Biogeosciences Discuss.,
https://doi.org/10.5194/bg-2018-314-RC1, 2018

Interactive comment on “Interspecific variation in tropical tree height and crown allometries in relation to life history traits” *by* Isabel Martinez Cano et al.

N. Picard (Referee)

nicolas.picard@fao.org

Received and published: 12 September 2018

General comments

This study develops allometric models for tree height and crown area that integrate species traits as co-variates to account for species differences in allometric scaling. Questions (ii) and (iii) addressed by this study (P2L32-34) are not new and have been addressed by other studies before. Related text in the manuscript could be shortened (e.g. P9L10-19). Question (i) is quite new, but a recently published paper by Loubota Panzou et al. (2018) also addressed it (with a slightly different approach, though). There are differences between the results reported by Loubota Panzou et al. (2018)

and those shown here. For instance, Loubota Panzou et al. (2018) found that large-statured canopy species tended to be light-demanding and small-statured understory species tended to be shade-tolerant, whereas the current study found light-demanding species to have smaller stature than shade-tolerant species (Fig. 2d). Rüger et al. (2012) also reported positive (but weak) correlation between the light response of species and their maximum height. Hence, the relationship between light requirements and maximum height may be more complex than that described at P9L24-27. It has often been reported that there are many small tree species on BCI, while large light-demanding species are common in central Africa. Could it be a confounding factor?

Loubota Panzou, G.J., Ligot, G., Gourlet-Fleury, S., Doucet, J.L., Forni, E., Loumeto, J.J., and Fayolle, A. 2018. Architectural differences associated to functional traits among 45 coexisting tree species in central Africa. Functional Ecology, in press. https://doi.org/10.1111/1365-2435.13198

The implication of species differences in height allometry for forest biomass estimation is not addressed by the study. Thus the statements at P11L6 and P12L28-31 is not fully supported by the current study. Rather than comparing the AGB estimates using different height models (power model vs. saturating model), it would be more interesting to compare the gain (both in terms of accuracy and precision of the estimate of forest biomass) of including species traits into the height model. The comparison should be done at plot level and not at tree level because practical needs are for estimates of forest biomass stocks. At plot level, random tree-level errors level off, so that reducing the residual error of the allometric model at the cost of greater uncertainty on the estimates of the parameters of the model is not necessarily the best option. Uncertainty on the species traits (in particular when it comes to forest inventory data where little information is available for most species) should also be considered when assessing the relevance of integrating species traits into allometric models.

The systematic bias of AGB prediction using the power model for tree height (Figures 4 and 5) is a bit surprising. Yellow dots in Figure 5 show the ratio AGBpow/AGBobs in log axes, where AGBpow is the biomass estimated using the power model for tree height. In other words, Fig. 5 shows log(AGBpow) $-$ log(AGBobs). Because log(AGB) = log(0.0559) + log(ρ) + 2log(D) + log(H), all terms except the one depending on height cancel out, so that Fig. 5 is actually showing log(Hpow) $-$ log(Hobs), where Hpow is the height predicted by the power model. In other words, yellow dots in Fig. 5 are showing the residuals of the fitted power model for log-transformed height. If the power model for tree height had been fitted by linear regression on log-transformed data, then, by definition, these residuals would have a zero sum, which does not seem to be the case in Fig. 5 (but the x-axis is truncated to dbh ≥ 30 cm, so maybe we do not have the right picture). The fact that the residuals of the power model for height (Eq. 1) are not centered on zero is a bit concerning and seems to contradict what is written at P6L16. Is it a consequence of the hierarchical approach where species-level models are averaged at community-level? Could you clarify how the community-level model is obtained from the species-level models? (Do all species have the same weight, or do all trees have the same weight? Etc.)

Specific comments

P2L19-20 and P10L28-29: these sentences are a bit misleading. The use of wood density as a way to account for specifies differences in multispecies biomass equation is an old idea (e.g. Brown et al. 1989) that is now commonplace. It is accordingly less common for height- and crown-diameter allometries, but see Loubota Panzou et al. (2018).

Brown, S., Gillespie, A.J.R., and Lugo, A.E. 1989. Biomass estimation methods for tropical forests with applications to forest inventory data. Forest Science 35(4): 881–902. https://doi.org/10.1093/forestscience/35.4.881

P5 Eq.(2)-(4): these expressions do not correspond to the f function in Eq.(1) but rather to its exponential transform, right? In fact, the confusion comes from P4L29: Should not it be “f predicts expected *log* tree height or crown area” rather than “f predicts expected tree height or crown area"? Please clarify.

P5L18: why a univariate linear function? Why not combining several traits?

P5L29: why using the same trait for all models? Why not using different traits for the different parameters of the allometric equations?

P5L29-30: the sentence is confusing. I guess "trait model" is referring to Eq.(5), but why call it a *trait* model? A model is usually called after its response variable, not after its predictors (e.g. AGB $= aD^b$ is called a biomass model, not a diameter model). Moreover, the fact that the "trait" models have twice the number of community-level parameters is not due to the fact that all models have the same predictor. It is due to the fact that each model has a single predictor.

P8L19 sqq., " (...) based on the power model": which power model? No power model to predict tree height has been presented so far (P8L2 only mentioned that power models did much worse than the other models). The power model for height is actually later given (P8L24) but without specifying on which species trait it is based (presumably the growth trait). Please clarify and present the power model before presenting the consequences for AGB estimates.

P8L24-27 and Table 3: comparing AGB estimates without specifying the estimation uncertainties does not make much sense. An AGB difference of 283 vs. 252 Mg ha^{-1} does not have the same meaning if its estimation error is 10 or 1 000 Mg ha^{-1}. Therefore, please complement Table 3 with the estimation uncertainties. Referring to P6L14-15, please also clarifies whether you are considering only the uncertainty on the parameter estimates (confidence interval) or also the residual error (prediction interval), and possibly if you are also propagating other sources of errors (e.g. measurement error, or the error in the estimation of the species traits).

P10L7-8: unclear. What is emerging? Model fitting shows that differences among species are not strong enough for the model with a species effect to be better than the model without a species effect. It does not show the emergence of a pattern at community level from species-level patterns. Moreover the power model for crown allometry in Farrior et al. (2016) is an assumption of the model, not an emerging property.

P10L12, P11L6 and P12L26-27: interspecific variation in crown allometry is not that “high”/“considerable”/“extensive” since the gain in predictive accuracy brought by the species trait does not even compensate for the increase in the effective number of parameters of the model.

P12L18-26: repetition of previous text.

Figure 4: what are the lines representing? I understand that you are using for height the community-level across-species relationship (Eq. 7), so that height is a function of diameter only. However the biomass equation (Eq. 6) still depends on wood density that varies across species. Therefore, one would expect to have different lines for the different species rather than a single line for all species.

Figure 5: what are the lines representing? Smoothing functions? Because Hobs is an individual tree-level data and not a one-to-one function of diameter, neither is the ratio Hmod/Hobs.

Figure 5: why are dbh starting from 30 cm instead of 1 cm?

Interactive comment on Biogeosciences Discuss., https://doi.org/10.5194/bg-2018-314, 2018.