



TreeMig Tutorial

**Simulate the forest landscape
in your own region**

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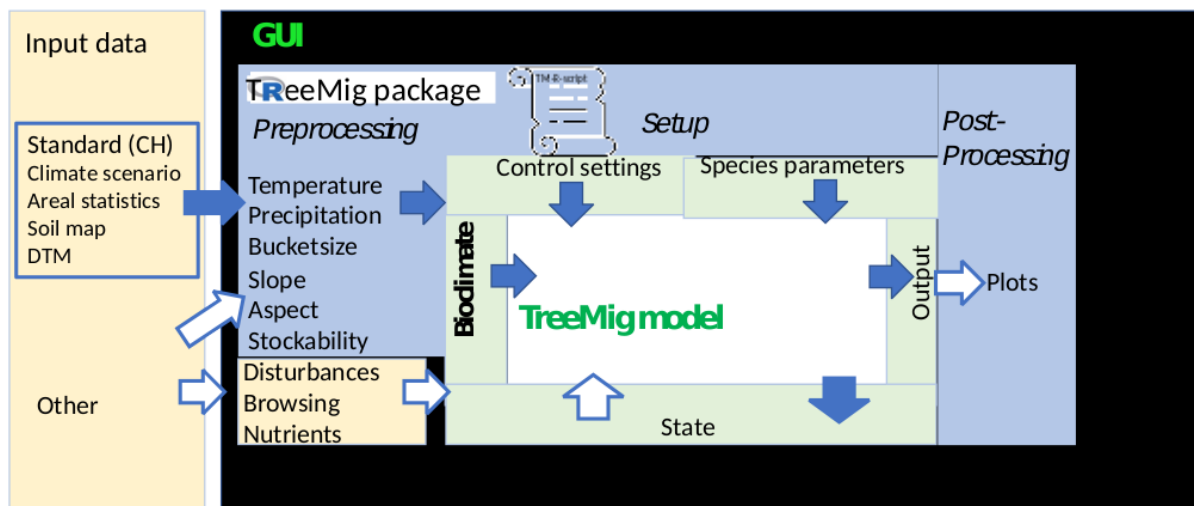
Try to perform at least the steps/exercises with a star ().*

If you manage to do the other exercises too, all the better! H: try at least to have a look into the additional scripts.

A. Overview

TreeMig:

The TreeMig-framework is an R package build around the TreeMig model. It allows you to run TreeMig simulations anywhere in Switzerland. A graphical user interface (GUI) facilitates the pre-processing of your input data, the execution of your simulation, and the post-processing of the results by creating print-ready diagrams.



Conventions:

In this tutorial the following conventions are consistently used:

- **GUI element**
- **Folder or Subfolder**
- Button
- "File"
- "text"
- "command"

Disclaimer:

You can use this GUI, the TreeMig-package, and the input data coming with it for your work. If you do so, be aware that it is a preliminary version, and that TreeMig [1,2], the TreeMig package [3] and the data [4] have to be cited, if you publish results based on them. It would be best if you would contact us for support.

Citations:

- [1] Lischke, H. 2020. Simulation der Baumartenmigration im Klimawandel. Schweiz. Z. Forstwes. **171**:151–157.
- [2] Lischke, H., N. E. Zimmermann, J. Bolliger, S. Rickebusch, and T. J. Löffler. 2006. TreeMig: A forest-landscape model for simulating spatio-temporal patterns from stand to landscape scale. Ecological Modelling **199**:409–420.
- [3] treemig.wsl.ch, citation will be included there later
- [4] see TMInputData/README_DescriptionInputData.pdf

B. Installation and Preparation*

1. Download ["TreeMig Simulation Environment and Input Data"](#) from EnviDat and unzip it ("tmenvandinputdata.zip"). Move this whole newly created TreeMig directory called **"TMEnvAndInputData"** to the place where you want to work. Inside you will find the Rscript ["installAndRunTreeMigWrapperAndGUI.R"](#) and three subfolders:

TMEnvironment with the TreeMig executable(s) and the necessary subfolders and files to run TreeMig (see box),

TMInputData with all necessary input data.

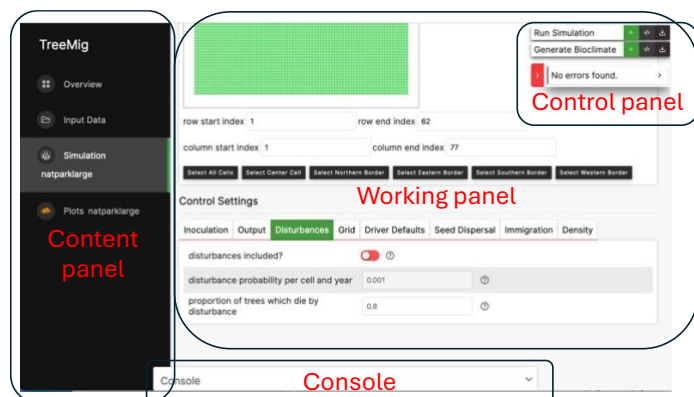
AdditionalRScripts with the Rscripts ["Stormtracks.R"](#) and ["Example Couple TM SpruceCut.R"](#).

