, roughly, a sufficiently overlapping set of taxa between trees, by  
<sup>151</sup> implementing definition 2.8 for n-overlap from Ané et al. (2009). In rare cases, a group of  
<sup>152</sup> trees can have multiple groves. By default, DateLife chooses the grove with the most taxa,  
<sup>153</sup> however, the “criterion = trees” flag allows the user to choose the grove with the most trees  
<sup>154</sup> instead. If source chronograms do not form a grove, the supertree reconstruction will fail.

<sup>155</sup> ***Dating the topology.***— Input topologies from OpenTree or the supertree approach  
<sup>156</sup> described above do not include branch length estimates of any kind. Optionally, to estimate  
<sup>157</sup> branch lengths proportional to substitution rates on these topologies, DateLife can mine the  
<sup>158</sup> Barcode of Life Data System, BOLD (Ratnasingham & Hebert, 2007) to obtain genetic  
<sup>159</sup> markers for the input taxa. These markers are aligned with MUSCLE (Edgar, 2004) (by  
<sup>160</sup> default) or MAFFT (Katoh, Asimenos, & Toh, 2009). This alignment can be used to  
<sup>161</sup> estimate branch lengths on input topologies that lack branch lengths. Currently, branch  
<sup>162</sup> length reconstruction in DateLife is performed using parsimony and the likelihood of the  
<sup>163</sup> phylogenetic tree given a sequence alignment is computed (Schliep, 2011). While relative  
<sup>164</sup> branch length information provides additional data for nodes without secondary date  
<sup>165</sup> calibrations, topologies without branch lengths can also be dated.

<sup>166</sup> Once a topology is chosen, DateLife applies the congruification method (Eastman,  
<sup>167</sup> Harmon, & Tank, 2013) to find nodes belonging to the same clade across source  
<sup>168</sup> chronograms, and extract the corresponding node ages from the patristic distance matrices  
<sup>169</sup> stored as `datelifeResult`. By definition, the matrices store total distance (time from tip to  
<sup>170</sup> tip), hence, node ages correspond to half the values stored in the patristic distance matrices.

171 This assumes that the terminal taxa are coeval and occur at the present. A table of  
172 congruified node ages that can be used as calibrations for a dating analysis is stored as a  
173 `congruifiedCalibrations` object.

174 For each congruent node, the pairwise distances that traverse that node are  
175 summarized into a single summary matrix using classic summary statistics (i.e., mean,  
176 median, minimum and maximum ages), and the Supermatrix Distance Method [SDM;  
177 Criscuolo, Berry, Douzery, and Gascuel (2006)], which deforms patristic distance matrices by  
178 minimizing variance and then averaging them. These single summary taxon pair age  
179 matrices (Summarized calibrations) can be applied as calibrations to date a tree topology,  
180 using different dating methods currently supported within DateLife: MrBayes (Huelsenbeck  
181 & Ronquist, 2001; Ronquist & Huelsenbeck, 2003), PATHd8 (Britton, Anderson, Jacquet,  
182 Lundqvist, & Bremer, 2007), BLADJ (Campbell O. Webb, Ackerly, & Kembel, 2008;  
183 Campbell O. Webb & Donoghue, 2005), and treePL (Stephen A. Smith & O'Meara, 2012).

184 By default, DateLife implements the Branch Length Adjuster (BLADJ) algorithm to  
185 obtain a fully dated topology. BLADJ fixes node ages that have calibration data, and  
186 distributes time between nodes with no data evenly between nodes with calibration data.  
187 This minimizes age variance in the resulting chronogram (Campbell O. Webb et al., 2008).  
188 BLADJ does not use branch lengths even when they are present in the input tree or  
189 summarizing topology. When there is conflict in ages between nodes with calibration data,  
190 the algorithm ignores node ages that are older than the age of a parent node. BLADJ  
191 requires a root age estimate. If there is no information on the age of the root in the  
192 chronogram database, users can provide an estimate from the literature. If none is provided,  
193 DateLife assigns an arbitrary age to the root as 10% older than the oldest age available  
194 within the group.

195 Alternative options supported in DateLife (MrBayes, PATHd8, TreePL) incorporate  
196 branch length information from the input topology in combination with the calibrations.

197 PATHd8 is a non-clock, rate-smoothing method (Britton et al., 2007) to date trees. treePL  
198 (Stephen A. Smith & O'Meara, 2012), is a semi-parametric, rate-smoothing, penalized  
199 likelihood dating method (Michael J. Sanderson, 2002). The MrBayes (Huelsenbeck &  
200 Ronquist, 2001; Ronquist & Huelsenbeck, 2003) approach in datelife uses the calibrations as  
201 priors on node ages.

202 **Visualizing results.**— Finally, users can save all source and summary chronograms in  
203 formats that permit reuse and reanalyses (newick and R “phylo” format), as well as visualize  
204 and compare results graphically, or construct their own graphs using `datelife`’s chronogram  
205 plot generation functions available from the R package `datelifeplot` (Sanchez-Reyes &  
206 O’Meara, 2022).

## 207 Benchmark

208 `datelife`’s code speed was tested on an Apple iMac with one 3.4 GHz Intel Core i5  
209 processor. We registered variation in computing time of query processing and search through  
210 the database relative to number of queried taxon names. Query processing time increases  
211 roughly linearly with number of input taxon names, and increases considerably if Taxonomic  
212 Name Resolution Service (TNRS) is activated. Up to ten thousand names can be processed  
213 and searched in less than 30 minutes with the most time consuming settings. Once names  
214 have been processed as described in methods, a name search through the chronogram  
215 database can be performed in less than a minute, even with a very large number of taxon  
216 names (Fig. 2). `datelife`’s code performance was evaluated with a set of unit tests designed  
217 and implemented with the R package `testthat` (R Core Team, 2018) that were run both  
218 locally with the `devtools` package (R Core Team, 2018), and on a public server –via GitHub,  
219 using the continuous integration tool Travis CI (<https://travis-ci.org>). At present, unit tests  
220 cover more than 40% of `datelife`’s code (<https://codecov.io/gh/phylotastic/datelife>). Unit  
221 testing helps identify potential issues as code is updated or, more critically, as services code  
222 relies upon may change.

223

## Case studies

224 We illustrate the DateLife algorithm using a family within the Passeriform birds  
225 encompassing the true finches, Fringillidae, as case study. The first example analyses 6 bird  
226 species and shows all steps of the algorithm. The second example is an application analysing  
227 289 species in the family Fringillidae that are included in the NCBI taxonomy.

228 **A small example**

229 ***Creating a search query.***- We chose 6 bird species within the Passeriformes. The  
230 sample includes two species of cardinals: the black-thighed grosbeak – *Pheucticus tibialis*  
231 and the crimson-collared grosbeak – *Rhodothraupis celaeno*; three species of buntings: the  
232 yellowhammer – *Emberiza citrinella*, the pine bunting – *Emberiza leucocephalos* and the  
233 yellow-throated bunting – *Emberiza elegans*; and one species of tanager, the vegetarian finch –  
234 *Platyspiza crassirostris*.

235 Processing input names found that *Emberiza elegans* is synonym for *Schoeniclus*  
236 *elegans* in the default reference taxonomy [Open Tree of Life Taxonomy v3.3, June 1, 2021].  
237 For a detailed discussion on the state of the synonym refer to Avibase (Avibase, 2022;  
238 Lepage, 2004; Lepage, Vaidya, & Guralnick, 2014). Discovering this synonym allowed  
239 assigning five age data points for the parent node of *Emberiza elegans*, shown as *Schoeniclus*  
240 *elegans* in figure 3A, which would not have had any data otherwise.

241 ***Searching the database.***- DateLife used the processed input names to search the  
242 local chronogram database and found 9 matching chronograms in 6 different studies (Fig.  
243 3B). Three studies matched five input names (Barker, Burns, Klicka, Lanyon, & Lovette,  
244 2015; Hedges, Marin, Suleski, Paymer, & Kumar, 2015; Jetz, Thomas, Joy, Hartmann, &  
245 Mooers, 2012), one study matched four input names (Hooper & Price, 2017) and two studies  
246 matched two input names (Barker, Burns, Klicka, Lanyon, & Lovette, 2013; Burns et al.,  
247 2014). No studies matched all input names. Together, matching chronograms have 28 unique

248 age data points. All nodes have age data.

