

Appendix

Tree regeneration in models of forest dynamics: a key priority for further research ECOSPHERE

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1 Model reports

1.1 4C

1.1.1 Authors

Nieberg M., Gutsch M., Reyer C.P.O., Lasch-Born P.

1.1.2 Model

The most complete reference resource for the 4C (v2.2) model and regeneration module is:

- Lasch-Bonn et al. 2020. Description and evaluation of the process-based forest model 4C v2.2 at four European forest sites. DOI: <https://doi.org/10.5194/gmd-13-5311-2020>)

1.1.3 Climate

We used the provided daily ERA5-CHELSA climate data set and complemented the CHELSA time series data regarding relative humidity with the model after [Eccel et al. \(2012\)](#) based on minimum and mean daily temperature to accomodate data needs of 4C. The missing data for January 2nd and 3rd 2013 were filled with data from January 1st and 4th 2013 respectively. For construction

of longer climate time series we looped through the provided time series from 1981 to 2018 up to the maximum simulation length of 2500 years. We amended situations where leap year inconsistencies arised by removing February 29 or duplicating data from February 28. Otherwise, the unaltered daily data were used to run 4C on a daily basis. We applied a constant atmopsheric CO₂ concentration of 380 ppm.

1.1.4 Soil

We used parametrized soils readily available for 4C from the EU soil data base. The link from parametrized soil to soil quality was done by extracting the plant available water storage capacity as the model bucket size of the rooted soil horizons. We excluded bucket size values of lower than 10 cm and larger than 35 cm. The bucket size was reprojected to the range from 0 to 1. In addition we tested the sensitivity of dominant tree height at age 100 years for monospecific stands of all five species simulated to the available soils using model simulations with 4C. The dominant tree height at age 100 years was then also reprojected to the range from 0 to 1 in order to derive a model specific soil quality indicator for all paramterized soils. Then we multiplied this relative model specific soil quality with the relative soil quality derived from the bucket size to the range from 1 to 5. The match between paramterized soil and plot was then done by finding the pair of soil quality with the minimum difference between simuation protocol prescribed soil quality and the soil quality of the paramterized soils as described above.

1.1.5 Topography

Topographical information was not considered in the simulations.

1.1.6 Tree species

We initialized stands with five out of the eleven proposed species/genera: *Fagus sylvatica* (fasy), *Picea abies* (piab), *Betula* spp. (betu; 4C parameters for *Betula pendula*), *Quercus* spp. (quer; 4C parameters for *Quercus robur*) and *Pinus sylvestris* (pisy) since only these are fully parameterized for an application as proposed in the simulation protocol. Each plot was initialized with all five tree species with similar distributions of height classes and number of individuals: 2000 individuals/ha with height around 0.25 m, 1000 individuals/ha with height around 0.75 m and 500 individuals/ha with height around 1.75 m. In total 17500 individuals/ha. *Carpinus betulus*, *Tilia cordata*, *Acer pseudoplatanus*, *Fraxinus excelsior*, *Alnus glutinosa* and *Abies alba* are not fully parameterized in 4C.

1.1.7 Simulations

1.1.7.1 Dispersal and seed input There is no explicitly modelled seed dispersal in a stand and between stands. We applied a constant sapling establishment rate every five years of 2000 individuals/ha for all five species; 10000 individuals/ha in total every five years. The constant sapling establishment provides constant regeneration potential if favorable conditions for sapling growth (especially light and water regime) are present. This approach enables regeneration of other species than only those present in the stand to establish if competition allows. The resulting recruitment patterns are an outcome of the dynamical processes from the sapling stage onward. Seed production and germination were not explicitly simulated.

1.1.7.2 Simulation length and equilibrium criteria To reach equilibrium and obtain dynamics in the equilibrium period, we simulated a maximum of 2500 years. 4C is usually applied for much shorter simulation periods and different technical as well as model-theory related issues arise when simulating longer than 100-150 years. Therefore 2500 years can be seen as the upper limit of continuous simulation in the defined simulation setup. The first 500 years were not sampled for recruitment as we assume the model needs this time to reach equilibrium. In this long simulation period 4C partially projects unrealistically large tree heights resulting in premature termination of the simulation (36 plots) so that not all plots were simulated for the full 2500 years. We started sampling the recruits after the first 500 simulation years from non-overlapping 10 year periods to obtain 200 samples. For shorter simulation periods we produced 200 samples from overlapping 10 year periods. In addition, we excluded those plots in which 4C simulated unrealistically high basal area values of over 150 m² (19 plots). We used this large threshold to give the model maximum flexibility to explore the solution space in these long simulation runs although we acknowledge that this is an unrealistic overestimation that is probably originating from misrepresented density dependent mortality processes in long simulation runs and misrepresented single tree dimensions due to wrong assumptions of tree geometry and biomass share of such old-aged individuals. Furthermore those plots with less than 1000 simulation years (16 plots) before termination were excluded because the sample space after the first 500 years was too small. Additionally we included another subset criterion removing all samples that have a $ba > 90$ to exclude unrealistically high samples without the need to exclude the full site. This resulted in discarding 0.8 % of the samples.

1.1.8 Outputs

We provide 200 samples each for 48 plots and at least 190 samples each for 117 plots while not simulating 35 plots (see reason for excluded plots in “Simulation length and equilibrium criteria”). These stem from 10 year periods that overlap partially (for < 2500 simulation years) or do not overlap (for 2500 simulation years). The number of recruits (`r.trees`) is the sum of individuals that cross the threshold diameter (7/10 cm) in the 10 year sample period per hectare that have not already died until the sample year. The recruit’s basal area (`r.ba`) is the sum of the basal area per hectare of the trees that cross the diameter threshold that have not already died until the sample year. The total stand basal area (`ba`) is the basal area per hectare of all trees in the stand > 0 cm diameter at breast height (no lower boundary) at the sample time per species. We provide the data for both diameter thresholds, 7 and 10 cm. In over 90 % of the decades no recruitment takes place.

[4C \(v2.2\)](#) is usually not used for simulations of forest equilibrium dynamics, potential natural vegetation assessment and long simulation periods but rather shorter-term simulations (up to 100-150 years). In addition, only five species out of the pool of eleven potentially relevant species here are parameterized in 4C so that projections of the potential natural vegetation done with 4C need to be considered in the light of model uncertainty. For example, the spatial homogeneity in the model leads to cyclic recruitment patterns. When the adult stands dies off, young individuals are recruited into the larger diameter classes because more light reaches lower canopy layer since larger (adult) trees do not anymore prevent the light reaching lower canopy layers. This results in increased growth of the regeneration layer during those times. In most stands *Fagus sylvatica* dominates the stand after some time but occasionally individuals of other species, like *Picea abies* or *Quercus* spp. cross the recruitment diameter threshold.

1.2 ForCEEPS & ForCEEPS(f)

1.2.1 Author

Xavier Morin & François de Coligny

1.2.2 Model

The most complete reference resource for the ForCEEPS & ForCEEPS(f) model and regeneration module are:

- Morin X., de Coligny F., Bugmann H., Limousin J.-M., Ourcival J.-M., Martin-StPaul N., Simioni G., Cailleret M., Prevosto B., Toïgo M., Vennetier M., Cateau E., Guillemot J. 2021. Beyond forest succession: a gap model to study ecosystem functioning and tree community composition under climate change. *Functional Ecology*. 35, 955-975.
- Jourdan M., Dreyfus, P., Riond C., Cordonnier T., Cornet B., de Coligny F., Morin X. 2021. Managing mixed stands can mitigate severe climate change impacts on French alpine forests. *Regional Environmental Change*. 21, 78.
- Morin X., Damestoy T., Toïgo M., Jactel H., Castagnéryrol B. Meredieu C. 2020. Using forest gap models and experimental data to explore long-term effects of tree diversity on the productivity of mixed planted forests. *Annals of Forest Science*. 77 <https://doi.org/10.1007/s13595-020-00954-0>.

1.2.3 Climate

ForCEEPS requires monthly data. A 4000-yr long time-series was obtained for each site by randomizing available years from the CHELSA database, with mean monthly temperature and monthly sum of precipitations (see 1.2.2).

1.2.4 Soil

Soil quality is represented by a continuous value between 1 and 5, as provided (see 1.2.3) Soil Field Capacity (SFC) was assessed as follows: $SFC = 8 + (X-1)*(25-8)/(5-1)$, in which X is the ‘soil_qual’ value in the provided ‘soil_quality_200.csv’ file.

1.2.5 Topography

Not considered.

1.2.6 Simulations

In each site, the simulation consists of 4000 yr-long simulation of 1ha of forest (ie. 10 patches of 1000 m²), starting from bare-ground. There was no dispersal between patches. Two kinds of simulations have been carried out in each of the 200 sites. In a first set of simulations, regeneration dynamics was simulated with a seed rain from a potential species list, thus independent from the actual forest composition, as classically done in gap models. Under this design, a number of seedling is randomly chosen for each patch, and a species identity is randomly sorted from a potential species list (defined at the start of simulation) assigned to each seedling. Then each seedling

tries to colonize the site depending on whether the suitability between species requirements and site conditions (climate, light, soil quality, browsing index). In a second set of simulations, regeneration dynamics was simulated with a seed rain whose composition depended on the actual forest composition. Under this design, a number of seedling is randomly chosen for each patch, but the species identity is assigned according to species relative abundance (calculated across all 10 patches according to species biomass). For instance, if at year i the adult trees of species j represent 60% of the total biomass across the 10 patches, then 60% of the seedlings that try to colonize the patches at year i will belong to species j. Then, similarly to the first design, each seedling tries to colonize the site depending on whether the suitability between species requirements and site conditions. In the two sets of simulations, simulations have been run for both thresholds for regeneration (7 and 10 cm).

1.2.7 Outputs

Outputs consisted in species specific regeneration rates per decade and per ha, by considering the last 2000 years of simulations to ensure that pseudo-equilibrium state is reached. Results were aggregated for every 10 years for the last 2000 years at the 1ha-level. Variables: - Site: numbers corresponding to the climate data file - Sample: one per decade, for a total of 2000 years = identified from 1 to 200 - Species: name specified as requested (eg. ‘fasy’) - r.trees: number of trees outcrossing the threshold (7 or 10 cm) during the decade, for the 10 patches simulated (= 1ha), per species - r.ba: summed basal area of the r.trees, per species - ba: summed basal area of all trees per species at the end of the decade - dbh: threshold used

1.3 FORMIND

1.3.1 Authors

Samuel M. Fischer, Friedrich Bohn, Rico Fischer

1.3.2 Model

A full description of the model can be found in Fischer et al (2016) . The basis for the parameterization we applied is described in Bohn et al (2014):

- Bohn, F. J., Frank, K., & Huth, A. (2014). Of climate and its resulting tree growth: Simulating the productivity of temperate forests. *Ecological Modelling*, 278, 9–17. <https://doi.org/10.1016/j.ecolmodel>.
- Fischer, R., Bohn, F., Dantas de Paula, M., Dislich, C., Groeneveld, J., Gutiérrez, A. G., Kazmierczak, M., Knapp, N., Lehmann, S., Paulick, S., Pütz, S., Rödig, E., Taubert, F., Köhler, P., & Huth, A. (2016). Lessons learned from applying a forest gap model to understand ecosystem and carbon dynamics of complex tropical forests. *Ecological Modelling*, 326, 124–133. <https://doi.org/10.1016/j.ecolmodel.2015>.

1.3.3 Climate

To incorporate climate, we used the data set ‘daily_era5_chelsa_200.csv’, which contains climate data on a daily resolution. We considered the covariates precipitation, temperature, and irradiance, the latter of which we converted to units used in Formind. Adding on to these data, we used a

constant and site-independent potential evapotranspiration (PET) value of $4\frac{\text{mm}}{\text{d}}$ and assumed that the mean day length was 12h at all sites.

Since we simulated longer time periods than the 38 years for which we had climate data, we used the provided data in a randomized fashion. For each simulation year, we applied the climate data of a randomly selected year. We neglected the existence of leap years, which led to a minor time shift in climate data of later years.

1.3.4 Soil

We modelled soil conditions by using the provided soil quality values as proxy for soil depth. To that end, we scaled the provided values to the typical range of soil depth values used in Formind for temperate forests. Specifically, we multiplied the soil quality values by factor 0.5 to obtain the modelled soil depth in meters.

1.3.5 Topography

We did not use any topography data.

1.3.6 Tree species

We considered each of the 11 species in the protocol explicitly. We chose the model parameters for the individual species based on the work by Bohn et al (2014). For species that were not covered by Bohn et al (2014), we used parameter values of similar species with known parameters. The species composition was not predefined and evolved solely from the seed input and the model dynamics.

1.3.7 Simulations

1.3.7.1 Simulation area We simulated a forest area of 1ha, which was divided into 25 patches of size 20m × 20m. No interactions between trees from different patches were considered in the model. That is, the 25 patches were independent replicates of one another.

1.3.7.2 Seed generation and dispersal We modelled seed generation as global external seed rain. Specifically, we assumed that for each species, there is a constant seed inflow of $250 \frac{\text{seeds}}{\text{ha}\cdot\text{yr}}$, which is distributed evenly among the 25 individual patches. We supposed that all seeds promptly establish to seedlings with initial stem diameters at breast height (DBH) of 5cm.

1.3.7.3 Simulation length and sampling approach We started the simulation at each site with a burn-in phase of 1000 years and collected samples of the output variables in subsequent years. The length of the burn-in phase was chosen based on earlier experiences with the model. To confirm that the model reached its limiting behaviour, we plotted the evolution of the output variables (e.g. the basal area) at selected sites over time and verified that no trends were visible after the burn-in phase. We computed the output variables in equidistant time intervals of 60 years. Before taking a sample, we saved parts of the model's state. Then, we simulated the forest for 10 years and computed the output variables, comparing the model's current state with the state saved earlier (see below). After taking the sample, we simulated the forest for another 50 years to reduce correlations between samples. Then, we repeated the procedure until the desired number of 200 samples was collected.

1.3.8 Outputs

To determine the number and basal area of recruits, we compared the set of large trees before and after the regeneration time period of 10 years. Prior to simulating the forest for the regeneration time period, we saved the internal IDs of all trees with DBHs above the thresholds of 0.07m or 0.1m, respectively. We stored these IDs in set data structures $S_{0.07}^{\text{prior}}$ and $S_{0.1}^{\text{prior}}$, corresponding to one threshold value each. After the regeneration time, we repeated the procedure, obtaining tree ID sets $S_{0.07}^{\text{posterior}}$ and $S_{0.1}^{\text{posterior}}$. We then computed the set differences $S_{0.07}^{\text{recruits}} = S_{0.07}^{\text{posterior}} \setminus S_{0.07}^{\text{prior}}$ and $S_{0.1}^{\text{recruits}} = S_{0.1}^{\text{posterior}} \setminus S_{0.1}^{\text{prior}}$ and determined both the number and cumulative basal area of the trees in $S_{0.07}^{\text{recruits}}$ and $S_{0.1}^{\text{recruits}}$ by considered species, respectively.