TMEnvironment structure:

TMEnvironment is a folder on your Harddisk. It contains the TreeMig program applications TM_Mac (for Mac), Tm.exe (for Windows), and TM_linux for Linux-Ubuntu, and the subfolders **C** for program control files, **E** for processed environmental inputs, mostly Bioclim(atic) files, **P** for species parameter files, **R** for simulation results, **Plots** for produced plots, and **S** for statefiles which store the state of the simulation at predefined time points. In **R**, **P**, and **Plots**, there will be subfolders for the different simulation experiments.

2. In R or RStudio run the Rscript ["installAndRunTreeMigWrapperAndGUI.R"](#) to install the TreeMig-package, to define the paths to the default input files and to start the GUI. For technical requirements, see Annex 4.

The GUI will open in your default browser. On the left side is the narrow, black **Content Panel** which allows to get an overview of the simulations and to select the main working steps from pre-processing to simulation to post-processing. The large white **Working Panel** on the right is the main working area and contains the tools to configure each step. On the very bottom you find the **Console**, a panel which reports about the output of the R scripts and the TreeMig program. The **Console** can be opened or closed at any time by clicking on the "v" symbol.



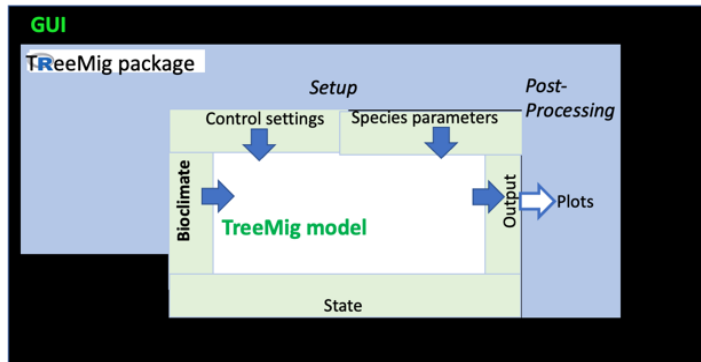
3. In the **Content Panel** select **Overview** and in the **Working Panel** under section **TreeMig Environment** select tab **Open TreeMig Environment** and enter the path to the subfolder **TMEnvironment**, either by clicking on the folder icon and searching the subfolder in the file system or by typing/pasting the path into the input field.

Then load the environment using the button Load Treemig Environment. A black box entitled "*natparklarge*" appears.

4. Select **Input Data** in the **Content Panel** and define the paths to the input data for the simulations in the **Working Panel**. (See Annex 2 for a detailed description of the input data.)
 - a. For this exercise, the input files – which are in the *subfolder* **TMInputData** – are predefined. Click on Add Default Paths (only once!) to add the input data paths. A black box appears for each of the seven input files.
 - b. Get an overview about the input files. What do you think, what kind of data are these? They all cover all of Switzerland, most are static, but two change over time.
 - c. Check that the boxes for the files are black. If a box is red, the file was not found, and you must assign the path to the file manually. Click the Edit button in each red box and set the correct path to the input file. (Alternatively, you can define more paths to other input data directories by clicking on Add Directory, and then combine these paths with the specific filenames.)

C. Set up and run the prepared simulation “Swiss National Park” *

We have prepared a ready-to-use simulation to get you used to the graphical interface. It uses a prepared area, a simulation time and a bioclimate input. Let's start by exploring and running this simulation without any changes.



- Go back to **Overview** in the **Content Panel**. Click button **View** in the simulation *"natparklarge"*. The **Content Panel** will switch to the **Simulation natparklarge** and the Working Panel is now filled with the settings for this simulation, grouped in several sections. Note the floating **Control Panel** at the top right. Let's go quickly through all sections and learn how the simulation is set up.



