

Interactive comment on “Harmonizing plant functional type distributions for evaluating Earth System Models” by Anne Dallmeyer et al.

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R: The introduction explains clearly why a model-generic PFT-based biomisation is needed, as opposed to other model-specific methods that have been used in the past. However, it is not obvious to me from the text why this new method that the authors are proposing is needed beyond the “classical approach” they compare to, and therefore how much this study is a novel contribution to the literature. All methods rely on subjective decisions as to how to classify vegetation into biomes, therefore adding another may only contribute to uncertainty in this area. This is particularly the case given that both the PFT-based and classical methods compare reasonably well; therefore, I am left wondering why the classical approach cannot be used and why a new method is needed? As the authors state in lines 338-340 “In general, the skill in represent-

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ing the individual mega-biomes is similar for the PFT- and the climate-based method. Both approaches have the same strengths and weaknesses, but the spread between the models is larger for the PFT-based biomisations.” And in lines 346-347 “Overall, the metrics indicate that the PFT-based method works similarly well as the classical approach of biomising climate states.” What then is the specific value of this new PFT-based biomisation method? I perhaps have misunderstood (but therefore likely some other readers will too) – so more clarity is needed on this in the introduction.

Our response: We have to admit that the main aim of the new method obviously got lost in the introduction. The main point is that General Circulation Models (or Earth System Models) usually calculate not only the climate but also (if a DGVM is coupled in the General Circulation Model) a vegetation pattern that is in quasi-equilibrium with this climate. This vegetation is represented in form of plant functional type cover fractions, but these PFTs are not used in the ‘classical’ biomisation. The classical biome models (such as BIOME1) only use the simulated climate as forcing and calculates PFT distributions and then biome distributions on its own. Most DGVMs are more complex and include more relevant processes, therefore a more appropriate way would be to use these DGVM-simulated PFTs and not the climate pattern for the biomisation. And this is exactly what our method aims for. We introduce a method that can directly biomise the DGVM-simulated PFT distributions and this method performs similar well as the classical method (which is not necessarily the case as biome models are highly tuned) We further stress the problem of the classical method: “Using this conventional method of biomisation, fundamental palaeo-vegetation analysis can be undertaken (e.g. Jolly et. al. 1998; Harrison et al., 2003; Wohlfahrt et al., 2008; Harrison et al., 2016, Dallmeyer et al., 2017) without requiring an explicit calculated vegetation distribution by the Earth System Models. On the other hand this also means that existing simulated plant functional type distributions calculated by the DGVMs being dynamically coupled in these models are neglected, since only the simulated climate pattern is taken into account. The biomisation via diagnostic biome models did not include any information on the original PFT-distribution simulated by the Earth System

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Models. As the DGVMs are generally more complex than the biome models and include more relevant processes, valuable information included in the PFT-distribution gets lost in the classical biomisation by the biome models. A more appropriate way of biomisation would be to use directly the PFT-distributions calculated by the DGVMs.” and: “Therefore these methods can not directly be adopted for all existing dynamic vegetation models. A consistent inter-model comparison of the simulated vegetation distribution and an evaluation of the models against reconstructions on biome level is so far not possible. “ and: “...we developed a biomisation technique that is based on the PFT-distributions simulated by the DGVMs and few input variables and simple differentiation rules. ...”

R: Biomisation itself should be defined in the introduction, and the classical approach needs to be defined there, and not at the end of Section 2.1, and a detailed explanation should be provided as to why we cannot use this method and instead need the new PFT-based method.

Our response: We agree that the introduction needs further clarifications. We have changed the paragraph to: “Pollen records are originally displayed in form of pollen percentages or pollen accumulation rates that can not be directly compared to plant functional type distributions, as pollen records do not reflect the actual plant abundances. For a systematic comparison of simulated plant functional type distributions and reconstructions, both need to be converted in a compatible format. In the last two decades, taxa to PFT assignment-methods and the method of ‘biomisation’ for pollen-based reconstructions have been developed (e.g. Prentice et al. 1996, Ni et al., 2010, Harrison et al. 2010), so that pollen assemblages can be grouped into biomes (e.g. tropical forest, temperate steppe, desert). Pollen-based biome syntheses have been provided (Prentice et al., 1998 and 2000, Bigelow et al., 2003; Ni et al. 2010, Harrison et al., 2017, Tian et al. 2017) that have extensively been used to evaluate simulated biome distributions obtained from diagnostic biome models such as BIOME1 or BIOME4 (e.g. Prentice et al., 1992, Haxeltine and Prentice, 1996, Kaplan et al., 2003). These biome

