

DateLife Workflows

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Taxon Cetacea

I. Query data

There are 198 species in the Open Tree of Life Taxonomy for the taxon Cetacea. Information on time of divergence is available for 89 of these species across 6 published and peer-reviewed chronograms from the following studies:

1. Toljagić O., Voje K.L., Matschiner M., Liow L., & Hansen T.F. 2017. Millions of Years Behind: Slow Adaptation of Ruminants to Grasslands. *Systematic Biology*, .
2. Bininda-Emonds, Olaf R. P., Marcel Cardillo, Kate E. Jones, Ross D. E. MacPhee, Robin M. D. Beck, Richard Grenyer, Samantha A. Price, Rutger A. Vos, John L. Gittleman, Andy Purvis. 2007. The delayed rise of present-day mammals. *Nature* 446 (7135): 507-512
3. 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
4. Steeman, M., Hebsgaard M., Fordyce R., Ho S., Rabosky D., Nielsen R., Rahbek C., Glenner H., Sørensen M., & Willerslev E. 2009. Radiation of Extant Cetaceans Driven by Restructuring of the Oceans. *Systematic Biology* 58 (6): 573-585.

All source chronograms are fully ultrametric. The proportion of Cetacea queried species found across source chronograms is as follows:

	Trees	Tips	Resolved
1	Open Tree of Life Subtree	198	99%
2	Dated Open Tree of Life Subtree	198	60%
3	Median Summary Chronogram	89	99%
4	SDM Summary Chronogram	89	99%

