Geoscientific
Model Development
Discussions

Open Access

Interactive
Comment

Interactive comment on "Upscaling with the dynamic two-layer classification concept (D2C): TreeMig-2L, an efficient implementation of the forest-landscape model TreeMig" *by* J. E. M. S. Nabel

Dr. Nabel

jemsnabel@gmail.com

Received and published: 7 September 2015

Thank you for your review and comments that help to clarify the manuscript. Below I duplicate your comments and respond to them point by point followed by the modifications that will be adopted in the revised manuscript.

Full Screen / Esc

Printer-friendly Version

Interactive Discussion

Discussion Paper

(1) P5537 L23
I cannot understand what "thematical" means here

Response:
Thematical means the represented content, i.e. how the objects of the real world are represented in the model, i.e. the modelled entities. For clarification, thematical has been replaced in the sentences. The sentences now state:

Aggregations can thereby be temporal, spatial or with regards to the representation of the modelled entities, i.e. the simulated processes and state variables. When the fine spatio-temporal resolution should be maintained (as recommended by Bocedi et al. 2012), remaining possibilities for cost reductions thus can only change the representation of the modelled entities.

(2) P5537 Para2 Following work should be adequately addressed here, as it is a pioneer work that adapted an approximation method on a forest dynamic model. Moorcroft, P. R., et al. (2001). A method for scaling vegetation dynamics: The ecosystem demography model (ED). Ecological Monographs 71(4): 557-586.

Response:
The work has been cited. The second part of the paragraph now reads:

One example finding broad application in DVMs is the aggregation of individuals with similar properties into cohorts (e.g. Scheller and Mladenoff, 2004; Smith et al. 2014). With cohorts solely one representative calculation, instead of multiple replicate calculations, needs to be conducted. Another more comprehensive example is the approximation of entire grid cell populations. Height-structured distributions (Lischke et al. 1998), as well as size- and age-structured approximations (Moorcroft et al., 2001), can be applied to upscale individual-based, stochastic models. By aggregating individuals of forest patches influenced by small scale stochastic processes, such approximations allow to dramatically reduce the number of calculations required to determine the veg-

etation dynamics in a grid cell. Both examples, cohorts and structured approximations, utilise similarities for within grid cell aggregations. The upscaling method presented in this paper – the dynamic two-layer classification concept (D2C) – is based on a more extensive similarity approach aiming to combine different grid cells with similar properties.

(3) P5542 L7-11 and L25-28 I cannot understand these sentences, where author try to explain how D2C organizes grid cells of the TreeMig-2L.

Response:
Following the suggestion of the second referee, the sentence L25-28 has been removed. Furthermore, because the second referee also had questions to this section, I did not only adapt the text, but also adapted the previous supplementary Figure A.2 and moved it to the main text (see Fig. 3). This Figure gives an example for the prestructuring. It shows the discretisation of the minimum winter temperature with the set E3 of bioclimate bins for one cell and how the bioclimate driver is then calculated from all associated cells. The new Figure includes the information of the previous Fig. 4, which I therefore removed. The sentence L7-11 and subsequent sentences were rephrased for clarification and now state:

One of the challenges for an efficient organisation of the elements on the non-spatial layer was that the number of elements is not known in advance, because it is an emergent property of the simulation. To allow for an arbitrary number of elements on the non-spatial layer, the elements are stored in linked lists, instead of using an array structure with a predetermined fixed size, as usually done in space discrete DVMs. However, using one large linked list, and comparing all elements with each other, would be very inefficient and would lead to a large organisational overhead. To reduce the organisational overhead required for the comparison of elements during runtime, TreeMig-2L uses several linked lists, and only elements in the same list are compared. To define the number of linked lists, the fact is used that the bioclimate drivers are an

Interactive
Comment

Full Screen / Esc

Printer-friendly Version

Interactive Discussion

Discussion Paper

input to TreeMig and can thus be used to pre-structure a simulation area (see Fig. 3 for an example, and Supplement Sect. A.2 for additional information). To pre-structure a simulation area, grid cells are classified into "bioclimate types". Each bioclimate driver is thereby discretised according to a set of pre-defined "bioclimate bins" (see e.g. Table 2). To limit the number of possible bioclimate types and to save computation time, the discretisation is only applied for temporal averages of the bioclimate drivers on a pre-defined set of "supporting periods". For each cell, one average per driver and supporting period is calculated. Two cells are classified into the same bioclimate type, if their averages fall into the same bioclimate bin for each driver and supporting period, whereby the bioclimate bins can differ in between supporting periods. For each existing bioclimate type, i.e. each type with which at least one cell is associated, an own linked list is used. The bioclimate drivers for a bioclimate type are calculated as the averages of all associated cells.

Caption of the new figure:
Visualisation of the pre-structuring into bioclimate types on the example of the minimum winter temperature (Min. winter temperature), one of TreeMig's three bioclimate drivers. **(a)** The minimum winter temperature driving $cell_k$ is averaged for each of the supporting periods (here P1: 1901–1930, P2: 1901–2100, P3: 2071–2100). **(b)** The range of the minimum winter temperature ($-14\,°C$ to $+10\,°C$) is discretised into 13 bins with a resolution of $2\,°C$ (as e.g. done for E3, the set of bioclimate bins with the coarsest resolution – Table 2). The averages of the supporting periods P1–P3 for $cell_k$ are classified according to these bins. **(c)** Cells whose averages fall into the same bin in each of the supporting periods for each of the bioclimate drivers are classified into the same bioclimate type. The bioclimate driver (here the minimum winter temperature) of the bioclimate type is calculated as the average (black line) of its 287 associated cells (grey lines).