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models can be forced by observed or simulated climate fields and calculate biome distributions in equilibrium to this input climate. Using this classical method of biomisation, fundamental palaeo-vegetation analysis can be undertaken (e.g. Jolly et.al 1998; Harrison et al., 2003; Wohlfahrt et al., 2008; Harrison et al., 2016, Dallmeyer et al., 2017) without requiring an explicit calculated vegetation distribution in the General Circulation or Earth System Models. On the other hand this also means that existing simulated plant functional type distributions calculated by the DGVMs being dynamically coupled in these General Circulation or Earth System Models are neglected, since only the simulated climate pattern is taken into account. The biomisation via diagnostic biome models did not include any information on the original PFT-distribution simulated by the models. As the DGVMs are generally more complex than the biome models and include more relevant processes, valuable information included in the PFT-distribution gets lost in the classical biomisation by the biome models. A more appropriate way of biomisation would be to use directly the PFT-distributions calculated by the DGVMs.”

R: It is clear the authors have thought in depth about performing a rigorous analysis and the caveats of their analysis are well detailed in the discussion. The analysis of the differences between models and comparison of different mega-biomes (as shown in Fig. 6 for example) is interesting and useful for the modeling community, particularly given the authors are testing whether the number of PFTs, model complexity, grid cell resolution, or simulation land use contribute to these differences. However, this is not a stated objective or important outcome of the paper. I understand the authors do not want to focus on a model comparison because the same climate data were not used to drive the models, and therefore the authors have chosen to focus on the introduction of the new PFT-based biomisation method. However, I am not sure this is a strong enough focus to sell the paper given the PFT-based and classical biomization methods produce similar results, as I discussed above.

Our response: In our revision we will more clearly outline how the new method differs from the classical biomisation method (i.e. the Biome Models) and why this new

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method is useful (see last comments). That the methods produce similar results has to be seen as one of the strength of the new method, it can keep up with the tuned biome models.

R: Furthermore, much of the text reads as a model comparison, thus causing confusion as to the objectives of the paper. And the authors claim this is a new powerful method that is needed in order to more readily compare models (as well as models with reconstructions), but then say this study cannot be a model comparison because they were not forced with the same climate states. It seems perhaps redundant to introduce a new method for a particular purpose and then not use it for that purpose. Clearly there is a lot of useful analysis and discussion in this paper, but I think it would be more useful if it were to be re-framed and re-structured with different objectives.

Our response: We agree that this is confusing. Unfortunately, no simulation setup exists in which all different DGVMs were forced with the same climate state. We had to confine our study to the available simulations. The lack of the same background climate lead to differences between the biome distributions that are neither related to the method nor to the dynamic global vegetation model. Therefore, this study can only be an introduction and evaluation of the biomisation method based on different models, but we can not judge which dynamic vegetation model is the best. We carefully go through the text again to avoid phrases that read as a model comparison, e.g. we now rather use terms such as 'the biomisation of model X' to underline that we only compare different biomisations and not the models.

R: Finally, the manuscript is somewhat dense in places, with many figures to digest, likely owing to the difficulty of describing complex and detailed analyses. The reader would likely benefit if the authors could spend some time editing the text to make it more concise.

Our response: We shorten the text by moving parts of the informations on the simulations and the preparation of the reference datasets to the Appendix (including Tab.5).

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We also move the comparison with the FPC-method to the Appendix. We furthermore deleted few sentences that were not so relevant. We deleted Tab.6 and Tab.2.

Specific comments

R: Lines 45-50: It might be useful if the authors detail the differences between diagnostic biome models forced with GCM-derived climate data vs DGVMs coupled to GCMs? Similarly, it might be useful to detail the difference between PFT and biome classifications. Examples could help with this. And finally, it might be useful in line 50 to clarify again that simulations from the DGVMs have been disregarded because PFT classifications are different to biome classifications.