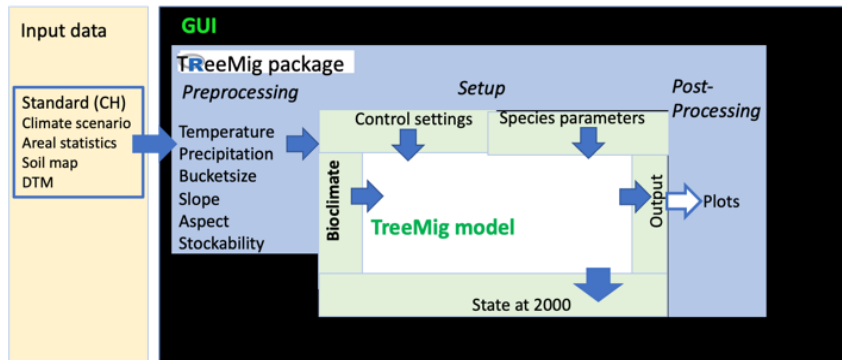
- Set up the simulation
 - Section **Simulation Configuration** contains the ID, time period and duration of the simulation *natparklarge*.
 - In section **StudyArea and Bioclimate** you can see a map of the prepared region, the Swiss National Park, and the surrounding area. Choose tab **Use Existing Bioclimate** and select the **Input Bioclimate** file *"BCNatParkLarge1700_2200.txt"* from the drop-down menu. Turn off Write Bioclimate to New File (red).
 - If for some reason the map does not appear, no problem!
 - Scroll further down and skip tab **Extend Bioclimate** and section **Apply Stockability**.
 - In section **Species Selection** choose tab **Select Species** and select the **Species Parameter File** *"TreePars3.txt"* from the drop down menu (In this file, species are characterized by their properties. (For the English, German or French species names, see Annex 3). A list of species appears. You can select the species to be simulated. For a start, Select All.
 - In section **State File**, tab **State-File**, the option **Read initial state from state-file?** should be switched off (red).
 - In section **Initial Cells**, tab **Select Initial Cells** you can define at which location within the study area seeds are put at the start of the simulation. Click on Select All Cells for this simulation.

- g. Section **Control Settings** allows to define even more settings to run the simulation. For now, don't change anything, but have a look at some of the tabs. Each setting is explained in a pop-up window if you point to the circled question mark. What is Inoculation time? (Point to the question mark!) Do disturbances occur?
Now you just have prepared your simulation, nothing is evaluated yet.
3. Run the simulation
 - a. Click Run Simulation > in the **Control Panel** at the top right of the page. (Mac users: A pop-up window may appear with a message like "*TM_Mac cannot be opened because the developer cannot be verified*". Click Cancel. Go to System Preferences/ Privacy & Security/General and click Allow anyway next to TM_Mac. Now click Run Simulation > again. When the window pops up again, click Open!)
 - b. The **Console** at the bottom of the page opens and you see the R-script that is executed:
 - i. First the already prepared file with the bioclimate is read in.
 - ii. Then TreeMig is started. You see the progress of the simulation by the "Year: idisp: T" lines.
 - iii. Hopefully at the end it will say: "*Job finished with no errors!*".
 - iv. You can fold away the **Console** by clicking on the "v" symbol at right.
4. The results of the simulation are stored in your TMEEnvironment in the folder **R**. Have a look!
5. Plots
 - a. Now select **Plots natparklarge** in the **Content Panel** on the left.
 - b. The results can be visualized in many ways. For a start, choose tab **Species Maps**.
 - c. Now you have to set the plot options:
 - i. Specify the **Species** to plot. First Select All species.
 - ii. You see a list of years for which the results will be plotted. You can use this list or remove it (x) and Add Year Sequence(s) of time intervals you want plots for, e.g. 1700 to 2200, in 100-year steps.
 - iii. In many visualizations you also must define which variable (e.g. biomass, LAI) you want to plot. Select **Biomass**.
 - iv. You can select a **Output threshold**, e.g. 30 t/ha, (only species with larger max. biomass are plotted) using the slider or by typing.
 - v. Turn on the **Species Comparison** option to create a common plot of all selected species.
 - d. Click on Generate Plot > in the **Control Panel**.
 - e. To see the plots (after "*Job finished with no errors!*") fold away the **Console**, scroll down and click on the leftmost plot to enlarge it. You'll see the change of the biomasses over time of the species in your simulation area. (The plots are stored as .jpeg files in the **Plots** folder.) To go back, click on the red cross at the top right of the page (never use the back arrow of your browser!).

- f. You can change the format of the plot by changing Width, Height and Scale in **ggplot2 Arguments**: and again, Generate Plot >. This is helpful, if e.g. the font is too large for the species names.
- g. You can also try to plot the **Species Along Gradients**, e.g. Gradient=custom, Custom raster=DHM CH 200, and Custom name="elevation", and Animate Plot=on to get the species' biomass vs. elevation plot. We recommend to plot 1700 to 2200 with a 10-year interval.
- h. Now try to plot **Species Limits**, with the same custom raster "DHM CH 200", Threshold Lines="Leading", for the upper treelines.
- i. You find interpretations of the plots in the Annex 1.
- j. If you have time, try out also **Species Summary**, **Bio Climate Summary**, and **Bio Climate Maps**, which will give you an impression about the used bioclimate.
- k. If your plot job finished with errors, with the message "Dimensions exceed 50 inches", try again with Limit Size off (red) in the **ggplot2 Arguments**.
- l. In many plot types, there is a field called Sub-Area Selection. Don't use it! It doesn't yet work.

