Response to decision letter

2023-11-07

Dear *Editor-in-Chief* Isabel Sanmartín,

Please find below response to each point raised by you and the *Associate Editor* Daniele Silvestro. We greatly appreciate your time and consideration for our resubmission.

Kind regards,

Luna L. Sanchez Reyes, on behalf of all coauthors.

30-Jun-2023

Dear Dr Sanchez Reyes:

Decision on USYB-2022-152.R1, DateLife: leveraging databases and analytical tools to reveal the dated Tree of Life:

Accept pending minor revisions.

I thank the authors for their extensive and careful revisions to the manuscript. It has been reviewed by Associate Editor Dr Daniele Silvestro and myself. We both agree that the manuscript has been greatly improved and meets all the previous requests of the referees and the AE. The AE has several other suggestions that you should find useful while preparing the revision, mainly concerning editorial and formatting issues.

I agree that some of your figures are difficult to visualize, for example Figs. 1 and 4, where you could use less color and more simple lines (they resemble a poster).

Thank you for your decision! We modified Figures 1 and 4, and consolidated into a single one. They are more streamlined now and usage of color was reduced; we followed all suggestions from AE.

Figure 5 is too large and detailed: it could never be published as an A4.

We reduced the number of tips shown in Fig 5 and moved the tree with all tips to supplementary data. Fig 5 is now Fig 3

I also wonder if all figures are necessary: for example, Figures 5 and 6 could be moved to the Supplementary; there is no limit in the number of figures in Software papers but we typically publish 4 figures per paper. Please consider these recommendations as you revise the manuscript.

We have now 4 figures in our paper. We achieved this by consolidating fig 1 and 3 into one single figure (now fig 2) and we moved figures 4 and 5 to supplementary material. We would like to request keeping Figure 6, which is now Figure 4 in the new submission, as we believe it adds good visual information for the cross validation analysis.

Please acknowledge (by email to sysbio.editorialoffice@oup.com, SYSBIO.OUP.EA@straive.com) receipt of the reviews and give a probable time frame for the return of your revised manuscript. Your revision should be submitted as soon as possible. Any revision not received in a timely manner may have to be considered a new submission.

Noted and done.

Your revision must comply with our instructions to authors (in this letter, with additional instructions at https://academic.oup.com/sysbio/pages/General_Instructions). This applies even if your original submission deviated from Systematic Biology style and corrections were not included in the notes from the editors or reviewers. Therefore, READ AND APPLY OUR INSTRUCTIONS BEFORE SUBMITTING A REVISION. Failure to do so will result in significantly delayed processing of your paper. If anything remains unclear after reading the instructions, use recent issues of the journal to find examples. If necessary, feel free to contact the Managing Editor at sysbio.editorialoffice@oup.com for help.

Noted and checked.

Log into https://mc.manuscriptcentral.com/systbiol and enter your Author Center, where you will find your manuscript title listed under "Manuscripts with Decisions." Under "Actions" click on "Create a Revision." Your manuscript number will be appended to denote a revision. Your original files are available to you. Delete the old files and replace them with your modified versions. Files that did not require revision can simply be retained.

Noted and done.

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Noted. We highlighted changes using latex and submitted the PDF file with track changes names manuscript-differences.pdf.

When submitting your revised manuscript, address each point made by the Editor, AE and Reviewers IN THE SPACE INDICATED (under "Response to Decision Letter"). Your revision cannot be processed if your responses to reviews are given only in a cover letter. The best way to address each point would be to copy this letter and insert your comments after each point made. Please do not change the order of or delete any of the comments because this makes it difficult to review again and would slow the process. The format of your responses must be compatible with ScholarOne Manuscripts text fields. For example, colored text is not an option, but you could use asterisks (and numbers, spacing, etc.) to clearly distinguish your responses from the text of the reviews.

Noted and done. We submitted response to reviews as a PDF file

Feel free to argue your case, with careful consideration and documentation, if you disagree with any of the suggestions. If you feel a reviewer did not understand a point you made, in your response keep in mind that as an author it is your responsibility to make your points clear to the readers.

Noted.

DO NOT submit your revision in .pdf format. This applies to the main text, tables, and appendices. Individual figures may be in .pdf format.

Noted.

In the specific case of papers written using LaTeX, in addition to the .tex (and associated style, bib, or etc. files) please include a .pdf generated from those files. Upload the .pdf in the ScholarOne Manuscripts category called Related Files. Figures must be uploaded separately, with each file name including the figure number. No figures may be imbedded in or tied to the .pdf or .tex files.

Noted and done.

After you've uploaded your revision, carefully view the ScholarOne Manuscripts version to verify that all figures and other files display correctly, and that you've followed all of our author instructions.

Noted and checked.

