# Model manual

## Modeling the long-term dynamics of tropical forests: from leaf traits to whole-tree growth patterns

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## Introduction

This manual is designed as a step-by-step manual to help you setting up the first model runs. The model was implemented using the open-source 3D modeling platform GroIMP. GroIMP is a Java application and should thus (theoretically) run on Linux, Windows and MacOS platforms. We used GroIMP on Windows 10 (64-bit) with Java version 1.8. When experiencing problems with GroIMP, please refer to https://sourceforge.net/projects/groimp/ or http://www.grogra.de/.

Please note that the model code and the configuration files are not necessarily user friendly (no professional computer scientist here), so please do not hesitate to contact us if you have problems applying the model.

## Installation

Please download the latest version of GroIMP (https://sourceforge.net/projects/groimp/) and the Java runtime environment (https://java.com/). We recommend using the 64-bit versions of GroIMP and the Java runtime environment. Install Java first, then GroIMP. During the installation process, GroIMP asks to set the Maximum Java heap size. This defines the maximum memory (RAM) GroIMP can use, i.e., if a GroIMP run requires more memory it will stop with an out-of-memory error. The predefined size (1.500 MB) might be enough for single tree models, but not for forest models. We recommend using a Maximum Java heap size of at least 10.000 MB for 50x50m forest models, preferably more if available. After installation, the Maximum Java heap size can be changed via the *Properties* dialog of the GroIMP shortcut (right-click on the GroIMP shortcut icon and chose *Properties* from the context menu). Here, chose the *Shortcut* tab and under *Target* and you should see something comparable to "C:\Program Files\Common Files\Oracle\Java\javapath\javaw.exe" -Xmx50000M -jar core.jar". The number after Xmx defines the Maximum Java heap size in MB and can be changed if desired.

Two sets of model files are available as zip-files at Github (https://github.com/julianoscabral/MoF3D). These files have the self-explanatory names "ForestModel.zip" and "TreeModel.zip". After unzipping these files, the basic folder structure of the model becomes apparent. There are three folders: *Pictures*, *Results*, and *Model*. The first two folders are initially empty and are used during model runs to store pictures and the model output files. The *Model* folder contains three files:

3DTreeAndForestModel.gsz, Forest_param_global.txt and Forest_param_pass0.txt. 3DTreeAndForestModel.gsz contains the actual model code, the two text files are files that can be used to control the model runs (more details below). Please note that the actual model code is the same whether you want to simulate forests or trees – only the parameter values in the Forest_param_global.txt and Forest_param_pass0.txt differ.

## Starting a GroIMP model run

Please start GroIMP. An initially empty window will appear. Select *File* and *Open* from the dropdown menu, navigate to the model code file (3DTreeAndForestModel.gsz) in the *Model* folder (We recommend starting with the tree model to familiarize yourself with GroIMP) and open it. There are different window layouts available, the most convenient one for the purpose of running the models is the RGG Layout, which can be selected from the dropdown menu (*Panels* => *Set Layout* => *RGG Layout*). Now, your GroIMP window should look similar to Fig. 1.