Finally, we computed the total basal area for each considered species by adding up the basal areas of all corresponding individuals. Note that the initial DBH of seedlings in our model was 0.05m. Consequently, smaller trees were not included in the basal area computation.

1.4 ForClim 1 & ForClim 11

1.4.1 Authors

Yannek Käber, Harald Bugmann

1.4.2 Model

The most complete reference resource for the ForClim 1 & ForClim 11 model and regeneration module is:

- Bugmann, H. (1994). On the ecology of mountainous forests in a changing climate: A simulation study.
- Huber, N., Bugmann, H., & Lafond, V. (2020). Capturing ecological processes in dynamic forest models: Why there is no silver bullet to cope with complexity. *Ecosphere*, 11(5).
<https://doi.org/10.1002/ecs2.3109>

1.4.3 Climate

Temperature and precipitation were aggregated to monthly means and sums, respectively, including their standard deviation. These values served as input for the weather generator within the model. The weather generator simulates wheather conditions in an annual time step based on the monthly average temperatures and precipitations sums.

1.4.4 Soil

Soil data were translated to bucket sizes values based on the assumption that the lowest soil quality value of 1 refers to a bucket size of 10 cm and the highest soil quality of 5 refers to a bucket size of 35 cm. Specifically we used the following formula to calculate the bucket size $\text{bucket_size} = 10 + (\text{soil_quality}-1) / 4 * 25$.

1.4.5 Topography

Topographic information was included by specifying the kSIAsp parameter. This parameter defines a value between -2 and 2 which affects the calculated Potential Evapotranspiration within the model. For details on the calculation of this value see Käber et. al. 2021.

1.4.6 Tree species

All species required were simulated: *Fagus sylvatica*, *Picea abies*, *Abies alba*, *Carpinus betulus*, *Tilia cordata*, *Acer pseudoplatanus*, *Betula spp.*, *Fraxinus excelsior*, *Quercus spp.*, *Alnus glutinosa*, *Pinus sylvestris*.

In addition the following species were simulated: *Acer campestre*, *Acer platanoides*, *Alnus incana*, *Alnus viridis*, *Castanea sativa*, *Corylus avellana*, *Larix decidua*, *Pinus montana*, *Populus nigra*, *Populus tremula*, *Salix alba*, *Sorbus aria*, *Sorbus aucuparia*, *Taxus baccata*, *Tilia platyphyllos*, *Ulmus glabra*, *Pinus cembra*

1.4.7 Simulations

All simulations were run according to the protocol. For each site we simulated on 16 ha (i.e., 100 patches of 0.08 ha). We defined a spin up phase of 1000 years. After the spin up we simulated 200 years of forest dynamics.

1.4.8 Outputs

We sampled in 10 year intervals between the simulation years 1010 to 1200, which resulted in 16 times 20 intervals each with one ha.

1.5 SIBYLA

1.5.1 Authors

Ján Merganič, Katarína Merganičová, Marek Fabrika, Peter Valent

1.5.2 Model

SIBYLA is the simulator of forest biodynamics. It belongs to the category of semi-empirical tree growth simulators. It consists of the set of mathematical models and algorithms that are transformed into an integrated software package SIBYLA Suite. The model has been developed at the Department of Forest Management and Geodesy, Technical University in Zvolen, Slovakia. The basis of the model was the modelling principle and algorithms implemented in SILVA 2.2 (Pretzsch 1992, Kahn 1994). The model is sensitive to climatic factors (length of growing season, mean temperature during growing season, annual temperature amplitude, and total precipitation during growing season). The climatic factors modify height and diameter growth potential, and consequently tree increment. The climatic factors also influence tree regeneration model.

The most complete reference resource for the SIBYLA model and regeneration module are:

- Fabrika (2005) “Simulátor biodynamiky lesa SIBYLA.” *Koncepcia, konštrukcia a programové riešenie. Habilitačná práca, Technická univerzita vo Zvolene*
- Materials available in <http://etools.tuzvo.sk/sibyla/english/model.htm>.

1.5.3 Climate

We used CHELSEA monthly and daily time series from 1981 to 2018 to derive climate variables necessary for simulations with SIBYLA as follows: Monthly average temperature (tas) values were used to derive the SIBYLA site-specific characteristic called the „annual temperature amplitude” (labelled as TAMPL or s5 in the model) that was calculated as a difference between the maximum and minimum monthly average temperatures. Monthly average temperature (tas) values for months

April to September were used to derive the SIBYLA site-specific characteristic called the „average temperature during the growing season” (labelled as TEMP or s6 in the model). Monthly precipitation sums (pr) for months April to September were summed up to derive the SIBYLA site-specific characteristic called the „precipitation total during the growing season” (labelled as PRECIP or s8 in the model). Daily average temperature (tas) values were used to derive the SIBYLA site-specific characteristic called the „length of the growing season” (labelled as DAYS or s4 in the model).

1.5.4 Soil

The information on site-specific soil quality (file name: soil_quality_200.csv) was used to define two SIBYLA site-specific characteristic called the „soil moisture” (labelled as MOIST or s7 in the model) and the „soil nutrient supply” (labelled as NUTR or s3). Since these two characteristics can obtain values in the range from 0 to 1, the provided values on soil quality were converted to this range by dividing each value with 5 (the maximum). We used the long-term average of CO₂ concentrations in air that represented the period 1981 – 2018. The long-term average of CO₂ was calculated from the annual CO₂ data obtained from Mauna Loa observations (Keeling et al. 1976). Similarly, we used the long-term NO_x concentration representing the time period 1981-2018. This was obtained by averaging annual values of NO_x concentration in air calculated using the equation by Kahn (1994), where the year is the driving variable.

1.5.5 Topography

The growth simulator SIBYLA uses the model of ecological classification applied in the growth simulator SILVA 2.2, which was derived by Kahn (1994). Site is specified using ecological site

characteristics describing climate, air, and soil, also called site variables:

- s1 (N2O) ... NOx concentration in air (ppb)
- s2 (CO2) ... CO2 concentration in air (ppm)
- s3 (NUTR) ... soil nutrient supply (relative value in the range from 0 to 1)
- s4 (DAYS) ... number of days in the vegetation period (days with daily mean temperature above 10°C)
- s5 (TAMPL) ... annual temperature amplitude (the difference between minimum and maximum monthly temperature in °C)
- s6 (TEMP) ... daily mean temperature in the vegetation period in °C (from April to September)
- s7 (MOIST) ...soil moisture (relative value in the range from 0 to 1)
- s8 (PRECIP) ... precipitation amount in the vegetation period in mm (from April to September)
- s9 (ARID)... aridity index according to de Martone in mm.°C-1 They directly influence the production capacity of a stand (tree height and diameter increment).

1.5.6 Tree species

At the beginning of the simulations we determined balanced tree species composition of all 12 tree species pre-defined in the „Regeneration workshop protocol”. It means that at the beginning each species was represented by the same volume, mean tree diameter, mean tree height, and age.

1.5.7 Simulations

The simulations were performed following the “Regeneration workshop protocol”. Hence, we simulated the pre-defined 200 sites with the model SIBYLA under current climate. The simulations were performed with the help of two software tools for automated handling of multiple sites to speed up the process called DBCreator and Automat (Valent et al. 2018).

1.5.7.1 Simulation area and site We set the simulation area to 1ha, i.e. each site was represented by an area of 1 ha, to enable a sufficiently large area for species interactions. Larger areas were not possible due to the restrictions in the number of trees per plot (the maximum number of trees per plot is 6,000). Due to the restriction in the maximum number of trees per plot we established a 40-year-old forest stand at each site with the balanced tree species composition as defined above. We used site-specific elevation and aspect obtained from the information on topography and elevation (file name: topo_data_200.csv).

1.5.7.2 Simulation length Each site was simulated for 3,000 years. Based on the analysis of the temporal development of multiple stand variables including number of trees, mean tree and stand characteristics, the simulation time until the equilibrium was set to 500 years. Hence, the first 500 simulated years were excluded from the results. The submitted output includes the required information per decade during the 2,500 years.

1.5.7.3 Dispersal Relevant aspects of the dispersal (if any) and seed input parameters in your model The regeneration model operates if there are mature trees able to produce seeds. Hence, the initial forest stand had to be established to allow the reproduction and regeneration module. The

seed yield of individual trees is predicted in relation to species-specific characteristics including tree age interval of seed production and fertility (age of start, optimum and end), seed production per adult tree, transmission distance, seed purity, seed quality, germination capacity, absolute weight of seeds. Seed tree production is further modified with the regulators and reduction factors, which describe other conditions necessary for the germination, survival, and the establishment of the next generation, e.g. stand canopy closure (Fabrika 2005, Merganič and Fabrika 2009, Fabrika et. al. 2009, 2011).

1.5.8 Outputs

To derive the required information, we worked with the model output for individual trees per decade. First, we calculated basal area of individual trees from the simulated diameter at breast height using the equation for the area of a circle. Total basal area (ba) was obtained by summing tree basal areas per species and decade. The number of recruits (r.trees) per species was derived by counting the trees that exceeded the diameter threshold (7 or 10 cm) in the specific time. The basal area of recruits (r.ba) per species was calculated by summing tree basal areas of recruits per species. NA was assigned if no trees of a specific species occurred in the period.

1.5.9 References

Fabrika M., Merganič J., Merganičová K., 2009: Natural regeneration density model developed for the purposes of the individual-tree growth simulator. *Acta Facultatis Forestalis Zvolen*, 51(3), p. 125-137, ISSN: 0231-5785

Fabrika, M., (2005): Simulátor biodynamiky lesa SIBYLA, koncepcia, konštrukcia a programové

riešenie. Habilitačná práca. Technická univerzita vo Zvolene, 238 p.

Kahn, M., (1994): Modellierung der Höhenentwicklung ausgewählter Baumarten in Abhängigkeit vom Standort. Forstliche Forschungsber. München, Vol. 141, 221 p.

Keeling C. D., R. B. Bacastow, A. E. Bainbridge, C. A. Ekdahl Jr., P. R. Guenther, L. S. Waterman, J. F. S. Chin 1976: Atmospheric carbon dioxide variations at Mauna Loa Observatory, Hawaii. Tellus. XXVIII, 6: 538-551, <https://doi.org/10.1111/j.2153-3490.1976.tb00701.x>

Merganič J., Fabrika M., 2009: Determination of climatic-site strata based on rectified climatic rasters for the purposes of natural regeneration density model. Acta Facultatis Forestalis Zvolen, 51(3), p. 113-124, ISSN: 0231-5785

Merganič, J., Fabrika, M., Merganičová, K., 2011: Submodel of height-diameter function for climatic-site strata of the model of natural regeneration in the growth simulator SIBYLA. Acta Facultatis Forestalis Zvolen, 53(1), p.155-168, ISSN: 0231-5785

Pretzsch, H., (1992): Konzeption und Konstruktion von Wuchsmodellen für Rein- und Mischtbestände. Forstliche Forschungsberichte München, Nr.115, 358 p.

Valent, P., Merganič J., Výbošťok J. 2018: Optimus – Software for Multi-criteria analysis. TU Zvolen.

1.6 xComp

1.6.1 Authors

Tobias Mette, LWF.

1.6.2 Model

The forest growth model xcomp was developed to simulate gap dynamics of monospecific stands with a strong emphasis on position-dependent individual tree competition. The model consists of three units: (1) the main growth phase which determines the growth and mortality of each individual tree above 5 cm dbh, (2) the old-growth phase where individual trees exceeding a certain dbh-limit decline in vitality and eventually die, and (3) the regeneration phase where seedling growth and mortality is modelled depending on light availability. The primary focus of the model was to establish a set of robust algorithms that can be flexibly calibrated for different species attributes. The model was used to simulate single-species stand development cycles for *Nothofagus pumilio* in Patagonia (Mette 2014), for European beech in NE-Bavaria (Mette et al. 2016) and a Norway spruce stand with different mortality algorithms (Bugmann et al. 2019). For the current article the model was (4) connected to a climate sensitive species distribution model to modify growth and mortality in dependence of the site conditions, and (5) extended from single to multi-species simulations (c.f. Section 1.6.7).

The most complete reference resource for the xComp model and regeneration module are:

- Mette, T. (2014). xcomp Tutorial (v2014_08). Technical Report, TUM. DOI: 10.13140/RG.2.2.32524.59529
- Mette, T. (2014) Using Reineke to self-calibrate mortality in individual tree based forest growth modelling. Beiträge zur Forstwissenschaftlichen Tagung, Dresden, 17.-20.09.2014. 10.13140/RG.2.2.11553.07527

1.6.3 Climate

The species parameterisation in xcomp is sensitive to long-term climate, i.e. 30-year averages of summer temperature, summer precipitation and winter temperature. Reactions to daily, monthly or periodic extremes are not implemented as deterministic but as stochastically processes functionally dependent on the long-term climate. The climate sensitivity of growth, mortality and regeneration is described in Section 1.6.7.

1.6.4 Soil

Soil moisture class MOIST was used to modify the climate sensitivity via summer precipitation PJJA by $PJJA(\text{mod}) = PJJA + 15 * \text{MOIST} - 45$ (in mm).

1.6.5 Topography

Topography is no input parameter in xcomp. It may only effect the simulation results indirectly through climate or soil parameters.

1.6.6 Tree species

From the suggested species spectrum *Alnus glutinosa* and *Fraxinus excelsior* were not included in the species mix. *Quercus spec* was split into *Q. petraea* and *Q. pubescens*, but united in the validation to meet the protocol.

