

#2 Response to : Interactive comment on “An analysis of forest biomass sampling strategies across scales” by Hetzer et al.

This manuscript assesses the ability of different sampling strategies to characterize the overall mean biomass of tropical forests. Although there have been previous studies looking at this, the multi-scale approach and the point-pattern simulation to replicate the spatial clustering of previous studies add novelty, and mean that there is enough new for this to be a useful contribution. There are a number of issues that need to be addressed, primarily through improved discussion.

Thank you for your very helpful comments. We will prepare a revision of our manuscript that will follow your recommendations closely. The main changes will be:

a) Restriction of sampling to forest biomes

Following your suggestion we analyzed the sampling strategies for each biome separately (covering moist broadleaf, dry broadleaf, conifer and mangrove forest). Results will be added and discussed in the revised manuscript.

b) Discussion about the impact of more variation in high biomass values

The current analysis leads to more conservative estimations. We agree that the tested maps have limitations concerning the fine scale variation. Assuming an increased variation in biomass values would lead to a moderate increase in the minimum sample size. We will add this aspect in the discussion.

We have added our responses to your comments in blue following each comment.

##Major comments

I agree with the major points raised by Ref1, and won't elaborate on them more here except to say that it would make more sense to me to restrict the allocation of sampling points to a single biome (i.e. moist tropical forests) and areas with forest cover (i.e. above a given threshold in the Baccini map) to more realistically reflect real sampling efforts.

Thank you for this comment. We will extend the study by analyzing the sampling strategies across different biomes. Therefore, the biomass map used for continental analyses (Baccini et al., 2012) is merged now with a global biome map (Dinerstein et al., 2017). To exclude rarely vegetated pixels within biomes, we assume a minimum above ground biomass threshold of 25 t/ha. Current results show that there are differences between biomes regarding the sampling effort (e.g., between moist broadleaf forests and conifer forests, see attached figure 1). We plan to include and discuss these additional results in the revised manuscript.

The analysis of clustered sampling strategies implies a very naïve analysis approach to get an overall mean – just taking an average across plots without considering their configuration. To what extent the performance of clustered plot networks at estimating the overall mean can be improved by analyses accounting of climate and soil covariates and/or spatial autocorrelation to account for this oversampling? I would assume that there would be considerable potential to remove the disruptive effect of non-random sampling, and instead move estimates to a point on the random sampling curve equivalent effective sample size of spatially random plots. Thus existing plot

networks, with appropriate analysis, may provide much better estimates of continental mean biomass than implied by this study.

This is a good point. We designed our analysis primarily to explore the effect of spatially clustered vs. random sampling. We therefore agree that existing plot networks, that stratified plots based on additional constraints, may provide better estimates than suggested by a “blind” clustered sampling.

A possible solution to this issue is to expand the pattern reconstruction approach to include additional criteria (ideally those used for selection of the real clustered plot networks, accounting e.g., for climate and soil covariates). If the covariates representing the additional criteria can be mapped in the entire study area, the pattern reconstruction approach can take the additional constraints into account and reject plot configurations that do not agree with these criteria.

However, we believe that such an analysis would be beyond the scope of our current study, but an interesting task for forthcoming studies. We therefore will briefly discuss in the discussion section that our clustered sampling strategies do not account for additional criteria that will be used for the design of real plot networks, and propose the above solution for a better assessment of the performance of clustered plot networks.

It is worth noting that the remote sensing maps used as reference have serious limitations (some pointed out by Ref1). Most importantly, they miss the effect of species composition on biomass, which is driven by wood density and leads to marked spatial patterns in Amazonia. This isn't so much of a problem for this study if the remote sensing reference maps are interpreted as providing realistic examples of large-scale spatial variation in biomass, rather than as real references. I do wonder if this means the large scale reference maps underestimate the extent of fine scale variation due to compositional differences across soil types (for example).

Thank you for your comment. We agree that continental biomass maps have their limitations especially in terms of fine scale variation. An higher variation of the biomass variation will lead to a higher sampling effort, such that our estimated plot number could be interpreted as a conservative estimation. We plan to add an additional analysis where we assume higher variations in high biomass values (see figure 1 in the response to the first Referee) and will discuss this important issue in the revised manuscript.

