

datelife package

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datelife is an R package for obtaining information on time of divergence of taxa from expert sources (i.e., peer-reviewed published research). It is also a service for time scaling phylogenetic trees. It leverages on chronograms already available on Open Tree of Life Database and on existing dating and analyzing tools to rapidly generate de-novo hypothesis of time divergence of taxa.

Installation

First, install **datelife** into your computer. You can install the stable version of the package from cran

```
install.packages("datelife")
```

or the development version from github

```
devtools::install_github("phylostatic/datelife")
```

Now load the package into the R workspace.

```
library("datelife")  
# devtools::load_all("~/Desktop/datelife/")
```

Getting all available chronograms

The main goal of **datelife** is to search chronograms from published peer reviewed studies (from now on *source chronograms*) available for a set of taxa of interest. This task is performed with the **datelife_search()** function. Taxa of interest are accepted as scientific names, either as a single character vector, as tip labels in a phylo object or as a character string in newick format. In any case, upper and lower case are ignored.

```
mamms <- datelife_search(input = c("Felis catus", "Delphinus delphus", "Homo sapiens", "Elephas maximus"))  
# > Source chronograms from:  
# > 1: Bininda-Emonds, Olaf R. P., Marcel Cardillo, Kate E. Jones, Ross D. E. MacPhee, Robin M. D. Beck  
# > 2: Bininda-Emonds, Olaf R. P., Marcel Cardillo, Kate E. Jones, Ross D. E. MacPhee, Robin M. D. Beck  
# > 3: Bininda-Emonds, Olaf R. P., Marcel Cardillo, Kate E. Jones, Ross D. E. MacPhee, Robin M. D. Beck  
# > 4: Nyakatura, Katrin, Olaf RP Bininda-Emonds. 2012. Updating the evolutionary history of Carnivora  
# > 5: Nyakatura, Katrin, Olaf RP Bininda-Emonds. 2012. Updating the evolutionary history of Carnivora  
# > 6: Nyakatura, Katrin, Olaf RP Bininda-Emonds. 2012. Updating the evolutionary history of Carnivora  
# > 7: Hedges, S. Blair, Julie Marin, Michael Suleski, Madeline Paymer, Sudhir Kumar. 2015. Tree of life  
# > Input taxa presence across source chronograms:  
# >          taxon chronograms  
# > 1 Elephas maximus      4/7  
# > 2 Homo sapiens        7/7  
# > 3 Felis catus          3/7  
# > Input taxa completely absent from source chronograms:  
# >          taxon  
# > 1 Delphinus delphus
```

