

Response to comments of Anonymous Referee #2

1. General comments

Reviewer comment: Most analyses using Neotoma or other archived pollen data are dependent, at least to some extent, on the chronologies. The available chronologies have variable quality: some records have an uncalibrated chronology, others have a Bayesian chronology. In many cases the uncertainty on the chronology is not available, or if it is, just the upper and lower credibility interval. To synthesise pollen data from several datasets, it may be necessary to harmonise the age-depth models, a huge amount of work. Once such harmonisation is presented in this current manuscript.

Reviewer comment: *(1) As far as I can tell, the chronologies are not archived, but instead the metadata needed to make the chronologies. This is probably a good idea as it encourages the user to check the parameters.*

Response: We are sorry for the misunderstanding. We provided the final chronologies as well as all metadata and scripts to recreate the chronologies. We also improved the documentation on accessing and using the dataset and code to avoid further misunderstandings.

New text (line 312-333):

‘4 Code and data availability

Seven supplementary datasets (Table S1-S7, in comma-separated values format) and one readme text about the LegacyAge 1.0 are accessible in the navigation bar ‘Further details’ of the PANGAEA page (<https://doi.pangaea.de/10.1594/PANGAEA.933132>; Li et al., 2021a). We provided the chronological control points metadata (Table S1), prior information of dates from publication (Table S2), Bacon parameter settings (Table S3), original chronology metadata from the Neotoma and Cao et al. (2013, 2020) (Table S4), LegacyAge 1.0 chronology (Table S5), description of the comparison of original chronology and LegacyAge 1.0 (Table S6), and record references (Table S7) respectively. All datasets are already in long data format that can be joined by the dataset ID.

The R-code for calculation and comparison of chronologies with embedded manual, metadata for code runs, Bacon output graphs of each record, graphs comparison of original chronologies and LegacyAge 1.0, and a short shared-screen video of the R-code to show the usage on two example records are accessible on Zenodo (<https://doi.org/10.5281/zenodo.5815192>; Li et al., 2021b).

5 How to use the LegacyAge 1.0 dataset and code

LegacyAge 1.0 provides the calibrated ages (mean, median, minimum, maximum) and uncertainties at each centimeter for each record with a 95% confidence interval (Supplement

Table S5). All users can apply some interpolation algorithms in the chronologies, subsetted from the LegacyAge 1.0 dataset or outputted by our code, to assign ages for proxy depths of records.

As for the R-code, users only need to set the working directory where the Bacon results will be stored and input the record ID of interest to run it successfully. The manual and shared-screen video on R-code usage could provide helpful guidance for users, with or without some R-experience’.

Reviewer comment: (2) *One important result is that "95.4% of records could be improved ". However, it is unclear what objective criteria were used to determine whether the new model represented an improvement. The criteria need to be explicitly stated.*

Response: We added the criteria for the preferred models in the new text.

New text (line 232-237): ‘We plotted our newly generated ‘best’ calibrated chronologies with 95% confidence intervals together with the original ones taken from the Neotoma and Cao et al. (2013, 2020) datasets (Supplement Table S4) to compare and evaluate the performance of the new models visually. The criteria for the preferred models are that the model fitted the dates well, had small uncertainties, combined dates with prior information (e.g., geological and hydrological setting, environmental history), and calibrated with the latest calibration curves’.

Reviewer comment: (3) *The metadata and code are available on github (Zenodo.org would be preferable for the final version).*

Response: We agree with your suggestion. Therefore, we moved to store metadata, code, and results from GitHub to Zenodo (<https://doi.org/10.5281/zenodo.5815192>).

2. Data (PANGAEA)

Reviewer comment: (1) *The data are arranged in wide format, with a set of columns for each date. This is not the ideal way to arrange the data, as it makes the code much more complicated to deal with this structure, and will need extra extra columns adding in the future to cope with new sites. A better setup would be to have the data in long format, perhaps in multiple files that can be joined by the dataset ID.*

Response: All datasets are already in long data format that can be joined by the dataset ID. To avoid misunderstanding, we provide this information now in the text.