249 **Summarizing search results.-** DateLife obtained OpenTree's synthetic tree  
250 topology for these taxa (Fig. 3C), and mapped age data to nodes in this chosen topology. As  
251 expected, more inclusive nodes (e.g., node "n1") have more age data than less inclusive nodes  
252 (e.g., node "n5"). The name processing step allowed including five data points for node "n4"  
253 (parent of *Schoeniclus elegans*; Fig. 3A) that would not have had any data otherwise due to  
254 name mismatch. Age summary statistics per node were calculated and used as calibrations to  
255 date the tree topology using the BLADJ algorithm. Age data for node "n2" was excluded as  
256 final calibration because it is older than age data of the more inclusive node "n1" (Fig. 3C4).

257 **The family Fringillidae**

258 **Creating a query.-** To obtain ages for all species within the family of true finches,  
259 Fringillidae, we ran a DateLife query using the "get species from taxon" flag, which gets all  
260 recognized species names within a named group from a taxonomy of choice. Following the  
261 NCBI taxonomy, our DateLife query has 289 Fringillidae species. This taxon-constrained  
262 approach implies that the final results of a full DateLife analysis will be done using a tree  
263 topology and ages for the species in a named group, which do not necessarily correspond to a  
264 monophyletic group. Users can change this behaviour by providing a monophyletic tree as  
265 input for a DateLife search, or as a tree topology for a DateLife summary.

266 **Searching the database.-** Next, we used the processed species names in our DateLife  
267 query to identify chronograms with at least two Fringillidae species. The DateLife search  
268 identified 13 chronograms containing at least two Fringillidae species, published in 9 different  
269 studies (Barker et al., 2013, 2015; Burns et al., 2014; Claramunt & Cracraft, 2015; Gibb et  
270 al., 2015; Hedges et al., 2015; Hooper & Price, 2017; Jetz et al., 2012; Price et al., 2014).  
271 Once identified, DateLife pruned matching chronograms to keep Fringillidae species names  
272 on tips only, and transformed these pruned chronograms to pairwise distance matrices.

**Summarizing search results.**- The final step is to summarize the age data available for Fringillidae species into single summary chronograms, using different types of summary ages, median and SDM. As explained in the “Description” section, a tree topology to summarize age data upon is required. By default, DateLife uses the portion of OpenTree’s phylogeny that contains the species provided as search query as summarizing phylogeny. According to this phylogeny, species belonging to the family Fringillidae do not form a monophyletic group (Fig. 4). Age data from source chronograms is summarised into a single patristic distance matrix and then the available node ages are used as fixed node distributions over a consensus tree topology, to obtain a fully dated phylogeny with the same BLADJ (Fig. 5). Median summary chronograms are older and have wider variation in maximum ages than chronograms obtained with SDM.

## Cross-validation test

We performed a cross validation analysis of the DateLife workflow using the illidae chronograms. We used the individual tree topologies from each of the 19 source nograms from 13 studies as inputs, treating their node ages as unknown. We then ated dates for these topologies using the node ages from the chronograms from the studies as calibrations and smoothing using BLADJ.

We found that node ages from original study, and ages estimated using all other age available are correlated (Supplementary Fig. 6).

For five studies, Datelife tended to underestimate ages for topologically deeper nodes (i.e. with many descendant taxa, aka ‘closer to the root’) relative to the original estimate, overestimate ages for nodes closer to the tips. Accordingly, root ages are generally older than the original study than estimated using cross-validated ages (Supplementary Fig. 7).

296

## Discussion

297        `datelife` makes state-of-the-art data on evolutionary time frame easily accessible for  
298 comparison, reuse, and reanalysis, to researchers in all areas of science and with all levels of  
299 expertise in the matter. It is an open service that does not require any expert biological  
300 knowledge from users –besides the names of the species or group they want to work with, for  
301 any of its functionality.

302        A total of 99474 unique terminal taxa are represented in `datelife`'s database.

303        Incorporation of more chronograms into `datelife`'s database will continue to improve its  
304 services. One option to increase the number of chronograms in the DateLife database is the  
305 Dryad data repository. Methods to automatically mine chronograms from Dryad could be  
306 designed and implemented. However, Dryad's metadata system has no information to  
307 automatically detect branch length units, and those would still need to be determined  
308 manually by a human curator. We would like to emphasize on the importance of sharing  
309 chronogram data, including systematically curated metadata, into open repositories, such as  
310 OpenTree's Phylesystem (McTavish et al., 2015) for the benefit of the scientific community  
311 as a whole.

312        **Primary vs Secondary calibrations in dating analyses**

313        While most chronograms in DateLife's database are constructed using primary  
314 calibrations (molecular substitution rates or ages obtained from the fossil record or geological  
315 events), DateLife summarizes chronograms using secondary calibrations only (ages coming  
316 from other chronograms).

317        Graur and Martin (2004) cautioned on the increased error and uncertainty in estimated  
318 ages when using secondary calibrations in dating analyses. Schenk (2016) showed that, in  
319 simulations, divergence times inferred using secondary calibrations are significantly younger  
320 than those inferred with primary calibrations, when obtained with Bayesian inference

321 methods, and when priors are implemented in similar ways in both analyses. Accordingly, the  
322 scientific community seems to have more confidence in chronograms obtained from a single  
323 analysis, using fossil data as primary sources of calibrations (Schenk, 2016), and using fossils  
324 that have been widely discussed and curated as calibrations to date other trees, making sure  
325 that all data used in the analysis reflect a coherent evolutionary history (Sauquet, 2013), as  
326 for example done by (Antonelli et al., 2017). There have been attempts to create fossil  
327 calibration databases (Ksepka et al., 2015), though these still have room to grow.

328        **LLSR: What does our cross validation analysis show in relation to diffs between**  
329 **primary and secondary calibrations?**

330        It seems that using several (as opposed to just a few) secondary calibrations can  
331 provide sufficient information to alleviate or even neutralize potential biases (Sauquet, 2013).  
332 Certainly, further studies are required to fully understand the effect of secondary calibrations  
333 on outputs from different tree dating methods, and on downstream analyses. It is possible  
334 that secondary calibrations can be safely used with dating methods that do not require  
335 setting priors, such as penalized likelihood (Michael J. Sanderson, 2003), methods that do  
336 not make any assumptions on the ages and fix them to a node on a tree topology, such as  
337 BLADJ (Campbell O. Webb et al., 2008; Campbell O. Webb & Donoghue, 2005), or  
338 methods that summarize age data unto a tree topology.

339 **Variation in source chronograms**

340        Conflict among alternative dating studies is common in the literature (see, for example,  
341 the robust ongoing debate about crown group age of angiosperms (Barba-Montoya, Reis,  
342 Schneider, Donoghue, & Yang, 2018; Magallón, Gómez-Acevedo, Sánchez-Reyes, &  
343 Hernández-Hernández, 2015; Ramshaw et al., 1972; Michael J. Sanderson & Doyle, 2001;  
344 Sauquet, Ramírez-Barahona, & Magallón, 2021)).

345        Source chronograms may have been estimated using different types of primary

346 calibrations (fossil record, geologic or biogeographic events, molecular substitution rates).  
347 These differences in approach can deepen the already substantial variation in time estimates  
348 between lineages, as observed from the comparison of source chronograms in the Fringillidae  
349 example. For example, the chronograms from Burns et al. (2014) tend to have much older  
350 date estimates for the same nodes than other inferences (Figure 5). This study inferred dates  
351 using molecular substitution rate estimates across birds (Weir & Schluter, 2008) **EJM:**  
352 **MORE ON the FINCH examples and the cross validation here**

353 Different chronograms might also imply fundamentally distinct evolutionary  
354 hypotheses. For example, two different researchers working on the same clade could both  
355 carefully select and argue for their choices of fossil calibrations. Still, if one researcher  
356 decides a fossil will calibrate the ingroup of a clade, while another researcher uses the same  
357 one to calibrate outside the clade, the resulting age estimates will often differ substantially,  
358 as the placement of calibrations as stem or crown group is proved to deeply affect estimated  
359 times of lineage divergence (Sauquet, 2013).

## 360 Sumarizing chronograms

361 By default, DateLife currently summarizes all source chronograms that overlap with at  
362 least two species names. Users can exclude source chronograms if they have reasons to do so.  
363 Strictly speaking, a good chronogram should reflect the real time of lineage divergence  
364 accurately and precisely. To our knowledge, there are no tested measures to determine  
365 independently when a chronogram is better than another. Yet, several characteristics of the  
366 data used for dating analyses, as well as from the output chronogram itself, could be used to  
367 score the quality of source chronograms.