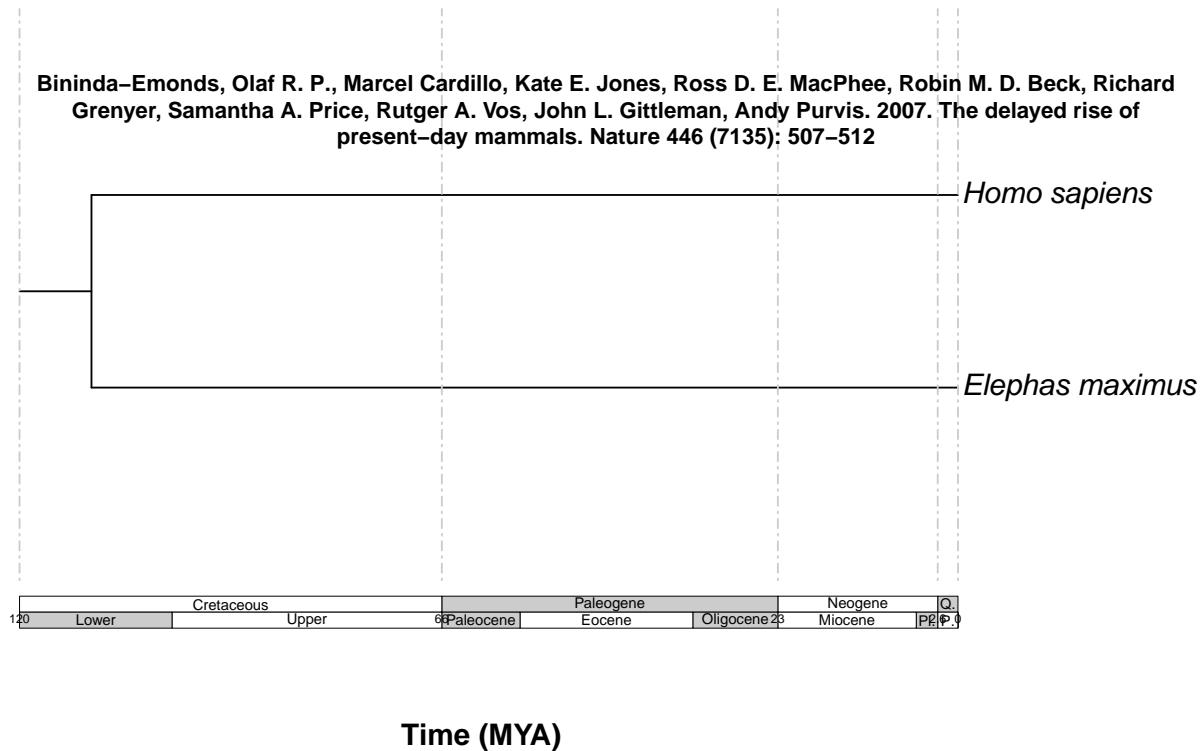


Figure 1:

You can plot all source chronograms on screen with the function `plot_phylo_all()` or save them into a pdf or png file with the argument `write`:

```
plot_phylo_all(mamms, write = "pdf", file = "mamms_phyloall")
```

Source chronograms come from Open Tree of Life tree store, this means that uncertainty from original studies is not yet available.

Explain the `datelife` object. It is composed by three elements. `datelifeQuery` `datelifeResults` `datelifeSummary`

You can get all trees in newick format. Chronogram search is performed at the species level. This means that source chronograms with subspecies are collapsed to present one exemplar per species.

```
# show how chronogram cache is constructed, do not eval, show one message example
```

Source chronograms are cached in the package as a data object called `opentree_chronograms`. This object is updated every two months approximately. If you want to manually update the object or save it as an object in your own computer, you can do:

```
update_datelife_cache <- function(file = "opentree_chronograms.RData")
```

The update will take approximately 10 secs.

Chronograms are downloaded from OToL and processed in various ways to be suitable for `datelife` use. Tip labels are standardized to Opentree of Life Taxonomy. Tips that cannot be automatically standardised are left alone as original. As of now, the percentage of standardised names is as follows:

For now, taxon names must be provided as scientific names. Common name searches are not yet implemented. Scientific names can be anything from species binomials to higher-taxon names. Subspecies names will not be considered. You can use the `datelife_query` function first to check that your names are accepted. If you are unsure about the spelling or synonyms, you can use arguments `use_tnrs` and `approximate_match`.