New text (line 319-320): ‘All datasets are already in long data format that can be joined by the dataset ID’.

Reviewer comment: (2) *At present, datasets are marked as being marine or otherwise. At least in principle, there could be datasets where some dates are on marine fossils, and others on terrestrial macrofossils. Marine should be a property of the date, not the core.*

Response: Thank you for this comment. After rechecking all sites marked as marine in the dataset, we did not find a single case where terrestrial material was dated. So we did not implement this suggestion.

Reviewer comment: (3) *Setting a constant reservoir age for a core without error seems risky to me. Do you check these are only occurring with bulk dates, as there should not normally be a problem with terrestrial macrofossils.*

Response: Although the reservoir ages with errors would be better, the reservoir ages reported by the original author through various methods are mostly without error. We fully respect the original authors' comments because we assume that they are more familiar with the sites than we are. As you can infer from the variable 'Material_Dated' in supplement Table S1, various dating materials were used for dating. Thus, we subtracted the reservoir age as a constant from all ^{14}C dates of an affected record, excluding those derived from terrestrial macrofossils.

New text (line 187-193):

'Reservoir effects: the uptake of old carbon by aquatic plants, mosses, or shells either originating from, e.g., limestone in the catchment ('hard-water effect') or slow ^{14}C exchange between the atmosphere and ocean interior, can result in too old radiocarbon dates (Philippsen, 2013; Philippsen and Heinemeier, 2013; Giesecke et al., 2014; Heaton et al., 2020). In addition to the reservoir ages reported by the original authors, we also identified some additional records for which there is likely a reservoir effect through modern correction and linear extrapolation (Wang et al., 2017). We then subtracted the reservoir age as a constant from all ^{14}C dates of an affected record, excluding those derived from terrestrial macrofossils'.

3. Code

Reviewer comment: (1) *The code is presented in a single script. This is fine if someone wants to make chronologies for all datasets, but often people will want to run a subset of the sites, and may find the script difficult to use. Breaking the script into functions than each do one task, perhaps compiled into a small package with help files and other documentation, would make the product more useful.*

Response: We apologize for this. We revised the code and rephrased this part of the text.

Description of the uploaded file in new text (line 321-324):

‘The R-code for calculation and comparison of chronologies with embedded manual, metadata for code runs, Bacon output graphs of each record, graphs comparison of original chronologies and LegacyAge 1.0, and a short shared-screen video of the R-code to show the usage on two example records are accessible on Zenodo (<https://doi.org/10.5281/zenodo.5815192>; Li et al., 2021b)’.

Description of code usage in new text (line 331-333):

‘As for the R-code, users only need to set the working directory where the Bacon results will be stored and input the record ID of interest to run it successfully. The manual and shared-screen video on R-code usage could provide helpful guidance for users, with or without some R-experience’.

Splitting the code into separate functions is an interesting idea, but getting this to universal usage (now it is very specific and focused on our data) would need more modifications. But to consider this, we separated the “Age Allocation” part into a standalone code (line 252-295 of code) that should be the most valuable part of the main script for other purposes.

New code (line 252-295):

```
‘#-----Age Allocation-----
```

```
# Define basic values for the age allocation
```

```
model.AWI <- read.table(paste0(folder, "/Ages.txt/", ID, ".txt"), header = TRUE)
```

```
model.rest <- round(model.AWI$depth[length(model.AWI$depth)] -
```

```
floor(model.AWI$depth[length(model.AWI$depth)]), 4)
```

```
new.memory <- data.frame(min = NA, max = NA, median = NA, mean = NA, stringsAsFactors = FALSE)
```

```
.....’.
```

Reviewer comment: (2) *The code includes fixes for issues the authors found in Neotoma. Please report these issues, and make sure the code to fix them (e.g. line 187) will work safely when the error is fixed.*

Response: We discovered wrong depth units of the four IDs (15669, 15671, 15673, 156750) reported it to the Neotoma team, which revised them. So this problem does not anymore apply.

4. Figure

Reviewer comment: (1) Figures 4-6. The x-axis, labelled 0-1, 1-2 etc, is rather cluttered and difficult to read. Please consider other ways to label them. The relative lack of outliers in the pre-LGM sediment is interesting, but probably represents over-fitting the models to sparse data.