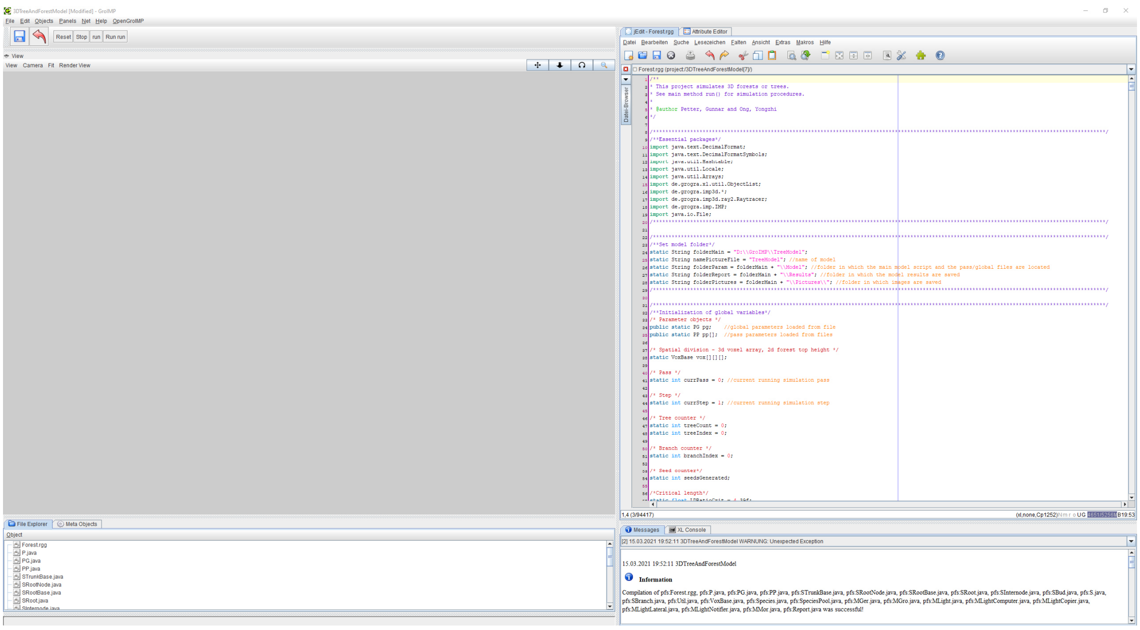

**Fig. 1.** Basic Layout of GroIMP after loading the main model file (3DTreeAndForestModel.gsz). The source code is shown on the top-right, the tree/forest will be visualized on the top-left. The main model file contains several files, please use the File Explorer on the bottom-left side to navigate through them. The *Forest.rgg* is the main source code file.

The model code will generally be displayed in the top-right window. The model itself consists of several files that are displayed in the *File Explorer* window (bottom-left). The *Forst.rgg* file is the main model file - if it is not loaded automatically, please double-click on it so it is shown on the top-right. In this file, the path to the main model folder, i.e., the folder that contains the *Pictures*, *Results*, and *Model* folders, has to be specified - please change it accordingly (source code line 24). After this, please save the altered model code by clicking on the save button (or choosing *File* and *Save* from the dropdown menu). Saving the file will automatically start the compilation process - if the altered model path is correct, the information that the compilation was successful should appear in the *Messages* windows (bottom-right). Now you can start the model run by clicking the *Run run* or the *run* button right above the *View* window on the top-left. The button *run* causes the model to run one time step at a time, the button *Run run* causes the model to run time step after time step automatically. After starting the model, messages like the current time step are displayed on the bottom-right, and the tree or the forest is visualized in the *View* window (Fig. 2). In the *View* window, you can choose between the Wireframe or the Shader view from the dropdown menu (*View* => *Display* => *Wireframe* or *OpenGL*). We recommend starting with the *Wireframe* view – the model runs faster and it is more convenient to adjust the view. You can adjust the view (e.g., zoom, rotate, shift) using the four buttons on the top-right of the *View* window. For this purpose, please hold down the left mouse button on the respective button and adjust the view by moving the mouse. If you should lose sight of your tree or forest, chose *Fit Visible* from in the *Fi*t dropdown menu. The *OpenGL* view is meant for the purpose of visualizing a rendered version of the forest or tree. This can be chosen if you want to make better-looking pictures of the simulated forest or tree. The pictures of the model runs are saved by default. This means, after each time step, the visualization as seen in the *View* window is saved in the *Picture* folder. Please adjust the *View* window according to your preferences. It is important to note that most existing output files and pictures in the *Results* and *Pictures* folders are overwritten when starting a model run. For instance, if you run a model until time step 10, stop it and run it again, most previous files will be replaced. Some outputs like the *Forest* output file (see below) will not be overwritten, rather the results of each model run will be appended to the existing one. If you adjusted a model run for your purposes, it is hence best to remove all files from the *Pictures* and *Results* folders before starting a model run to get "clean" results.

In general, if you want to stop a model run, click the stop button. If you want to restart the model run, click the save button (the model code will be compiled) and restart the model again (*run* or *Run run*). You might experience problems when clicking the *Reset* button – Use the save button instead if this should be the case, it will have the same effect.

More information about controlling the model runs is provided in the following section.