D. Simulate in your own region in Switzerland * ("standard simulation")

Now, you apply TreeMig to a region of your own choice in Switzerland. This can be somewhere in the mountains, or in the lowlands.



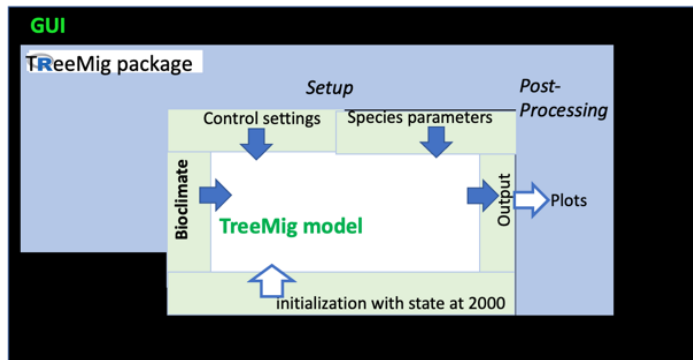
1. Go back to **Overview** in the **Content Panel**.
2. In section **Simulations** you see the black box **Create New Simulation**. First select as **Template** "natparklarge", then click on the big plus sign. The display immediately switches to the newly created simulation.
3. Give your simulation a "Simulation ID", ideally with "Std" for standard, e.g. "ZuerichStd".
4. Define the **Simulation Period**, e.g. 1700 to 2200. Be aware that simulation time scales linearly with the simulated years.
5. In section **StudyArea and Bioclimate** select tab **Create New Bioclimate**.
6. Now use your mouse and the three buttons below the displayed map to select the region where you want to simulate the future forest development. To select the area more precisely, you can first zoom in. Click on **Start StudyArea Selection** to define the area. To zoom out or if you get lost click on **Focus Switzerland**. Finally click **Focus StudyArea**. If you are not satisfied with the result, just repeat this step.
 - a. If for some reason you don't see a map, go in another tab of your browser to map.geo.admin.ch, set at the bottom left the coordinate system to CH1903 / LV03, navigate to your study area, note its bottom left and top right coordinates, and type these in **Latitude/Longitude start/end** under **Crop Bioclimate**.
7. Select a **Grid cell side-length** to the left of the map. Be aware that simulation time scales quadratic with 1/grid cell side-length. (Check grid dimensions **rows x cols** just below the Projection information. An area with less than 1000 cells and 500 years is reasonable for this exercise.)

8. Set up the Bioclimate. This time, the bioclimate will be newly calculated from the input data about slope, aspect, temperature, precipitation, soil properties and areal statistics.
 - a. Choose a new, descriptive **Bioclimate Output Name**, e.g. *"ZueriBC1700_2300.txt"*.
 - b. Now check the input data by clicking on the file specification to see the file content and path to the file (according to the R list "default_files" in the Rscript *"installAndRunTreeMigWrapperAndGUI.R"*.)
Don't change anything now! For later applications, you can choose other formats and other files, which you have to first add to **Input Data**, or even set constant values.
 - c. Scroll down to tab **Extend Bioclimate**. The climate input data ranges from 1981:2099 ("*values in range*"), but you probably want to run the simulation for a longer period, e.g. from 1700 to 2300. Thus, for the missing times, the bioclimate will be sampled from the beginning and end of the available period. Under **Sample years** write e.g. 1981:2010 and 2070:2099 in the **Extend into the past** and **Extend into the future** fields respectively.
9. The standard simulation should not include land use. Therefore, in section **Apply Stockability** there should be no stock file listed. (If so, just remove it!)
10. In section **Species Selection** choose a parameter file, e.g. *"TreePars3.txt"* and click on Select All.
11. In section **State File** and tab **State-File** switch "Read initial state from state-file?" to OFF (red).
12. In section **Initial Cells** and tab **Select Initial Cells**, click on Select All Cells.
13. At the end of the page in section **Control Settings** select the **Output** tab
 - a. Change the **report intervals**: we recommend to choose 1, although the output files tend to be huge, but you don't have to care about resolution during the plotting later.
 - b. Indicate to write out the state of the simulation at a specific year (e.g. 2000) to a statefile. For this, write the year in **specific years for statefile output**.
14. Click on Run Simulation > in the **Control Panel**!
 - a. This time, the input data are read in, and afterwards the bioclimate is calculated from them and stored in the folder E under the name you gave it.
 - b. After that the simulation starts.
 - c. This might take some time, maybe drink a coffee in the meantime! If it is more the time for a whole lunch including preparation, consider changing simulation time, spatial extent, spatial resolution, or the number of simulated species.
15. Make Plots. (You can try different plots)

16. After the simulation, you will find the newly created statefile in the folder ***TMEnvironment/S/<simulationID>/***. The statefile contains the state of the simulation at your chosen year, e.g. 2000, and is named accordingly, e.g. "statefile 2000.txt". This statefile saves computing time in the next simulations!