368 Some measures that have been proposed are the proportion of lineage sampling and the  
369 number of calibrations used Magallón et al. (2015). Some characteristics that are often cited  
370 in published studies as a measure of improved age estimates as compared to previously

371 published estimates are: quality of alignment (missing data, GC content), lineage sampling  
372 (strategy and proportion), phylogenetic and dating inference method, number of fossils used  
373 as calibrations, support for nodes and ages, and magnitude of confidence intervals.

374 DateLife provides an opportunity to capture concordance and conflict among date  
375 estimates, which can also be used as a metric for chronogram reliability. Its open database of  
376 chronograms allows other researchers to do such analyses themselves reproducibly, and  
377 without needing permission. Though, of course, they should follow proper citation practices,  
378 especially for the source chronogram studies.

379 The exercise of summarizing age data from across multiple studies provides the  
380 opportunity to work with a more inclusive chronogram, that reflects a unified evolutionary  
381 history for a lineage, by putting together evidence from different hypotheses. The largest,  
382 and taxonomically broadest chronogram currently available from OpenTree was constructed  
383 summarizing age data from 2,274 published chronograms using NCBI's taxonomic tree as  
384 backbone (Hedges et al., 2015). A summarizing exercise may also amplify the effect of  
385 uncertainty and errors in source data, and blur parts of the evolutionary history of a lineage  
386 that might only be reflected in source chronograms and lost on the summary chronogram  
387 (Sauquet et al., 2021). **EJM: ??? it's not clear to me what this last part means! What might**  
388 **you be losing? LLSR: I changed loosing to blurring. But I will elaborate more on it**  
389 Choosing source chronograms that we are going to keep and the ones that we are going to  
390 discard might be key. **LLSR: Example**

### 391 Effects on downstream analyses

392 For downstream analyses, using alternative chronogram may deeply affect our  
393 inferences (Title & Rabosky, 2016), particularly when studying phenomena dependent on the  
394 timing of species diversification events, such as macroevolutionary processes.

395 In ecology and conservation biology, incorporating at least some data on lineage

396 divergence times represents a relevant improvement for testing alternative hypothesis using  
397 phylogenetic distance (Campbell O. Webb et al., 2008). Hence, DateLife's workflow features  
398 different ways of estimating node ages in the absence of calibrations and branch length  
399 information for certain taxa. "Making up" branch lengths is a common practice in scientific  
400 publications: Jetz et al. (2012), created a time-calibrated tree of all 9,993 bird species, where  
401 67% had molecular data and the rest was simulated; Rabosky et al. (2018) created a  
402 time-calibrated tree of 31,536 ray-finned fishes, of which only 37% had molecular data;  
403 Stephen A. Smith and Brown (2018) constructed a tree of 353,185 seed plants where only  
404 23% had molecular data.

405 Notably, risks come with this practice. Taken to the extreme, one could make a fully  
406 resolved, calibrated tree of all modern and extinct taxa using a single taxonomy and a single  
407 calibration, using polytomy resolution and branch estimation methods. There has yet to be  
408 a thorough analysis of what can go wrong when one extends inferences beyond the data in  
409 this way, so we urge caution; we also urge readers to follow the example of the large tree  
410 papers cited above, by carefully considering the statistical assumptions being made, and  
411 assessing the consistency of the results with prior work.

## 412 Conclusions

413 Knowledge of the evolutionary time frame of organisms is key to many research areas:  
414 trait evolution, species diversification, biogeography, macroecology and more. It is also  
415 crucial for education, science communication and policy, but generating chronograms is  
416 difficult, especially for those who want to use phylogenies but who are not systematists, or  
417 do not have the time to acquire and develop the necessary knowledge and skills to construct  
418 them on their own. Importantly, years of primarily public funded research have resulted in  
419 vast amounts of chronograms that are already available on scientific publications, but hidden  
420 to the public and scientific community for reuse.

The DateLife project allows for easy and fast summary of public and state-of-the-art data on time of lineage divergence. It provides a straightforward way to get an informed idea on the state of knowledge of the time frame of evolution of different regions of the tree of life, and allows identification of regions that require more research, or that have conflicting information. It is available as an R package, and as a web-based R shiny application at [www.datelife.org](http://www.datelife.org). Both summary and newly generated trees are useful to evaluate evolutionary hypotheses in different areas of research. The DateLife project helps with awareness of the existing variation in expert time of divergence data, and will foster exploration of the effect of alternative divergence time hypothesis on the results of analyses, nurturing a culture of more cautious interpretation of evolutionary results.

## Availability

The `datelife` software is free and open source and it can be used through its R shiny web application at <http://www.datelife.org>, through the `datelife` R package, and through Phylotastic's project web portal <https://phylo.cs.nmsu.edu/>. DateLife's web application is maintained using RStudio's shiny server and the shiny package open infrastructure, as well as Docker and Open Tree of Life's infrastructure ([dates.opentreeoflife.org/datelife](https://dates.opentreeoflife.org/datelife)). `datelife`'s R package stable version is available for installation from the CRAN repository (<https://cran.r-project.org/package=datelife>) using the command `install.packages(pkgs = "datelife")` from within R. Development versions are available from the GitHub repository (<https://github.com/phylotastic/datelife>) and can be installed using the command `devtools::install_github("phylotastic/datelife")`.

## Supplementary Material

<sup>443</sup> Code used to generate all versions of this manuscript, the biological examples, as well  
<sup>444</sup> as the benchmark of functionalities are available at datelifeMS1, datelife\_examples, and  
<sup>445</sup> datelife\_benchmark repositories in LLSR's GitHub account.

446

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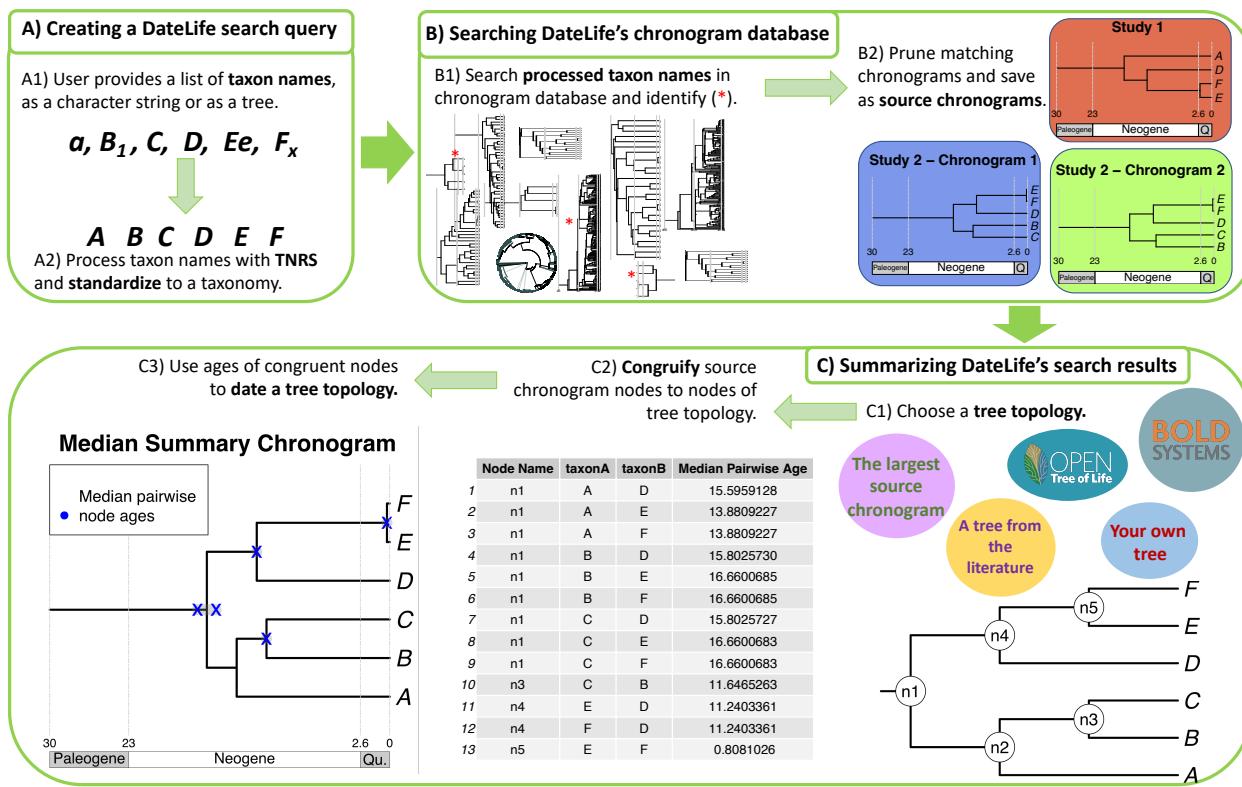


FIGURE 1. Stylized DateLife workflow. This shows the general workflows and analyses that can be performed with `datelife`, via the R package or through the website at <http://www.datelife.org/>. Details on the functions involved on each workflow are shown in `datelife`'s R package vignette.