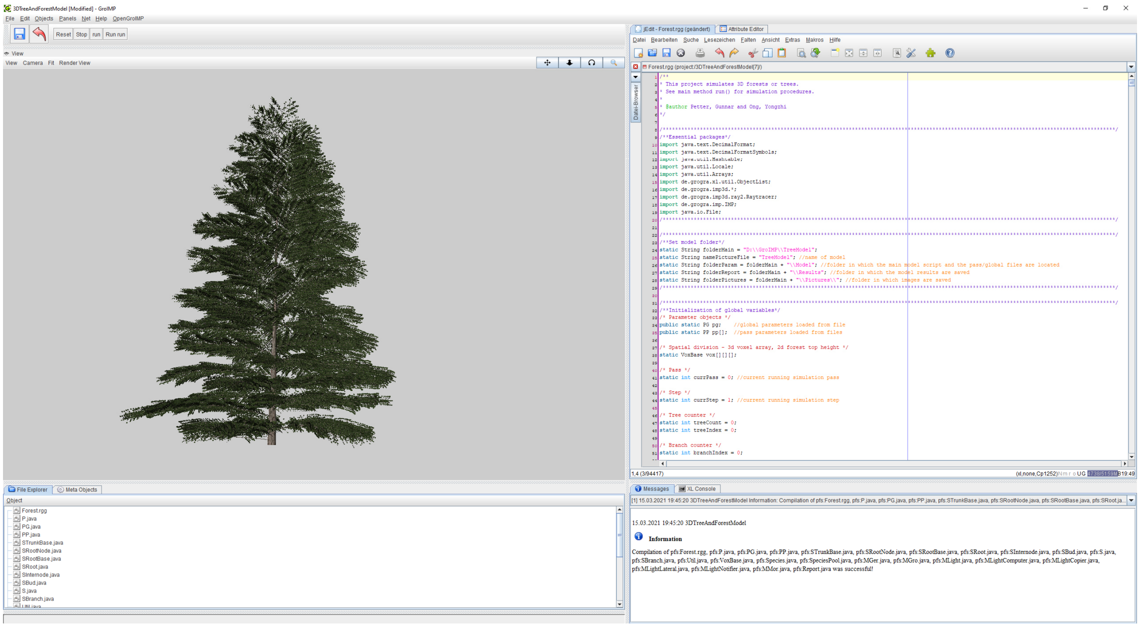

**Fig. 2**. Basic Layout of GroIMP when simulating a tree or a forest. In this example, the *OpenGL* view is activated in GroIMP and the option to visualize leaves (*VisualizationShader*=1) is selected in the global file.

## Controlling a GroIMP model run

This model is designed as flexible tool that can be controlled by the user via simple text files, which allows manipulation and customization for simulation experiments without source code changes. There are two different types of text files, the *global* (Forest_param_global.txt) and the *pass* (Forest_param_pass0.txt) file.

The ***global*** file contains a set of parameters defining the basic set up of the model. This includes the general decision whether a forest stand or an individual tree shall be simulated, the spatial extent and resolution of the model space, the number of time steps and the number of replicates. Information on all parameters in the global file are provided in Table 1.

**Table 1.** Parameters of the global file. The global file is a text file located in the main model folder and contains a set of parameters defining the basic set up of the model, such as the spatial extent or the number of time steps to be simulated. In addition, it can be specified in which time intervals different types of model results shall be save (*Report…*; please enter 0 if you do not want to save the specific results). Please note that only integer values are allowed in the global file. The Symbol refers to the symbol used in the model description (Appendix A of the main paper)

| Parameter | Explanation | Unit | Symbol |
|---|---|---|---|
| Timesteps | Number of simulated annual time steps for each replicate run | a | $t_{max}$ |
| Replicates | Number of replicate runs to be simulated successively | - | - |
| MaxX | Spatial extent of core model area (in X direction) | m | $MaxX$ |
| MaxY | Spatial extent of core model area (in Y direction) | m | $MaxY$ |
| MaxZ | Spatial extent of core model area (in Z direction) | m | $MaxZ$ |
| WidthCorridor | Width of corridor around core model area | m | $L_{Cor}$ |
| VoxelSize | Side length of voxels | m | $L_V$ |
| ReportForest | Time interval in which forest variables are saved | a | - |
| ReportLight | Time interval in which light variables are saved | a | - |
| ReportMortality | Time interval in which mortality variables are saved | a | - |
| ReportShoots | Time interval in which shoot variables are saved | a | - |
| ReportTrees | Time interval in which trees variables are saved | a | - |
| ReportVoxel | Time interval in which voxel variables are saved | a | - |
| SimulateForest | Parameter specifying whether a forest (*SimulateForest*=1) or an individual tree (*SimulateForest*=0) is simulated | a | - |
| ThreadCount | Number of threads that are used in parallel in light model calculations | - | - |
| VisualizationShader | Parameter specifying whether rendered trees are shown (*VisualizationShader* =1) or not (*VisualizationShader* =0) | - | - |
| VisualizationMethod | Parameter specifying visualization method (see Figure 3 for possible options) | - | - |

The time intervals in which different types of model results are saved can also be determined in the global file (Table 1). In general, trees in the model consist of tree components such as trunks, branch segments and leaf compartments. In forest stands, the number of these components can be substantial. For instance, forest stands may consist of several million branch segments, the amount of data to be saved can thus be large. As such detailed outputs are not always needed, higher level outputs are also calculated and can be saved in addition or instead of the low-level outputs. The user can specify if and in which time intervals the following six model result shall be saved - *Shoots*: state variable of branch segments, *Trees*: tree level results, *Forest*: forest level results, *Voxels*: leaf biomass and light in voxels, *Mortality*: causes of mortality for each tree, *Light*: light in all voxels at forest floor. In addition, the species pool is saved by default. Please see Table 2 for more information about the specific variables saved in each of the result file.