E. Simulate in your own region from a given state * ("standard short")

Now run the same simulation in the same region but start at a given year (e.g. 2000). The first part of the standard simulation is used as spinup, and you start at year 2000 with your simulation experiments.



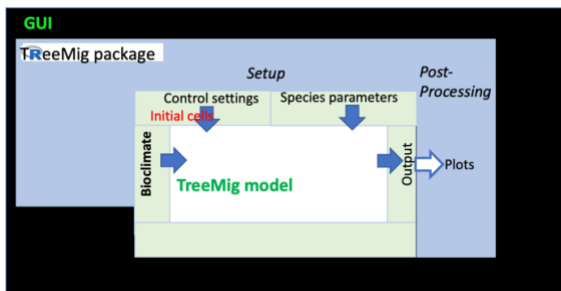
1. Go to **Overview**, create a **new simulation**, and use the simulation you just created as template. Give your new simulation a new, informative name, e.g. "MyRegionStdShort".
2. Start the **Simulation Period** only at a later year (e.g. 2000).
3. Use the same bioclimate as before. In section **StudyArea and Bioclimate** select tab **Use Existing Bioclimate** and in the **Input Bioclimate** drop-down menu select the "Bioclimate file" you created in your standard simulation. Choose Write Bioclimate to New File and give it a new name, e.g. "BCMyRegion2000_2200.txt"
4. Start from the initial state at the year, for which you have created the statefile in your standard simulation.
 - a. In section **State File** and tab **State-File** switch on the **Read initial state from state-file?** Option (green).
 - b. In the drop-down menu **State-file Path** select the statefile you have created in your standard simulation, e.g. "statefile 2000.txt".
5. Run and plot.

F. Simulate different scenarios

Now we will stay in the same region but test out different scenarios, i.e. vary the simulation setup. You can run your simulation over the entire period ("standard") or start from a given year as before ("standard short").

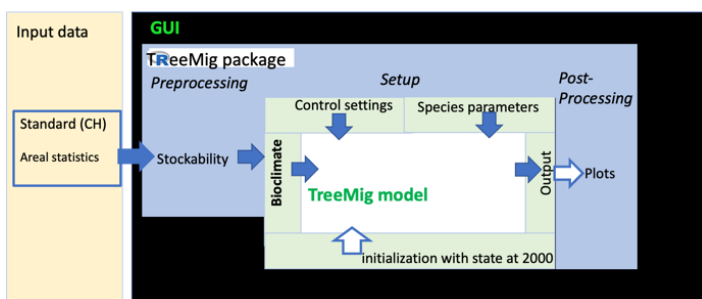
1. For each type of scenario create a new simulation, using your "standard" or "standard short" one as template. Use new and meaningful names for these simulations.
2. Use the same bioclimate as before in the "standard" simulation.
3. Define two or more of the scenarios 1-4 described below. Do them one at the time.
4. Run and plot. Don't forget to look at different output variables, not always only biomass.

Scenario 1: Migration from one or a few cells *



TreeMig is primarily a tree-migration model. To simulate tree migration, use the settings of your "standard" simulation (i.e. use this as template), but now start the simulation only in one single cell, e.g. the center cell of your simulation domain, or from a border in section **Initial Cells**. Make sure you select the Bioclimate of the "standard" simulation and switch the **Read initial state from state-file?** Option off.

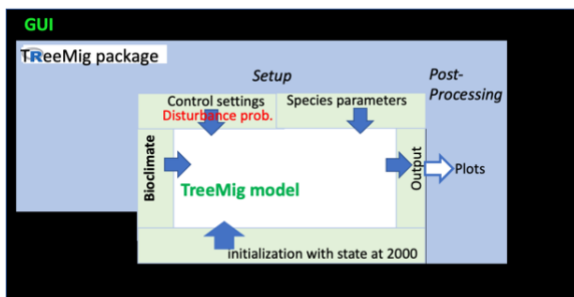
Scenario 2: Land use *



Up to now, the simulations did not include any land use, i.e. they were run without a **Stockability** file. Now, based on your "standard short" simulation, include a land-use filter ("stockability") in section **Apply Stockability** and tab **Add Stockability**.