Response: We replotted figures.

New Figures:

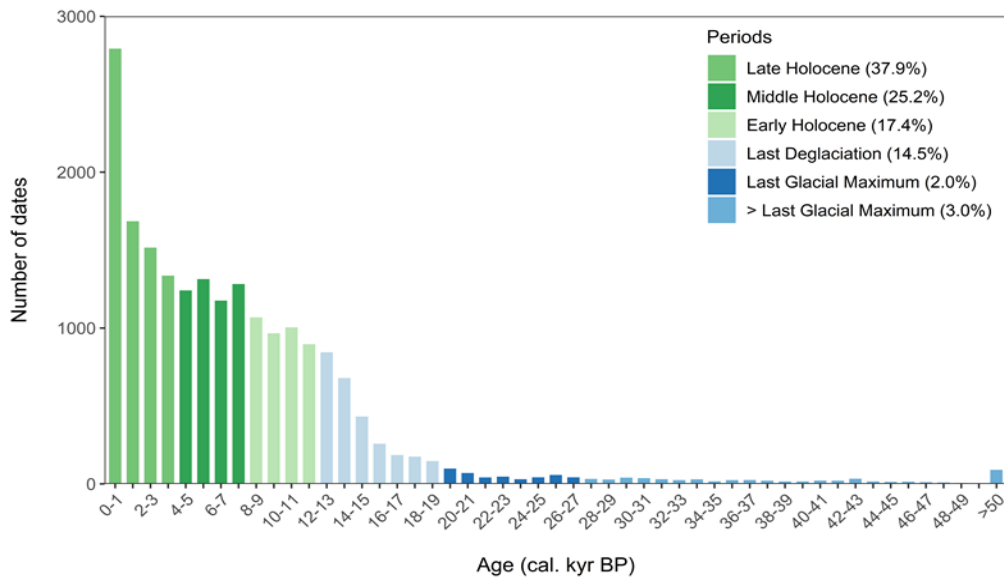


Figure 4. Histogram showing the number of available dates in distinct time slices.

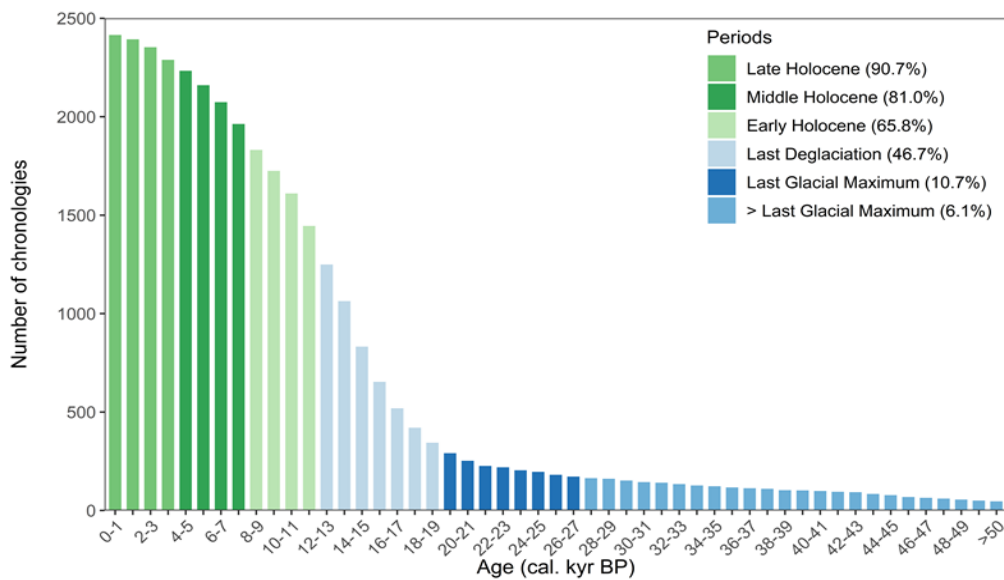


Figure 5. Histogram showing the number of available chronologies in distinct time slices.

