REVISION

We thank the editor and the reviewers for giving us the opportunity of revising and improving our manuscript. We have addressed all the comments below.

# Reviewer #1

We thank the reviewer for providing these thorough comments that helped us clarify and address several important points in the manuscript, especially in the abstract. We have replied to all the comments below.

This article should make clear that the list of techniques used is not fixed but should be completed. The short list in the abstract is misleading. In my opinion it should be indicated that it is a selection of the authors but for me the risk is that less scientific researchers use only the few indicators instead of the whole list of parameters.

We agree that the abstract can indeed be improved and have added further clarification that the selection of techniques used is non-exhaustive but are those predominantly used by researchers for analyses and available for computation via the open-source Neurokit2 Python package.

“*In this study, we systematically compared a non-exhaustive list of 125 complexity indices that are predominantly used in research analyses (available via Neurokit2) by their computational weight, their representativeness of a multidimensional space of latent dimensions, and empirical proximity with other indices*”

Note also that there are also recent articles, to mention only a few, such as those on the notions of symmetry (linking in recurrences -RQA and entropies (palindrome, symmetropy, symmetrical quantification analysis)) that would also deserve to be mentioned.

We recognize that in the attempt to keep our article as concise and to the point as possible, we did not include an extensive literature review on all the available complexity methods, including some that were in fact used in the analyses, such as RQA. To address this, we have added more information on the use of other methods of quantifying complexity that were not included in the analyses. This addition can be found on line ..

“ *For instance, in using palindromic analyses (the study of sequences that read the same forward and back) in complexity quantification, new tools like symmetropy (i.e, a measure of the global level of symmetry) and symmentropy (an indicator of the different types of palindromes) have been developed based on binarized signals with differing types of symmetry (e.g., translation symmetry, inversion symmetry etc.,) (Girault & Menigot, 2022).”*

To improve the paper, the abstract should be corrected because the abstract is a review, so the results are missing, please correct.

We have amended this by adding the results in the abstract as follows:

*“Twelve indices which explained 91.01% of the total variance of the entirety of the indices was thus selected and organized in the order that maximized the variance explained”*

The size of the signals is missing (unless I am mistaken).

It is an oversight of our part that we missed out on including the specific sizes of the signals in the manuscript. We have added this information in line..

*“Each of this signal was iteratively generated at 4 different lengths of 500, 1000, 1500 and 2000 sampling points.”*

There is either a problem in the numbering of the figures in the "factor analysis" part or the description is not clear and should be corrected

Indeed, there is a mistake made in the numbering of the figures due to a repetition in one of the figure numbers. This has been rectified accordingly.

# Reviewer #2

We thank the reviewer for the constructive comments as well as the suggestions made to include other complexity methods that had prompted us to delve deeper into the extensive literature of complexity quantification and other available open-sourced software for running such comparative analyses.

The authors may like to cite and discuss some work by Fulcher et al. on highly comparative time series analysis (HCTSA), particularly their 2022 paper as it directly speaks to this cause.

We agree that Dr Fulcher’s work on developing the HCTSA toolbox should indeed be cited seeing its relevance to the objective of our manuscript, which is to provide researchers a guide to selecting complexity indices most pertinent to their research. However, we note also that there lies distinctions in the use of this software from that of Neurokit, which we used to derive our analyses. To address this, we have included some clarification in line..

*“Furthermore, although there exists open-source software that allows comparison of various types of time series analyses functions, such as HCTSA (Fulcher & Jones, 2017), such software usually by default administers all its features relevant to the inputted data, before returning a set of the top performing features. While this may be well-suited for exploratory data-driven analyses, it may be computationally redundant and lead to results that are difficult to interpret*.”

The authors never account for multifractal nonlinearity or tMF which quantifies multifractality due to nonlinearity obtained by comparison of the original spectrum with that of surrogates (Kelty-Stephen et al., 's work has been using this index as a predictor for a decade now). While I do not expect the authors to redo their modeling, this variable is something they may keep in mind for a follow-up study.

In trying to keep the scope of our manuscript targeted, there were multiple other parameters we did not take into account. However, this is indeed a factor worth looking into in a follow-up study.