**Table 2.** Export parameters of the model. This table contains all parameters that are saved in each of the different types of result files (Forest, Mortality, Shoots, Species, Trees and Voxels). The time interval at which each of this result files shall be saved to the hard disk can be defined by the user in the global file (Table 1).

| Parameter | Explanation | Unit | File |
|---|---|---|---|
| year | Year / time step | a | Forest |
| numberTrees | Number of trees | $ha^{-1}$ | Forest |
| basalArea | Basal area | $m^2\,ha^{-1}$ | Forest |
| maxHeight | Maximum tree height | m | Forest |
| meanHeight | Mean tree height | m | Forest |
| maxDiameter | Maximum tree diameter | m | Forest |
| meanDiameter | Mean tree diameter | m | Forest |
| woodyBiomass | Total biomass of all woody parts (trunks, branches) | $Mg\,ha^{-1}$ | Forest |
| trunkBiomass | Total trunk biomass | $Mg\,ha^{-1}$ | Forest |
| branchBiomass1stOrder | Total biomass of first order branches | $Mg\,ha^{-1}$ | Forest |
| branchBiomass2ndOrder | Total biomass of second order branches | $Mg\,ha^{-1}$ | Forest |
| leafBiomass | Total leaf biomass | $Mg\,ha^{-1}$ | Forest |
| trunkBiomassProduction | Total trunk biomass produced in one year | $Mg\,ha^{-1}\,a^{-1}$ | Forest |
| branchBiomass1stOrderProduction | Total biomass of first order branches produced in one year | $Mg\,ha^{-1}\,a^{-1}$ | Forest |
| branchBiomass2ndOrderProduction | Total biomass of second order branches produced in one year | $Mg\,ha^{-1}\,a^{-1}$ | Forest |
| leafBiomassProduction | Total leaf biomass produced in one year | $Mg\,ha^{-1}\,a^{-1}$ | Forest |
| branchBiomass1stOrderLoss | Total biomass of first order branches lost in one year | $Mg\,ha^{-1}\,a^{-1}$ | Forest |
| branchBiomass2ndOrderLoss | Total biomass of second order branches lost in one year | $Mg\,ha^{-1}\,a^{-1}$ | Forest |
| leafBiomassLoss | Total leaf biomass lost in one year | $Mg\,ha^{-1}\,a^{-1}$ | Forest |
| treeID | Tree ID | - | Mortality |
| speciesID | Species ID | - | Mortality |
| height | Tree height | m | Mortality |
| diameter | Tree diameter | m | Mortality |
| basalarea | Basal area of tree | m | Mortality |
| x | Position in core model area in X direction | m | Mortality |
| y | Position in core model area in Y direction | m | Mortality |
| age | Tree age | a | Mortality |
| causeDeath | Cause of death | - | Mortality |
| shootID | ID of branch segment | - | Shoots |
| branchID | ID of branch | - | Shoots |
| treeID | Tree ID | - | Shoots |
| speciesID | Species ID | - | Shoots |
| length | Length of branch segment | m | Shoots |
| diameter | Diameter of branch segment | m | Shoots |
| order | Branch order | - | Shoots |
| xbegin | Start position of branch segment (X direction) | m | Shoots |
| ybegin | Start position of branch segment (Y direction) | m | Shoots |
| zbegin | Start position of branch segment (Z direction) | m | Shoots |
| xend | End position of branch segment (X direction) | m | Shoots |
| yend | End position of branch segment (Y direction) | m | Shoots |
| zend | End position of branch segment (Z direction) | m | Shoots |
| SpeciesID | Species ID | - | Species |
| SLA | Specific leaf area | $cm^2\,g^{-1}$ | Species |
| rhoW | Wood density | $g\,cm^{-3}$ | Species |
| LL | Leaf lifespan | d | Species |
| Nmass | Nitrogen concentration | % | Species |
| RL | Respiration rate per gram of leaf dry mass | $gC\,g^{-1}d^{-1}$ | Species |
| Gmax | Maximum gross photosynthetic rate (g C per g dry mass per day) | $gC\,g^{-1}\,d^{-1}$ | Species |
| k | Light intensity at which the gross photosynthetic rate is half of its maximum | $\mu mol\,m^{-2}\,s^{-1}$ | Species |
| FirstOrderPhyllotaxis | Angle between first order branches from top view | ° | Species |
| FirstOrderPhyllotaxisNum | Number of first order branches arranged in a 360° circle | - | Species |
| FirstOrderAngleSide | Angle of first order branches from side view | ° | Species |
| HigherOrderAngle | Angle between second and first order branch from top view | ° | Species |