Specific comment

The barplots in Figures 3 and 4 could be misinterpreted as giving strong evidence that big plots are best, as they show that the smaller plot size the more plots are needed. It would be good to also display the change in the area of sampling needed (as is done in the text and table), as that is more relevant to sampling effort.

Thank you. We will revise these figures and will show than also total sampling area.

Figures

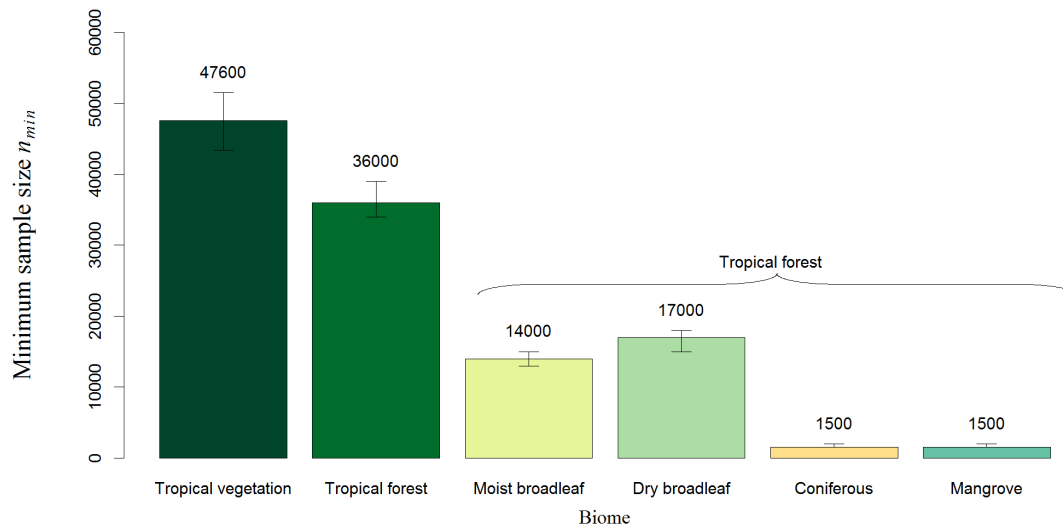


Figure 1: Necessary number of samples to derive accurate mean estimations for different forest biomes of South America by applying the transect sampling (former remote sensing sampling). Samples (25 ha each) were taken with regular distances of 1 km between plots. The first bar shows the results for South America as implemented in the current study (Tropical vegetation). The second bar displays the number of plots when sampling is carried out exclusively in forest biomes. Therefore we merged the biomass map used (Baccini et al., 2012) with a biome map (Dinerstein et al., 2017), restricting sampling to moist broadleaf, dry broadleaf, coniferous and mangrove forest. The last four bars give the minimum sample size if forest biomes are sampled separately. Error bars reflect the range of 10 repetitions.

Literature

Baccini, A., Goetz, S. J., Walker, W. S., Laporte, N. T., Sun, M., Sulla-Menashe, D., Hackler, J., Beck, P. S. A., Dubayah, R., Friedl, M. A., Samanta, S. and Houghton, R. A.: Estimated carbon dioxide emissions from tropical deforestation improved by carbon-density maps, *Nat. Clim. Chang.*, 2(3), 182–185 [online] Available from: <http://dx.doi.org/10.1038/nclimate1354>, 2012.

Dinerstein, E., Olson, D., Joshi, A., Vynne, C., Burgess, N. D., Wikramanayake, E., Hahn, N., Palminteri, S., Hedao, P., Noss, R., Hansen, M., Locke, H., Ellis, E. C., Jones, B., Barber, C. V., Hayes, R., Kormos, C., Martin, V., Crist, E., Sechrest, W. E. S., Price, L., Baillie, J. E. M., Weeden, D. O. N., Suckling, K., Davis, C., Sizer, N., Moore, R., Thau, D., Birch, T., Potapov, P., Turubanova, S., Tyukavina, A., Souza, N. D. E., Pintea, L., Brito, J. C., Llewellyn, O. A., Miller, A. G., Patzelt, A., Ghazanfar, S. A., Timberlake, J., Klöser, H., Shennan-farpón, Y. and Kindt, R.: An Ecoregion-Based Approach to Protecting Half the Terrestrial Realm, *Bioscience*, 67(6), doi:10.1093/biosci/bix014, 2017.