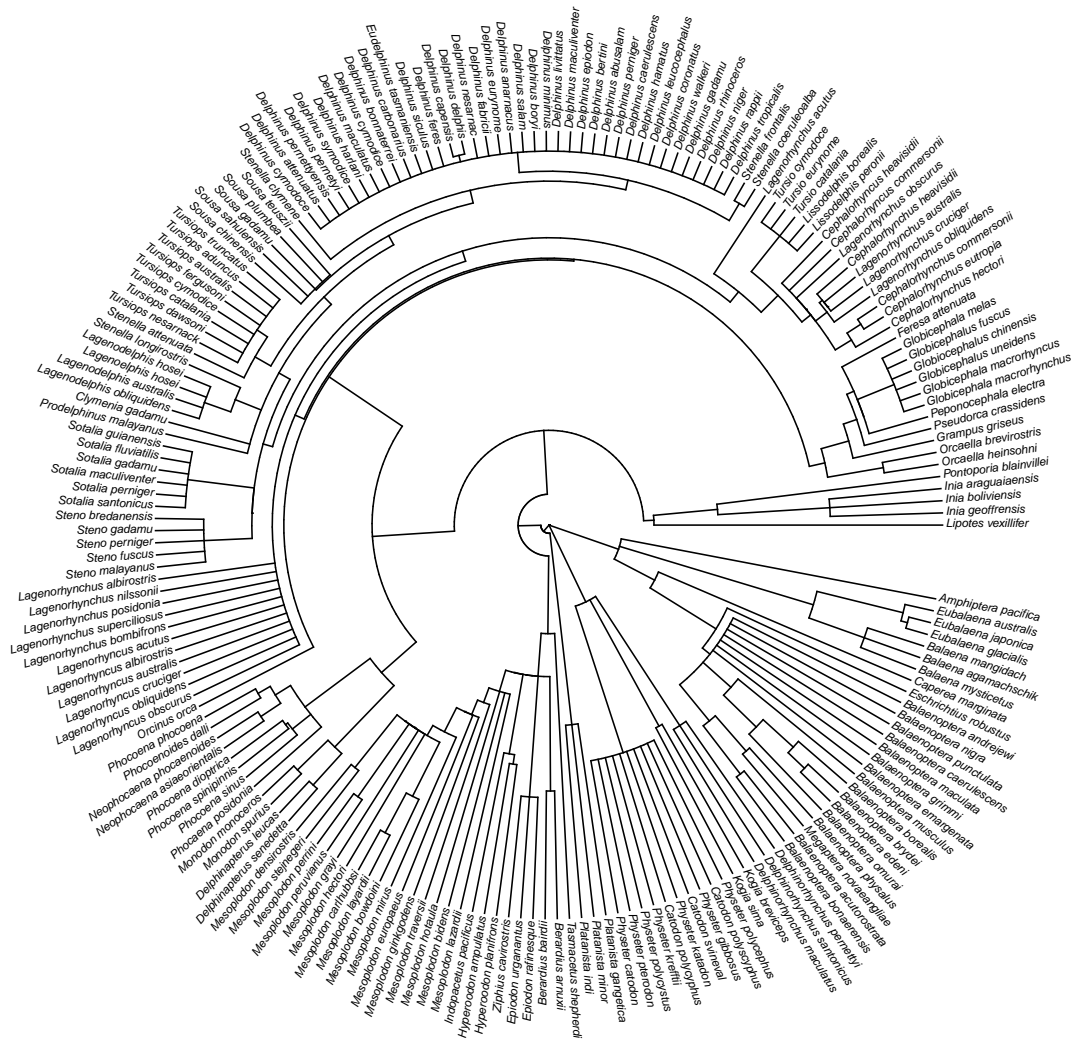


Figure 1: Cetacea Species Dated Open Tree of Life Induced Subtree. This chronogram was obtained with `get_dated_oto1_induced_subtree()` function.

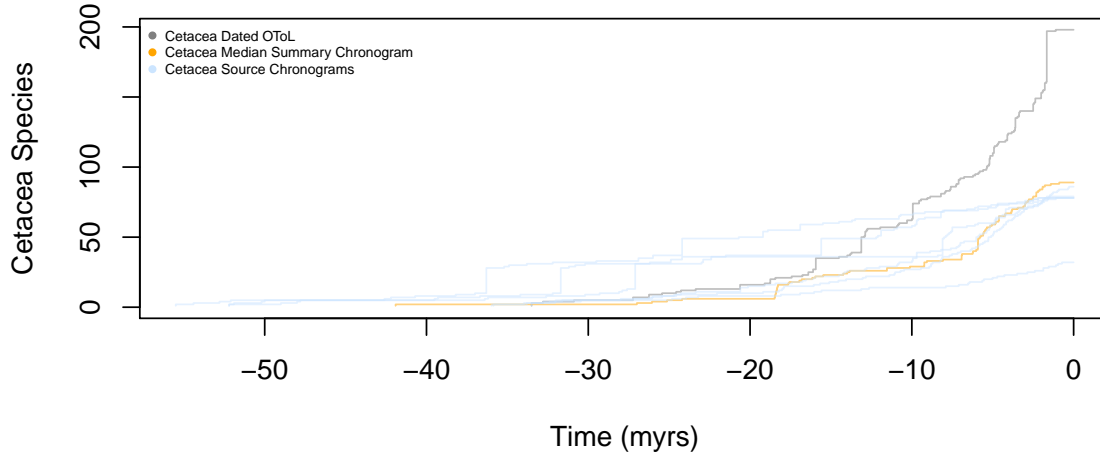


Figure 2: Cetacea lineage through time (LTT) plots from source chronograms, summary median chronogram and dated Open Tree of Life chronogram.

II. Summarize results.

II.A. Diagnosing clustering issues.

We identified some issues with chronograms coming from SDM and Median summary matrices. First, clustering algorithms implemented to go from a summary distance matrix to a tree return trees that are too old (generally with UPGMA algorithms) or non-ultrametric (generally with Neighbour Joining algorithms). In most studied cases, UPGMA returns fully ultrametric trees but with very old ages (we had to multiply the matrix by 0.25 to get ages approximate to source chronograms ages, however this is a number chosen at random, it was just the number that worked well. NJ returned reasonable ages, but trees are way non ultrametric, as you can see in Fig. 3 and Fig. 4.

This taxon's SDM matrix has some negative values in the following taxa: *Eubalaena japonica*, *Eubalaena glacialis*. This taxon's Median matrix has NO negative values.