| | | | |
|---|---|---|---|
| InternodeLengthTrunkMin | Species-specific minimum trunk internode length | cm | Species |
| InternodeLengthTrunkMax | Species-specific maximum trunk internode length | cm | Species |
| InternodeLengthBranchMin | Species-specific minimum branch internode length | cm | Species |
| InternodeLengthBranchMax | Species-specific maximum branch internode length | cm | Species |
| kInt | Factor controlling the relationship between internode length and total annual length growth | - | Species |
| TropismStrength | Strength of tropism (negative values: phototropism; positive: gravitropism) | - | Species |
| LDRatioTrunk | Length-diamter ration of trunk | - | Species |
| ApicalDev | Maximum relative increase in height growth when IM < IT | | Species |
| IApical | Light intensity threshold regulating apical dominance of trunk apical meristem | µmol $m^{-2}$ $s^{-1}$ | Species |
| ShorteningFactor | Factor regulating the shortening of branches with their order | - | Species |
| maxPipeLength | Maximum pipe length of tree (emergent property) | m | Species |
| StochasticityTwisting | Maximal rotation along the main growth axis (if *Stochasticity*=1) | ° | Species |
| StochasticityBranchingAngle | Maximum deviation from $\alpha_{TSO}$ (if *Stochasticity*=1) | ° | Species |
| StochasticityTropism | Maximum deviation from $S_{Trop}$ (if *Stochasticity*=1) | - | Species |
| StochasticityAnglePlane | Maximum deviation from $\alpha_{SFO}$ (if *Stochasticity*=1) | ° | Species |
| StochasticityPhyllo | Maximum deviation from $\alpha_{TFO}$ (if *Stochasticity*=1) | ° | Species |
| ALProdMax | Absolute maximum leaf area production per leaf compartment | $cm^2$ | Species |
| PipeReuseFactor | Pipe-reuse factor | - | Species |
| treeID | Tree ID | - | Trees |
| speciesID | Species ID | - | Trees |
| height | Tree height | m | Trees |
| diameter | Tree diameter | m | Trees |
| basalArea | Basal area of tree | $m^2$ | Trees |
| x | Position in core model area in X direction | m | Trees |
| y | Position in core model area in Y direction | m | Trees |
| age | Tree age | a | Trees |
| heightDelta | Height increase in one time step | m | Trees |
| heightRGR | Relative height increase in one time step | % | Trees |
| diameterDelta | Diameter increase in one time step | m | Trees |
| diameterRGR | Relative diameter increase in one time step | % | Trees |
| basalareaDelta | Basal area increase in one time step | m | Trees |
| basalareaRGR | Relative Basal area increase in one time step | % | Trees |
| woodyBiomass | Biomass of all woody tree parts (trunk and branches) | Mg | Trees |
| trunkBiomass | Biomass of trunk | Mg | Trees |
| branchBiomass1stOrder | Biomass of first order branches | Mg | Trees |
| branchBiomass2ndOrder | Biomass of second order branches | Mg | Trees |
| leafBiomass | Total leaf biomass of tree | g | Trees |
| leafArea | Total leaf area of tree | g | Trees |
| trunkBiomassProduction | Total trunk biomass produced in one year | Mg $ha^{-1}$ $a^{-1}$ | Trees |
| branchBiomass1stOrderProduction | Total biomass of first order branches produced in one year | Mg $ha^{-1}$ $a^{-1}$ | Trees |
| branchBiomass2ndOrderProduction | Total biomass of second order branches produced in one year | Mg $ha^{-1}$ $a^{-1}$ | Trees |
| leafBiomassProduction | Total leaf biomass produced in one year | Mg $ha^{-1}$ $a^{-1}$ | Trees |
| branchBiomass1stOrderLoss | Total biomass of first order branches lost in one year | Mg $ha^{-1}$ $a^{-1}$ | Trees |
| branchBiomass2ndOrderLoss | Total biomass of second order branches lost in one year | Mg $ha^{-1}$ $a^{-1}$ | Trees |
| leafBiomassLoss | Total leaf biomass lost in one year | Mg $ha^{-1}$ $a^{-1}$ | Trees |
| apicalLight | Light conditions at apical stem meristem | µmol $m^{-2}$ $s^{-1}$ | Trees |
| crownArea | Crown area of tree | $m^{-2}$ | Trees |
| crownWidth | Crown width of tree | m | Trees |
| crownDepth | Crown depth of tree | m | Trees |
| crownWidthRelative | Crown width relative to tree height | % | Trees |
| crownDepthRelative | Crown depth relative to tree height | % | Trees |
| heightFirstBranching | Height of first branching | m | Trees |
| x | Position of Voxel (in X direction) | m | Voxels |
| y | Position of Voxel (in Y direction) | m | Voxels |
| z | Position of Voxel (in Z direction) | m | Voxels |
| leafarea | Leaf area in Voxel | $cm^2$ | Voxels |

Visual control of simulated trees or forests is an important additional method to evaluate the quality of the model. Therefore, a picture showing the tree/forest structure is saved to disk at each time step by default. The perspective from which the picture is taken can be configured in the *View* window GroIMP. Two general methods how trees are visualized are implemented, and they can be specified in the *global* file. First, trees can be represented by woody components and leaves (*VisualizationShader*=1). If you choose this option, the *OpenGL* view in GroIMP is best suited. Please note that we are not simulating single leaves in our model - However, for aesthetic purposed, we integrated a technique which allows visually representing leaf compartments by leaf shaders. Second, trees can be represented by their woody components only (*VisualizationShader*=0), whereby second order branches connected to leaf compartments can be colored according to the state of the leaf compartment. If you choose this option, the *Wireframe* view in GroIMP is best suited. In addition, for this option, three different methods to represent the leaf compartments attached to second order branches are available (*VisualizationMethod*), which are presented in Fig. 3.