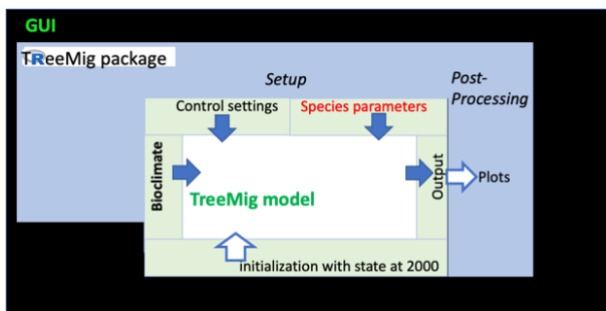
1. In a first simulation, choose the tab **From NOAS04**, i.e. the land use from the Swiss areal statistics. Select the whole simulation period, e.g. 2000-2201 as **Affected years**. Under **File**, select the "stock data" file and filter the land use classes from 50 to 60, i.e. c(50:60), using the range filter from the drop-down-menu. These are the current forest classes from areal statistics and will mask out every area except forest. (You can see the codes for the land use classes under the provided link (sorry, only in German); click on a class in the popup window to unfold the subclasses and their codes.) Since a new bioclimate file is created with the land use filter, make sure to store the bioclimate under a new file name in Write Bioclimate, not to overwrite your original bioclimate file.
2. In another simulation, first select only a few land use **Affected Years**, e.g. 2000-2005 with filter c(50:60). Then add a second **Stockability** with **Affected years** 2006:2200, and filter c(45:60,64,65,70). This will extend the areas which allow forest growth also to alpine meadows and other areas prone to land abandonment. (Remark: If your simulation is in the lowlands, the effects of this land use change will be minor.)

Scenario 3: Random small scale disturbances



In section **Control Settings** and tab **Disturbances**, switch on the random cell scale **disturbances** and maybe change the **disturbance probability per cell and year**.

Scenario 4: Different species parameters



In section **Species Selection** and tab **Edit Species Parameters** set one or several species parameters to different values. For example, change kDrT, the drought stress tolerance (0

$<kDrT<1$), for one or a few species, e.g. to a lower value for *Picea abies* and/or a higher value for *Quercus petraea*. By clicking on a cell, you get the information about this parameter, and you can also use the slider there to change the value.

You can also add new species. To do this, create a copy of the species parameter file in the folder P, add new lines for the new species with their parameter values,

Load Treemig Environment anew in **Overview**, create a new simulation based on your long Std (not Std short!) simulation and use this modified file in **Select Species**.

Scenario 5: Fine resolution and FFT

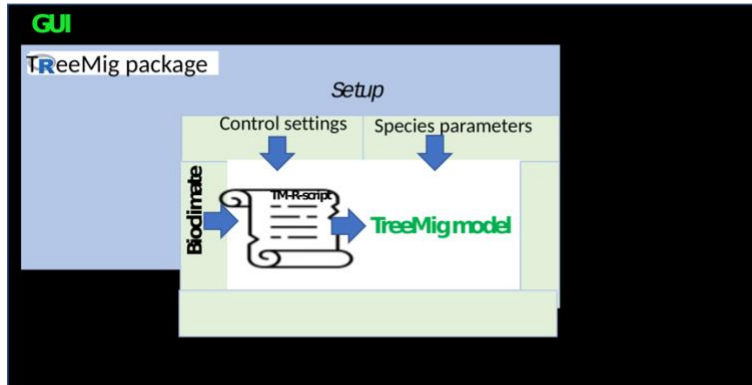
If the spatial resolution is fine ($\sim \leq 100\text{m}$) and the area is comparably large ($\sim 10'000$ grid cells), simulations with the standard ("brute-force") seed dispersal become very time consuming, because the seeds are dispersed from each grid cell to each other. In this situation, the use of the Fast Fourier Transform (FFT) can considerably speed up the simulation.

1. Create in **Overview** a new simulation from your "standard" simulation, with "_fine" at the end of the name. Now set the grid cell side-length to a lower value, e.g. 100m instead of 500m. Make sure that the total number of grid-cells is still $\leq 10'000$.
2. Then first **Create New Bioclimate** (analogue to D.3-D.9), give it a suitable name, e.g. with "_fine" in the end, and then **Generate Bioclimate**.
3. Once this is finished, prepare the simulation using this new existing Bioclimate, analogously to D.10-D.13. In the **Control Settings** under the **Seed Dispersal** tab, set **Dispersal by FFT (T) or brute force (F)** to **FFT**.
4. Now run the simulation. Note the time. Plot.
5. If you are very patient, you can create a new simulation with exactly the same settings, but with **Dispersal by brute force (F)**. Run the simulation and compare the time and the plots. It will take considerably longer.

For coarser resolutions or very small areas, the FFT does not make sense and is error prone because of boundary effects.

G. Working with the TM-R script

With the TreeMig-package you can do more than just using the GUI. The GUI is mainly used to create and execute an R script ("*TM-R-Script*"). This R script then calls the TreeMig model, i.e. the executable *TM_Mac* or *TM.exe* depending on your OS.