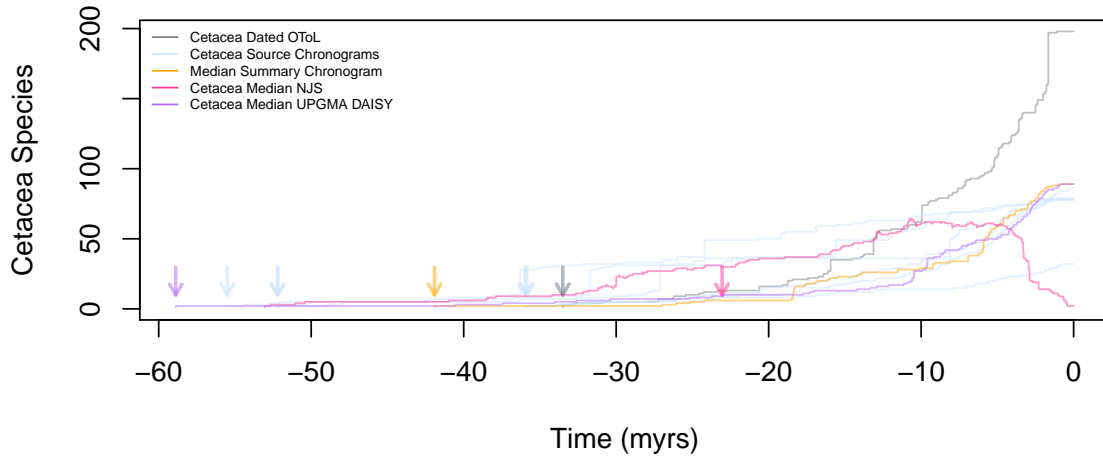


Figure 3: Cetacea lineage through time (LTT) plots from source chronograms and Median summary matrix converted to phylo with different methods (NJ and UPGMA). Clustering algorithms used often are returning non-ultrametric trees or with maximum ages that are just off. So we developed an alternative algorithm in `datelife` to go from a summary matrix to a fully ultrametric tree.

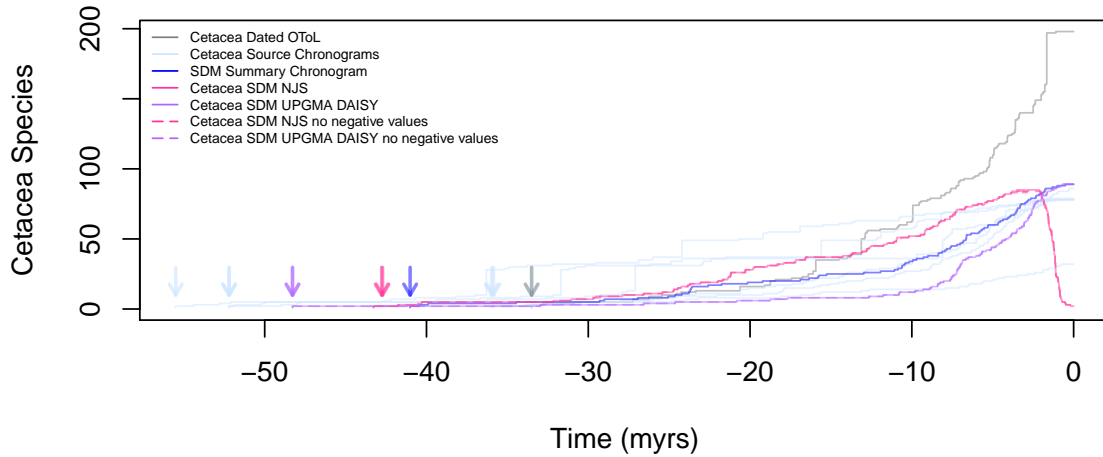


Figure 4: Cetacea lineage through time (LTT) plots from source chronograms and SDM summary matrix converted to phylo with different methods (NJ and UPGMA). As you can note, dashed lines and solid lines from trees coming out from both types of clustering algorithms implemented are mostly overlapping. This means that removing negative values does not change results from clustering algorithms much. Clustering algorithms used often are returning non-ultrametric trees or with maximum ages that are just off. So we developed an alternative algorithm in `datelife` to go from a summary matrix to a fully ultrametric tree.

III. Create new data

As an example, we're gonna date the Open Tree Synthetic tree (mainly because the taxonomic tree is usually less well resolved.)

Now, let's say you like the Open Tree of Life Taxonomy and you want to stick to that tree. Dates from available studies were tested over the Open Tree of Life Synthetic tree of Cetacea and a tree was constructed, but all branch lengths are NA. We also tried each source chronogram independently, with the Dated OToL and with each other, as a form of cross validation in Table 2. this is not working perfectly yet, but we are developping new ways to use all calibrations efficiently.