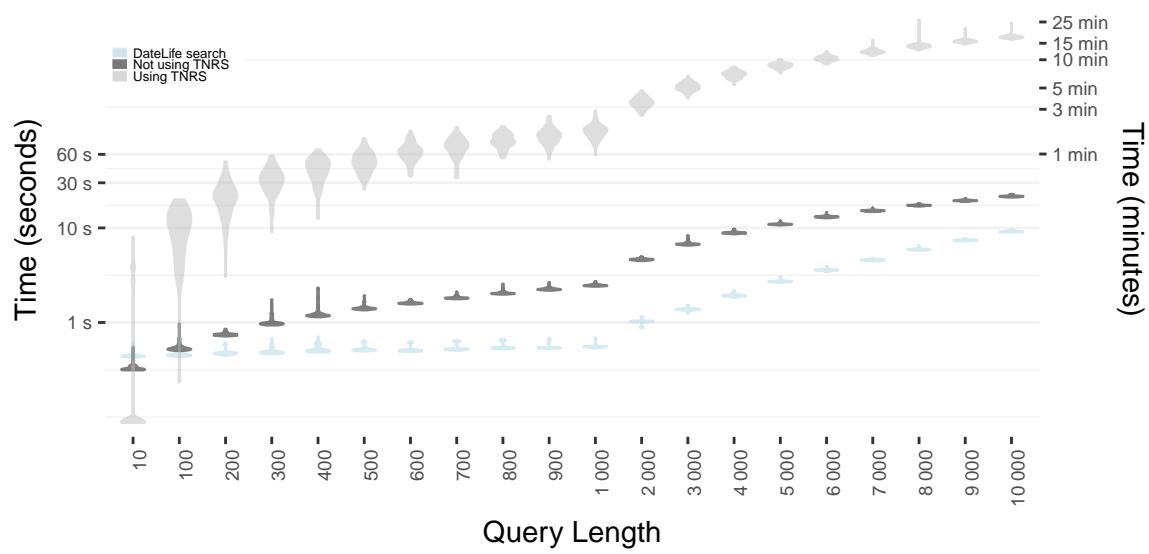


FIGURE 2. Computation time of query processing and search across **datelife**'s chronogram database relative to number of input taxon names. We sampled N names from the class Aves for each cohort 100 times and then performed a search with query processing not using the Taxon Names Resolution Service (TNRS; dark gray), and using TNRS (light gray). We also performed a search using the already processed query for comparison (light blue).

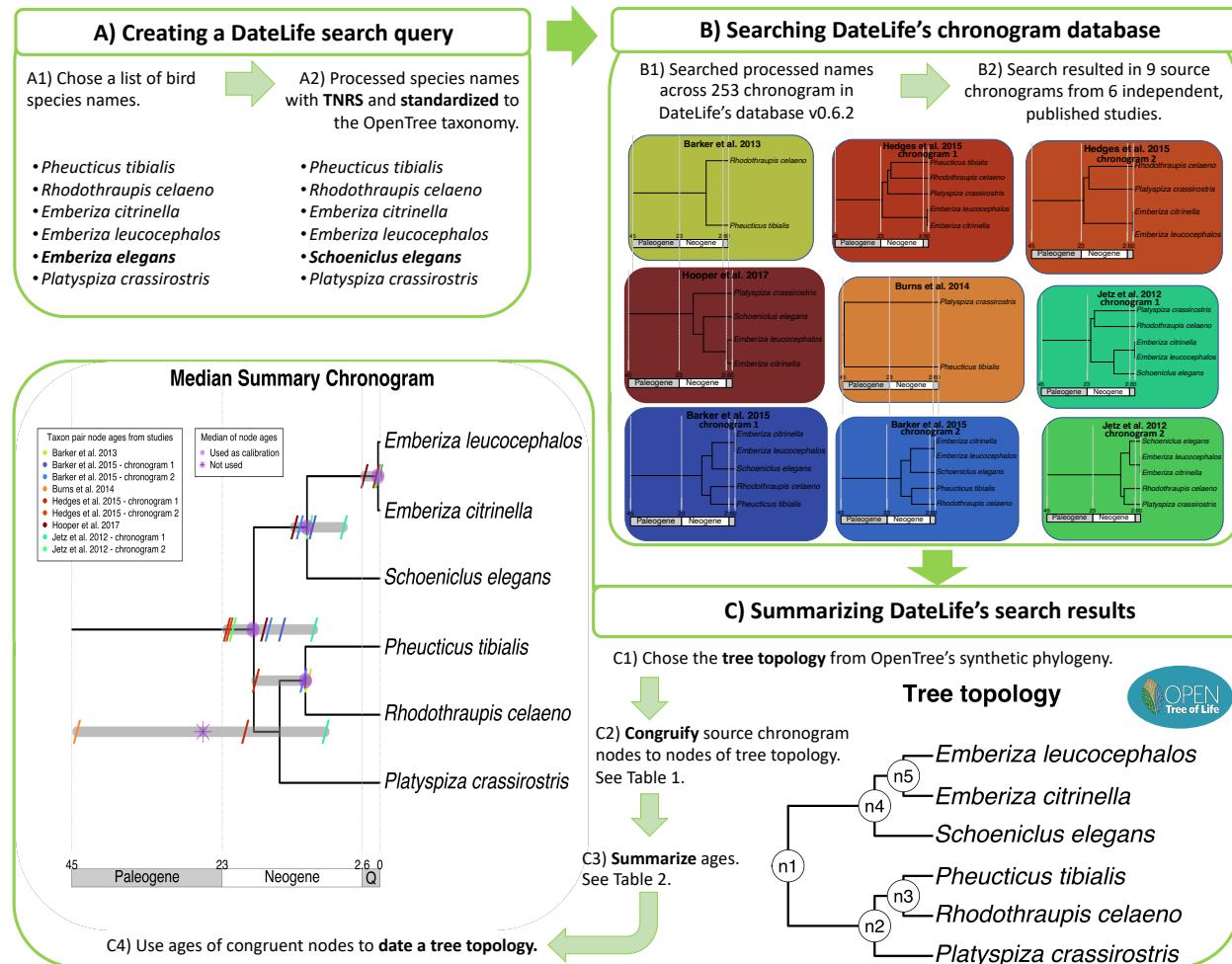


FIGURE 3. DateLife analysis results for a small sample of A) 6 bird species within the Passeriformes. B) Processed species names were found across 9 chronograms within 6 independent studies (Barker et al. (2012), Barker et al. (2015), Burns et al. (2014), Hedges et al. (2015), Hooper and Price (2017), Jetz et al. (2012).) C) This revealed 28 source age data points for the queried species names. Summarized age data is used as secondary calibrations to date a tree topology obtained from OpenTree's synthetic tree, resulting in a summary chronogram of source ages.