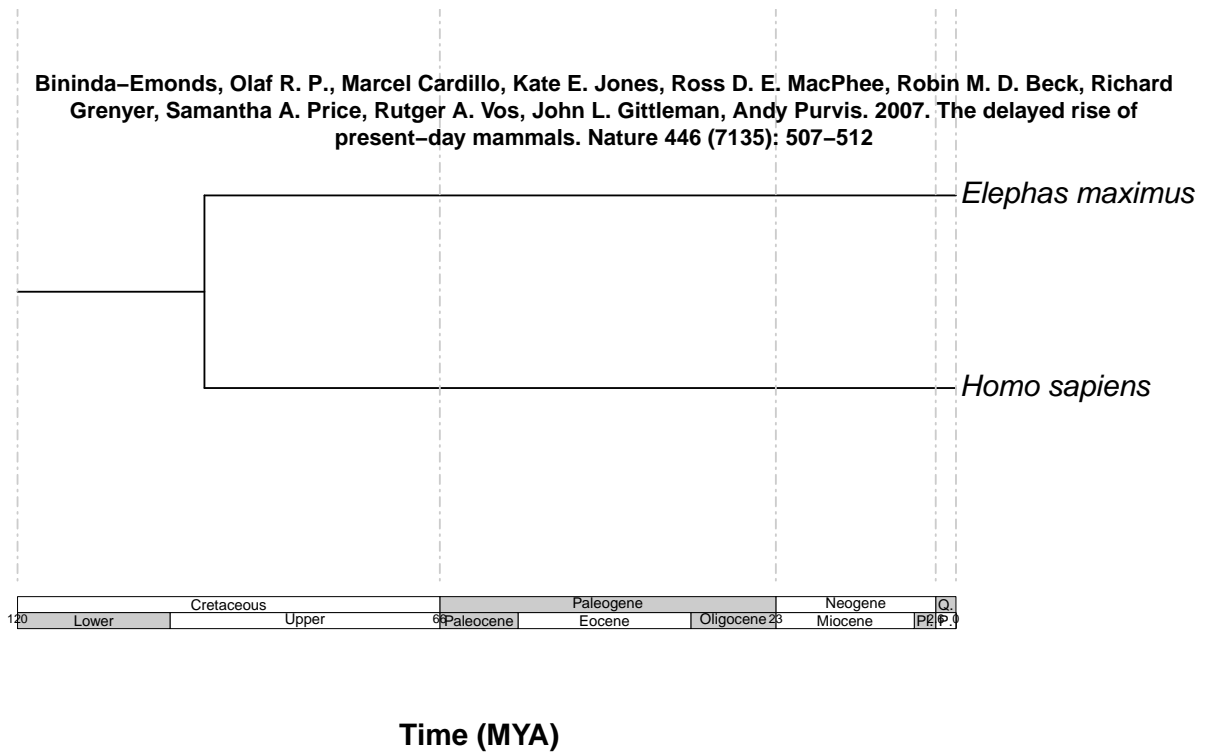


Figure 2:

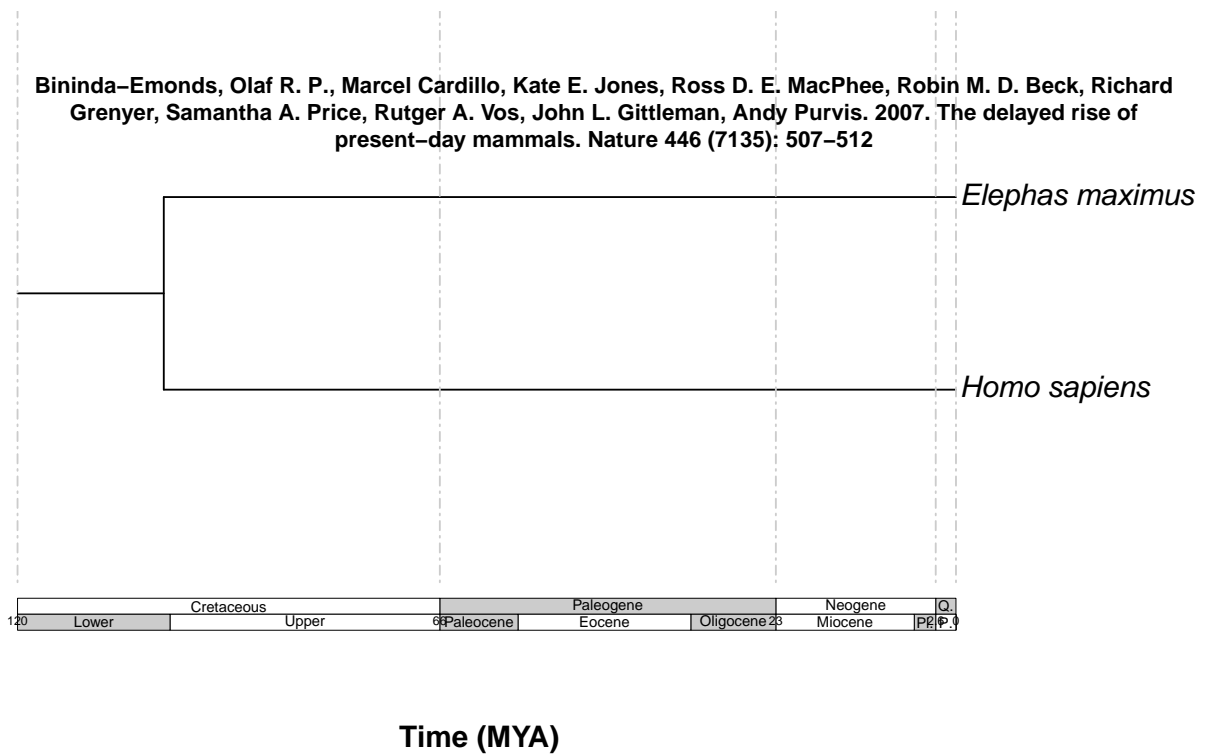


Figure 3:

Nyakatura, Katrin, Olaf RP Bininda-Emonds. 2012. Updating the evolutionary history of Carnivora (Mammalia): a new species-level supertree complete with divergence time estimates. BMC Biology 10 (1): 12

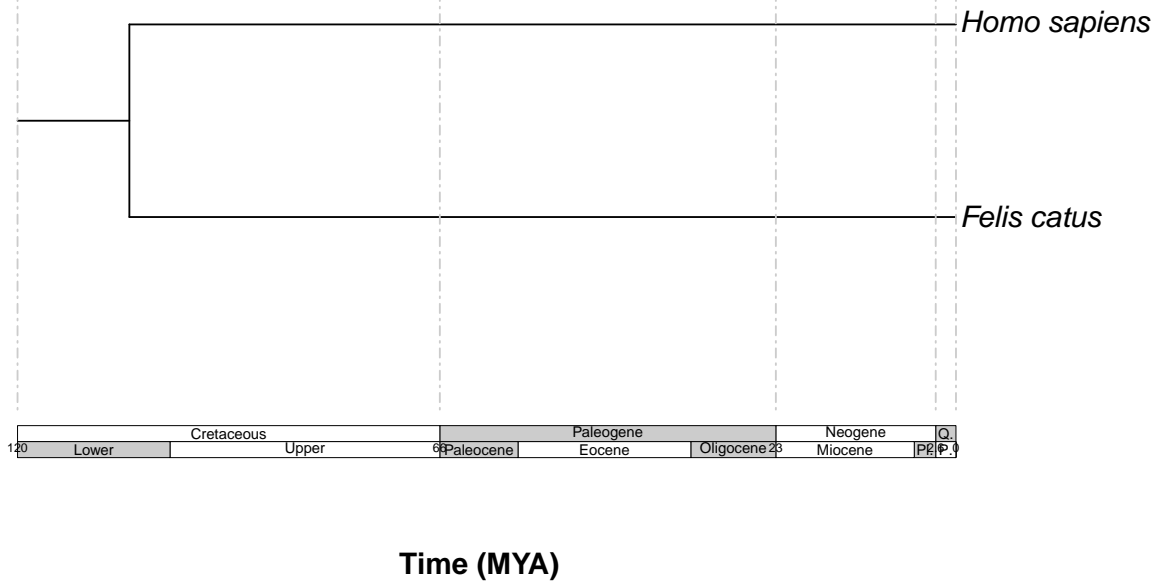


Figure 4:

Nyakatura, Katrin, Olaf RP Bininda-Emonds. 2012. Updating the evolutionary history of Carnivora (Mammalia): a new species-level supertree complete with divergence time estimates. BMC Biology 10 (1): 12

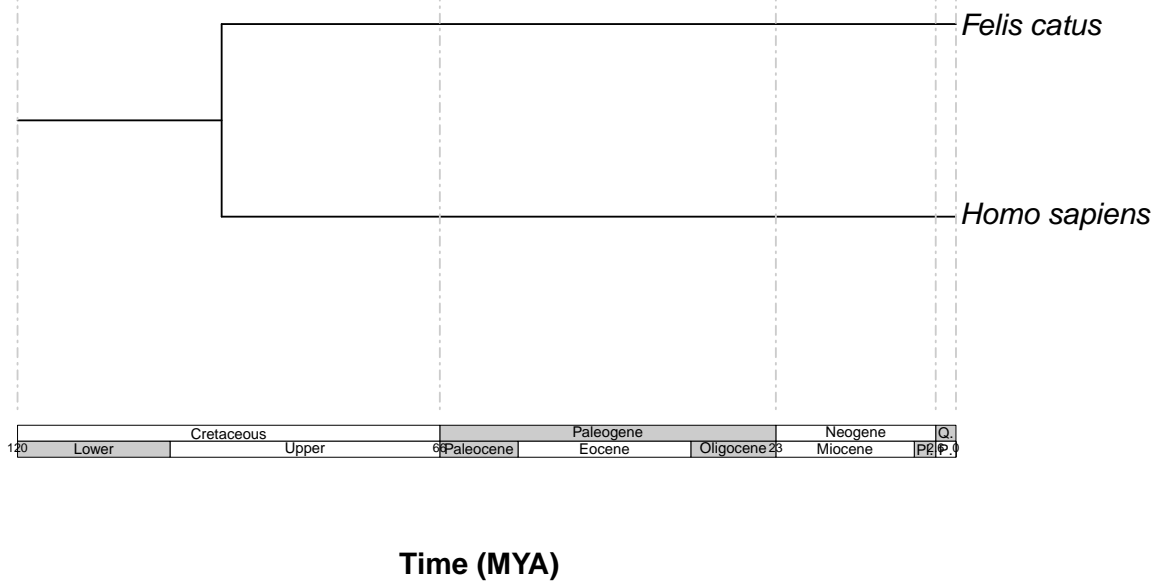


Figure 5:

Nyakatura, Katrin, Olaf RP Bininda-Emonds. 2012. Updating the evolutionary history of Carnivora (Mammalia): a new species-level supertree complete with divergence time estimates. BMC Biology 10 (1): 12

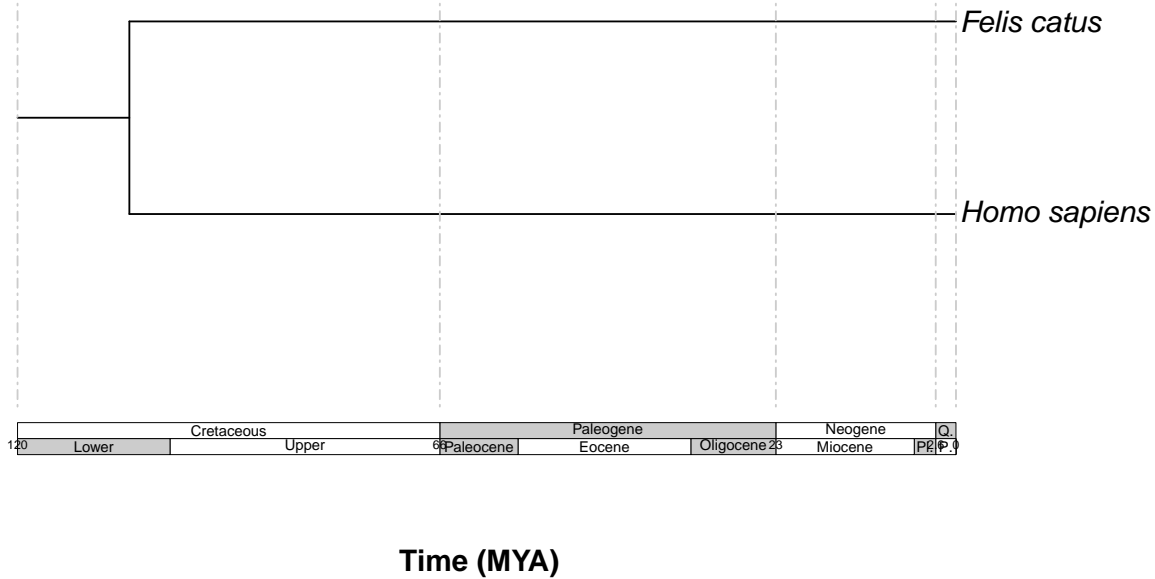


Figure 6:

Hedges, S. Blair, Julie Marin, Michael Suleski, Madeline Paymer, Sudhir Kumar. 2015. Tree of life reveals clock-like speciation and diversification. Molecular Biology and Evolution 32 (4): 835–845