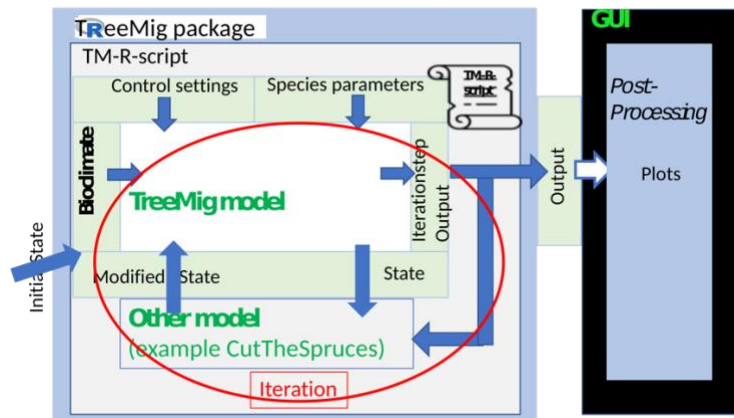
G.1 Get the TM-R-script *

1. Go to your "standard short" simulation in **Overview, View**.
2. In the **Control Panel**, next to the command Run Simulation > click the view button (</>) to view the "*TM-R Script*" and the download button (⬇) to download it. Move the downloaded script to the **TMEnvironment**.
3. Open a new window (i.e. a new session) of RStudio (Otherwise you would have to terminate the GUI).
4. In this new session, open the "*TM-R script*" and have a look at it. In this script you will see much of the information you have previously entered in the GUI, including the RunTreeMig call at the end.
5. The manual execution of this script leads to the same results as the entire simulation part, which ends with the Run Simulation > in the **Control Panel** of the GUI.

G.2 Plotting from the TM-R script *

1. You can also generate the plots from the script by calling the plot functions of the TreeMig-package, e.g. `plotSpeciesMaps()`, `plotBioClimateSummary()`, `plotBioClimateMaps()`, `plotSpeciesSummary()`, `plotSpeciesAlongGradients()`, or `plotSpeciesLimits()`.
1. For a detailed description of the functions you can use the "?"- help command in the console of RStudio, e.g. `?plotSpeciesMaps` (Note: Make sure that `"library(TreeMig)"` is loaded in the new session!).
2. To see how the plot functions were called in your simulation, go back to the GUI, set the **Console** to Code, and choose one of the successful Plot jobs on the right. Now the **Console** shows the function call. You can copy it, paste it into your script and adapt it to your needs. You can also download ⬇ the script snippets for plotting in the **Control Panel** at **Plots**.
3. The documentation (vignette) of the TreeMig-package including the plot functions will later be made available on treemig.wsl.ch.

G.3 Soft-Coupling with another model



You can also couple TreeMig with another model with a timestep larger than 1 year. TreeMig is then called iteratively and writes out a statefile and output files at the end of each iteration. The other model uses the TreeMig output files as input, runs and manipulates the TreeMig statefile according to its result. This manipulated statefile is then used to initialize the next TreeMig iteration.

Example: soft-coupling TreeMig with a toy management model

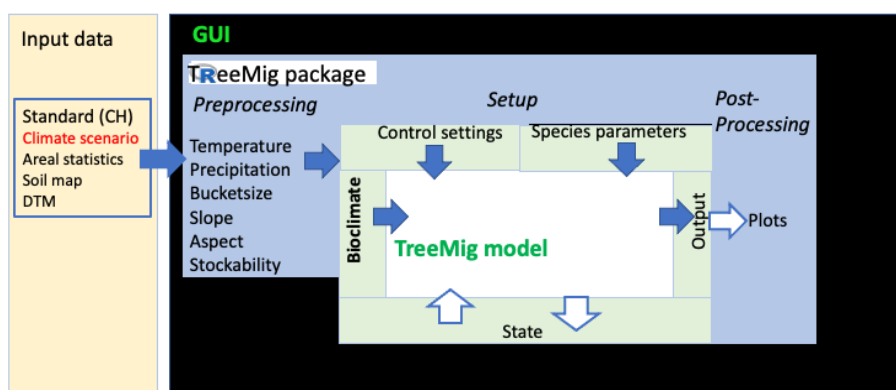
As a demonstration, we couple TreeMig to a simple, not very realistic model that every e.g. 20 years cuts out spruces. This checks the total biomass and share of spruce in the TreeMig biomass output file and selects grid cells whose total biomass is above a certain threshold and whose share of spruce is within a certain range. Of these, some are selected at random with a given probability, with all spruce trees over 1.37 m being felled. This of course is very unrealistic, but the important point here is that there is feedback from the forest to the management and vice versa.

1. Create a new simulation with the Simulation ID extended by "_couple", using the template of your "standard short" simulation. In **Control Settings** and tab **Output**, set the output format to "txt" instead of "netcdf" and Output with tabs or commas to "commas". Run Simulation >!
2. Download the "TM-R-script", move it to the **TMEnvironment folder** and open it in a new, second RStudio instance.
3. Run the script except for the `runTreeMig()` statement (comment it out)! This stores the correct settings in the new RStudio instance.
4. Copy the statefile from the "standard simulation" (e.g. "statefile 2000.txt"; you used it for your "standard short" simulations.) to the **S folder** of your current simulation (the one with extension "_couple") and rename it exactly to "statefile.orig.txt".
5. Open the script "AdditionalRScripts/Example Coupl TM SpruceCut.R".
6. Have a look at it! Find the iteration, the call of TreeMig, the reading of the statefile, the call of the coupled model `CutTheSpruces()`, and the saving of the statefile. Within function `CutTheSpruces()`, find where the statefile is modified.