1.6.7 Simulations

The simulation was carried out according to the protocol by Bugmann et al. (2022). I.e. the simulation is initiated for mixed species stands of 1 ha size at 200 sites of with given climate and soil conditions. The initial species mix consists of up to 10 species of equal shares with an initial root mean square diameter dq of 8 cm. Xcomp simulates forest growth in 5 year intervals. Data are validated after having reached a climate dependent equilibrium – which is typically the case after 750 years (= 150 simulation periods). Starting with year 760, data are read out for 200 10 year intervals (until year 2750, simulation period 550). Further simulation relevant model details:

- (1) The main growth phase is determined by the processes growth and mortality. Mortality is determined by the Reineke exponent rke and the stand density sdi and calibrated over a range of 8 cm to 50 cm dq (= root mean square diameter) so that stem number N equals: $N = sdi * (dq/25)^{rke}$. A tree's resource acquisition area res (m²) is approximated as $res = 1e4 / (sdi * (dbh/25)^{rke})$. As the Reineke exponent is fixed to $\square 1.6$, species with higher/ lower sdi have a lower/ higher resource acquisition area for a given dbh. Potential dbh growth dd is calculated by multiplying a reference dbh growth with a site specific temperature dependent modifier. The individual dbh growth in the stand is further modified by the neighbourhood competition.
- (2) The old growth phase sets in when a tree passes a certain old growth dbh (ogDbh) which depends on the site conditions. Having passed this threshold dbh a tree is assigned a mortality period that assumes a value not greater than a site independent maximum ogPer. The maximum old growth time span ranges from 100 years (birch) to 350 years (fir). During the old growth phase dbh growth declines and more light becomes available for regeneration.
- (3) The regeneration phase allows seedling development on a 1x1 m grid over the entire stand.

First, a light availability matrix (1x1 m) is calculated from a cumulative crown shadow which decreases with increasing distance to the tree center. Next, regeneration matrices (1x1 m) are created for each of the stand's species. In the initial period, the regeneration matrix of each species is empty, but at the end of each period, a light dependent dbh growth and mortality is calculated for each 1m raster cell. The dbh growth is scaled so that under full light 5 cm dbh is reached in a defined regeneration period (regnPer) that depends on the site conditions. The default value is set to 15 years and equal for all species. Dbh growth is modified by the light availability and the species' regeneration light demand. This is a decisive difference between the species and favours shadow-tolerant trees like fir and beech in the absence of large gaps. However, each raster cell is afflicted with a species bonus or malus that provides local variation to the global regeneration parameters. Mortality in the regeneration raster occurs as a random process, the likelihood of which depends on the climate.

(4) The climate sensitivity was calculated by methods of species distribution modelling. Effectively species abundance in European NFI-plots (Mauri et al. 2017) was related to climate of the plots (Karger et al. 2017) using generalized additive models as in Thurm et al. (2018). Input variables were summer temperature mean (Jun-Aug), winter temperature mean (Dec-Feb) and summer precipitation sum (Jun-Aug). Abundance was transformed into prevalence () so that the values for each species can assume a range from 0 to 1. The prevalence values modify dbh growth dd, old growth dbh ogDbh, the regeneration period regnPer, and the regeneration mortality regnMort.

(5) The extension from single to multiple species simulation introduced no technical changes to the single-species growth and mortality behaviour. Competition as the main interaction between trees depends on the crown size and density of the neighbouring trees and can turn out an dis/advantage for one or the other species. But species calibration parameters were not changed due to mixture-

specific interaction.

1.6.8 Outputs

Since the simulation output tables contain all biometric variables on an individual tree basis, all required outputs can be derived directly from the output tables. Being a very deterministic model what typically happens in xcomp is that the equilibria consist of one or two species. Shade tolerance favours fir and beech in the absence of large gaps creating disturbances. The second most important parameter is the site suitability which is estimated by the modelled species prevalence and affects growth and thereby competitiveness. As it is the first time that xcomp is used in a multiple species application there is room for improvements. The automation of a robust calibration of the main growth phase is a precondition to investigate how for instance larger disturbances, a weighted regeneration potential oriented at the main stand, higher or selective mortality of the regeneration affect the species composition and turnover.

1.6.9 References

1. Bugmann, H., Seidl, R., Hartig, F., Bohn, F., Brůna, J., Cailleret, M., ... & Reyer, C. P. (2019). Tree mortality submodels drive simulated long-term forest dynamics: Assessing 15 models from the stand to global scale. *Ecosphere*, 10(2), e02616.
2. Karger, D. N., Conrad, O., Böhner, J., Kawohl, T., Kreft, H., Soria-Auza, R. W., ... & Kessler, M. (2017). Climatologies at high resolution for the earth's land surface areas. *Scientific data*, 4(1), 1-20.
3. Mauri, A., Strona, G., & San-Miguel-Ayanz, J. (2017). EU-Forest, a high-resolution tree

- occurrence dataset for Europe. *Scientific data*, 4(1), 1-8.
4. Mette, T., Falk, W., Blaschke, M., Förster, B., Walentowski, H. (2016). Modelling natural forest dynamics in individual tree based forest growth simulators. *Beiträge zur Forstwissenschaftlichen Tagung*, Freiburg, 26.-29.09.2016. 10.13140/RG.2.2.29169.15201
 5. Thurm, E. A., Hernandez, L., Baltensweiler, A., Ayan, S., Rasztovits, E., Bielak, K., ... & Falk, W. (2018). Alternative tree species under climate warming in managed European forests. *Forest Ecology and Management*, 430, 485-497.

1.7 PICUS

1.7.1 Authors

Christian Hochauer, Manfred J. Lexer

1.7.2 Model

The core elements of PICUS are described in Lexer and Hönniger (2001) and Seidl et al. (2005).

Specific details regarding the regeneration module can be found in Woltjer et al. (2008).

The most complete reference resource for the SIBYLA model and regeneration module are:

- Lexer MJ, Hönniger K (2001) A modified 3D-patch model for spatially explicit simulation of vegetation composition in heterogeneous landscapes. *For Ecol Manag* 144:43–65. doi: [10.1016/S0378-1127\(00\)00386-8](https://doi.org/10.1016/S0378-1127(00)00386-8)
- Seidl R, Lexer MJ, Jäger D, Hönniger K (2005) Evaluating the accuracy and generality of a hybrid patch model. *Tree Physiol* 25:939–951. doi:[10.1093/treephys/25.7.939](https://doi.org/10.1093/treephys/25.7.939)

- Woltjer M, Rammer W, Brauner M, Seidl R, Mohren GMJ, Lexer MJ (2008) Coupling a 3D patch model and a rockfall module to assess rockfall protection in mountain forests. *J Environ Manag* 87:373–388. [doi:10.1016/j.jenvman.2007.01.031](https://doi.org/10.1016/j.jenvman.2007.01.031)

1.7.3 Climate

We used the provided monthly climate data (monthly_era5_chelsa_200.csv). The provided solar radiation rsds was converted to MJ per m². Additionally, vpd was calculated.

1.7.4 Soil

Based on the provided continuous value for soil quality between 1 and 5 minimum (soil quality = 1) and maximum (soil quality = 5) values for soil water holding capacity (80mm, 200mm), plant available Nitrogen (40 kg ha⁻¹ yr⁻¹, 100 kg ha⁻¹ yr⁻¹) and soil pH (4.2, 5.6) were defined. Linear interpolation was used to scale between the minimum and maximum values.

1.7.5 Topography

Not considered.

1.7.6 Tree species

The species composition was defined by the given species from the protocol: *Fagus sylvatica*, *Picea abies*, *Abies alba*, *Carpinus betulus*, *Tilia cordata*, *Acer pseudoplatanus*, *Betula spp.*, *Fraxinus excelsior*, *Quercus spp.*, *Alnus glutinosa* and *Pinus sylvestris*. For *Betula spp.* *Betula pendula* was simulated, for *Quercus spp.* the species *Quercus petraea* and *Quercus robur* where used. The

establishment from bare ground was achieved via external seed input (see also in section seed dispersal), so depending on the environment and random components all the given species had a chance to grow into the respective simulation. In addition, on site production of seed is considered depending on age and size of potential parent trees.

1.7.7 Simulations

1.7.7.1 Simulation Area In PICUS the area is defined via the number of 10 m by 10 m patches. For this simulation we used an area of 12 by 12 patches resulting in an area of 1.44 ha. This size of the simulated forest provides relatively stable species composition & structure and reasonable simulation time.

1.7.7.2 Seed dispersal For the experiment seed input to the simulated forest happens via 2 pathways: (1) external seed input to every patch in any simulated year (fixed number of seed per patch per species). (2) locally produced seed by parent trees growing in the simulated forest. Seed production depends on species, and tree size and a random component accounting for mast years. Seed dispersal depends on whether a species is anemochorous or zoolochorous. If anemochorous tree height and seed characteristics determine the maximum dispersal range and the shape of the dispersal function. Based on germination rate, the environmental factors (temperature, soil moisture, Nitrogen, light) and the amount of seeds in combination with a random component seedling establishment is calculated per patch in any given year. Seedling cohorts grow through 4 height classes and are then eventually recruited into the tree population.

1.7.7.3 Simulation length We decided to use the temporal sampling. We first run the model into a quasi equilibrium and continue afterwards with another 2000 years. The simulation time until equilibrium was chosen with 600 years from experience in other projects and a few simulations with test sites where 600 years was a sufficiently long simulation time to reach an equilibrium state.

1.7.8 Output

Output consisted of species-specific regeneration rates per decade and per ha. Oak species were aggregated. A sample was taken for every 10 years for a total period of 2000 years once the model had reached equilibrium (see 1.7.7.3). Ingrowth was determined by counting the trees passing the 7cm and 10cm DBH thresholds every 10 years. Basal area of the ingrowth was determined at the end of each decade.

1.8 iLand

1.8.1 Authors

Werner Rammer, Kristin Braziunas

1.8.2 Model

The most complete reference resource for the iLand regeneration module is:

- Seidl, R., Spies, T. a. T. A. T. a., Rammer, W., Steel, E. A. A., Pabst, R. J. R. J. R. J., & Olsen, K. (2012). Multi-scale Drivers of Spatial Variation in Old-Growth Forest Carbon

Density Disentangled with Lidar and an Individual-Based Landscape Model. *Ecosystems*, 15(8), 1321-1335. <https://doi.org/10.1007/s10021-012-9587-2>

1.8.3 Climate

Climate inputs for iLand are at daily temporal resolution. We used daily climate from the CHELSA dataset for maximum and minimum temperature, precipitation, and surface shortwave radiation. We calculated daily vapor pressure deficit (VPD) from these inputs assuming daily minimum temperature is dewpoint temperature, a reasonable assumption except under very arid conditions (Campbell and Norman 2000). We calculated vapor pressure from temperature using the Tetens formula with different coefficients for temperatures above or below 0° C (Murray 1967). We then followed methods outlined by the Food and Agriculture Organization of the United Nations (Allen et al. 1998) to calculate vapor pressure deficit as the difference between average daily saturation vapor pressure (derived from minimum and maximum temperature) and ambient vapor pressure derived from dewpoint temperature. Some daily VPD values were negative because there were days in the CHELSA dataset where minimum temperature exceeded maximum temperature; negative VPD values were set to 0.

As recommended by workshop organizers, we filled in daily values for two missing days in 2013 (Jan 2 and Jan 3) with daily values for Jan 1 and 4, respectively.

Atmospheric CO₂ concentration was set to 380 ppm and latitude was set to 50° N for all sites. Annual climate year was drawn randomly with replacement from the full dataset (1981-2018) for each site for the duration of the simulation.

1.8.4 Soil

Inputs for soil depth, texture, and fertility (plant available nitrogen) were extracted from a previously compiled Europe-wide dataset (unpublished dataset). We averaged values in a 1 km buffer around blurred site coordinates provided by workshop organizers. Relationships between ranked site quality provided by workshop organizers and soils data from our Europe-wide dataset were weak (Pearson's $|r|$ ranged from 0.04 to 0.34), but followed expected trends with lower sand content, higher water holding capacity, and higher fertility associated with higher site quality. Albeit the weak correlation, we chose to use our available data set because we could avoid additional assumptions as it included all site variables needed for the model.

1.8.5 Topography

Topographic information was not used.

1.8.6 Tree species

Tree composition is defined at the species level. All individually requested species (*Fagus sylvatica*, *Picea abies*, *Abies alba*, *Carpinus betulus*, *Tilia cordata*, *Acer pseudoplatanus*, *Fraxinus excelsior*, *Alnus glutinosa*, *Pinus sylvestris*) were included. For the two taxa where species was not defined, we identified a representative species (*Betula pendula* for *Betula* spp. and *Quercus robur* for *Quercus* spp.). No other species were included in model simulations.

1.8.7 Simulations

1.8.7.1 Simulation area The simulation extent for each site was 1000 m x 1000 m (total area = 100 ha). Environmental conditions were homogeneous for each site.

1.8.7.2 Dispersal Dispersal parameters are species-specific and include maturity age, fecundity (seedling potential per m² crown area), masting (lower seed production in non-mast years), and dispersal distance (probabilistic dispersal kernel). A small fraction of seeds are dispersed over longer distances (long distance dispersal algorithm). Dispersal is calculated at 20 m spatial resolution. Seedling establishment is further modified by other environmental constraints and is stochastically spatially distributed at finer (2 m) resolution. The simulation extent is treated as a spatially explicit landscape, so neighboring cells can serve as seed sources for each other.

We initialized our simulation experiments from bare ground with uniform probability of seed availability set to a low level (0.001) for all species. Once trees reached maturity, they also contributed to seed availability and dispersal.

1.8.7.3 Simulation length Simulations were run for 2010 years, and equilibrium was reached at year 1500. We assessed temporal patterns of species composition and basal area and defined equilibrium as when forest composition and structure stabilized across all sites (“potential natural vegetation”). Some sites had high interannual variation, especially in basal area, after equilibrium; this variation did not represent directional change and appeared instead to be related to sites with extreme growth conditions and variation in randomly selected annual climate.

1.8.7.4 Simulation approaches Only one simulation was run per site.

1.8.8 Output

For each site, we generated decadal outputs for the full simulation extent every 100 years after equilibrium was reached (i.e., 1500-1509, 1600-1609, ..., 2000-2009). This resulted in outputs for a total of 600 ha (100 ha simulation extent x 6 decades). From this list, we randomly sampled 200 ha without replacement.

We derived recruit density and basal area annually by species. Trees > 4 m in height are represented as individuals in iLand, so we were able to identify individual trees that crossed the DBH threshold of either 7 or 10 cm each year. We summed the number of annual recruits and their basal area in the year they crossed the recruitment threshold for each 10-year output period.

We averaged total density and basal area by species for each decade. We further included 0 values (complete cases) for species that were missing from a given sample and site.

1.8.9 References

Allen, R. G., L. S. Pereira, D. Raes, and M. Smith. 1998. Crop evapotranspiration - Guidelines for computing crop water requirements. FAO - Food and Agriculture Organization of the United Nations, Irrigation and drainage paper 56. Campbell, G. S., and J. M. Norman. 2000. An Introduction to Environmental Biophysics. Springer Science & Business Media. Murray, F. W. 1967. On the computation of saturation vapor pressure. Journal of Applied Meteorology 6:203–204.

