

## RESEARCH

# Physcraper: A Python package for continually updated phylogenetic trees using the Open Tree of Life

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## Abstract

**Background:** Phylogenies are a key part of research in many areas of biology. Tools that automate some parts of the process of phylogenetic reconstruction, mainly molecular character matrix assembly, have been developed for the advantage of both specialists in the field of phylogenetics and non-specialists. However, interpretation of results, comparison with previously available phylogenetic hypotheses, and selection of one phylogeny for downstream analyses and discussion still impose difficulties to one that is not a specialist either on phylogenetic methods or on a particular group of study.

**Results:** Physcraper is a command-line Python program that automates the update of published phylogenies by adding public DNA sequences to underlying alignments of previously published phylogenies. It also provides a framework for straightforward comparison of published phylogenies with their updated versions, by leveraging upon tools from the Open Tree of Life project to link taxonomic information across databases. The program can be used by the nonspecialist, as a tool to generate phylogenetic hypotheses based on publicly available expert phylogenetic knowledge. Phylogeneticists and taxonomic group specialists will find it useful as a tool to facilitate molecular dataset gathering and comparison of alternative phylogenetic hypotheses (topologies).

**Conclusions:** The Physcraper workflow demonstrates the benefits of doing open science for phylogenetics, encouraging researchers to strive for better sharing practices. Physcraper can be used with any OS and is released under an open-source license. Detailed instructions for installation and usage are available at <https://physcraper.readthedocs.io>.

**Keywords:** gene tree; interoperability; open science; reproducibility; public database; dna alignment

## Content

Text and results for this section, as per the individual journal's instructions for authors.

## Section title

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In this section we examine the growth rate of the mean of  $Z_0$ ,  $Z_1$  and  $Z_2$ . In addition, we examine a common modeling assumption and note the importance of considering the tails of the extinction time  $T_x$  in studies of escape dynamics. We will first consider the expected resistant population at  $vT_x$  for some  $v > 0$ , (and temporarily assume  $\alpha = 0$ )

$$E[Z_1(vT_x)] = \int_0^{v \wedge 1} Z_0(uT_x) \exp(\lambda_1) du.$$

If we assume that sensitive cells follow a deterministic decay  $Z_0(t) = xe^{\lambda_0 t}$  and approximate their extinction time as  $T_x \approx -\frac{1}{\lambda_0} \log x$ , then we can heuristically estimate the expected value as

$$\begin{aligned} E[Z_1(vT_x)] \\ = \frac{\mu}{r} \log x \int_0^{v \wedge 1} x^{1-u} x^{(\lambda_1/r)(v-u)} du. \end{aligned} \quad (1)$$

Thus we observe that this expected value is finite for all  $v > 0$  (also see [1, 2, 3, 4, 5, 6]).

## Appendix

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### Acknowledgements

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### Funding

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### Abbreviations

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### Availability of data and materials

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### Ethics approval and consent to participate

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### Competing interests

The authors declare that they have no competing interests.

### Consent for publication

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### Authors' contributions

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Figures



Tables

**Table 1** Sample table title. This is where the description of the table should go

	B1	B2	B3
A1	0.1	0.2	0.3
A2	...	..	.
A3	..	.	.

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Additional file 1 — Sample additional file title  
Additional file descriptions text (including details of how to view the file, if it is in a non-standard format or the file extension). This might refer to a multi-page table or a figure.

Additional file 2 — Sample additional file title  
Additional file descriptions text.