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Interactive comment on "Ages and transit times as important diagnostics of model performance for predicting carbon dynamics in terrestrial vegetation models" *by* Verónika Ceballos-Núñez et al.

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We appreciate the time that Referee 1 dedicated to review our manuscript. In the text below we quote the referee's comments in italics and provide our response below in blue:

General comments : The research article 'Ages and transit times as important diagnostics of model performance for predicting carbon dynamics in terrestrial vegetation models' promotes using the distribution of C ages and C transit times of different tree

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organs for improving performance of vegetation model. In order to do so, the authors tested three different carbon allocation schemes into a simple vegetation model with the aim to discriminate the three allocation models in terms of C stock, C flux, radiocarbon, C ages and C transit times distribution. The paper concludes that C ages and C transit times distribution can indeed be used to evaluate the skill of the allocation schemes. Furthermore, the authors encourage the scientific community to use their approach for future model comparison or validation. In my opinion the authors did a good job in developing a powerful method to help reducing uncertainty in model output as well as facilitating model development.

We appreciate the motivating comments from Referee No. 1. This referee's impression from the manuscript captures what we intended to communicate with it.

I really appreciate that the R scripts are clear and easy to use by someone interested in applying this method to their own model. I'm convinced that the ideas presented in this paper our of interest to the readership of biogeosciences, but the presentation itself needs to be improved. The methods and result sections lack essential information. Before resubmitting the manuscript, a senior researcher should carefully edit these sections such that they meet the minimal requirements for publication.

We agree that there were some explanations missing and that there were certain points of the methods section that could be improved. Thus, we made major modifications to this section, which can be found in the suplementary material of this response.

Furthermore, the following concerns should be addressed in the manuscript:
1) The study relies on theoretical simulations from an unrealistic vegetation model to match the requirements of the mathematical calculation of ages and transit time. I understand and agree with the need for this approach. This caveat should, however, be addressed in the discussion and the conclusion where it was argued that the method can be useful for evaluating more complex vegetation models. In my opinion this suggestion is overly simple and this statement is not needed for the study. I would rec-

ommend the authors to stick to the more theoretical conclusions. Based on my understanding of complex vegetation models, the numerical and conceptual work required to implement the proposed method into a vegetation model with full complexity is too large to be downplayed. If the authors disagree, I would expect at least a paragraph dedicated to how this functionality could be integrated into a model with phenology, environmental changes, forest management i.e. forest structure and genetics. This would really enhance the impact of the manuscript as it may convince modellers to apply your method in their models.

The explanation on how this approach could be applied to more complex models was shortly examined on page 17 line 17. In order to calculate mean ages and transit times of non-autonomous models (inputs and process rates change over time), we would need a different set of equations. Rassmusen et al. (2016) have provided equations for the mean age and mean transit time for non-autonomous models, which require knowledge on the entire history of inputs and cycling rates for the duration of the simulation. This information is not available for Harvard forest, and for this reason we did not include these computations in our analysis. However, for complex models in which process rates vary over time due to phenology, environmental change, forest management, etc., one would obtain nevertheless age and transit time distributions. These distributions would be time-dependent, i.e. one would obtain a different distribution for each time-step. Since this manuscript is an introduction to the main concept of age and transit time distributions in vegetation models, we believe it is better to keep it simple and show these distributions for the steady-state case only. This would allow the reader to grasp the main concept, and if needed, apply to the more general case in which process rates change over time.

2) The method section is concise, which in general I like, but the current description of the methods is too concise making it hard to follow. Each time the authors refer to a method described by another study they referring to it without a explanation or at least the reason why they choose this one. As a general guideline readers should be able *to understand the method section without having to consult any other papers. What justifies the use of a two-step instead of one step optimization? Why do you need Bayesian optimization?*

As mentioned before, we admit that the Methods section needed some improvements and we have worked on that for the new version of the manuscript. The Bayesian optimization gave us the possibility of exploring the parameter space, because it searches for alternative parameter sets that can result in a good fit of the model to the data. In order to have a good starting point for this search, we used the output of the classical optimization as an initial constraint. The parameter sets that we obtained were used in the uncertainty analysis, as explained in the P7L10.

Why do you test co-linearity between parameters (answered too late in the discussion)

We agree that the explanation of why we test collinearity should be included in the methods, specially because it is not a common practice in the field. The new version of the manuscript includes a rationale for the use of the collinearity analysis early in the Methods section.

3) Since the authors use a lot of R packages to manage complex statistical methods, I guess that they are familiar with statistics and coding. Surprisingly, simple tests such as the t-test, anova, or metrisc like Root Mean Squared Error are not used to highlight their finding. The conclusions are not backed-up by any statistics, which is mandatory for publication in a journal like Biogeosciences.

This is an interesting point because it is customary to support empirical findings with statistics. However, we are dealing with a completely different case here. In empirical studies one has data that is assumed to be random draws from an unknown distribution. Here, we have known distributions and no samples are drawn from them, only calculated mean values from the distributions. Unfortunately, in this case the usual t-test or even the Kolmogorov-Smirnov test for comparisons of samples from different distributions are not appropriate because we are not dealing with samples whose dis-

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tribution is unknown; we are actually within the rare case in which the distribution is known and we not only have it's equation, but also the parameter values. We have to admit that we are not aware of any statistical test designed to compare two or more distributions without having to draw samples from them. But even if there would be a test, the results would be trivial. We know that the distributions are different because we have different parameter values from all of them. Therefore, we would always reject the null hypothesis that the distributions are different. Since this would be a trivial result, we refrain from adding any statistical comparison to our analysis.

Detailed comments on the tables and figures:
Table 1: the column called 'final' is not clear! Why this column differs from 'Best2' column ? I guess it is because of the constraint optimization on C stock but it is not described in the caption. Do not show the median and the quantiles of Best2 if you will not use these values in the next step.

We agree that the names that we used for the parameter sets were confusing. We now describe them in a better way in table 1 as well as in the Results section. 'Final' is the parameter set that was most frequently chosen by the Bayesian optimization method and was used for all of the simulations, unless otherwise noted. Furthermore, the above mentioned 'quantiles' are the quantiles of the distribution of the values of each parameter, as a result of the parameter space exploration performed with the Bayesian optimization.

Table 2:I am not sure this one is necessary ...

We moved it to the appendix

Figure 3: Two figures instead of one can be better to avoid the compressing of the leaf C stock.

This is a good point, we followed the recommendation of the reviewer here.

Figure 5,7: Put some statistics to highlight your results. You argue that mean ages and *transit time are different across allocation model. Support it with a probability! Figure 8: Again show that mean ages are significantly different.*

Please see our response above regarding the applicability of statistical tests in this case.

We hope that we addressed all comments from Referee 1 adequately, and improved the clarity of this manuscript.

Please also note the supplement to this comment:
https://www.biogeosciences-discuss.net/bg-2017-308/bg-2017-308-AC1-supplement.pdf

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