1.9 LandClim

1.9.1 Authors

Olalla Díaz-Yáñez, Harald Bugmann

1.9.2 Model

We used LandClim version 2.0, which calculates forest dynamics at a decadal time step. The complete reference resources for the LandClim model and its regeneration module are:

- SCHUMACHER, S., H. BUGMANN, AND D. J. MLADENOFF. (2004). “Improving the formulation of tree growth and succession in a spatially explicit landscape model” Ecological Modelling 180: 175-194.
- SCHUMACHER, S. AND H. BUGMANN. (2006). “The relative importance of climatic effects, wildfires and management for future forest landscape dynamics in the Swiss Alps” Global Change Biology 12: 1435-1450.
- SCHUMACHER, S., B. REINEKING, J. SIBOLD, AND H. BUGMANN. (2006). “Modeling the impact of climate and vegetation on fire regimes in mountain landscapes” Landscape Ecology 21: 539-554.
- Manual available on the model web page: <https://ites-fe.ethz.ch/openaccess/products/landclim>

1.9.3 Climate

Climate inputs for LandClim are at monthly temporal resolution. We used monthly climate from the CHELSA dataset provided in the protocol, using temperature and precipitation variables. During the simulations, we randomly sampled the annual climate data from the CHELSA time series.

1.9.4 Soil

We used the soil quality provided in the protocol to infer the Available Water Holding Capacity (WHC) needed in LandClim. We assigned WHC = 8 cm for soil quality one and WHC = 25 cm for soil quality five, and interpolated the values for the other categories linearly between these two extremes.

1.9.5 Topography

We used the altitude and soil information provided in the protocol to create 200 landscapes, one per site. However, each landscape created per site had no slope, altitude, or aspect variation.

1.9.6 Tree species

We simulated forest dynamics considering only the 11 species proposed in the protocol: *Fagus sylvatica*, *Picea abies*, *Abies alba*, *Carpinus betulus*, *Tilia cordata*, *Acer pseudoplatanus*, *Betula* spp., *Fraxinus excelsior*, *Quercus* spp., *Alnus glutinosa*, and *Pinus sylvestris*.

1.9.7 Simulations

We simulated forest dynamics from bare ground for each site, using patches (pixels) with a size of 20x20 cm². We prepared landscapes of 250x250 m without topographical variation for each site. The simulations we run from bare ground to 2000 years, and the samples were taken starting in the year 2000. In the regeneration module, we used (1) a base seeding probability of 0.001, which defines if seeds are available due to background seed rain; (2) a dispersal mode based on the formulation ‘random asymmetric’; and (3) the same establishment probability of 0.9 for all species included in the simulation of, which sets the same probability for all the species to regenerate successfully, provided that the abiotic and light conditions are suitable for establishment.

1.9.8 Outputs

We estimated the outputs based on a sample of 25 random cells every ten years from the simulation years 2010 to 4000 for one simulation per site, thus providing the required 200 samples per site.

1.10 Landis II

1.10.1 Authors

Josef Brúna, Paola Mairotta, Marco Mina, Giorgio Vacchiano

1.10.2 Model

Landscape scale forest simulation model LANDIS-II (Scheller et al. 2007) with PnET-Succession extension (version 4.1). PnET-Succession is based on the Biomass Succession extension of Scheller

and Mladenoff (2004), embedding elements of the PnET-II ecophysiology model of Aber et al. (1995) to mechanistically simulate growth as a competition for available light and water (De Bruijn et al. 2014). PnET-Succession simulates the competition among cohorts for water and light at a monthly time-step as a function of photosynthetic processes and maintenance respiration that are explicitly linked to environmental drivers such as temperature, precipitation, photosynthetic active radiation (PAR), and CO₂ concentration. Regeneration depends on distance from a seed source, soil water, and subcanopy light, while competition is modeled by partitioning incoming light through multiple canopy layers. Growth of specific cohort biomass components is allocated in the following order: non structural carbon, first, then foliage then root and stem. Biomass growth decreases as cohorts approach their longevity age but mortality can occur at any time when carbon reserves production is insufficient to support growth due to shading, water competition, and/or drought (Gustafson et al. 2015), or by any disturbance or management extension used. For output, we selected Biomass Community Output Extension version 2.0.1, which generates output in the format: species age biomass (g / m²) at specified time steps.

The most complete reference resources for the LANDIS-II model and regeneration module are:

- Scheller R.M. & Mladenoff D.J. (2004) A forest growth and biomass module for a landscape simulation model, LANDIS: design, validation, and application. Ecological Modelling 180: 211–229. <https://doi.org/10.1016/j.ecolmodel.2004.01.022>
- Scheller, R. M., Domingo J. B. , Sturtevant B. R. , Williams J. S. , Rudy A. , Gustafson E. J. & Mladenoff D. J. (2007) Design, development, and application of LANDIS-II, a spatial landscape simulation model with flexible temporal and spatial resolution. Ecological Modelling 201(3-4): 409–419. <https://doi.org/10.1016/j.ecolmodel.2006.10.009>

- de Bruijn A., Gustafson E.J., Sturtevant B.R., Foster J.R., Miranda B.R., Lichti N.I. & Jacobs D.F. (2014) Toward more robust projections of forest landscape dynamics under novel environmental conditions: Embedding PnET within LANDIS-II. Ecological Modelling (287): 44–57 <https://doi.org/10.1016/j.ecolmodel.2014.05.004>
- Petter G., Mairota P., Albrich K., Bebi P., Brůna J., Bugmann H., Haffenden A., Scheller R.M., Schmatz D.R., Seidl R., Speich M., Vacchiano G. & Lischke H. (2020) How robust are future projections of forest landscape dynamics? Insights from a systematic comparison of four forest landscape models. Environmental Modelling & Software 134: 104844. <https://doi.org/10.1016/j.envsoft.2020.104844> (supplementary material)
- Gustafson E.J., De Bruijn A.M.G., Pangle R.E., Limousin J.M., McDowell N.G., Pockman W.T., Sturtevant B.R., Muss J.D. & Kubiske M.E. (2015) Integrating ecophysiology and forest landscape models to improve projections of drought effects under climate change. Global Change Biology 21: 843–856. <https://doi.org/10.1111/gcb.12713>

1.10.3 Climate

Climate input was generated by randomly selecting entire years from the monthly data from the CHELSA dataset and collating them one after the other to create a 2000 years series. The sampling was repeated 10 times with different random order of years to create the 10 climate replicates. Selecting a year at a time eliminates inconsistent seasons (especially summer). We used monthly mean, minimum and maximum temperatures and precipitation as input for PnET succession extension. PnET-Succession also requires mean monthly values of PAR during daylight hours, which

we calculated by dividing the monthly rsds data by the number of daylight seconds in each month for latitude 47 to get W/m². We then multiplied this by 4.6 to get $\mu\text{mol}/\text{m}^2/\text{s}$ and multiplied by 0.5 to get PAR part of the spectrum, based on the approximation by Tsubo et al. (2005). Leap years were not considered. The PAR distribution across all sites and years is in range with values that are typical for temperate regions.

CO_2 concentration with yearly timestep was added from the concentrations table available from EEA (2019). For years 0-1750 CO_2 concentration was maintained fixed to 278 ppm. As for the period 1750-1975 there was only one value each 5 years, we used a constant value for each 5-year period. CO_2 concentration was added to the climate input file after randomization of temperature, precipitation and PAR (see above), so it reflects realistic values for the simulated years. Simulations were run from year 0 to 1990 but sampled outputs did not exceed year 1910. Thus, the drastic increase in CO_2 concentration during the second half of the 1900s did not affect the delivered results.

1.10.4 Soil

Soil type was set to LOAM at all sites. Rooting depth was calculated from soil quality codes (1-5, original values ranged from 1.13 to 4.87) multiplicatively by 205. This produces a soil depth in the range 231 - 998 mm, that are within the typical range for PnET-Succession (maximum 1000 mm). A clear trend emerged - deeper soils resulted in higher biomass, although with some exceptions.

1.10.5 Topographhy

The ecoregion-specific parameter Precipitation Loss Fraction denotes the water lost to runoff induced by topographic slope. We estimated this parameter for each site from topo_data_200 dataset as slope * 0.01 (e.g., 12% slope = 0.12 PrecLossFrac). We acknowledge that this is a simplification and that better parameterization would be possible if soil types were available for each site. Tests showed that sites with extreme slope tended to have lower biomass, but the signal was not that clear. The correlation between slope and elevation was 0.6 which could obscure the results.

Some sites at very high elevation had, correspondingly, very low temperature. At these sites, the model showed a visible trend in producing lower biomass (down to zero at a few sites). Yet this was probably not apparent in the regeneration results, as extremely low biomass could still support regeneration, even if cohorts do not live long, due to our modification of sexual maturity age.

1.10.6 Tree species

As LANDIS-II cannot start from bare ground, initial communities were set to include all species defined in the protocol at all sites starting with 10-years old cohorts of the following species: fasy (*Fagus sylvatica*), pabi (*Picea abies*), abal (*Abies alba*), cabe (*Carpinus betulus*), tico (*Tilia cordata*), acps (*Acer pseudoplatanus*), betu (*Betula spp.*), frex (*Fraxinus excelsior*), quer (*Quercus spp.*), alg1 (*Alnus glutinosa*), pisy (*Pinus sylvestris*). The species-specific parameter denoting sexual maturity was set to 10 years equally for all species, so that seed source of all species is available from the onset of the simulations at all sites and to maintain seed in the ladscape pool. Vegetative regeneration (resprouting) was prevented, since this would have an effect on allometry and regeneration.

Some species may be under or overrepresented because their occurrence in LANDIS-II simulations is typically due to small-scale disturbances or management which were not included in the simulations.

The model requires two sets of parameters representing species-specific life traits. The first set is used by the LANDIS-II core module. The species-specific parameter denoting “longevity” and “sexual maturity” were the only parameters of this set considered in the current exercise. The “sexual maturity” was set to 10 years equally for all species, so that seed source of all species is available from the onset of the simulations at all sites and to maintain seed in the landscape pool. Vegetative regeneration (resprouting) was prevented since this would influence allometry and regeneration.

The second set is used by the PnET-Succession extension and includes several ecophysiological parameters. For this second set we started with the values already applied in Petter et al. (2020) with a previous version of PnET. The values of some of the parameters to which PnET is most sensitive and/or for which the range of variation had been modified for PnET4.1 were then iteratively adjusted (individually and then in combination) to meet the requirements of PnET version 4.1 used in this exercise. The changes were implemented one by one in simulations with the exercise data and those leading to an output deemed realistic and to a relative stabilization of the biomass trend through the simulation were retained for the implementation of the full set of replicates. The retained changes include: 1) decreased percentage of foliar nitrogen for algl (*Alnus glutinosa*); 2) rescaling to the new ranges for all species of the values of the Halfsat and the FracBelowG. The first of these parameters represents shade tolerance and its value affects the probability of establishment of a species (Half saturation light level for photosynthesis.); the latter regulates allocation between

above and below ground pool (Fraction of non-foliar biomass that is belowground (root pool)) ; 3) a slight decrease of the value of the parameter (Fracfol) affecting the yearly allocation to foliage of the active total woody biomass for the three conifers abal (*Abies alba*), piab (*Picea abies*), pisy (*Pinus sylvestris*).

1.10.7 Simulation

Simulation area was defined as a rectangle of 10×20 dimension with sites (i.e., cells) of 1-ha. Each site is an individual ecoregion (i.e., one cell - as in our case - or group of cells sharing similar climate and soil conditions, as a way in LANDIS-II to define differences in biophysical conditions across landscapes) with specific values for soil quality, topography and climate, based on the data provided. The model runs with a yearly timestep using monthly climate. We started each model run with initial communities of all species at age 10 at all sites. Each run was simulated for 1980 years.

1.10.7.1 Dispersal We have used the non-spatial seeding algorithm “universal dispersal” for all the model runs. This way, every species can seed any forest site in the landscape (across all the 200 sites). This mode does not take into account the spatial arrangement and contiguity of cells (i.e., no active seed dispersal), which is proper for the sake of the model comparison exercise. Yet in real landscape seed limitation can also play a role in species composition. The seed number is affected by species-specific age of maturity, which we have modified. This setting ensures an influx of seeds from outside consistent with the original settings.

1.10.7.2 Sampling design We have sampled each site 20 times along the simulation run in two time windows starting 50 years after the first cycle following typical species longevity. After the year 700, biomass of most species was relatively stable and we sampled every 50 years, starting at 750 until the year 1200. The next sampling period started from 1450 and continued until 1900, i.e., after the next longevity peak, again every 50 years. At each selected sampling time, we extracted cohorts of each species according to the age related to the two DBH thresholds (7cm/10cm). Additionally, we extracted cohorts that were up to 9 years older than these thresholds, to get the expected results for a 10-year interval. For example, *Fagus sylvatica* reaches DBH 7cm at 17 years, therefore we have selected all cohorts with age 17-26.

To deliver more than one simulation per site, we created 10 replicates with different climate replicate and random number generator seed number to account for stochastic processes in PnET-Succession. This resulted in the expected 200 samples for each site.

1.10.8 Outputs

Sample number code

Number (1-200) was defined as sample in time + (replicate-1)*20, with sample in time (1-20) according to the sample order. Replicate (1-10) combines random number and climate sequence. For example sample number 25 was taken from the climate replicate 2 and the fifth sample in time (year 950).

r.trees

As LANDIS-II outputs are expressed in terms of cohort age and mean biomass per site, we have calculated the mean DBH and biomass of each species based on age. We estimated the age when

each species reaches 7 cm and 10 cm DBH and the number of individuals using allometric models from the Italian forest inventory collected in R package ForIT (Puletti et al. 2014), and unpublished data from the study by Mina et al. (2021). Please note that the equations used predict DBH >0 already for a tree with age 1, this is because it is based on forestry data and tree cores. The real age when reaching 1.3 m height is species specific and we did not implement this offset. For each cohort, we divided the cohort biomass reported by LANDIS-II, recalculated to kg/ha by the mean biomass of a tree of the same species and age to obtain the number of trees of each species per site. We rounded all results up to the nearest integer to avoid any fraction of trees. The number of individuals was aggregated for all the cohorts of the age of reaching 7 cm or 10 cm DBH and all cohorts of the same species that were up to 9 years older. This approach does not reflect influence of site conditions or stand densities on Age-DBH and Age-Biomass. Relationships between age and DBH were derived by fitting asymptotic regressions using individual tree measurements from an ensemble of forest inventory plots distributed across south-eastern Canada (see Supporting information of Mina et al. 2021). This was the only public dataset for which we could relate tree age, derived from stem coring and tree ring analysis, to measured DBH. Although tree age measurements were obtained with a robust methodology, these functions do not disentangle the influence of site conditions or stand densities. Additionally, they reflect growing conditions of tree genera in Eastern North America.

r.ba basal area of regeneration Calculated as a sum of r.ba of all the cohorts selected in r.trees using the following formula: $DBH^2 * \pi/4 * r.tree$.

ba: total basal area We have not calculated this since our allometric equations do not cover older ages. Therefore, we produced the following two biomass variables as a surrogate. The basal area

was later calculated as a sum of r.ba and estimated ba based on biomass. The estimation includes transformation of kg into tonnes / ha and expansion factor 12.5 to transform ba m²/ha.