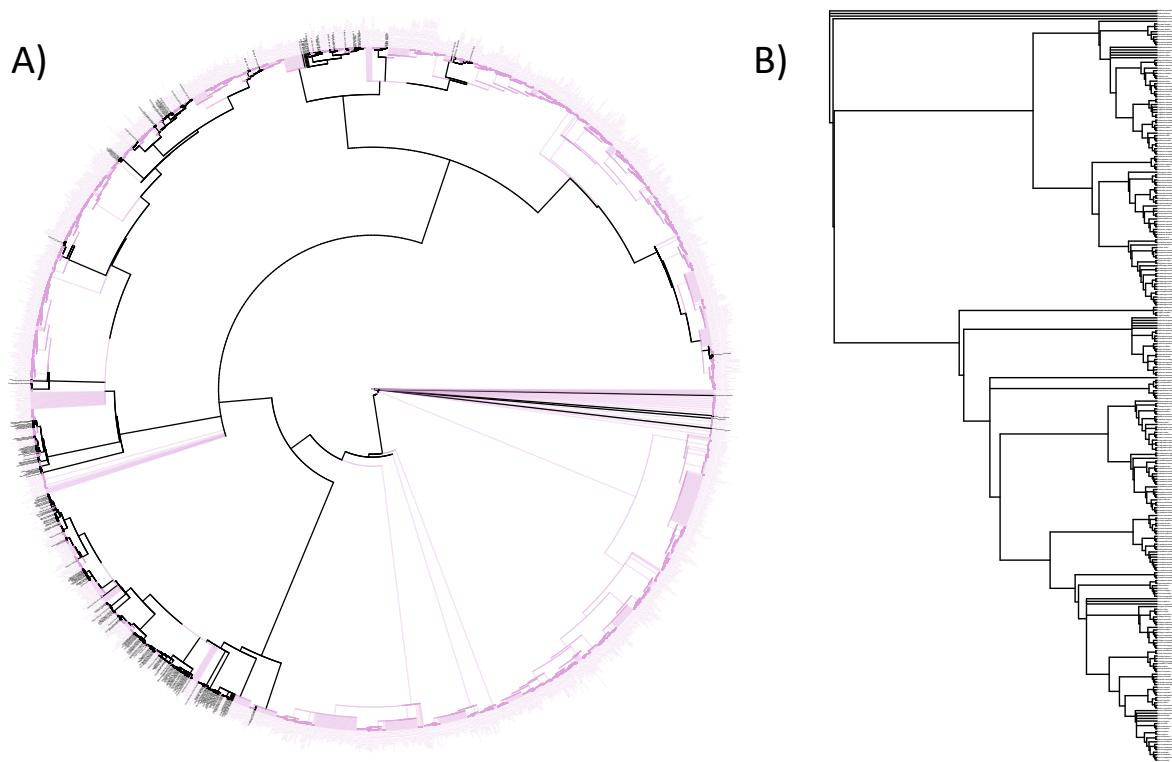


FIGURE 4. Tree topologies obtained from Open Tree of Life's (OpenTree) synthetic phylogenetic tree. A) Topology of 2,333 tips and 1,305 internal nodes, encompassing bird species within the family Fringillidae following the NCBI taxonomy (black), as well as all other bird species that share the same mrca node in OpenTree's synthetic tree (purple). B) Topology of 289 tips and 253 internal nodes, encompassing bird species within the Fringillidae only, resulting from pruning purple branches from topology A. Bird species within the Fringillidae do not form a monophyletic group (Alström et al. 2014, Barker, Cibois, Schikler, Feinstein, & Cracraft 2004, Barker et al. 2013, Barker 2014, Barker et al. 2015, Beresford, Barker, Ryan, & Crowe 2005, Bryson Jr et al. 2014, Burleigh, Kimball, & Braun 2015, Burns et al. 2014, Chaves, Hidalgo, & Klicka 2013, Claramunt & Cracraft 2015, Gibb et al. 2015, Hackett et al. 2008, Jetz et al. 2012, Johansson, Fjeldså, & Bowi 200, Kimball et al. 2019, Klicka et al. 2014, Lamichhaney et al. 2015, Lerner, Meyer, James, Hofreiter, & Fleischer 2011, Lovette et al. 2010, Moyle et al. 2016, Ödeen, Håstad, & Alström 2011, Oliveros et al. 2019, Päckert et al. 2012, Parchman, Benkman, & Mezquida 2007, Powell et al. 2014, Price et al. 2014, Pulgarín-R, Smith, Bryson Jr, Spellman, & Klicka 2013, Selvatti, Gonzaga, & Moraes Russo 2015, Tietze, Päckert, Martens, Lehmann, & Sun 2013, Treplin et al. 2008, Zuccon, Prŷs-Jones, Rasmussen, & Ericson 2012).

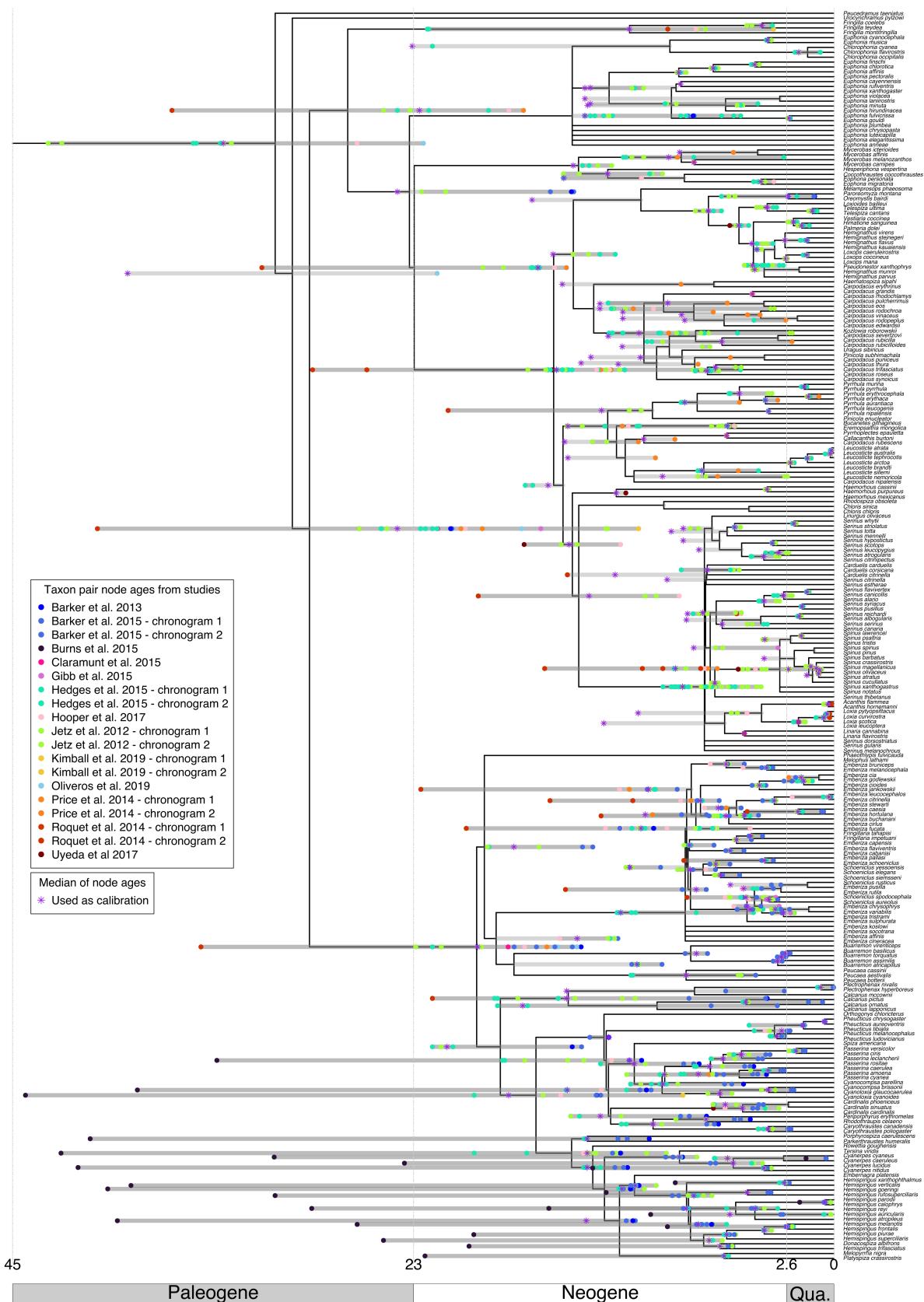


FIGURE 5. Fringillidae median summary chronogram generated with DateLife. It has 256 tips and 233 nodes.