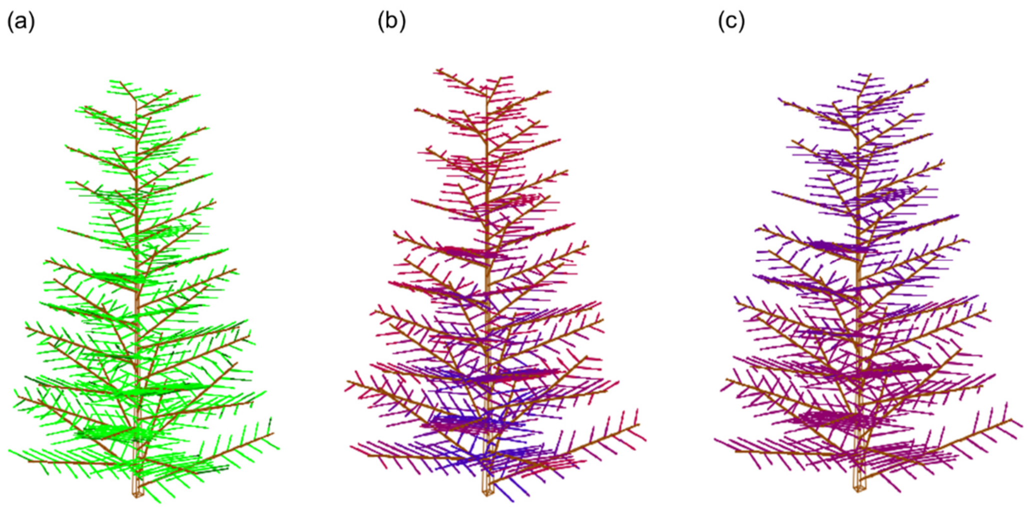


**Fig. 3.** Visual representation of trees. If *VisualizationShader*=0 is chosen, three different methods to represent the leaf compartments attached to second order branches can be specified: (a) second order branches are colored in different shades of green depending on the associated leaf biomass (*VisualizationMethod*=0); (b) second order branches are colored according to the light conditions at the leaf compartments, with red colors representing high light intensities (*VisualizationMethod*=1); (c) second order branches are colored according to the net carbon assimilation in the leaf compartments, with red colors representing higher values (*VisualizationMethod*=2).

The ***pass*** files contain a set of parameters for each replicate run (The number of replicate runs is specified in the global file: *Replicates*). For a single model (replicate) run, only one pass file is needed (Forest_param_pass0.txt). For additional replicate runs after finishing the first run, additional pass files are needed (please name them Forest_param_pass1.txt, Forest_param_pass2.txt, etc.). Each pass file includes global model parameters, ranges of functional and structural traits, but also parameters to select a specific optional model mechanism. An exhaustive list with explanations of all parameters in the pass file is provide in Table 3. Please note that for some parameters, minima and maxima have to be specified. These parameters are usually traits and the species pool (the parameter *NumberSpecies* defines the total number of species in this pool) is generated by randomly sampling from the defined ranges for each trait. If you want to simulate a single tree with defined traits, the minima and maxima should be the same, and *NumberSpecies* should be set to 1. When a species pool of several species is generated but only a single tree is simulated, its species identity is randomly chosen from the species pool.

**Table 3.** Parameters of the pass file. The pass file is a text file located in the main model folder and contains a set of parameters for each replicate. Each pass file includes global model parameters, ranges of functional and structural traits, but also parameters to select a specific optional model mechanism. The parameter values shown in this table are the values of the model shown in the main manuscript. The Symbol refers to the symbol used in the model description (Appendix A of the main paper)