((landis\$sum.bio - landis\$r.bio.sum)* 0.001) / 12.5). This includes

sum.bio

Biomass of all cohorts of the species on site including the regeneration and even younger regeneration (units kg/ha).

r.bio.sum Biomass of the regeneration cohorts corresponding to the r. ba and r.trees on site (units kg/ha).

Please notice that we included 0 values for species missing in a given sample and for samples in sites where Landis did not simulate any tree.

1.10.9 References

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1.11 TreeMig

1.11.1 Authors

Heike Lischke

1.11.2 Model

The model TreeMig (see treemig.wsl.ch) was originally based on the ForClim model, then aggregated by a distribution based approach (Lischke et al. 1998), and extended to a forest landscape model by including seed production, seed dispersal, seed bank dynamics and seedling establishment (Lischke and Loffler 2006, Lischke et al. 2006).

The most complete reference resource for the TreeMig model and regeneration module are:

- Lischke, H., T. J. Loffler, and A. Fischlin. 1998. Aggregation of individual trees and patches in forest succession models: Capturing variability with height structured, random, spatial distributions. *Theor Popul Biol* 54:213-226.
- Lischke, H., N. E. Zimmermann, J. Bolliger, S. Rickebusch, and T. J. Loffler. 2006. TreeMig: A forest-landscape model for simulating spatio-temporal patterns from stand to landscape scale. *Ecological Modelling* 199:409-420.

- Lischke, H., and T. J. Loffler. 2006. Intra-specific density dependence is required to maintain species diversity in spatio-temporal forest simulations with reproduction. *Ecological Modelling* 198:341-361.
- The online resources available at treemig.wsl.ch

1.11.3 Climate

As climatic input, the monthly time series of mean temperature and precipitation sum were used. With these climatic variables and additional data about slope, aspect and soil field capacity, yearly time series of the following bioclimatic variables were calculated: (1) DDSum, the yearly day degree sum above 5.5°C , (2) MinWiT, the lowest mean monthly temperature, (3) DrStr, drought stress according to a bucket model that estimates a monthly PET following (Thornthwaite and Mather 1957), using temperature, latitude, slope and aspect as input, and calculates the monthly soil water content based on soil water content in the previous month, precipitation, interception, and field capacity (“bucketsize”) (Bugmann 1994, Fischlin et al. 1995). Drought stress is then given by 1- the ratio between demand (PET-interception) and the supply, a function of the soil water content. To get climate data also for the spin-up, bioclimate was calculated from the monthly data as given, and then extended by sampling from the given data from the end of the climate data to get 1000 years. The same sequence of sampling years was used in all simulations and sites.

1.11.4 Soil

The soil bucketsize (available water capacity of the upmost 1m soil layer) required for the drought stress calculation, was derived from the soil quality data set, by $\text{Bucketsize} = 10 + (\text{soil_quality}-1)$

/4 * 25 , to covert the range from 10 cm to 35cm

1.11.5 Topography

Slope and aspect were taken from the topographic data set and converted to a common variable entering the PET calculation, by $\text{slasp} = 2\cos(\text{aspect} \pi/180) * \min(1, \text{slope}/60)$

1.11.6 Tree species

Thirty Central European tree species were simulated, including the standard species of the project . Only *Betula pubescens* was not simulated, because we did not have a parametrization for this species at hand. Species: *Abies alba*, *Larix decidua*, *Picea abies*, *Pinus cembra*, *Pinus montana*, *Pinus sylvestris*, *Taxus baccata*, *Acer campestre*, *Acer platanoides*, *Acer pseudoplatanus*, *Alnus glutinosa*, *Alnus incana*, *Alnus viridis*, *Betula pendula*, *Carpinus betulus*, *Castanea sativa*, *Corylus avellana*, *Fagus sylvatica*, *Fraxinus excelsior*, *Populus nigra*, *Populus tremula*, *Quercus petraea*, *Quercus pubescens*, *Quercus robur*, *Salix alba*, *Sorbus aria*, *Sorbus aucuparia*, *Tilia cordata*, *Tilia platyphyllos*, *Ulmus glabra*

1.11.7 Simulation

The simulations were carried out on a grid of 15 x 15 cells, each with 200 m side length.

1.11.7.1 Dispersal The seeds produced by the mother trees are transported from the source cell according to a double negative exponential, species specific that determines the share of the seeds in the source cell landing in a sink cell in a given distance to the source cell. In the sink cells,

the seeds enter the seed bank . At the start of the simulation for 10 years seeds of all species are available in all grid cells, from then on, the normal seed dispersal starts.

1.11.7.2 Regeneration processes TreeMig simulates the full feedback from seed production to ingrowth. Some of the involved processes depend on environment. (1) Overall seed production in TreeMig is described by multiplying a species specific seed production per tree that depends on tree size and thus indirectly on the growth, which depends on DDsum, drought stress, nutrients and light and the adult tree number that depends on survival that depends on DDsum, drought stress, nutrients and light. (2) Seed dispersal is independent of environment. (3) Seed bank dynamics – also environment independent - is given by seed input, seed mortality, and germination. Additionally, the number of seeds S of a species in the seed bank of this species (SB) is limited to a carrying capacity C of 1000, by

$$SB = C + (SB - C) * \text{Exp}(-S/C).$$

(4) Germination and seedling survival depend on browsing, drought, winter temperature, DDSum and light. (5) The saplings up to 1.37 die and grow like adult trees, depending on DDsum, drought stress and light. Only the parameter value of the light dependence differs from that of the adult trees.

The regeneration processes were simulated annually in the order 1. germination, 2. germinated seeds leave the seed bank, 3. mortality of seeds in the seed bank, 4. seed entry by seed dispersal. The ingrowth numbers were very sensitive to this order. Simulations with another sequence, in which the seeds in the seed bank died first and then the remaining ones germinated, resulted in about half the ingrowth.

1.11.7.3 Simulation length The simulations were started on bare ground and run for 1000 years, when at all sites the equilibrium was reached.

1.11.7.4 More simulations per site TreeMig simulates directly the mean dynamics of entire stands, but based on the variability of light conditions within the stand (distribution based approach, cf. Lischke et al. 1998). To come up with the required 200 random patches of 1 ha, temporal and spatial variability intrinsic to TreeMig were combined. Temporal variability was given by sampling from each decade of the last 100 years of the simulation, i.e. years 900-1000. For each of these 10 decades, 20 grid cells were sampled from the simulated grid, reflecting spatial variability, results from demographic stochasticity and short-range spatial interactions

1.11.8 Outputs

In contrast to gap models, TreeMig is based on the concept of frequency distributions of tree densities classes in different tree heights on ca. 1/12 ha (833m^2) patches, and the resulting frequency distributions in discrete light. During the simulation, in each height class the frequencies of the different light classes were recorded, as well as the ingrowth of each species in the height-light class. By sampling 12 times from the height-light class ingrowths according to the height-light class frequency distribution and summing up, the stochastic ingrowths into all TreeMig height classes for one ha were calculated for each grid cell. Then the height class boundaries were translated into DBH and the ingrowths into the height classes linearly interpolated to 7cm and 10cm. The ingrowth basal areas into the height classes were obtained by multiplying the interpolated ingrowth numbers with the basal areas at 7cm and 10cm, i.e. $r.\text{trees} * \text{Pi} * (0.07/2)^2$ and $r.\text{trees} * \text{Pi} * (0.1/2)^2$. The species specific basal area (at 1.37m) sums are a standard output of TreeMig, given by multi-

plying the state variables (number of trees per grid cell, height class, and species) with the species specific basal area of each height class. To account for the ingrown trees dying within a decade, as an approximation the survival in each year to the power of 5 was used. Thereby, it was assumed that the trees have to survive in average 5 years in each decade, and that the current mortality is valid for these 5 years.

1.11.9 References

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1.12 LPJ-GUESS

1.12.1 Authors

Tim Anders, Jessica Hetzer, Thomas Hickler

1.12.2 Model

The model was originally developed by Ben Smith of Lund University in a collaboration also involving the Potsdam Institute for Climate Impact Research and the Max-Planck Institute for Biogeochemistry. Over the years, many people from institutes around the world have contributed to the refinement and further development of the model.

We used the process-based mechanistic model LPJ-GUESS to simulate vegetation dynamics considering tree species, age cohorts, gap dynamics and biogeochemical cycles. Parameters of the model reflect an updated version of the most common European tree species as well as typical shrub PFTs as described by Hickler et al. (2012).

The most complete reference resource for the LPJ-GUESS model and regeneration module is:

- Smith, B. (2001). LPJ-GUESS-an ecosystem modelling framework. Department of Physical Geography and Ecosystems Analysis, INES, Sölvegatan, 12, 22362.
- Smith, B., Wårlind, D., Arneth, A., Hickler, T., Leadley, P., Siltberg, J., & Zaehle, S. (2014). Implications of incorporating N cycling and N limitations on primary production

in an individual-based dynamic vegetation model. Biogeosciences, 11(7), 2027-2054.

- Source code is available on demand (see <https://web.nateko.lu.se/lpj-guess/>).

1.12.3 Climate

We used the provided daily time series of climatic variables from 1981 to 2018. The climatic variables base on the CHELSA data set with a spatial resolution of $0.008^\circ \times 0.008^\circ$ (~ 1 km) (Karger et al., 2021). Daily average temperature (tas) [$^\circ\text{C}$], daily average maximum temperature (tasmax) [$^\circ\text{C}$], daily average minimum temperature (tasmin) [$^\circ\text{C}$], precipitation sum (pr) [mm] and surface solar (shortwave) radiation (rsds) were taken to set up the LPJ-GUESS simulation. Used climatic variables were converted to netCDF files. As LPJ-GUESS requires the climatic variables in specific units, temperature variables (tas, tasmax, tasmin) [$^\circ\text{C}$] were converted to Kelvin and surface solar radiation (rsds) [Jm^{-2}] was converted to W/m^2 by dividing rsds by 86400 s (3600 s/h * 24 h). Nitrogen deposition was considered to be constant at a level of 10 kgN/ha/year. Atmospheric carbon dioxide concentration data from 1900 to 2018 was taken from the global carbon project (Quéré et al. 2018).

1.12.4 Soil

All sites were simulated with default values for a medium textured soil type (sand: 0.35, clay: 0.15, 823 silt: 0.5) in LPJ-GUESS.

1.12.5 Topography

Topography was not considered.

1.12.6 Tree species

LPJ-GUESS can be run in different modes, with different levels of abstraction of the population and community processes. For this study, the more detailed ‘cohort’ mode was used, in which individuals, patches and vertical canopy structure are represented explicitly, but living individuals within a cohort (age class) of a given tree species in a given patch are assumed to be identical (in terms of all state variables, such as height and stem diameter). Simulations consider the main tree species as well as other PFTs yielding an appropriate representation of European vegetation, including only tree and shrub species that are widely distributed across Europe and can become dominant in some areas (Hickler et al., 2012). Mediterranean rain-green small shrubs with shallow roots (e.g. *Lavendula* spp., *Rosmarinus* spp.) and alpine/arctic shrubs (e.g. *Vaccinium* spp.) were represented as PFTs in the model. As in earlier applications of LPJ-GUESS, herbaceous vegetation was represented by two ‘generic herb’ PFTs, with C3 and C4 photosynthesis, respectively. The final set included 16 tree species, one Mediterranean shrub PFT, one boreal/alpine shrub PFT, and the two herbaceous PFTs described earlier (Table 2). To increase the chances of shade-intolerant species becoming established, patch-destroying disturbances were allowed as described in Hickler et al. 2012. *Acer pseudoplatanus* and *Alnus glutinosa* are not parameterized in LPJ-GUESS and therefore not considered.

1.12.7 Simulation

In this study, vegetation is simulated in so called patches that represent forest areas of fixed size. Patches can be regarded as sample stands in a grid cell, each of which represents an 0.1 ha (comparable to figure 1 of the tree regeneration workshop protocol). In this study, vegetation dynamics

were simulated by 2000 replicate patches each 0.1 ha in size. To match the required sample size, we processed the data so that ten 0.1 ha patches were merged to one 1 ha sample.

1.12.7.1 Dispersal Model formulations of establishment are based on those employed within the ‘forest gap’ model FORSKA (Leemans & Prentice, 1989; Prentice et al., 1993). The number of new saplings of each woody PFT/species and in each patch each year is drawn at random from the Poisson distribution, with an expectation influenced by a PFT/species-specific maximum establishment rate and by the ‘propagule pool’, i.e. the amount of carbon allocated to reproduction by all individuals of the PFT/species at all patches in the previous year. No saplings are established in a given patch if the minimum PAR level at the forest floor is below a PFT/species-specific threshold, which is higher for more light-demanding PFTs/species.

1.12.7.2 Simulation length What is the simulation length, and how have you determined the simulation time until the equilibrium?

The simulations were initialized from bare ground (no biomass) and the model was spun up for 500 years until the modelled vegetation was in approximate equilibrium with the climate and CO₂ around the year 1900 (Smith et al., 2001; Hickler et al., 2012).

If you have run more than one simulation per site, please describe the differences of the approaches used. We performed one simulation per site.

1.12.8 Output

The generated output file is called Output_SGN_LPJGUESS.txt. Each row of the output dataset contains variables regarding the decade 2008-2018. The first two columns describe the study site

(column “site”, values reflect site ID) and the 1 ha samples of that specific site (column “sample”, values range from 1 to 200). Output variables are species-specific. Although we simulated a total of 20 European tree species and PFTs, our output file considers only the species required by the protocol (column “species”, values are the abbreviations for the species name (“abal” for *Abies alba*, “cabe” for *Carpinus betulus*, “fasy” for *Fagus sylvatica*, “frex” for *Fraxinus excelsior*, “pabi” for *Picea abies*, “pisy” for *Pinus sylvestris*, “tico” for *Tilia cordata*, “betu_pen” for *Betula pendula*, “betu_pub” for *Betula pubescens*, “quer_il” for *Quercus ilex*, “quer_pub” for *Quercus pubescens*, and “quer_rob” for *Quercus robur*). Since *Acer pseudoplatanus* (“acps”) and *Alnus glutinosa* (“algl”) are not parameterized for LPJ-GUESS so far, we have not included these species in the output. Further we excluded shrubs (alpine/arctic shrubs and *Quercus coccifera*) and herbaceous vegetation from the final output as this study focusses on tree regeneration only. The first variable is the number of 7 cm recruits “r_7cm.trees” calculated as the sum of all trees of the same species that cross the threshold of 7 cm DBH between 2008 and 2018 in that specific sample of that specific site. The variable “r_10cm.trees” refers to 10 cm threshold respectively. The 7 cm recruits’ basal area „r_7cm.ba” is calculated as a weighted sum of r_7cm.trees multiplied by recruits basal area at that time (with $ba=(dbh/2)\cdot\pi$). Similarly, r_10cm.ba was calculated for 10 cm recruits. The last two columns describes the mean annual basal area and the mean number of trees per site, sample, and species overall years between 2008 and 2018 (column “ba”).