Our response: We changed the text to: "In the last two decades, taxa to PFT assignment-methods and the method of 'biomisation' for pollen-based reconstructions have been developed (e.g. Prentice al. 1996, Ni et al., 2010, Harrison et al. 2010), so that pollen assemblages can be grouped into biomes (e.g. tropical forest, temperate steppe, desert). Pollen-based biome syntheses have been provided (Prentice et al., 1998 and 2000, Bigelow et al., 2003; Ni et al. 2010, Harrison et al., 2017, Tian et al. 2017) that have extensively been used to evaluate simulated biome distributions obtained from diagnostic biome models such as BIOME1 or BIOME4 (e.g. Prentice et al., 1992, Haxeltine and Prentice, 1996, Kaplan et al., 2003). These biome models can be forced by observed or simulated climate fields and calculate biome distributions in equilibrium to this input climate. Using this classical method of biomisation, fundamental palaeo-vegetation analysis can be undertaken (e.g. Jolly et. al., 1998; Harrison et al., 2003; Wohlfahrt et al., 2008; Harrison et al., 2016, Dallmeyer et al., 2017) without requiring an explicit calculated vegetation distribution in the General Circulation or Earth System Models. On the other hand this also means that existing simulated plant functional type distributions calculated by the DGVMs being dynamically coupled in these General Circulation or Earth System Models are neglected, since only the simulated climate pattern is taken into account. The biomisation via diagnostic biome models did not include any information on the original PFT-distribution simulated by the models.

As the DGVMs are generally more complex than the biome models and include more relevant processes, valuable information included in the PFT-distribution gets lost in the classical biomisation by the biome models. . .”

Methods R: Section 2.1 Tables 2 and 3 and for all bioclimatic thresholds (lines 99-111): Is there a reference for the bioclimatic limits used here? Why have these bioclimatic limits been used? Is there evidence to suggest these are better descriptors of bioclimatic limits than used in other studies?

Our response: We added the references to the figure captions. Most bioclimatic limits were taken from the BIOME4 model.

R: Lines 115-119: Please could the authors give more detail here? Perhaps they could provide more detail as to what they mean by “biomise the underlying climate”. An illustrative example would be helpful.

Our response: We now write: "To assess the performance of the biomisation based on simulated PFTs, we additionally biomise the simulated climate fields corresponding to the PFT-distributions for each model. This is the conventionally used procedure to biomise GCM or ESM output (further referred to as classical approach or method). For this purpose, we use the biome model BIOME1 (Prentice et al., 1992) that calculates the biome distribution in equilibrium to the input climate. As forcing, BIOME1 needs the monthly mean climatological precipitation, near-surface temperature and cloudiness, which were taken from each simulation considered in this study, respectively“

R: Section 2.2 It would be interesting to denote which simulations in Table 4 are run with dynamic vs static vegetation.

Our response: We mark the simulation with static vegetation.

R: Lines 154-156: Please could the authors briefly explain what is the difference between a gap model and a tiling approach. This will aid a reader who is less familiar with these models. Further, please could they describe how the PFT distribution has been

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determined via the NPP of the vegetation categories for SEIB and why the vegetation categories do not already correspond to the PFT distribution?

Our response: We further explain the model SEIB. The calculation of the PFT fraction from the original (species-based) output was performed by the Japan Agency for Marine-Earth Science and Technology, Atmosphere and Ocean Research Institute (The University of Tokyo), and National Institute for Environmental Studies within the framework of CMIP5, the technique goes beyond the scope of this paper. We now write: "SEIB deviates from the other DGVMs in this study as it does not use the tiling approach of calculating PFT fractional coverage for each grid-cell. It is a so called forest gap-model, simulating the interactions among individual trees that compete for light and space in arising gaps (e.g. due to disturbances) within a spatially explicit virtual forest. The model was built for capturing the vegetation dynamics on local scale. The application of the model for larger (e.g. global) scales is possible, but global simulations partly disagreed with observations (Sato et al., 2007). The PFT distribution used in this study has been calculated in the post-processing for CMIP5 via the relative net primary productivity of the vegetation categories, it was not explicitly calculated by the model, which may lead to additional biases in the vegetation distribution."

