Biogeosciences Discuss.,
https://doi.org/10.5194/bg-2019-262-AC1, 2019
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Biogeosciences Discussions

Interactive comment on "Validation of demographic equilibrium theory against tree-size distributions and biomass density in Amazonia" *by* Jonathan R. Moore et al.

Jonathan R. Moore et al.

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Received and published: 17 December 2019

1. I think that this manuscript would be more impactful if it were organized around an explicit scientific question or hypothesis. In its current form, the manuscript is focused on the implicit question of whether DET or MST better fits the Amazon plot data. This implicit question strikes me as too technical. I would like to challenge the authors to develop a question that is more focused on the fundamental biology rather than a close-ended question of which model is better.

2. Most of the Discussion is a re-statement of the Results. This is a major weakness of the manuscript because the significance of the results is left unexplained.

Response to 1 & 2: In the revised manuscript (see attached supplement with just the revised intro and discussion) we have reduced the emphasis on the comparative performance of DET and MST, instead focusing on the implications of the DET fits to the data. We have introduced new histograms to show the range of best-fit parameter values across all 124 ForestPlots sites. These show that: (a) best-fit values for the exponents relating tree-size to growth-rate have mean and median values close to those predicted by Metabolic Scaling Theory; (b) when the growth exponent is fixed at the MST value, the remaining fitting parameter (which represents the ratio of mortality to growth) clusters strongly around a common value across the ForestPlot sites.

We also discuss the relationship between the fitting parameters φ and $\mu 1$ as a possible life-history trade-off within forest plots, resulting in dominance of either live-fast die-young or grow-slow live-long strategies based on local conditions.

These findings, and their possible consequences, are now more prominent in heavily reworked versions of the Abstract, Discussion and Conclusions sections. Also, we now more clearly separate the use of MST to define the allometric relationship between tree size and growth-rate (West et al., 1997) for which we find some observational support, from the MST size-distribution (MSTF, West et al., 2009) for which we do not.

3. At the end of the paper, the authors discuss the work of Zhou and Lin (2018), who discuss a "fundament flaw" in the MST model. If the authors knew this, why did they bother with MST model at all in their own analysis? The way that the text is currently framed, one is left with the impression that the MST model was a straw man

Response to 3: In our revised manuscript we have significantly reduced the emphasis on the comparison of the DET and MSTF models, in favour of focusing on the implications of the DET fits across the 124 ForestPlots sites. We also feel there is no issue with replicating the result of others, that MSTF is a poor model, especially with a dataset we believe has not been tested this way before.

4. Artificial imposition of a maximum tree size seems unsatisfying to me. That it is

needed suggests that there is a problem with the size-dependence of the mortality and/or growth rates. How might mortality (and/or growth) rates be modified so that maximum tree size would be a predictive outcome of the model?

Response to 4: The largest tree size in any dataset is largely driven by the statistical effect of large trees being rarer and therefore appearing less often in datasets with smaller sample size. However, the reviewer raises an interesting point regarding the largest possible tree size. Trees cannot grow infinitely large due to physical constraints (mechanical, hydraulic etc) but it an open question as to whether mortality prevents trees reaching these limits. While this is somewhat outside the scope of this study, we see this as an interesting avenue for future study.

5. Page 1, line 5: Here and elsewhere in the manuscript, it is stated that one model is "better" than another. But "better" in what sense? Blanket assertions that one model is better than another seem unwarranted to me.

Response to 5: We have reduced the use of the word 'better' and made changes to be more explicit regarding the basis of each comparative statement in the manuscript.

6. Page 1, line 16: I did not see any whole-continent analysis.

Response to 6: We have modified the text throughout to change the term continent to "all plots". While all plots is loosely a continental scale, to be more precise we have made this change. As the abstract has been heavily rewritten the specific line mentioned no longer exists.

7. Page 5, line 25: Please explicitly describe your algorithm.

Response: There is no algorithm, seems that the line was not clear enough. Have now clarified this by changing the line last two lines of that paragraph to read: "The 124 selected plots all had a consistent lower cut-off in measurements at 10 cm trunk diameter. Two available upper montane plots with very few measurements above 10 cm were not included in the 124 plots used, as they did not have enough measurements

to allow a reliable fit."

8. Page 8, line 13: What is a "data point"? A stem? A size class? Something else?

Response: Have now clarified this by changing the line to read:- "where Di is tree trunk diameter measurement of stem i in the dataset."

9. Equation 14: I do not see how the second equality follows from the first. Please be more explicit.

Response: We have clarified this point, explaining that the second equality does not follow from the first, but instead describes the range of validity of the equation. The equation is not valid for phi = 1. We have changed the comma separating the equation and the equality to instead read "for".

10. Equation 15: What is S?

Response: Our apologies this was a typo. This should have been D not S - now corrected.

11. Page 9, lines 9-11: from the text, it looks like the two parameters were not estimated jointly: the parameter mu1 was estimated first, and then the estimate of mu1 was used to estimate phi. The problem with this procedure is that the estimation of mu1 itself depends on phi, which is initially unknown. I am left confused about exactly what the authors did.

