

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

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## Abstract

Time of evolutionary origin is fundamental for understanding biological processes.

The combination of new analytical techniques, availability of more fossil and molecular data, and efforts to improve data sharing practices in biology has resulted in a steady accumulation of time of lineage divergence in public and open databases such as TreeBASE, Dryad, and Open Tree of Life for a large quantity and diversity of organisms in the last few decades.

However, getting a tree with branch lengths proportional to time remains difficult for many biologists and the non-academic community, despite its importance for biological research, medicine, education, and science communication.

Here we present **datelife**, a service implemented via an R package and a web site (<http://www.datelife.org/>) for efficient reuse, summary and reanalysis of expert, peer-reviewed, public data on time of lineage divergence.

Main results: 1. blah 2. blah 3. blah

Results in a general context: All source and summary chronograms can be saved in formats that permit easy reuse and reanalysis. Summary and newly generated trees are potentially useful to evaluate evolutionary hypothesis in different areas of research in biology. How well this trees work for this purpose still needs to be tested.

**datelife** will be useful to increase awereness on the existing variation in expert time of divergence data, and might 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.

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

<sup>40</sup> Congruification; Supertree; Calibrations

<sup>41</sup> Word count: 55

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## Warning in data(opentree_chronograms): data set 'opentree_chronograms' not found
```

## Introduction

## Description

We report how we determined our sample size, all data exclusions (if any), all manipulations, and all measures in the study.

## Benchmark

## Example

We used R (Version 4.1.0; R Core Team, 2021) and the R-package *papaja* (Version 0.1.0.9997; Aust & Barth, 2020) for all our analyses.

## Discussion

## Conclusions

## Availability

**datelife** is free and open source and it can be used through its current website <http://www.datelife.org/query/>, through its R package, and through Phylotastic's project web portal <http://phylo.cs.nmsu.edu:3000/>. **datelife**'s website is maintained using RStudio's shiny server and the shiny package open infrastructure, as well as Docker. **datelife**'s R package stable version will be 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

Code used to generate all versions of this manuscript, the biological examples, as well as the benchmark of functionalities are available at `datelifeMS1`, `datelife_examples`, and `datelife_benchmark` repositories in LLSR's GitHub account.

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