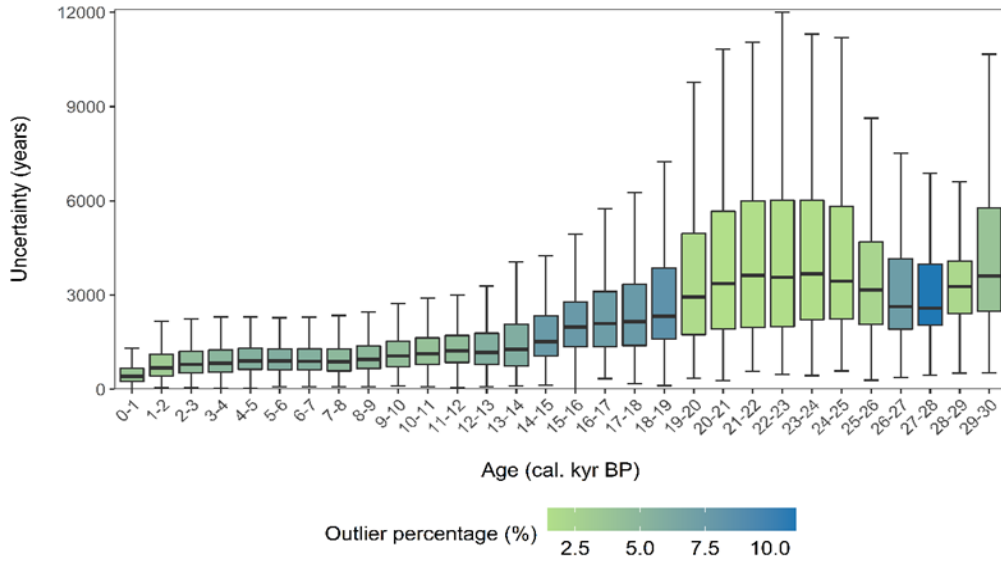


Figure 6. Boxplots of age uncertainties and outlier percentages in distinct time slices.

As we can see from the figure below (Figure R1), the outliers appear on the maxima side of the boxplot. After examining these outliers, we found that most of them came from chronologies with sparse age control points and significant dating errors. For example, the maxima values in all distinct time slices are from the *Nachtigall* record (Dataset ID 41435; Figure R2), with only three significant-error dates.

New text (line 280-282): **‘The boxplots show wide boxes, i.e., a more extensive data range, for the LGM period, characterized by fewer outliers, mostly from chronologies with sparse age control points and significant dating errors, than the periods with small box sizes’.**

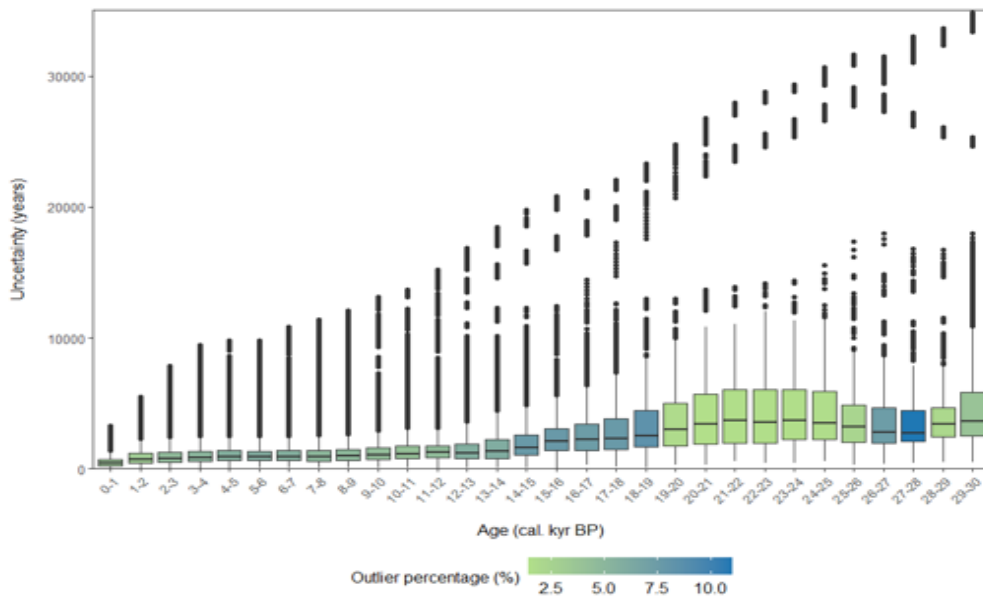


Figure R1. Boxplots of age uncertainties and outlier percentages in distinct time slices (with outliers).