Table 1: Species/PFT characteristics and parameter of Hickler et al. 2012. r base respiration rate, kallm1 constant in allometry equations, Tc,min minimum winter temperature for establishment, Tc,max maximum coldest-month temperature for establishment, GDD5 minimum degree-day sum above 5 °C for establishment, fAWC minimum growing-season fraction of available soil

water holding capacity in the first soil layer, rfire fraction of individuals surviving fire, k_{leaf}:sa leaf longevity, CA_{max} maximum woody crown area. Parameter that are associated with establishment processes are marked in bold. Species/PFT

Species/PFT	Short name	Geographic range	r^* (gCgN 'day')	Growth form	k_{allow}^* (°C)	$T_{c,\min}^*$ (°C)	$T_{c,\max}^*$ (°C)	GDD_5^* (°Cd)	fAWC	Chilling requirement*	Shade tolerance class	r_{fire}	k_{leaf} ^a	Z_t^{**} (yr)	a_{leaf}^* (yr)	a_{end}^* (yr)	CA_{\max}^b (m ²)
<i>Abies alba</i>	abal	temperate	0,055	tree	150	-4,5	-2	1450	0,35	-	tolerant	0,1	4000	0,8	4	350	40
<i>Betula pendula</i>	betu_pen	temperate	0,055	tree	250	-30	-	700	0,42	intermediate	intolerant	0,1	5000	0,8	0,5	200	40
<i>Betula pubescens</i>	betu_pub	boreal	0,11	tree	250	-	-	350	0,5	intermediate	intolerant	0,1	5000	0,8	0,5	200	40
<i>Carpinus betulus</i>	cabe	temperate	0,055	tree	250	-8	-	1200	0,33	high ^b	intermediate	0,1	5000	0,7	0,5	350	40
<i>Corylus avellana</i>	cor_ave	temperate	0,055	tree	250	-8	-	800	0,3	intermediate	intolerant	0,1	4000	0,7	0,5	300	15
<i>Fagus sylvatica</i>	fasy	temperate	0,055	tree	250	-3,5	-	1500	0,3	high ^b	tolerant	0,1	5000	0,8	0,5	500	40
<i>Fraxinus excelsior</i>	frex	temperate	0,055	tree	250	-16	-	1100	0,4	low	intermediate	0,1	5000	0,8	0,5	350	40
<i>Juniperus oxycedrus</i>	jun_oxy	Mediterranean	0,055	shrub	150	0	-	2200	0,01	-	intolerant	0,4	1500	0,5	1,5	200	10
<i>Picea abies</i>	pabi	boreal	0,11	tree	150	-30	-1,5	600	0,43	-	tolerant	0,1	4000	0,8	4	500	40
<i>Pinus halepensis</i>	pin_hal	Mediterranean	0,055	tree	150	3	-	3000	0,05	-	intolerant	0,4	2000	0,6	2	350	40
<i>Pinus sylvestris</i>	pisy	boreal	0,11	tree	150	-30	-1	500	0,25	-	intermediate	0,4	2000	0,6	2	500	40
<i>Quercus coccifera</i>	quer_coc	Mediterranean	0,055	shrub	250	0	-	2200	0,1	-	intermediate	0,3	2500	0,5	1,5	350	10
<i>Quercus ilex</i>	quer_il	Mediterranean	0,055	tree	250	-2	-	1800	0,1	-	intermediate	0,3	3000	0,5	2	350	40
<i>Quercus pubescens</i>	quer_pub	supra-Mediterranean	0,055	tree	250	-5	-	1900	0,2	low	intermediate	0,2	4000	0,6	0,5	500	40
<i>Quercus robur</i>	quer_rob	temperate	0,055	tree	250	-16	-	1100	0,25	low	intermediate	0,2	4000	0,6	0,5	500	40
<i>Tilia cordata</i>	tico	temperate	0,055	tree	250	-18	-	1000	0,33	high ^b	intermediate	0,1	5000	0,8	0,5	350	40
Boreal evergreen shrub ^e	BES	boreal	0,11	shrub	250	-	-1	300	0,25	-	intolerant	0,1	500	0,8	2	50	3
Mediterranean raingreen shrub ^e	MRS	Mediterranean	0,055	shrub	250	0	-	2200	0,01	low	intolerant	0,3	1500	0,9	1	100	10
C ₃ herbaceous		temperate-boreal	0,055	herbaceous	-	-	-	-	0,01	-	-	0,5	-	0,9	1	-	-
C ₄ herbaceous		tropical	0,011	herbaceous	-	15,5	-	-	0,01	-	-	0,5	-	0,9	1	-	-

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1.13 aDGVM2

1.13.1 Authors

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1.13.2 Model

We used aDGVM2, an individual-based dynamic vegetation model that is based on concepts from community assembly theory and uses a functional trait approach (Langan et al., 2017; Scheiter et al., 2013). The model simulates growth, reproduction, and mortality of individual plants while keeping track of state variables, such as biomass, height, and leaf area. Each plant in aDGVM2 is characterized by a plant-specific set of trait values. Traits describe growth form, leaf characteristics, hydraulic characteristics, resource allocation, architecture, reproduction, mortality, and

response to disturbance. Most plant traits are linked by trade-offs to constrain possible trait combinations. Selection and trait inheritance assemble plant communities that are adapted to biotic and abiotic conditions. Plants with trait combinations that allow sufficient growth and reproduction rates, and that allow plants to cope with competition and disturbances can contribute their trait values to the community trait pool. Trait mutation and recombination may alter trait values in the community trait pool. Randomly drawn seeds from the trait pool are added to the plant population and new plants start growing from seeds. Plants that are not adapted to the prevailing disturbance regimes, biotic and abiotic conditions, or that do not allocate enough carbon to reproduction disappear from the population. Therefore, successful ecological strategies emerge dynamically from these community assembly and reproduction process. Due to the trait-based approach, species or plant functional types (PFTs) are not pre-defined and hard-coded in aDGVM2. Rather, different PFTs or ecological strategies that are adjusted to the prevailing biotic and abiotic conditions emerge from community assembly processes (Scheiter et al., 2013), and plants can be classified into PFTs or ecological strategies based on their trait values in a post-processing step. The aDGVM2 has primarily been developed for tropical and sub-tropical ecosystems and it has not been tested and benchmarked for Europe. We applied the model in the original version. Data-model comparisons with model results were not done and the model was not changed to improve agreement with any data for Europe.

The most complete reference resource for the aDGVM2 model and regeneration module is:

- Scheiter S, Langan L, Higgins SI (2013) Next generation dynamic global vegetation models: learning from community ecology. NEW PHYTOLOGIST, 198, 957-969.

1.13.3 Climate

The aDGVM2 simulates vegetation at daily temporal resolution. We therefore used daily climate input data for the period 1981-2018 according to the modeling protocol.

1.13.4 Soil

Soil quality data was converted to maximum rooting depth. Specifically, the soil quality value multiplied by 2 and the result was used as maximum rooting depth. We used the multiplication, as we typically use maximum soil depth and maximum rooting depth of 10m. Previous model simulations showed that rooting depth and soil dept have strong impacts on vegetation dynamics by influencing water availability to plants (Langan et al., 2017). We therefore considered it as adequate representation of soil quality. Other soil characteristics including volumetric water-holding capacity, soil hydraulic conductivity, soil bulk density, soil depth, soil texture, soil carbon content, soil wilting point and field capacity were taken from the FAO (<http://www.fao.org>, Nachtergael et al., 2009).

1.13.5 Topography

We used elevation according to the modeling protocol. In aDGVM2, elevation is used to calculate atmospheric pressure which in turn influences ecophysiological processes related to water and carbon fluxes at leaf and canopy level. Information on slope and aspect was not used, as related processes (e.g., impacts on runoff or radiation balance) are not implemented in aDGVM2.

1.13.6 Tree species

The aDGVM2 does not simulate pre-defined species or PFTs. The 11 tree species included in the modeling protocol cannot be implemented and parametrized with reasonable effort. We therefore classified simulated trees into different ecological strategies as a post-processing step. We used all combinations of evergreen/deciduous, light/water triggered phenology, low/high SLA. Evergreen/deciduous phenology and light/water triggered phenology are traits implemented in aDGVM2. The threshold to distinguish high and low SLA was defined as 20 m²/kg. We used these traits as previous simulation experiments showed that patterns of these traits emerge along environmental gradients while patterns of other traits implemented in aDGVM2 are often less clear. Ecological strategies considered are: low SLA, deciduous, rain-triggered; low SLA, deciduous, light-triggered; low SLA, evergreen, rain-triggered; low SLA, evergreen, light-triggered; high SLA, deciduous, rain-triggered; high SLA, deciduous, light-triggered; high SLA, evergreen, rain-triggered; high SLA, evergreen, light-triggered.

1.13.7 Simulations

Simulations followed the modeling protocol. Simulations were conducted for all sites using the provided daily climate and soil data. By default, aDGVM2 simulates 1ha stands. To implement the modeling protocol, adjustments to scale model results to 1 ha level were therefore not required. The model was initialized by default initialization routines, i.e., traits of individual plants were drawn randomly from a pre-defined range of values for each trait. Ranges of trait values are provided in Langan et al. (2017). The model was initialized with bare ground and 2880 tree seedlings with 100g each. The aDGVM2 simulates both trees and grasses. As the simulation experiment aims at

tree/forest regeneration, simulations were conducted only with trees while grasses were removed.

We conducted 5 replicates for each of the 200 sites to account for stochastic processes in aDGVM2.

Stochastic processes include random initialization of trait values of initial plant populations, demographic processes such as plant mortality or selection of seeds from seed bank, or the community assembly processes including mutation and cross-over. Climate time series used for different replicates were identical such that variation between replicates can be attributed by stochastic processes in aDGVM2.

Although aDGVM2 includes routines to simulate fire, simulations were conducted in the absence of fire. Management was not simulated.

1.13.8 Dispersal

The aDGVM2 does not simulate seed dispersal.

1.13.9 Simulation length

We first conducted a 600-year spin-up with a randomized order of years 1981-2018 provided in the CHELSA daily climate data. Spin-up is required to ensure that both state variables such as biomass and tree cover and community trait composition have stabilized and are in a dynamic equilibrium with climate. Previous model simulations showed that a 600-year spin-up is sufficient to reach such an equilibrium state (Langan et al., 2017). Following the spin-up, we simulated transient vegetation dynamics with daily CHELSA climate data for the period 1981-2018.

1.13.10 Outputs

To create output variables, we randomly selected 10-year periods within the transient phase (i.e., period 1981-2018 after spin-up phase) and calculated averages of all required output variables following the modeling protocol. The selected 10-year periods differed between sites and replicates.

The aDGVM2 does not simulate pre-defined species or PFTs and trees were classified into different ecological strategies (see section Tree species). Codes for the ecological strategies in the species column of the output files are: 1 - low SLA, deciduous, rain-triggered 2 - low SLA, deciduous, light-triggered 3 - low SLA, evergreen, rain-triggered 4 - low SLA, evergreen, light-triggered 5 - high SLA, deciduous, rain-triggered 6 - high SLA, deciduous, light-triggered 7 - high SLA, evergreen, rain-triggered 8 - high SLA, evergreen, light-triggered

Simulations were conducted for all 200 sites. We conducted 5 replicates per site to account for stochastic processes in aDGVM. In the output files, replicates are given as follows: Replicate 1 – sample 1:200 Replicate 2 – sample 201:400 Replicate 3 – sample 401:600 Replicate 4 – sample 601:800 Replicate 5 – sample 801:1000

1.13.11 References

Langan L; Higgins SI; Scheiter S (2017) Climate-biomes, pedo-biomes or pyro-biomes: which world view explains the tropical forest - savanna boundary in South America? JOURNAL OF BIOGEOGRAPHY, 44, 2319-2330.

Nachtergael, F., van Velthuizen, H., Verelst, L., Batjes, N., Dijk- shoorn, K., Van Engelen, V., Fischer, G., Jones, A., Montanarella, L., and Petri, M.: Harmonized world soil database (version

1.1), FAO, Rome, Italy, IIASA, Laxenburg, Austria, 2009.

Scheiter S, Langan L, Higgins SI (2013) Next generation dynamic global vegetation models: learning from community ecology. *NEW PHYTOLOGIST*, 198, 957-969.

2 Supplementary figures and tables

2.1 Ingrowth levels, tree diversity and mortality in tree establishment

Table S1: Number of total samples, samples with zero recruitment and the proportion of zero recruitment per model and observed data.