Figures: Each figure must be submitted as an individual file. The name of the file should include the figure number. Numbers and letters on figures should be as large and clear as possible, without overlapping any text. No figures may be imbedded in the document. Captions should not be placed on the figures. Figure portions should be referred to in the text and figure captions using lowercase letters. On the figures themselves, portions should be labeled by a lowercase letter followed by a single parenthesis (e.g., "a)"), located in the upper left area of the figure portion. Line thickness (including graph axes) should be a minimum stroke weight of 0.5pts, and 1.0pts is recommended for most lines. We prefer vector rather than bitmap figure formats. If desired, see http://systbio.org/?q=node/138 for an explanation of the difference. If bitmapped figures are necessary, they should be created at a minimum of 300 dpi and should be about 8 inches wide. We accept a wide variety of figure file types, as long as the figures are of sufficiently high resolution.

Noted and done.

The cost of printed color figures is $600 each. Authors are normally expected to cover this cost, but we do have limited funds available for authors who are SSB members, and cannot pay the full amount. If you feel your circumstances create an unusual financial need, please explain in your cover letter. The maximum allowance is one color figure per paper. All color costs can be avoided if you decide to have the figures printed in black and white, but be shown in color in the online version of the paper. If you do this, the captions must be worded such that they are appropriate for both situations (e.g., descriptions should not name colors), because the captions in print and online will be identical even if color is used online only. Do not submit two versions of any figure. Instead, make sure the color figure is also easily legible in grayscale, then submit only the color version. In your cover letter, please make your intentions regarding the use of color clear.

Noted.

Journal Covers: Please consider submitting a suggested cover image. They can be illustrations of theory, photos of organisms, a combination of the two, or alternatives. These can be uploaded with a revision of the manuscript or may be sent later. Only images for which you have copyright permission or that are not under copyright may be submitted. The color figure fee does not apply to images chosen by the Editor to be on the cover of the issue. If you have questions about possible cover designs, please email sysbio.editorialoffice@oup.com. We encourage and greatly appreciate cover image suggestions.

Noted.

Data and Online Appendices: All such files should be deposited in the Dryad data repository. Also, before the manuscript can be published, data accession numbers must be in the text. Nucleotide sequence data and alignments must be submitted to GenBank (http://www.ncbi.nlm.nih.gov/genbank) or EMBL (http://www.ebi.ac.uk); alignment, input file and tree files must be submitted to TreeBASE (http://www.treebase.org); morphological data must be submitted to either Morphbank or MorphoBank. Check over your online appendices or supplemental material (if any) carefully, because they will not be copyedited or proofread, and cannot be changed later.

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We added the DOI of our Dryad package containing all Supplementary Material at the en dof the manuscript (https://datadryad.org/stash/dataset/doi:10.5061/dryad.cnp5hqc6w).

Make sure all section headings conform to Systematic Biology style for first, second and third levels. Use of incorrect styles is potentially confusing and, in any case, is likely to delay processing of the manuscript.

Noted, checked and done.

Tables should have a single-sentence informative title above the table, with any other descriptive information located below the table in the form of notes and/or specific footnotes.

Noted, checked and done.

When references are grouped together in parentheses in the text, they should be listed in ascending chronological order. Multiple references in a single year should be alphabetized.

Noted, checked and done.

All funding used for this work should be listed in a "Funding" section preceding the Acknowledgements. Please give the full official name of each funding body.

Added in "Funding" section, after "Supplementary Material".

Our accepted abbreviation for millions of years ago is Ma. The abbreviation for millions of years duration is myr.

Checked and implemented.

Our full instructions are accessible via the link in the upper right area of the ScholarOne Manuscripts page (the link goes to https://academic.oup.com/sysbio/pages/General_Instructions). In case of a discrepancy between the information at that site and this letter, follow the instructions in this letter.

Noted.

If you are the first author and your manuscript is based on work done while you were a student, you would be eligible for the "Publisher's Award for Excellence in Systematic Research." When submitting your revised version be sure to indicate student work in the checkbox provided. If two student researchers were heavily involved in the manuscript, please briefly describe the situation in your cover letter.

This work was done while the first author was a Postdoctoral researcher.

I think that your paper will be a valuable contribution to Systematic Biology once the comments provided below are addressed. Thank you very much for your submission.

Sincerely,

Dr Isabel Sanmartín Editor-in-Chief, Systematic Biology isanmartin@rjb.csic.es

Thanks so much for your decision! We made sure to address all comments carefully and hopefully you find the manuscript and figures improved.

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Associate Editor: Dr Daniele Silvestro

Associate Editor Recommendation: Accept with minor revisions

Comments to the Author: Dear Dr Sanchez Reyes and co-authors,

Many thanks for the thorough revisions of your paper, which I find nearly ready for acceptance and have decided not to send it back to the reviewers. I do have a few additional comments, which I would like you to address in a minor revision.

Thanks you for your decision! We addressed all your comments as follows.

Lines 24-25 "A service [. . .] that provide services" rephrase?

Rephrased to "a phylogenetic software that provides services"

Line 33: how is the topology chosen? User defined?