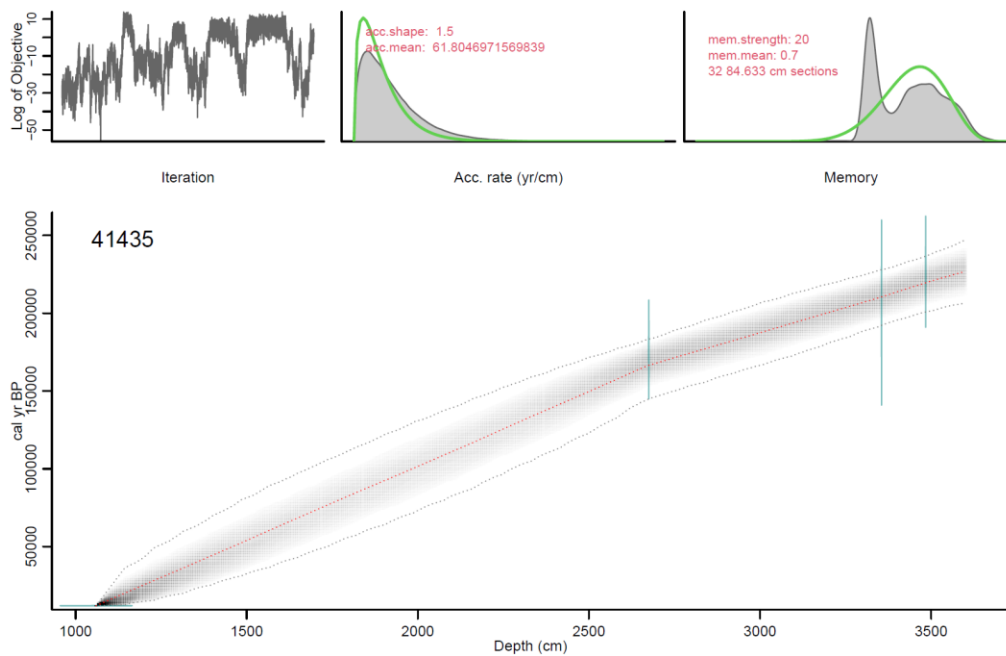


Figure R2. Bacon output graph of the *Nachtigall* record (Dataset ID 41435).

Reviewer comment: (2) *Figure 7 has a minuscule font: I need to view it at 200% before I can read it. No need to repeat the legend four time - once is enough and leaves more space for everything else.*

Response: We laid out this figure on a whole page. As suggested by reviewer #3, we have newly provided the section thicknesses in the title of each figure. Also, one additional age-depth model created by Bacon with relatively poor performance has been included for comparison.

5. Specific comments

Reviewer comment: *Line 202 "with fewer than 2" Maybe rewrite as "only one" for clarity. Consideration should be given as to the minimal number of dates that can give a good chronology - I would be cautious using a model based on only two dates.*

Response: Thanks for your suggestion. We rephrased this part of the text to avoid further misunderstandings.

New text (line 241-243): ‘We discarded 640 records with fewer than two reliable dates (i.e., no reliable date or only one reliable date), evaluated based on prior information from original literature, leaving chronologies for 2831 records’.

It is well known that the quality of the chronology is closely related to the quality and quantity of the date. As a rule, the more high-quality dates a chronology has, the more reliable it is.

Therefore, it is difficult to give the minimum number of dates to establish a chronology. As you read from column '*Dates_Number*' of the supplement Table S5, 9.7% of the records have only two dates. We have kept these to keep as many records as possible.