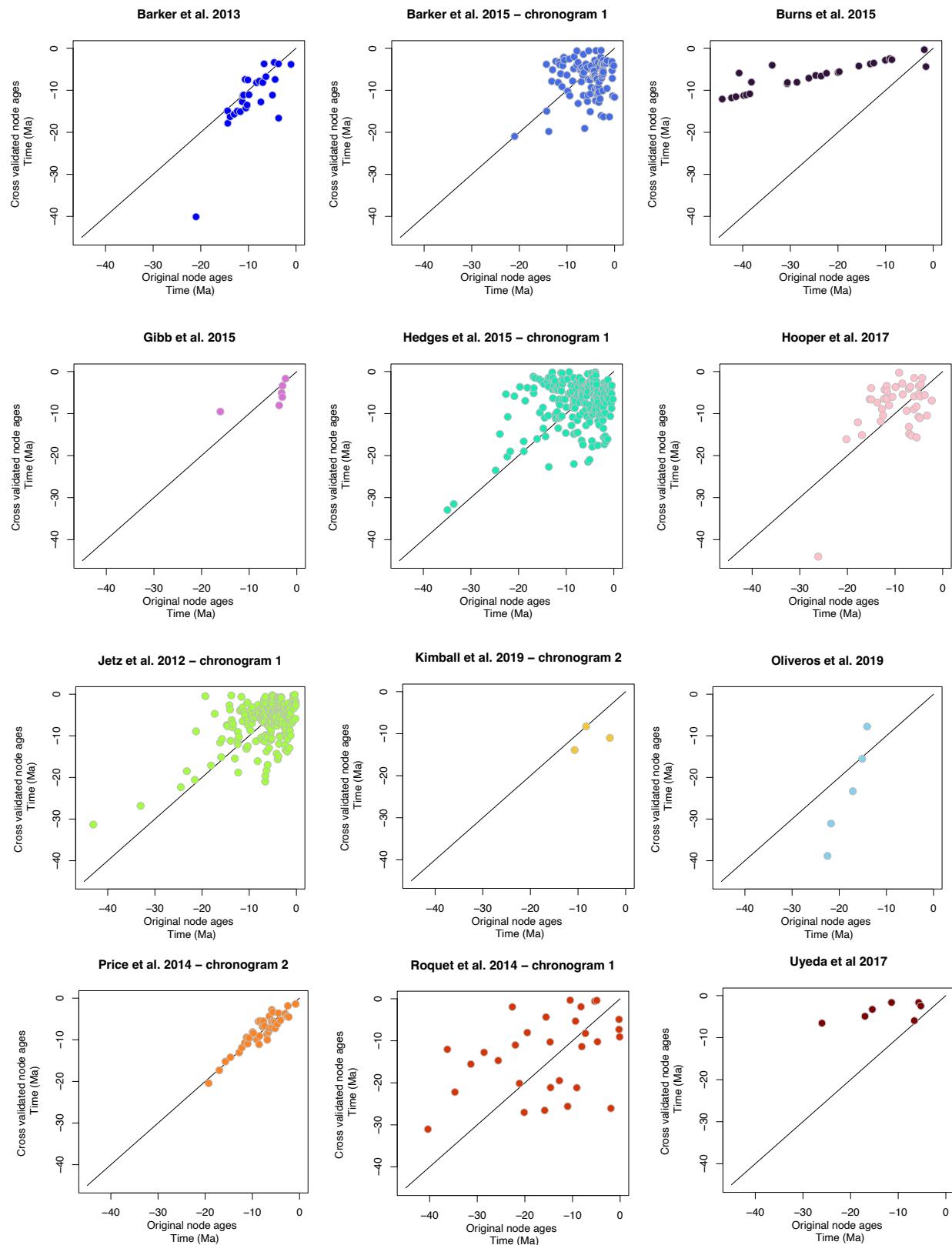


FIGURE 6. Results from cross validation analysis.

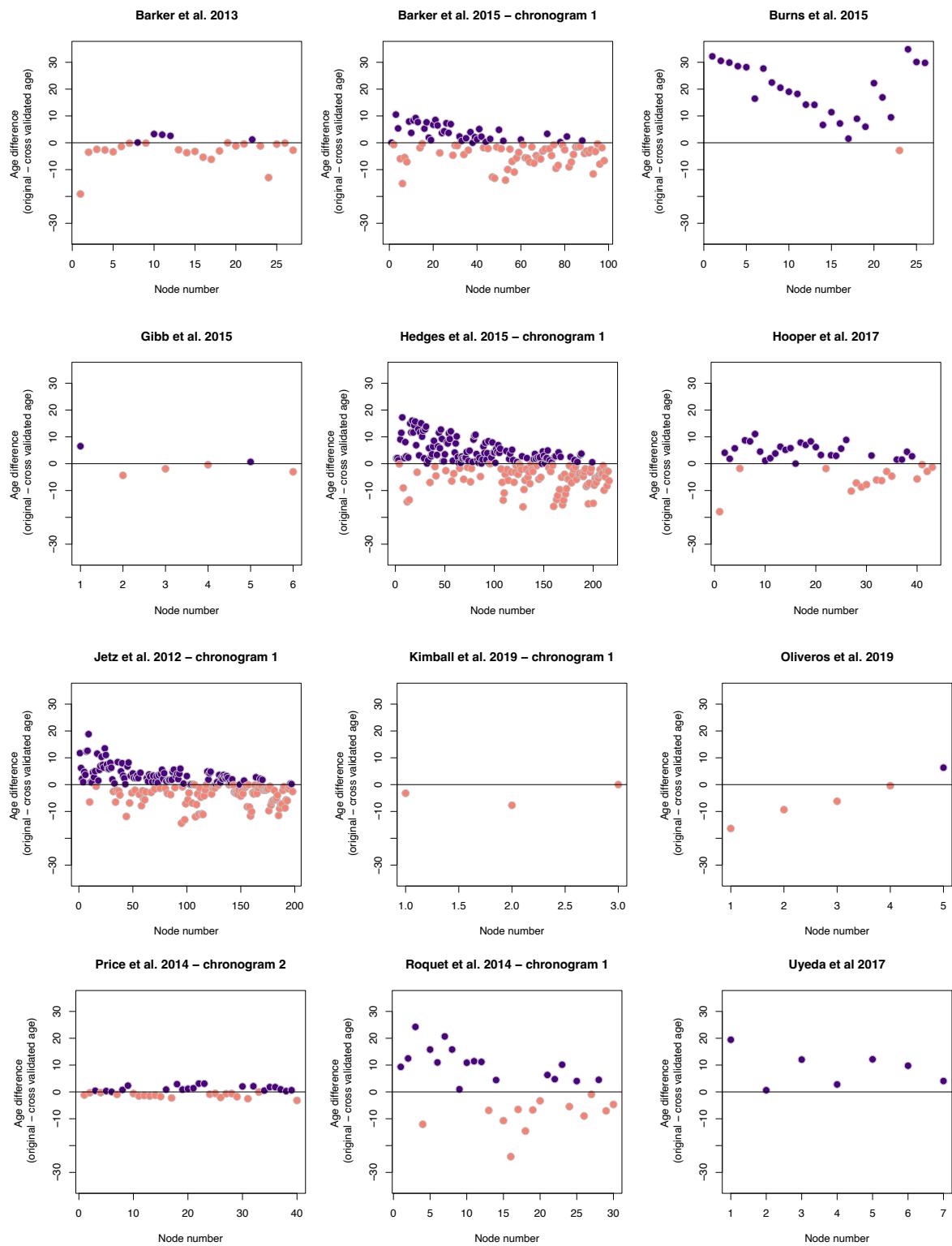


FIGURE 7. Results from cross validation analysis.

Barker et al. 2015 - chronogram 1



FIGURE 8. Cross validation of second source chronogram. The chronogram shown in black corresponds to the dates published in the original study. The gray chronogram corresponds to

## Barker et al. 2015 - chronogram 2

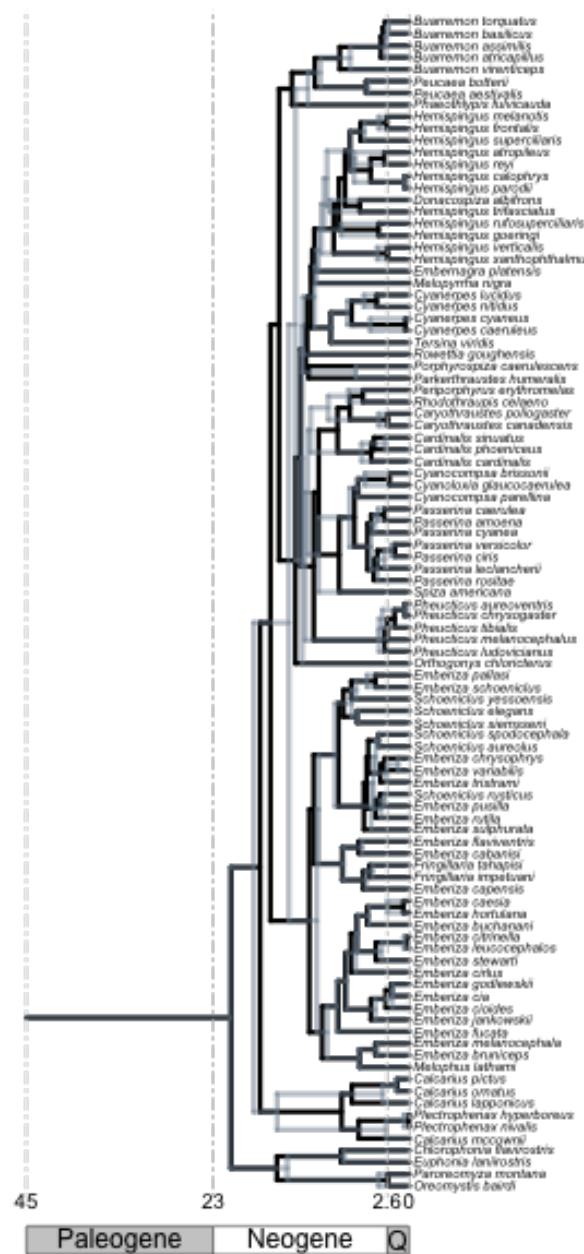


FIGURE 9. Cross validation of third source chronogram. The chronogram shown in black corresponds to the dates published in the original study. The gray chronogram corresponds to the dates calculated with BLADJ, i.e., the same for all the nodes.