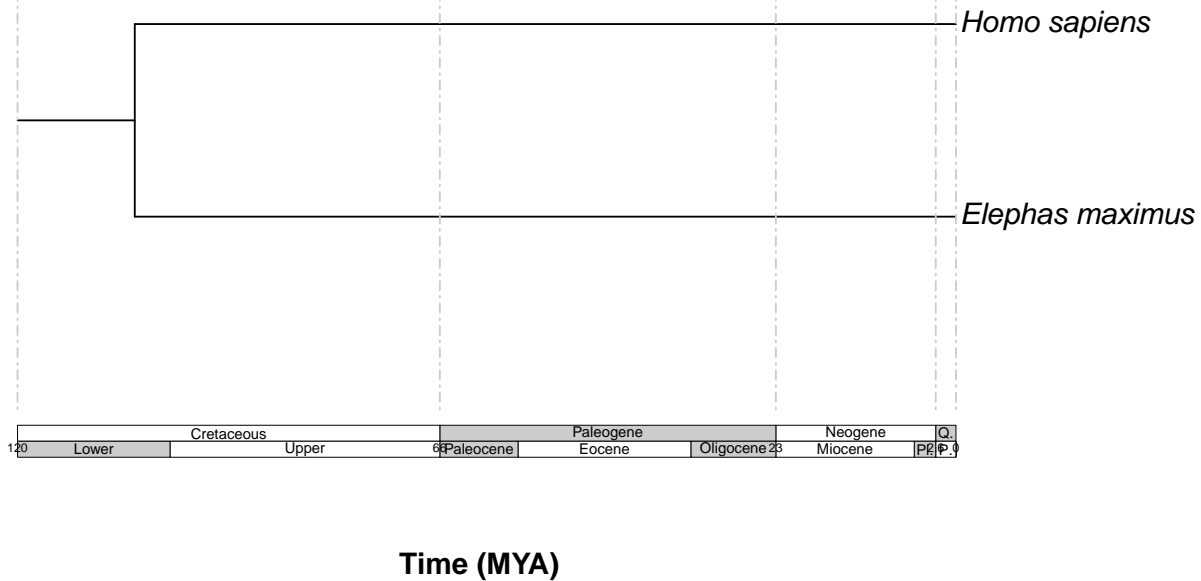


Figure 7:

```

# datelife query function
make_datelife_query(c("cat", "dog"))
# > $cleaned_names
# > [1] "cat" "dog"
# >
# > $ott_ids
# > NULL
# >
# > $phy
# > [1] NA
# >
# > attr("class")
# > [1] "datelifeQuery"
make_datelife_query(c("Felix", "Caniss"), use_tnrs = TRUE)
# >
# |
# |
# |
# |=====| 50%
# |
# |=====| 100%
# > $cleaned_names
# > [1] "Felix" "Canis"
# >
# > $ott_ids
# > NULL
# >
# > $phy
# > [1] NA
# >
# > attr("class")
# > [1] "datelifeQuery"
make_datelife_query(c("Felix", "Canis"), get_spp_from_taxon = TRUE)
# >
# |
# |
# |=====| 50%
# |
# |=====| 100%
# >
# |
# |
# |=====| 100%
# >
# |
# |
# |=====| 100%
# >
# |
# |
# |=====| 100%
# > $cleaned_names
# >
# >          Felis1          Felis2          Felis3
# > "Felis margarita" "Felis chaus"  "Felis silvestris"

```

```

# >          Felis4          Felis5          Canis1
# >    "Felis nigripes"    "Felis catus"    "Canis mesomelas"
# >          Canis2          Canis3          Canis4
# >    "Canis aureus"    "Canis anthus"    "Canis rufus"
# >          Canis5          Canis6          Canis7
# >    "Canis lycaon"    "Canis lupus"    "Canis latrans"
# >          Canis8          Canis9          Canis10
# >    "Canis adustus"    "Canis indica" "Canis himalayensis"
# >          Canis11
# >    "Canis simensis"
# >
# > $ott_ids
# >    Felis margarita    Felis chaus    Felis silvestris
# >          983177          983181          563163
# >    Felis nigripes    Felis catus    Canis mesomelas
# >          983179          563166          666235
# >    Canis aureus    Canis anthus    Canis rufus
# >          621168          5835572          113383
# >    Canis lycaon    Canis lupus    Canis latrans
# >          948004          247341          247331
# >    Canis adustus    Canis indica Canis himalayensis
# >          621176          346728          346723
# >    Canis simensis
# >          752755
# >
# > $phy
# > [1] NA
# >
# > attr(,"class")
# > [1] "datelifeQuery"

```

If higher-taxon names are provided, you can use option `get_spp_from_taxon = TRUE`, which is also a service of `rphylotatsic` that gets all species within a higher taxon. If you choose this option, all species within the higher-taxon names provided will be included in the search.

```
# datelife query function
```

Summarizing source chronograms: getting a single tree

You can summarize all source chronograms found by `DateLife` with the median method.

You can also summarize source chronograms with a supertree approach. In here we have implemented `SDM` method.

Within `DateLife`, we have also wrapped the `OToL` scaling service available from <http://141.211.236.35:10999>.

See also the [Time Tree of Life](#) web for getting time of divergence of a pair of taxa or a synthetic chronogram of lineages within a single taxon.

Generating chronograms

Alternatively, new chronograms can be generated using available information as secondary calibrations.

```
# ``{r, fig.align = 'center', fig.retina = 2, fig.margin = TRUE}
```

theme

theme

Citing

The datelife manuscript is still being written.