

(R1 comments in normal typeface; **responses in bold**)

After reviewing this manuscript, I have a mixed feeling about its quality. The introduction is clear and well written. The discussion section is also interesting and well presented. But the method section, with its description of the synchronisation method is in my opinion unclear, and probably contains some mistakes. An effort is therefore needed in my opinion to better describe this method. If I understood correctly, the age transfer function is supposed to be continuous and linear by parts with only 4 segments, which is a very restrictive assumption that should be discussed in greater detail. Moreover, I am personally not convinced that current automated synchro methods can better synchronize than the human brain when the signal-to-noise ratio is low.

**Many thanks for the detailed scrutiny of the methodology section. This is welcome and much appreciated. I agree that there are points that can be improved and I will address all the specific points and typesetting mistakes that the reviewer has brought up. As to the point about potential noise in the data, I will present a new CLIM synchronization that combines multiple speleothem d18O records (please see my responses to R2 and R3).**

**Replies to specific comments of particular concern:**

Eq. (2): First, on the general expression of this cost function. I am personally unfamiliar with this way of adding the  $R^2$  and the RMSD. Where does this come from?

**Thank you for bringing this up. I understand that the combination of  $R^2$  and RMSD can be confusing. Accordingly, the algorithm was modified and the synchronizations were performed again after re-defining the log-likelihood using only the minimum distance between the observed (obs) and simulated (sim) data –i.e. the most commonly employed formulation of the misfit in inverse problem studies:**

$$M(\mathbf{X}) = \sum_i \frac{|D_i^{obs} - D_i^{sim}|}{\sigma_i}$$

344: To constrain the ages to be strictly increasing, it would be more convenient to invert positive sedimentation rates.

**Thank you, this is a valid point that should be addressed when dealing with records of cosmogenic radionuclide fluxes. Given R2's comments, the revised manuscript will only focus on the climate synchronization. However I will certainly consider this in future cosmogenic synchronizations.**

Eq. (7): Why are there only 4 segments in the synchronisation, with the last two segments having a slope equal to the average slope (l. 352)? This seems to be a very restrictive way to define a synchronisation. I could not understand if this is a global formulation of the transfer function or only a local formulation. If this is global, it is a very restrictive assumption that should be discussed in greater detail.

**I agree that the formulation is simplistic and I have been open about the fact that the forward model may not provide a realistic representation of the alignment process (see**

lines 356-357, and 391-395). However, employing random restarts and only a handful of parameters, makes the algorithm computationally much more efficient than other automated methods (e.g. Lin et al., 2014). Furthermore, random restarts minimize the constraints of a 4-segment linear function (see lines 412-429) and effectively allow the algorithm to explore alignment pathways in a fashion that is qualitatively comparable to other more sophisticated routines – capabilities that have been demonstrated in other seminal works (Sessford et al., 2019; Cutmore et al., 2021; West et al., 2021). Although it is hoped that in the future the same synchronizations will be done using more refined automated methods, it is unlikely that the results will be fundamentally different from those presented in this paper. That being said, as recommended by the reviewer, I will discuss strengths and limitations of the forward model in more detail and more upfront in the manuscript. In particular, the importance of random restarts in relaxing the restrictions associated with the piecewise linear function synchronization will be further highlighted.

Finally, I would like to point out that I have improved the algorithm and re-performed the synchronizations (see also comments to R2 & 3). Model mixing is now improved using a differential-evolution (DE) MCMC sampler (ter Braak and Vrugt, 2008) – whereby multiple chains are run in parallel in such a way that some can move around the parameter space more easily– while the number of random restarts was increased.

Section 2.3.5: Nothing is said about the computation time to get the posterior distribution, it would be interesting to know that, since it is generally the Achilles' heel of MCMC methods.

**The runtime of MCMC algorithms is heavily dependent on computer specs. To give the reviewer a ballpark estimate, in the particular case of CLIM using a DE-MCMC sampler in RStudio (v1.3.1093) on a late 2017 MacOS system, the algorithm runs ~1.7k simulations per second.**

## References

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