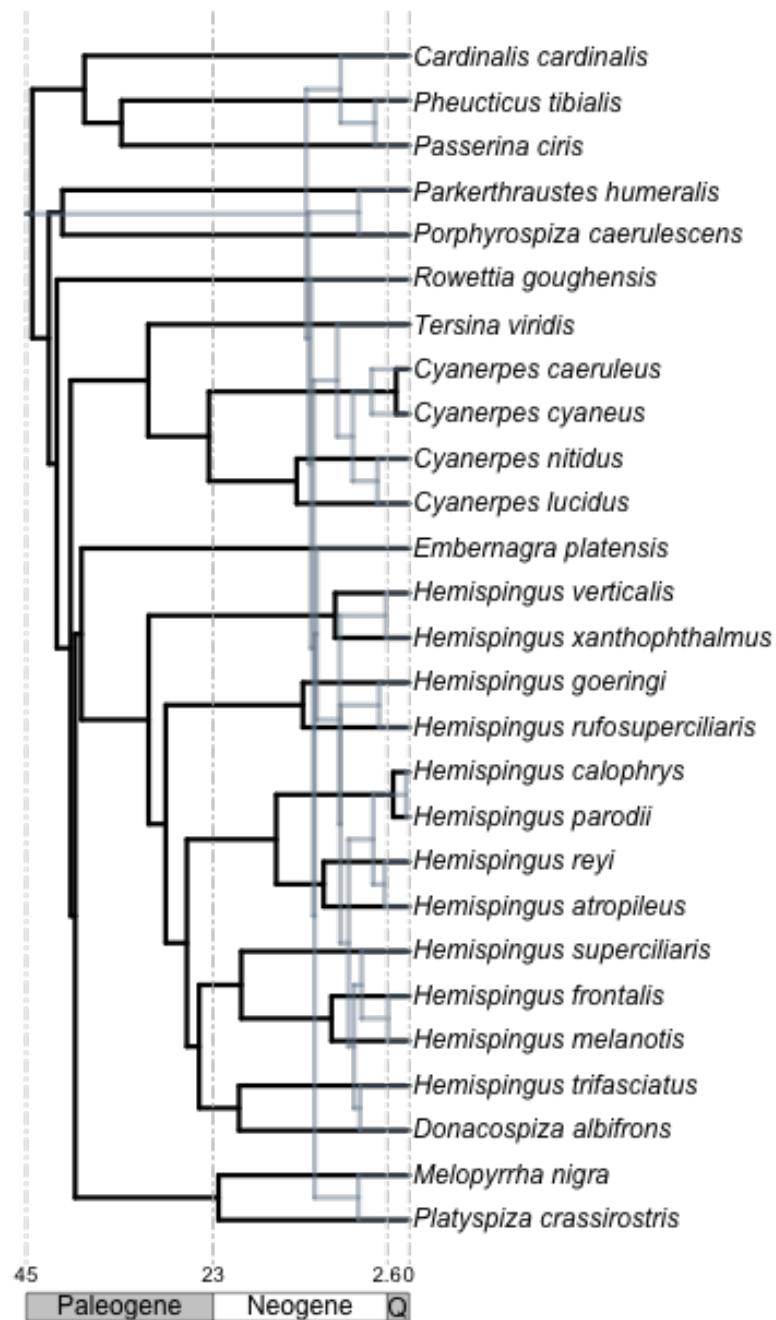
**Burns et al. 2015**

FIGURE 10. Cross validation of fourth source chronogram. The chronogram shown in black corresponds to the dates published in the original study. The gray chronogram corresponds to the dates calculated with BLADJ in each run of the cross-validation.

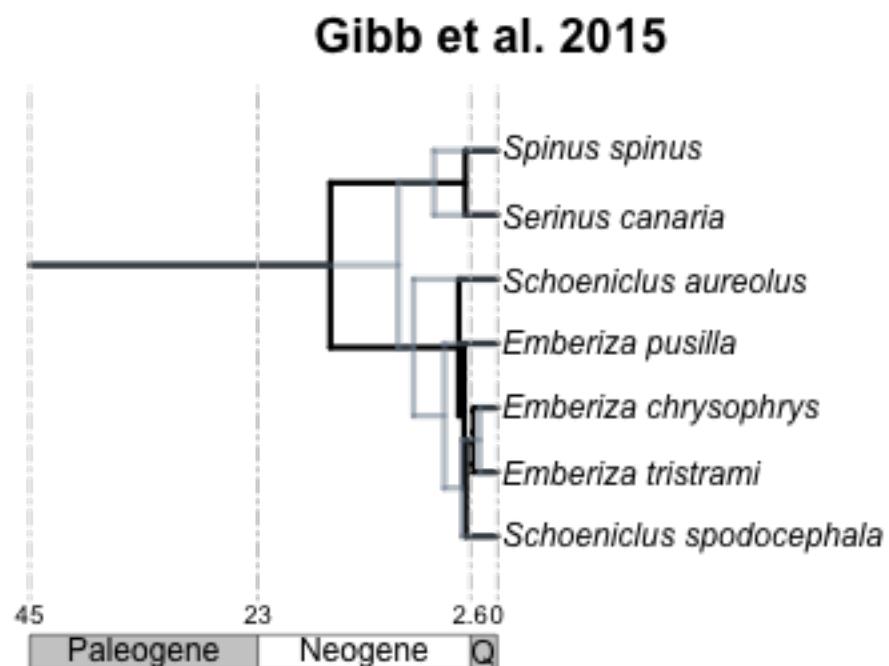


FIGURE 11. Cross validation of sixth source chronogram. The chronogram shown in black corresponds to the dates published in the original study. The gray chronogram corresponds to the same tree topology dated with BLADJ using node ages from all other source chronograms as secondary calibrations.

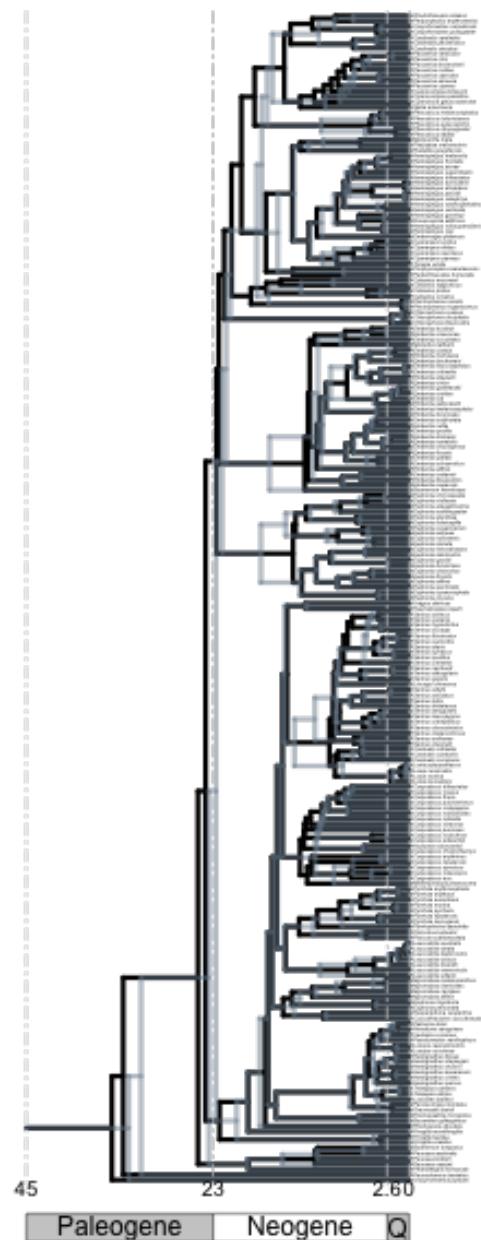
**Hedges et al. 2015 - chronogram 1**

FIGURE 12. Cross validation of seventh source chronogram. The chronogram shown in black corresponds to the dates published in the original study. The gray chronogram corresponds to the dates calculated with BLADeL. In order to facilitate the comparison, the