| Parameter | Explanation | Unit | Symbol | Value |
|---|---|---|---|---|
| ALMax | Maximum leaf area in voxel | $cm^2$ | $A_{\mathrm{LMax}}$ | 15000 |
| ALProdMax (Min/Max) | Absolute maximum leaf area production per leaf compartment | $cm^2$ | $A_{\mathrm{LProdMax}}$ | 65000/65000 |
| AngleFirstOrderSideView (Min/Max) | Angle of first order branches from side view | ° | $\alpha_{\mathrm{SFO}}$ | 0/40 |
| AngleSecondOrderTopView (Min/Max) | Angle between second and first order branch from top view | ° | $\alpha_{\mathrm{TSO}}$ | 20/60 |
| BetaD (Min/Max) | Maximum relative increase in height growth when $I_{\mathrm{M}} < I_{\mathrm{T}}$ | - | $\beta_{\mathrm{D}}$ | 0.1/0.3 |
| BetaS | Shape parameter regulating apical dominance of trunk apical meristem | - | $\beta_{\mathrm{S}}$ | 3 |
| BranchMortMassRate | Parameter of biomass-based branch mortality rate (if *BrMortMethod*=2) | $g^{-1}\ a^{-1}$ | $m_{BB}$ | 0.02 |
| BranchMortMassScalingExponent | Scaling exponent in biomass-based branch mortality rate (if *BrMortMethod*=2) | - | $M_{BS}$ | 0.2 |
| BranchMortMethod | Parameter specifying whether branches are removed only if the lost all leaf compartments (*BrMortMethod*=0), or if they are additionally removed randomly (*BrMortMethod*=1) or based on their biomass (*BrMortMethod*=2) | - | *BrMortMethod* | 0 |
| BranchMortRandomRate | Random branch mortality rate (if *BrMortMethod*=1) | $a^{-1}$ | $m_{\mathrm{BR}}$ | 0 |
| BrCollide | Parameter specifying whether branches stop to grow in length if the collide with surrounding trees (*BrCollide* =1) or not (*BrCollide* =0) | - | *BrCollide* | 1 |
| CarbonOverheadCosts | Carbon overhead costs | - | $C_0$ | 1.45 |
| CBLratio | C-mass to biomass ratio of leaves | $gC\ g^{-1}$ | $CBL_{\mathrm{ratio}}$ | 0.5 |
| CBWratio | C-mass to biomass ratio of wood | $gC\ g^{-1}$ | $CBW_{\mathrm{ratio}}$ | 0.5 |
| DistanceVoxelLightCal | Maximal distance of surrounding voxels to be considered in light calculation | m | $LR$ | 4 |
| EdgeC | Parameter specifying whether a forest fragment with a real edge (*EdgeC*=1) or a forest patch within a forest matrix (*EdgeC*=0) is simulated | - | *EdgeC* | 0 |
| FormFactorWood | Form factor used to calculate trunk biomass | - | - | 0.55 |
| Hsun | Assumed number of sun hours per day | h | $h_{sun}$ | 8 |
| Imax | Light intensity above canopy | $\mu mol\ m^{-2}\ s^{-1}$ | $I_{\mathrm{max}}$ | 900 |
| InitialDiamter | Initial diameter of seedling (fixed value) | m | $D_{\mathrm{ini}}$ | 0.0005 |
| InternodeLengthBranchMax (Min/Max) | Species-specific maximum branch internode length | m | $L_{IBMax}$ | 0.4/0.6 |
| InternodeLengthBranchMin (Min/Max) | Species-specific minimum branch internode length | m | $L_{IBMin}$ | 0.3/0.4 |
| InternodeLengthTrunkMax (Min/Max) | Species-specific maximum trunk internode length | m | $L_{ITMax}$ | 0.5/0.7 |
| InternodeLengthTrunkMin (Min/Max) | Species-specific minimum trunk internode length | m | $L_{ITMin}$ | 0.3/0.5 |
| KInt (Min/Max) | Factor controlling the relationship between internode length and total annual length growth | - | $k_{int}$ | 0.01/0.02 |
| LDBranch | Allometric parameter of length-diameter relationship of branches | - | $LD_{\mathrm{B}}$ | 3 |
| LDTreeDev (Min/Max) | Allometric parameter of length-diameter relationship of branches, LDT=LDB+LDRatioDev | - | $LD_{\mathrm{T}}$ | -0.8/0.8 |
| LightC | Parameter specifying method to calculate average light intensity; *LightC*=[1,2,3] | - | *LightC* | 1 |
| LightExtinctionCoeff | Light extinction coefficient (Lambert-Beer equation) | - | $k_{\mathrm{L}}$ | 0.6 |