Table 2: Was it successful to use each source chronogram independently as calibration (CalibN) against the Dated Open Tree of Life (dOToL) and each other (ChronoN)?

	dOToL	Chrono1	Chrono2	Chrono3	Chrono4	Chrono5	Chrono6
Calibrations1	TRUE	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE
Calibrations2	TRUE	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE
Calibrations3	TRUE	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE
Calibrations4	TRUE	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE
Calibrations5	TRUE	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE
Calibrations6	TRUE	TRUE	FALSE	TRUE	FALSE	TRUE	TRUE

III. Simulate data

An alternative to generate a dated tree from a set of taxa is to take the available information and simulate into it the missing data. We will take the median and sdm summary chronograms to date the Synthetic tree of Life:

```
#> Error in paste0("\n![" , figcap_lttplot_sdm, "](plots/", taxon, "_LTTplot_sdm.pdf)\n"): object 'fig'
#> Error in cat(lttplot): object 'lttplot' not found
```

Appendix

The following species were completely absent from the chronogram data base: *Amphiptera pacifica*, *Balaena agamachschik*, *Balaena mangidach*, *Balaenoptera andrejewi*, *Balaenoptera caerulea*, *Balaenoptera emarginata*, *Balaenoptera grimmii*, *Balaenoptera maculata*, *Balaenoptera nigra*, *Balaenoptera punctulata*, *Catodon polycyphus*, *Catodon polyscyphus*, *Catodon svineval*, *Cephalorhynchus commersonii*, *Cephalorhynchus heavisidii*, *Clymenia gadamu*, *Delphinapterus senedetta*, *Delphinorhynchus maculatus*, *Delphinorhynchus pernettyi*, *Delphinorhynchus santonicus*, *Delphinus abusalam*, *Delphinus anarnacus*, *Delphinus attenuatus*, *Delphinus bertini*, *Delphinus bonnaterrei*, *Delphinus boryi*, *Delphinus caerulea*, *Delphinus carbonarius*, *Delphinus coronatus*, *Delphinus cymodice*, *Delphinus cymodoce*, *Delphinus epiodon*, *Delphinus eurynome*, *Delphinus fabricii*, *Delphinus feres*, *Delphinus gadamu*, *Delphinus hamatus*, *Delphinus harlani*, *Delphinus leucocephalus*, *Delphinus livittatus*, *Delphinus maculatus*, *Delphinus maculiventer*, *Delphinus minimus*, *Delphinus nesarnac*, *Delphinus niger*, *Delphinus pernettyensis*, *Delphinus pernettyi*, *Delphinus perniger*, *Delphinus rappii*, *Delphinus rhinoceros*, *Delphinus salam*, *Delphinus siculus*, *Delphinus symodice*, *Delphinus walkeri*, *Epiodon rafinesque*, *Epiodon urganantus*, *Eudelphinus tasmaniensis*, *Globicephala macrorhynchus*, *Globicephalus fuscus*, *Globicephalus unoidens*, *Globiocephalus chinensis*, *Inia araguaiaensis*, *Inia boliviensis*, *Lagenodelphis australis*, *Lagenodelphis obliquoidens*, *Lagenodelphis hosei*, *Lagenorhynchus bombifrons*, *Lagenorhynchus nilssonii*, *Lagenorhynchus posidonia*, *Lagenorhynchus superciliosus*, *Lagenorhynchus acutus*, *Lagenorhynchus albirostris*, *Lagenorhynchus australis*, *Lagenorhynchus cruciger*, *Lagenorhynchus obliquoidens*, *Lagenorhynchus obscurus*, *Mesoplodon hotaula*, *Mesoplodon lazaridii*, *Monodon spurius*, *Neophocaena asiaeorientalis*, *Phocaena posidonia*, *Physeter gibbosus*, *Physeter katadon*, *Physeter krefftii*, *Physeter polycephalus*, *Physeter polycystus*, *Physeter pterodon*, *Platanista indi*, *Prodelphinus malayanus*, *Sotalia gadamu*, *Sotalia maculiventer*, *Sotalia perniger*, *Sotalia santonicus*, *Sousa gadamu*, *Sousa plumbea*, *Sousa sahalensis*, *Steno fuscus*, *Steno gadamu*, *Steno malayanus*, *Steno perniger*, *Tursio catalania*, *Tursio cymodoce*, *Tursio eurynome*, *Tursiops australis*, *Tursiops catalania*, *Tursiops cymodice*, *Tursiops dawsoni*, *Tursiops fergusonii*, *Tursiops nesarnack*