(4) P5547 Para2 The model versions 2 and 3 would be explained more. It is very difficult to understand what they are at first reading.

Response:
The paragraph has been adapted and now states:

To disentangle the effects of the pre-structuring into bioclimate types and of dynamic associations between the layers, simulations of four model versions with increasing complexity were compared (Table 3). (1) 1L-ORG: the original one-layer approach with the original bioclimate driver. Simulations with this version were conducted to obtain reference values for the comparisons. (2) 1L-PB: a model version in which bioclimate types were used to derive averaged bioclimate drivers, but in which all processes were still simulated on one layer. Simulations with this version thus isolate the loss in accuracy due to the averaging of the bioclimate drivers. (3) 2L-NDA: a model version using bioclimate types and two layers but no dynamic associations, i.e. in this version each bioclimate type has only one element. Because dynamic associations are switched of, differences in the number of germinated seeds between cells associated with the element do not lead to splits, and a species introduced in one of the cells will thus occur in all associated cells. Therefore, simulations with this version can elucidate if there is a necessity to track species. Furthermore, having no costs for splitting and merging, this version can be used to derive the maximum CPU time reduction that can be achieved. (4) 2L: the full TreeMig-2L model with two layers and with dynamic associations.

(5) P5548, L15-17 The term "peak element-cell ratio" is not defined anywhere in the manuscript. Also, please proved brief explanation for the "callgrind".

Response:
The paragraph was extended to incorporate the suggested changes:

Two further measurement were taken to assess the applicability of D2C in view of the three aspects listed at the end of Sect. 2. Firstly, the maximum number of elements

reached during a simulation was tracked, here referred to as the peak element-cell ratio. Secondly, the ratio of the time spent on different processes was profiled with callgrind, a tool which records function calls in a program during runtime (Weidendorfer, 2008).

(6) P5564, caption of the table 3 Need more words. According to GMD's "manuscript preparation guidelines for authors", tables should be self-explanatory and include a concise, yet sufficiently descriptive caption.

Response:
The caption of the table has been improved. Furthermore, the model versions in the table have been re-ordered to better reflect the changes in reaction to comment (4). See Table 3.

References

Moorcroft, P. R., Hurtt, G. C., and Pacala, S. W.: A Method for Scaling Vegetation Dynamics: The Ecosystem Demography Model (ED), Ecol. Monogr. 71, 557–586, 2001.

Interactive comment on Geosci. Model Dev. Discuss., 8, 5535, 2015.
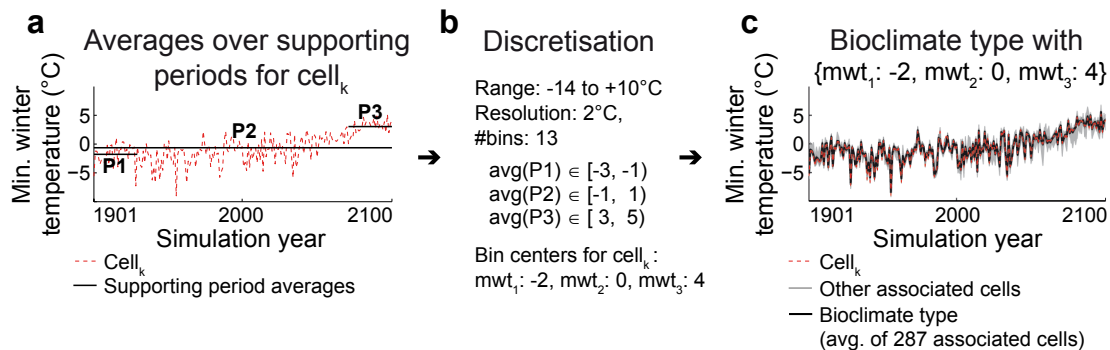
Table 3. Simulations of four model versions with increasing complexity were compared. The model versions differ in whether they (1) use the pre-structuring to bioclimate types, (2) do simulations on two layers and (3) apply dynamic associations between the two layers, i.e. allow for splitting an merging of elements on the non-spatial layer. 1L-ORG refers to the original one-layer approach with the original bioclimate driver. 1L-PB introduces the averaging of the bioclimate drivers according to the bioclimate types, but still runs on one layer. 2L-NDA applies the averaging and runs on two layers, albeit without dynamic associations. 2L, finally, refers to the full TreeMig-2L model with two layers and with dynamic associations.

	Bioclimate types	Two layers	Dynamic associations
1L-ORG	no	no	–
1L-PB	yes	no	–
2L-NDA	yes	yes	no
2L	yes	yes	yes

a Averages over supporting periods for cell$_k$

Min. winter temperature (°C)

P1, P2, P3

1901 2000 2100
Simulation year

--- Cell$_k$
— Supporting period averages

b Discretisation

Range: -14 to +10°C
Resolution: 2°C,
#bins: 13

avg(P1) ∈ [-3, -1)
avg(P2) ∈ [-1, 1)
avg(P3) ∈ [3, 5)

Bin centers for cell$_k$:
mwt$_1$: -2, mwt$_2$: 0, mwt$_3$: 4

c Bioclimate type with {mwt$_1$: -2, mwt$_2$: 0, mwt$_3$: 4}

Min. winter temperature (°C)

1901 2000 2100
Simulation year

--- Cell$_k$
— Other associated cells
— Bioclimate type
   (avg. of 287 associated cells)

Fig. 3. See response to comment (3) P5542 L7-11 and L25-28 for the figure caption