| | | | | |
|---|---|---|---|---|
| LightThreshApical | Light intensity threshold regulating apical dominance of trunk apical meristem | $\mu mol\ m^{-2}\ s^{-1}$ | $I_T$ | 30/100 |
| LPratio | Ratio between leaf area and pipe cross-sectional area | $cm^2\ cm^{-2}$ | $LP_{ratio}$ | 40000 |
| MinLeafArea | Minimum leaf area below which leaf compartment is removed from branch. The leaf area/biomass dynamics are calculated based on a differential equation that only converges to zero if the leaf area/biomass is reduced. The MinLeafArea can thus be understood as the size of a single leaf - if the leaf area drops below this value, the last leaf of a branch compartment is removed. | $cm^2$ | $B_{LMin}$ | 30 |
| MinLeafAreaRatio | Ration of leaf area to branch diameter below which the branch is removed. This only applies to first order branches and was mainly introduced for aesthetical purposes: Sometimes, only few leaf compartments remain at a first order branch, and only if all were removed, the first order branch would drop. This threshold increases the speed at which the first order branch is removed. | - | $B_{LMin}$ | 100 |
| MortalityBiomassRate | Parameter of biomass-based tree mortality rate | $g^{-1}\ a^{-1}$ | $m_{TB}$ | 0.032 |
| MortalityBiomassScalingExponent | Scaling exponent in biomass-based tree mortality rate | - | $M_{TS}$ | 0.13 |
| MortalityDisturbanceFrequency | Frequency of disturbances (average number of years between two events) | a | $F_{Dist}$ | 0 |
| MortalityDisturbanceRate | Average relative mortality rate in a disturbance event (if *TrMortDist=1*) | $a^{-1}$ | $m_{Dist}$ | 0 |
| MortalityNeighMinDiameter | Trees with a diameter > $D_{NMin}$ can create gaps (if *TrMortNeight=1)* | cm | $D_{NMin}$ | 0.15 |
| MortalityNeighRate | Trees affected by falling trees die with a probability of $m_{Neigh}$ | $a^{-1}$ | $m_{Neigh}$ | 0.05 |
| NumberSeedlingPerHa (Min/Max) | Number of seedlings dispersed at each time step (per hectare) | $ha^{-1}\ a^{-1}$ | $n_{Seed}$ | 500/500 |
| NumberSpecies | Number of species in species list | - | $n_{Spec}$ | 1000 |
| PhyllotaxisFirstOrder (Min/Max) | Number of first order branches arranged in a 360° circle | - | $Ph_{FO}$ | 3/5 |
| PipeLengthMethod | Parameter specifying whether pipe length is calculated based on within-tree position (*PipeLengthMethod*=1) or based on height only (*PipeLengthMethod*=0) | - | - | 1 |
| PipeReuseFactor (Min/Max) | Pipe-reuse factor | - | $P_{RU}$ | 0.6/0.6 |
| RespirationRateWood | Respiration rate per gram of sapwood | $gC\ g^{-1}\ d^{-1}$ | $R_w$ | 0.0005 |
| SafetyFactorTrunk | Safety factor for trunk growth. | - | $ST$ | 0.3 |
| ShorteningFactor (Min/Max) | Factor regulating the shortening of branches with their order | - | $S_F$ | 0.7/0.9 |
| SiteIndex | Site index describing the relative quality of the forest patch | - | $SI$ | 0.9 |
| SLA (Min/Max) | Specific leaf area | $cm^2\ g^{-1}$ | $SLA$ | 50/200 |
| Stochasticity | Parameter specifying whether stochastic variations of structural traits are simulated (*Stochasticity*=1) or not (*Stochasticity*=0) | - | *Stochasticity* | 1 |
| StochasticityAngleFirstOrderSideView (Min/Max) | Maximum deviation from $\alpha_{SFO}$ (if *Stochasticity*=1) | ° | $St_{\alpha SFO}$ | 5/10 |
| StochasticityAngleFirstOrderTopView (Min/Max) | Maximum deviation from $\alpha_{TFO}$ (if *Stochasticity*=1) | ° | $St_{\alpha TFO}$ | 0/20 |
| StochasticityAngleSecondOrderTopView (Min/Max) | Maximum deviation from $\alpha_{TSO}$ (if *Stochasticity*=1) | ° | $St_{\alpha TSO}$ | 0/10 |
| StochasticityTropismStrength (Min/Max) | Maximum deviation from $S_{Trop}$ (if *Stochasticity*=1) | - | $St_{Trop}$ | 0/0.02 |
| StochasticityTwisting (Min/Max) | Maximal rotation along the main growth axis (if *Stochasticity*=1) | ° | $St_{Tw}$ | 2/7 |
| StopCriterionBasalArea | Model stops and continues with next replicate if the total basal area exceeds $BA_{Stop}$ | $m^2\ ha^{-1}$ | $BA_{Stop}$ | 80 |
| TreeCompetionDist | Distance of additional competing trees from tree (only if SimualteForest=0) | | - | 0 |

| | | | | |
|---|---|---|---|---|
| TreeCompetionNum | Number of additional trees competing with tree (only if SimualteForest=0) | - | - | 0 |
| TreeMortBiomass | Parameter specifying if the biomass-based mortality following the MTE is simulated (*TrMortDist*=1) or not (*TrMortDist*=0) | - | $m_T$ | 1 |
| TreeMortCarbon | Parameter specifying if tree mortality due to carbon starvation is simulated (*TrMortDist*=1) or not (*TrMortDist*=0) | - | *TrMortCarbon* | 1 |
| TreeMortDist | Parameter specifying if tree mortality due to disturbances is simulated (*TrMortDist*=1) or not (*TrMortDist*=0) | - | *TrMortDist* | 0 |
| TreeMortNeigh | Parameter specifying if tree mortality due to falling neighboring trees is simulated (*TrMortNeight*=1) or not (*TrMortNeight*=0) | - | *TrMortNeigh* | 1 |
| TropismStrength (Min/Max) | Strength of tropism (negative values: phototropism; positive: gravitropism) | - | $S_{\mathrm{Trop}}$ | -0.02/0.02 |
| Tyear | Number of days per year suitable for photosynthesis | d | $t_{year}$ | 270 |
| WoodDensity (Min/Max) | Wood density | g cm$^{-3}$ | $\rho_{\mathrm{W}}$ | 0.5/0.7 |