Model	Total (7 cm)	Total (10cm)	No recruitment (7 cm)	No recruitment (10cm)	Percentage of no recruitment (7 cm)	Percentage of no recruitment (10 cm)
Observed	5676	6564	203	238	3.63	3.58
4C	133000	165000	23898	30177	18.29	17.97
ForCEEPS	363000	440000	1	137	0.03	0.00
ForCEEPS(f)	363000	440000	42	202	0.05	0.01
FORMIND	363000	440000	8663	10082	2.29	2.39
ForClim 1	396000	480000	7	28	0.01	0.00
ForClim 11	396000	480000	77	192	0.04	0.02
SIBYLA	363000	440000	1565	5539	1.26	0.43
xComp	297000	360000	0	0	0.00	0.00
PICUS	363000	440000	400	400	0.09	0.11
iLand	363000	440000	26	143	0.03	0.01
LandClim	363000	440000	378	1347	0.31	0.10
Landis II	363000	440000	28621	34844	7.92	7.88
TreeMig	396000	480000	0	0	0.00	0.00
LPJ-GUESS	328000	398000	6742	7140	1.79	2.06
aDGVM2	6600	8000	603	824	10.30	9.14

Table S2: Test of the significance of the differences of Shannon index in each model for 7 and 10 cm threshold.

model	y	Group 1	Group 2	p	p.signif
Observed	ShannonIndexRecruit	7	10	0.5752324	ns
4C	ShannonIndexRecruit	7	10	0.0112379	*
ForCEEPS	ShannonIndexRecruit	7	10	0.0022439	**
ForCEEPS(f)	ShannonIndexRecruit	7	10	0.0001502	***
FORMIND	ShannonIndexRecruit	7	10	0.0018175	**
ForClim 1	ShannonIndexRecruit	7	10	0.0000000	****
ForClim 11	ShannonIndexRecruit	7	10	0.0000078	****
SIBYLA	ShannonIndexRecruit	7	10	0.0017112	**
xComp	ShannonIndexRecruit	7	10	0.0089858	**
PICUS	ShannonIndexRecruit	7	10	0.0343325	*
iLand	ShannonIndexRecruit	7	10	0.0539118	ns
LandClim	ShannonIndexRecruit	7	10	0.0000000	****
Landis II	ShannonIndexRecruit	7	10	0.3486993	ns
TreeMig	ShannonIndexRecruit	7	10	0.4182782	ns
LPJ-GUESS	ShannonIndexRecruit	7	10	0.8213248	ns

7 cm diameter threshold

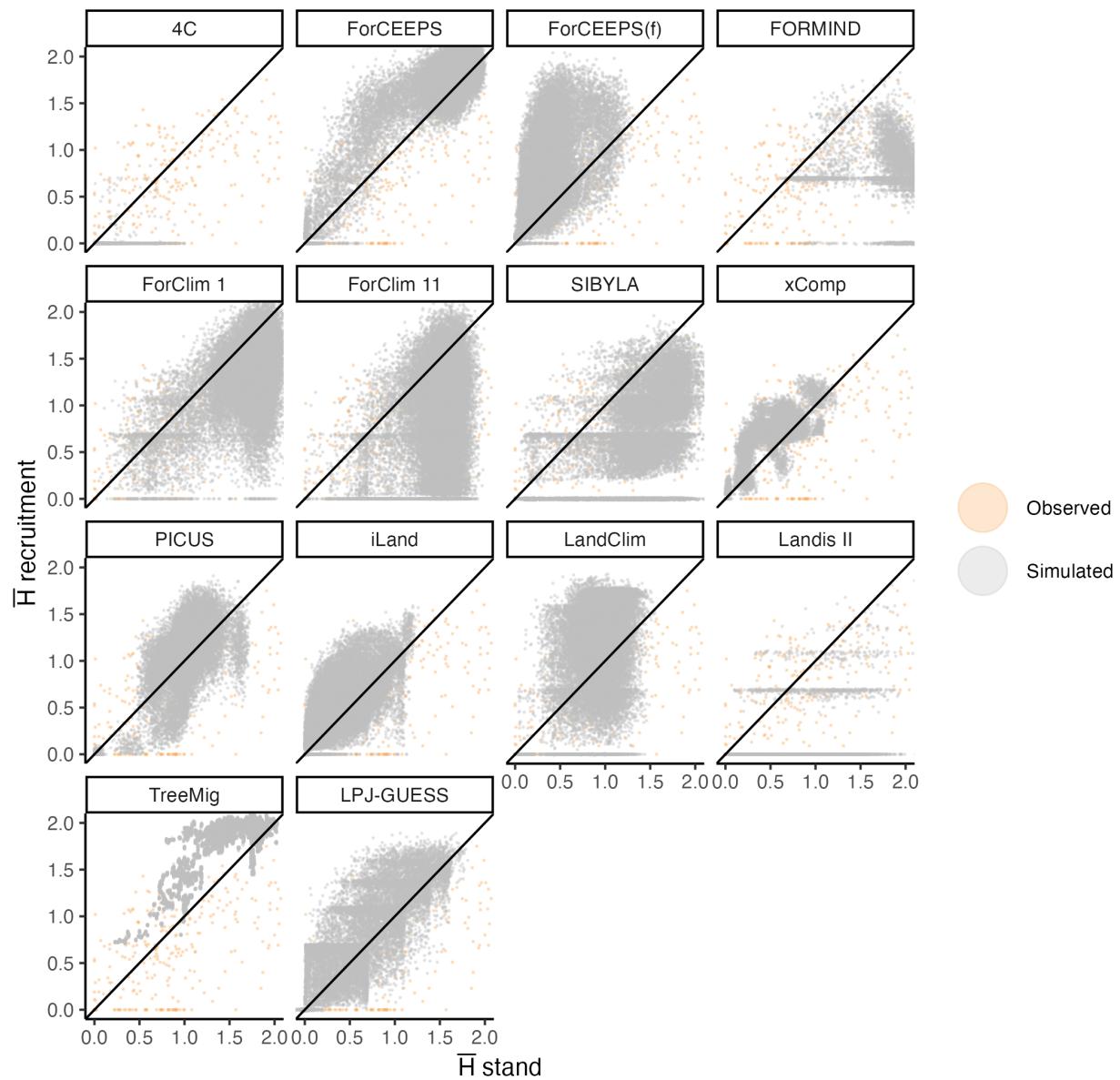


Figure S1: Mean Shannon index per site at recruitment and at the stand level both for observed and simulated values for the diameter threshold of 7cm. The black line marks where the mean Shannon index per site at recruitment and at the stand level would be equal.

10 cm diameter threshold

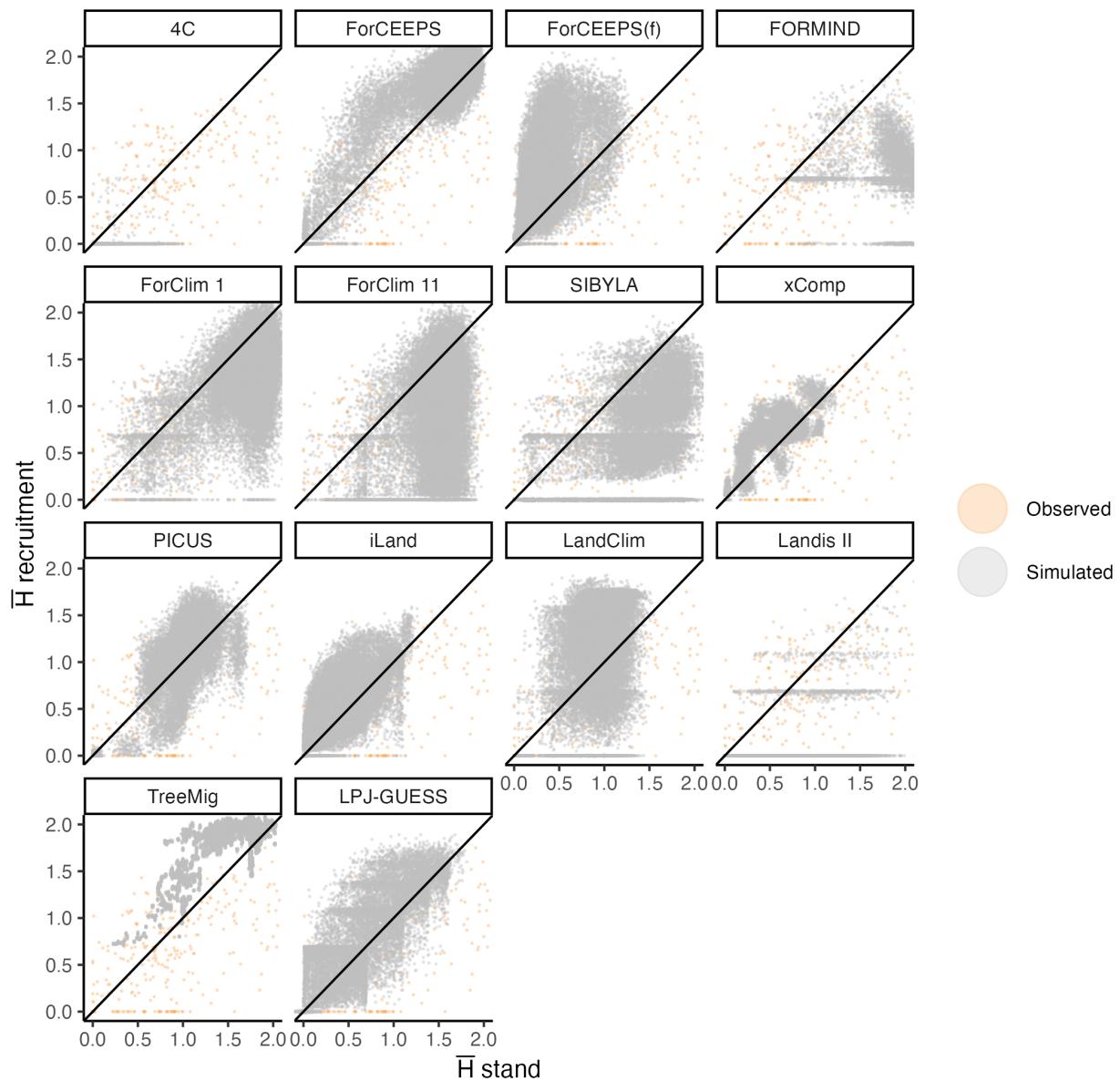


Figure S2: Mean Shannon index per site at recruitment and at the stand level both for observed and simulated values for the diameter threshold of 10cm.

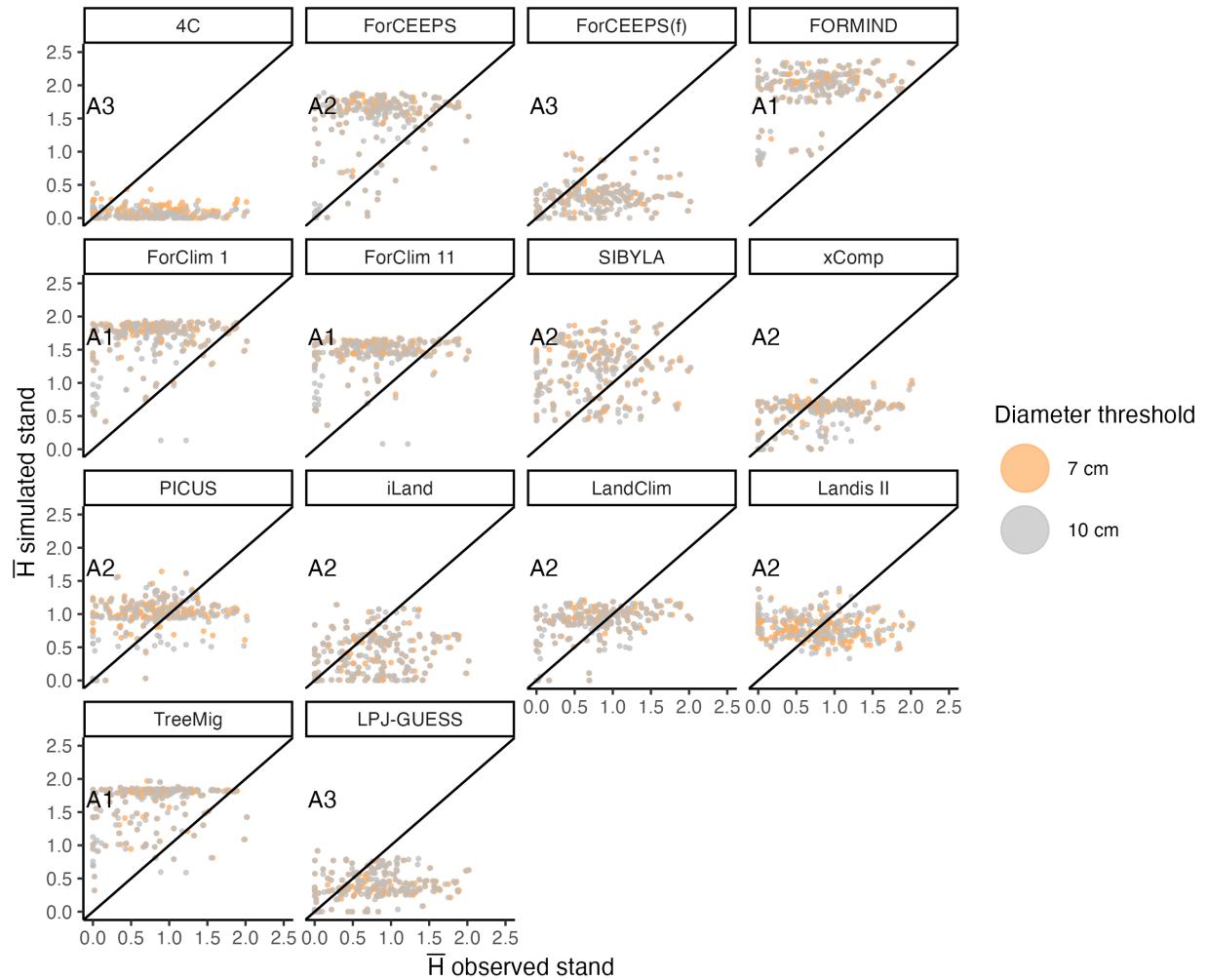


Figure S3: Mean species richness at the stand level per site in the simulated versus observed species richness. The species richness is estimated using the Shannon index calculated by basal area. A1) groups models where the simulated species composition in adults is higher than the observed, A2) groups models where the simulated species composition in adults is similar to the observed, A3) groups models where the simulated species composition in adults is lower than the observed. NOTE: The recruitment threshold recruitment for threshold 7 cm in the empirical data has several sites with no recruitment or no data and the Shannon index for those sites is NA.