Response: Text has been modified to clarify. Now reads: - "Substituting Eq. (16) into Eq. (17) creates a function only of c and therefore φ. This allows minimisation of -L in terms of φ by using Brent's bounded algorithm (Brent, 1973a). Once the optimum φ has been found then $\mu 1$ can be calculated from equation 16. As equation 16 is included in the minimisation of -L, then it means we are in fact solving for both parameters at once and are finding the maxima of L. This algorithm was tested both with real data and data generated by computer from known LTWD distributions, by plotting the L values against φ and $\mu 1$, to confirm the maxima was found correctly.

Once the parameters μ1 and φ are estimated, then this allows nL, the tree density per size class at DL, to be obtained from these parameters and the known quantities of the total number of trees N and the plot area A. This can be derived by integrating the equation for n (Eq. 4), to give: -"

12. Page 9, line 19: The inequality is not sufficient to justify the assumption. Rather, the entire argument of the exponential must be small. For example, what if Dmax Âż DL, but c Âż mu1? I know it did not turn out that way, but it could have.

Response: For c » μ1 that would imply either φ being a highly negative value or μ1 being very small (suggesting either very low mortality or very high growth). Both these scenarios are unlikely, but we have added a clarifying statement to the text to acknowledge this. Now reads: - "For this study it was found that as Dmax » DL for most cases (and that c is never much larger than μ1), n L could assumed to be: -"

13. Page 10, line 24 through Page 11, line 1: It would help to justify this statement.

Response: Text has been modified to clarify. Now reads: - "This is because these equations only evaluate the mass up to but not including the trees with mass equal to the largest value in the dataset. Therefore, to comply with the definition above it is necessary to add the mass of the largest trees back into the total biomass.

As the large trees are so rare this correction will be equivalent to adding just one tree of the largest mass mmax in the dataset divided by A, the total area of plots in the dataset."

14. Page 27, lines 3-4: The text is misleading because the biomass was not actually observed.

Response: Have changed all references from "observed biomass" to "allometric biomass" to emphasise that this is the sum of masses obtained from observed trunk diameter measurements converted by allometry to mass.

15. I found numerous typos, to list a few: page 3 line 9; Fig 1 x-axis label; page 10 line

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Response: All corrected.

Please also note the supplement to this comment:
https://www.biogeosciences-discuss.net/bg-2019-262/bg-2019-262-AC1-supplement.zip

Interactive comment on Biogeosciences Discuss., https://doi.org/10.5194/bg-2019-262, 2019.

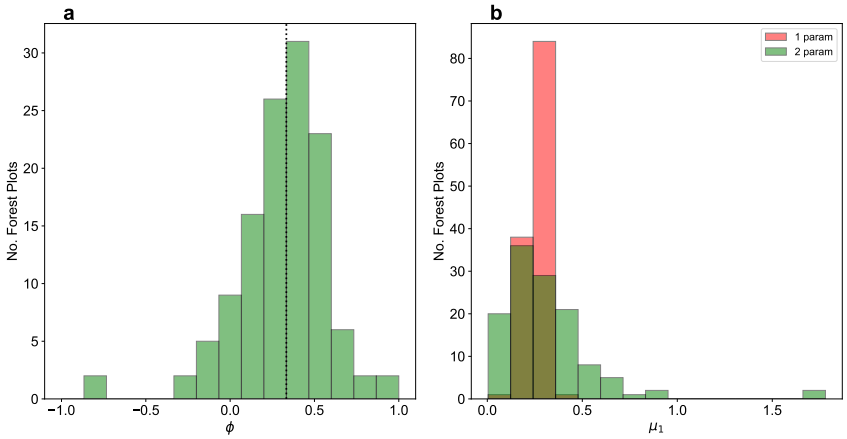
a
b
No. Forest Plots
No. Forest Plots
ϕ
μ_1
1 param
2 param

Fig. 1.

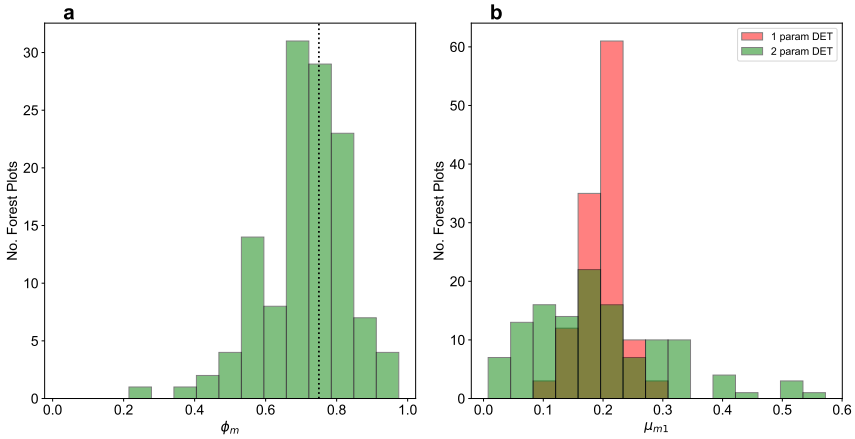
a
b
No. Forest Plots
No. Forest Plots
ϕ_m
μ_{m1}
1 param DET
2 param DET

Fig. 2.