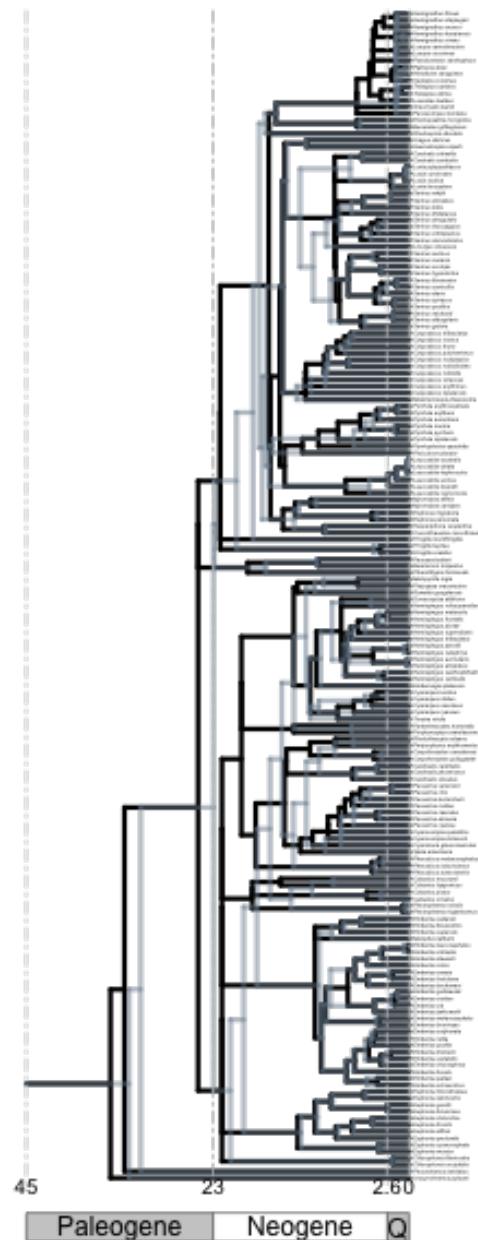
**Hedges et al. 2015 - chronogram 2**

FIGURE 13. Cross validation of eight source chronogram. The chronogram shown in black corresponds to the dates published in the original study. The gray chronogram corresponds to the dates calculated with BLADJ, i.e., the cross-validation procedure.

### Hooper et al. 2017

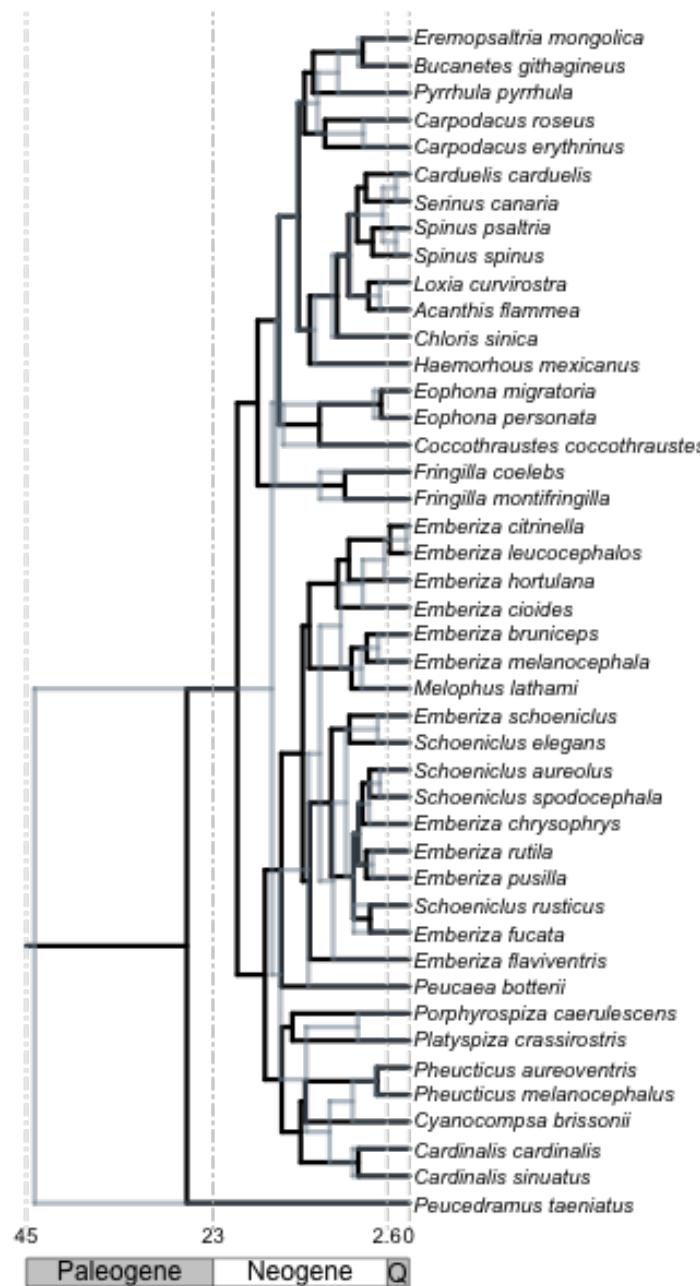


FIGURE 14. Cross validation of ninth source chronogram. The chronogram shown in black corresponds to the dates published in the original study. The gray chronogram corresponds to the dates calculated with BLADJ, i.e., the ones from the ninth source chronogram.

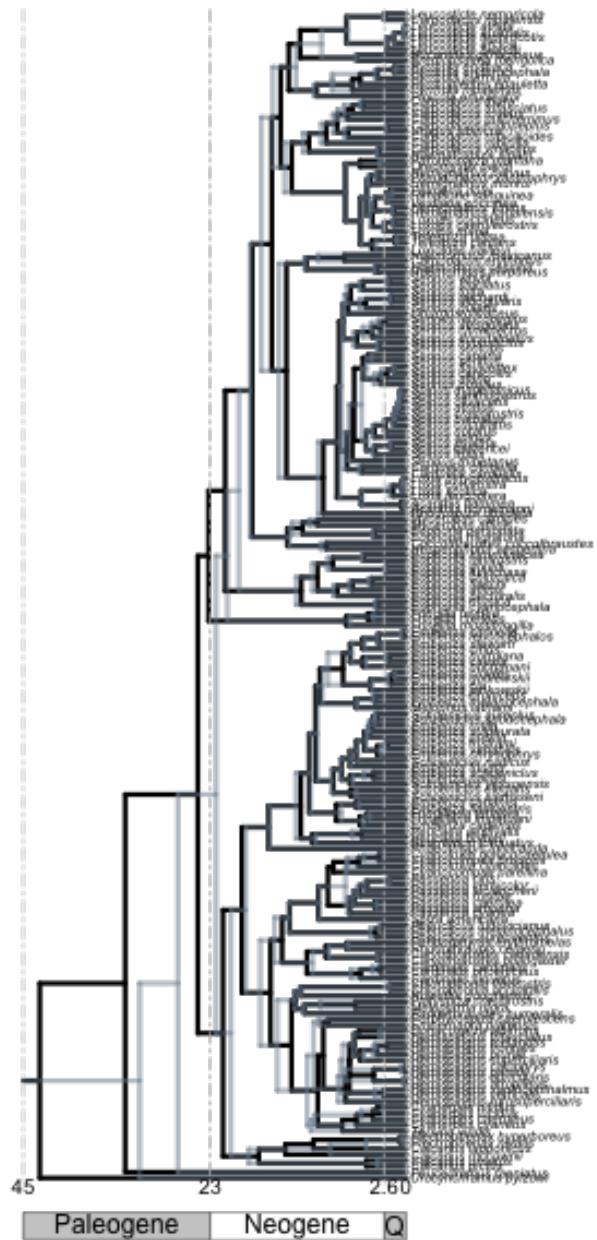
**Jetz et al. 2012 - chronogram 1**

FIGURE 15. Cross validation of tenth source chronogram. The chronogram shown in black corresponds to the dates published in the original study. The gray chronogram corresponds to the dates calculated with BLADe. In each case, the tree is the same.