R: Section 2.3 Line 175: Please could the authors briefly explain how Haxeltine and Prentice (1996) derived their vegetation compilation and what it includes?

Our response: This is not the scope of the paper, for details we refer to the publication of Haxeltine and Prentice (1996), Section 3.2.

R: Line 180: I do not understand this "on a basis of 5°C being higher than 900°C derived from modern observations". Please could the authors explain what they mean here? Does this correspond with Table 3? If so, it might be useful to say that. Our response: We further describe this: "RF99 additionally includes the biome 'Evergreen/Deciduous Mixed Forest/Woodland'. Here, this biome is assigned to the mega-biomes 'temperate forest' in warm regions and 'boreal forest' in colder regions

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via the modern growing degree days distribution ($GDD5 \geq 900^{\circ}\text{C}$ for warm region, $GDD5 < 900^{\circ}\text{C}$ for cold region, cf. Tab.2), derived from observations (University of East Anglia Climatic Research Unit Time Series 3.1, University of East Anglia, 2008, Harris et al., 2012).“

R: Line 203: “biomisation of simulated climate states (i.e. the classical method)”. This is the first time the classical method has been referenced. It might be useful to the reader to describe it earlier and to detail how the authors’ method differs from this classical method – particularly as it is used to compare the new method with throughout the results section. Otherwise, it appears somewhat out of the blue here.

Our response: We now mention the classical method already in the introduction (see comment above) and enlarge the part explaining the classical method in the Method part: “To assess the performance of the biomisation based on simulated PFTs, we additionally biomise the simulated climate fields corresponding to the PFT-distributions in each model. This is the conventionally used procedure to biomise GCM or ESM output (further referred to as classical approach or method). For this purpose, we use the biome model BIOME1 (Prentice et al., 1992) that calculates the biome distribution in equilibrium to the input climate. As forcing, BIOME1 needs the monthly mean climatological precipitation, near-surface temperature and cloudiness, which were taken from each simulation considered in this study, respectively. This classical biomisation approach can only handle climate data as input, the simulated PFT-distributions from the ESMs used in the here introduced PFT-based method are ignored. The original biomes has been grouped into the same mega-biome classification that is used for the PFT-based approach.“

Results R: Section 3.1 It might be more constructive to compare the PFT- and classical climate- based biomisation methods for each model side by side in one figure, and not the former in Figure 3 and latter in Figure 4, given the authors compare the two. It is hard to compare each model given they are on separate pages.

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Our response: We see this point. Our intention to plot all results based on the classical method on one page and the results based on the PFT-method on the other page was that we wanted to compare the methods and not the models. We did not change the order in the figures.

R: Line 287: It would be instructive to reference that “better represented” means in comparison to observations that are provided in Figure 2.

Our response: We now write: "As a consequence, the North American prairie fits better to observations for the PFT-based biome distributions."

Discussion R: Section 4.1 is well described and an honest and comprehensive view of the caveats of the methods.

Our response: Thank you.

Technical corrections R: Ni et al. (2010) missing most of the reference, Dallmeyer et al (2017) reference missing → check all references in the bibliography

Our response: We apologize that we had not update the reference list. We have now carefully checked all references in the text and add the missing references.

R: Line 97: additionally → additional Our response: done.

R: Line 147: has → have Our response: done.

R: Line 148: what is the importance of knowing that the simulations have been re-done on a new computer? Will they be better as a result?

Our response: We further explain it: The simulations used here has been conducted in a similar model-setup as described in Kleinen et. al. (2010), but has been re-done on a new computer (T. Kleinen, personal communication), which may lead to very small deviations from the original runs.

R: Line 159: extra → specifically Our response: done. R: Line 168: “than the other

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simulations ...” It would be helpful to add “that were run with dynamic/interactive vegetation”. Our response: done. R: Line 187: details → detail Our response: done. R: Line 399: works →work Our response: done. R: Line 420: “very rudimentary” → “in a very rudimentary manner” Our response: done. R: Line 521: coverage→cover Our response: Do you mean L531? There we changed coverage to cover

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