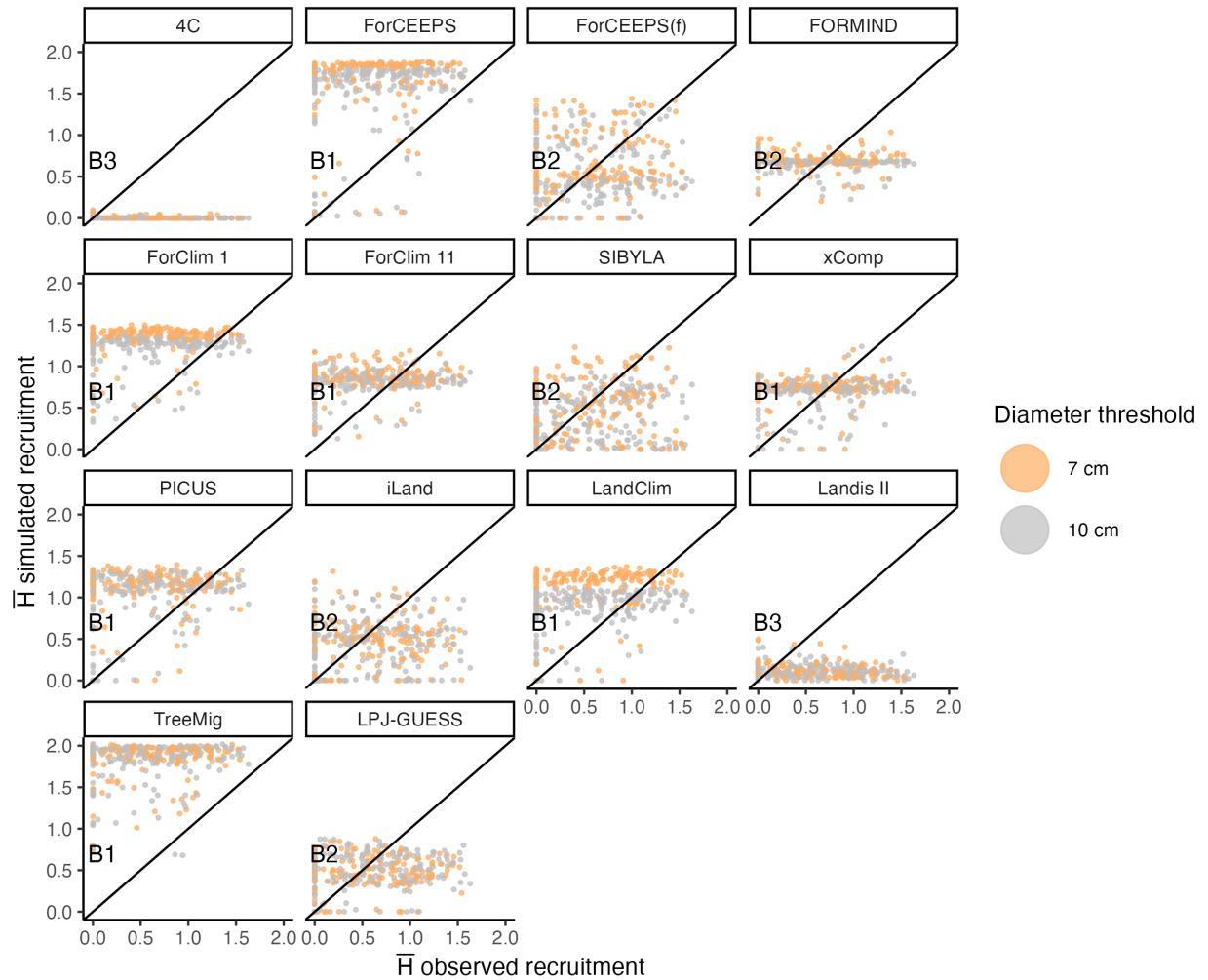


Figure S4: Mean species richness per site in the simulated recruitment versus observed species richness in the recruitment. The species richness is estimated using the Shannon index using the basal area. B1) groups models where the simulated species composition in recruitment is higher than the observed, A2) groups models where the simulated species composition in recruitment is similar to the observed, A3) groups models where the simulated species composition in recruitment is lower than the observed. NOTE: The recruitment threshold recruitment for threshold 7 cm in the empirical data has several sites with no recruitment or no data and the Shannon index for those sites is NA.

Table S3: Test of the significance of the differences of rate of recruitment at 7 cm threshold over 10 cm threshold between the observed values and the simulated values per model.

Y	Group 1	Group 2	p	p.signif
nn710	Observed	4C	0.00291	**
nn710	Observed	ForCEEPS	0.89835	ns
nn710	Observed	ForCEEPS(f)	0.02535	*
nn710	Observed	FORMIND	0.05994	ns
nn710	Observed	ForClim 1	0.59614	ns
nn710	Observed	ForClim 11	0.25164	ns
nn710	Observed	SIBYLA	0.00014	***
nn710	Observed	xComp	1.7e-15	****
nn710	Observed	PICUS	< 2e-16	****
nn710	Observed	iLand	0.07631	ns
nn710	Observed	LandClim	7.7e-05	****
nn710	Observed	Landis II	0.00021	***
nn710	Observed	TreeMig	5.7e-10	****
nn710	Observed	LPJ-GUESS	0.00137	**
nn710	Observed	aDGVM2	0.13992	ns

Table S4: Models trends in mortality between 7 and 10cm (represented in Figure S5), and the ingrowth at 7cm, based in the mean per site. The slope is the rate of change from the linear model between recruitment ratio 7-10 cm and the initial recruitment tree number.

model	Slope	Significance
Observed	0.0038	0.0280
4C	0.0054	0.0145
ForCEEPS	0.0010	0.0009
ForCEEPS(f)	0.0010	0.0000
FORMIND	0.0014	0.4006
ForClim 1	0.0007	0.2244
ForClim 11	-0.0016	0.0000
SIBYLA	0.0537	0.0000
xComp	0.0035	0.0000
PICUS	0.0066	0.0000
iLand	0.0027	0.0000
LandClim	-0.0028	0.0000
Landis II	0.0340	0.0001
TreeMig	0.0006	0.0090
LPJ-GUESS	0.0021	0.0018
aDGVM2	1.6130	0.3680

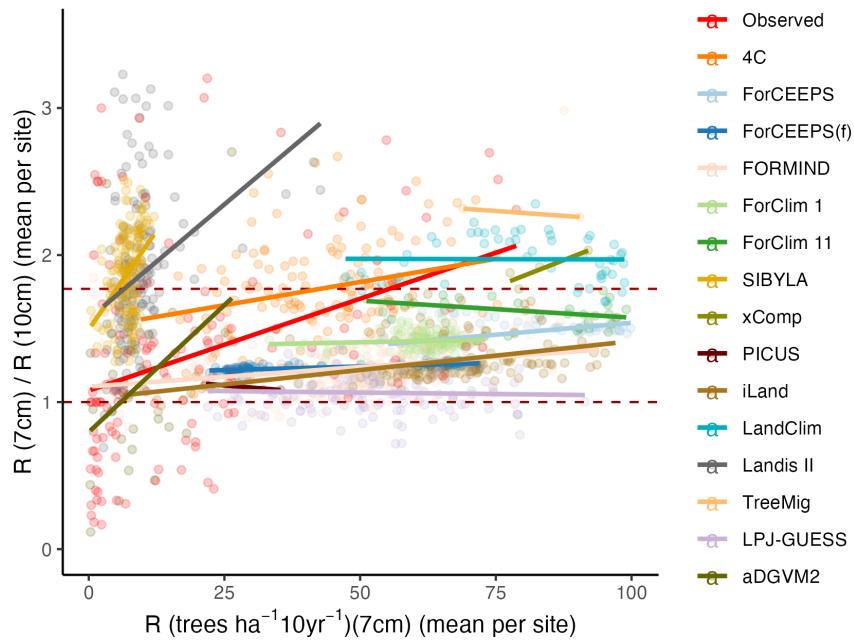


Figure S5: Recruitment ratio between 7 and 10cm and the initial recruitment tree number at 7cm. Dashed red lines mark a ratio equal to 1 indicating no decrease between 7 and 10cm tree recruitment and ratio equal to 1.77 corresponding with the Reineke self-thinning ratio under evenaged conditions.

2.2 Model traits and model performance

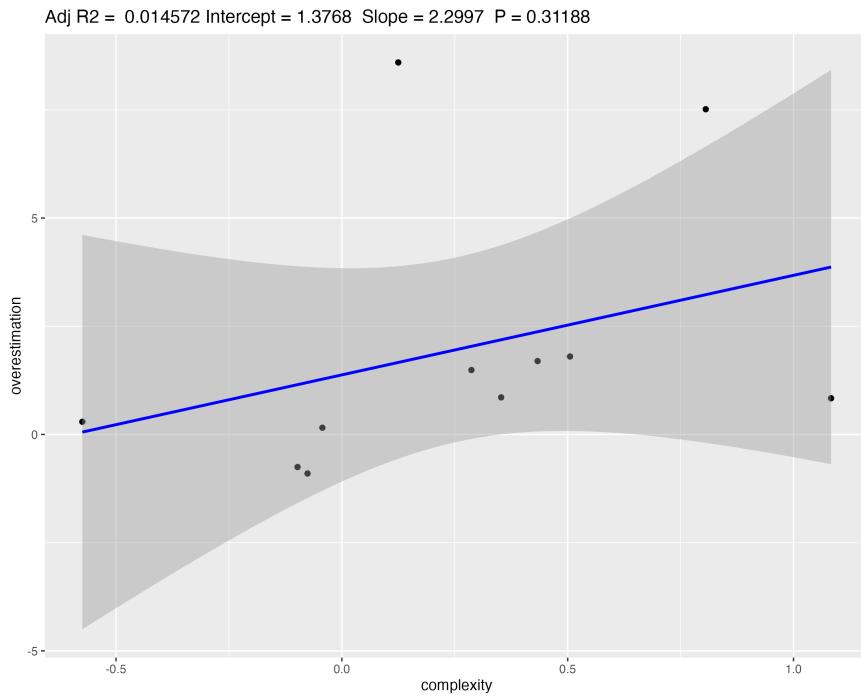


Figure S6: Plot and summary statistics of the linear model between the overestimation proportion in ingrowth levels and the mean complexity value of the establishment modules.

Table S5: Test of the significance of the differences of rate of recruitment at 7 cm threshold of the observed values and the simulated values per model.

Y	Group 1	Group 2	p	p.signif
r.trees	Observed	4C	0.256	ns
r.trees	Observed	ForCEEPS	< 2e-16	****
r.trees	Observed	ForCEEPS(f)	0.027	*
r.trees	Observed	FORMIND	0.036	*
r.trees	Observed	ForClim 1	< 2e-16	****
r.trees	Observed	ForClim 11	< 2e-16	****
r.trees	Observed	SIBYLA	7.9e-09	****
r.trees	Observed	xComp	< 2e-16	****
r.trees	Observed	PICUS	< 2e-16	****
r.trees	Observed	iLand	3.9e-08	****
r.trees	Observed	LandClim	< 2e-16	****
r.trees	Observed	Landis II	7.8e-08	****
r.trees	Observed	TreeMig	< 2e-16	****
r.trees	Observed	LPJ-GUESS	3.3e-07	****
r.trees	Observed	aDGVM2	2.8e-10	****

Table S6: Test of the significance of the differences of rate of recruitment at 7 cm threshold of the observed values and the simulated values per model.

Y	Group 1	Group 2	p	p.signif
ShannonIndexRecruit	Observed	4C	< 2e-16	****
ShannonIndexRecruit	Observed	ForCEEPS	< 2e-16	****
ShannonIndexRecruit	Observed	ForCEEPS(f)	0.17856	ns
ShannonIndexRecruit	Observed	FORMIND	0.07378	ns
ShannonIndexRecruit	Observed	ForClim 1	< 2e-16	****
ShannonIndexRecruit	Observed	ForClim 11	4.5e-10	****
ShannonIndexRecruit	Observed	SIBYLA	0.01610	*
ShannonIndexRecruit	Observed	xComp	0.02709	*
ShannonIndexRecruit	Observed	PICUS	< 2e-16	****
ShannonIndexRecruit	Observed	iLand	0.00462	**
ShannonIndexRecruit	Observed	LandClim	< 2e-16	****
ShannonIndexRecruit	Observed	Landis II	< 2e-16	****
ShannonIndexRecruit	Observed	TreeMig	< 2e-16	****
ShannonIndexRecruit	Observed	LPJ-GUESS	0.00063	***

2.3 Total ingrowth and individual species regeneration niches

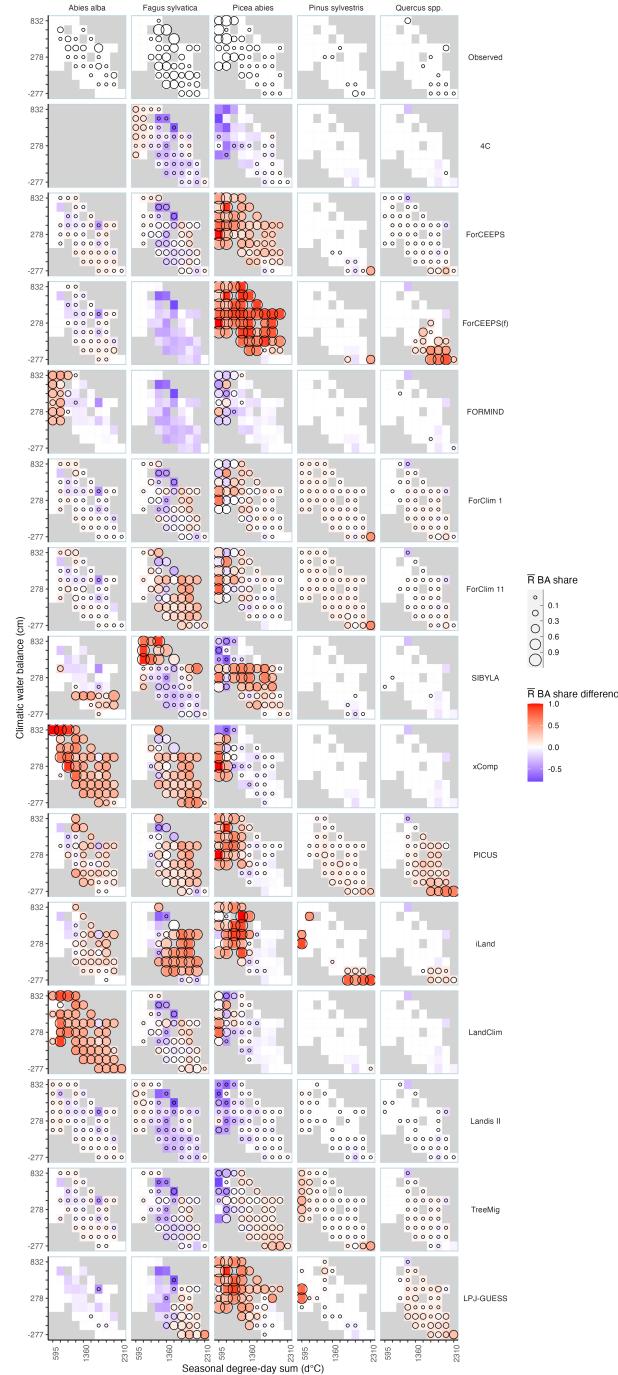


Figure S7: Departure of each model in the representation of the main species recruitment relative abundance from the observations across the environmental gradients for a 10cm threshold. The values shown are the mean of samples per site and across sites in bins, where the range of the climatic water balance (cm) and seasonal degree-day sum ($d^{\circ}\text{C}$) was divided in 10 bins. The point sizes represent ratio between recruited basal area of the species and the total recruited basal area for all the species. The color gradient shows the difference between the simulated and observed ratio between recruited basal area of the species and the total recruited basal area: grey cell represent areas of the environmental gradient in which the model had R BA share and the empirical data did not because both recruitment and stand level recruitments were equal to zero.