By default it uses OpenTree's tree topology, ig the user does not provide a topology that they want. We specified this as "to corresponding nodes on a tree topology, either extracted from Open Tree of Life's synthetic phylogeny or one provided by the user"

Line 40: I would rephrase to something like "Since the results of any [. . .], we highlight that [. . .]"

Thanks for pointing this out, we rephrased to "Because the results of any [. . .], we highlight that [. . .]"

Line 43: "DateLife can help [. . .]"

Yes, we changed to "DateLife can help to increase [. . .]"

Line 116: can you provide more information about the taxonomic scope of the available phylogenies? How many species are included? Can a researcher working on e.g. plants or invertebrates still use it? What happens if none of the user's species are found?

We address this on the manuscript, section "Searching a chronogram database", second paragraph (L 126-132). Briefly, it depends on the taxonomic scope that the researcher is looking for. The chronogram database encompasses close to 100 k (99 474) different species. The chronograms in datelife's database encompass almost the same amount of tips with phylogenetic information in OpenTree's synthetic tree (112 669), in which Chordata and Embryophyta are nearly fully sampled. In contrast, Bacteria, Fungi, Nematoda, and Insecta, present a large gap between the estimated number of species and what has phylogenetic information in OpenTree's synthetic tree. We would expect that users working with the former groups will always get results from datelife. If none of the user's species are found, datelife will return a message saying that there are no chronograms containing any of those species in the database. It will also encourage users to submit chronograms to a public database, so that their taxon of interest can be included in future searches.

Can a user choose to include a chronogram of their own? I think this would be useful if you want to plug a clade you are working on into a broader taxonomic scope.

Yes! They can add any chronograms they want to the database, or by providing an initial chronogram, node ages and tip names will be used as input for the analysis.

Line 206-207: Equally spacing branches does not mean "not requiring any assumptions". I think it's OK to use it as default as it does not require prior estimates of speciation and extinction rates, but it is still making an assumption. The assumption translates into a possibly strange distribution of non-homogenous branching rates. I would focus on the fact that it does not require additional input (the rates) rather than on the assumption aspect.

Thanks for pointing it out! We changed it to:

"BLADJ is an agnostic way to assign ages to nodes with no available genetic or branch length data, as it does not require initial diversification rates to draw from a branch length distribution"

An alternative to BLADJ to date tree topologies in the absence of initial branch lengths that is common practice in the literature is to use a birth-death model to draw branch lengths [@Jetz2012; @rabosky2018inverse; @smith2018constructing]. In addition to the initial tree topology and nodes with age data, these methods require initial values of speciation and extinction rate parameters provided by the user. DateLife implements this approach with MrBayes [@Huelsenbeck2001; @Ronquist2003], using nodes with published age data as calibration priors on nodes of a tree topology with no branch lengths, a simple birth-death model with speciation and extinction rate parameters that are provided by the user, and no genetic data. However, BLADJ is the default option in DateLife, as it does not require any information on diversification rates for the phylogenetic sample to draw from a branch length distribution.

Line 217: I think you mean branches that are proportional to the expected number of substitutions per site, i.e. substitution rate multiplied by elapsed time.

In this instance we are referring to branch lengths from phylogenetic trees that have not been dated yet. We modified the phrasing to make it more clear.

Line 218: orthology hypothesis?

Yes! we clarified that, too.

Lines 460-462: I don't have strong opinion on this, but the statement seems unnecessary.

We removed it.

I think the figures require some work. They look nice but are currently way too packed and I wonder if they need to include so much detail. I don't know if anybody is still reading printed papers, but I doubt the figures would be readable on an A4. I recommend reducing the amount of text and substantially simplifying the graphics in general.

We simplified all figures and reduced the number of final figures in the main manuscript.

Fig. 1. I like the trees in the background, but they contribute to making the figure really busy. Also, there is a lot of text and tables, I think this should be strongly streamlined.

Fig. 3. Way too much text, tip labels not readable. In b2 I would reduce the trees to like 4 examples and make sure all the boxes have the same size and are aligned. Again, consider removing the trees in the background, especially in the colored boxes. In c) fonts in references are way too small, the numbers on the time axis are not explained. In a figure I would not expect to see full sentences like "We used median summary ages of congruent nodes to date [...]". Font types and sizes seem inconsistent.

We consolidated Fig 1 and 3 and streamlined the figure by removing text in the figure and adding it to the figure caption. We removed the tables ad only reference them. We hope this new version of the figure is considerably clearer now.

Arguably none of the text in Figs. 4 and 5 is readable without a 200% magnification and the title of the plot is unnecessary. Tip labels should not be shown if they can't be read, consider summarizing them by e.g. higher taxonomy.

We reduced the number of tips shown in Figure 5 and sent the full figure (as well as Figure 4) to supplementary material. Figure 5 is now Figure 3.

I hope this helps and look forward to seeing your revised version of the paper.

Thanks so much!

Best regards, Daniele

We greatly appreciate your consideration of our resubmission.

Luna Sanchez-Reyes on behalf of all coauthors.