7. In the "## Settings for the iteration ##" you can use the given values or set reasonable values.
8. Run the "Example Coupl TM SpruceCut.R" script.
9. Either plot the results directly in RStudio or use the GUI (Go to the new simulation you created before (the one which ends with "_couple") and plot.). Attention: If there is already a .nc file from a previous simulation in the R folder, rename it before plotting, because otherwise this file will be used for plotting.

H. Working with own input data

H.1 Enter own input data in the GUI



We have provided you with input data for Switzerland consisting of one climate-change scenario, parts of the Swiss Soil Fertility Map for deriving the soil bucketsize, areal statistics for deriving land use masks (stockability). From these, the actual input data, the bioclimate, is calculated automatically.

But you can also provide own input data for slope, aspect, temperature, precipitation, and water capacity ("bucketsize"), and stockability. If you want to perform a simulation with inputs that are constant in time and space, this is easy. Under **Simulation/Study Area and Bioclimate/Create New Bioclimate**, you can use the **Constant** tab for every data type and just type in a constant value. Otherwise, you must define the input files and their storage locations under **Input Data** in the **Content Panel**. There, you can enter the paths to other input files for temperature, precipitation, DEM, slope, aspect, bucketsize, and stockability. These data are then harmonized in extent and resolution by the GUI.

Table 1: *Formats and ranges of Swiss input data which could be altered in the GUI. Netcdf and raster files must be readable with the terra package, text files with the data.table::fread function (e.g. .txt, .csv, .xls).*

Kind	Unit	Temporal Resolution	Value range	Format(s)	Explanation
Temperature	°C	Monthly average	>= -272	Raster/Netcdf, text (lon,lat,year, T1:T12), const.	
Precipitation	cm	Monthly sum	>= 0	Raster/Netcdf, text (lon,lat,year, P1:T12), const	
Slope	degrees		0:90	Raster/Netcdf, text, (lon,lat,slope), const	Slope
Aspect	degrees		0:360	Raster/Netcdf, text, (lon,lat,aspect), const	Aspect (compass direction)
Digital elevation model				must be readable with the terra package	Used to derive elevation for plotting
Bucketsize			>=0 <=40	Swiss Soil Fertility Map database, Raster/Netcdf, text, (lon,lat,bucketsize), const	Either derived from Swiss Soil Fertility Map database, or directly provided
Stockability			0 not stock-able 1 stock-able	NOAS04, Raster, text, shapefile (lon, lat, stockability)	Whether abiotic environment (except climate) and land use allow forest growth. Either derived from Swiss Areal Statistics (NOAS04), or directly provided. Make sure to use the settings matching your data in the "filter criterion" in the GUI

Example: Artificial Transect through Europe

As a demonstration how to use other input data, we run TreeMig on a 4000 km long transect from Europe. The climate (change) input data are given as lon, lat, year, T1-T12 (P1-P12) text files. They very roughly correspond to those from Gibraltar to Hammerfest, always over land (ignoring the little gaps in the Baltic sea) and stretched to a line. Also, the species are only a selection of the standard species in TreeMig plus a generic and artificial Mediterranean species and generic grasses and shrubs. Don't take these input data and parameters for real!

1. Go to **Input Data** in the **Content Panel**
2. Click **Add File** below the already listed black input files.
3. Under Display Name write something like "Temp_Transect" and fill in the path to the artificial temperature data file "TMInputData/Transect Temp.txt".
4. Do the same for the artificial precipitation data ("TMInputData/Transect Prec.txt"), call it "Prec_Transect".
5. Create in **Overview** a new simulation, e.g. with your Standard simulation as template, name it "*Transect*" with the Simulation Period 1700-2300.

6. Under **StudyArea and Bioclimate/Create New Bioclimate** enter Latitude start *1000*, Latitude End *4000000*, Longitude Start *1000*, Longitude End *2000*, grid cell side Length *1000*. On the map, this transect will be east of Greenland, this has no meaning!
7. Call the bioclimate output file name *"Transect 1700 2300.txt"*.
8. Now go to **Slope Data**. Use the **Constant** value 0.
9. **Aspect Data: Constant** 0.
10. **Temperature Data: From Text File** and **Choose a Text-File** *"Temp Transect"*.
11. **Precipitation Data: From Text File** and **Choose a Text-File** *"Prec Transect"*.
12. **Water Capacity Data Constant** 15. This is a medium value.
13. **Select Species/Select All** from **Species Parameter File** *"TreeParsTransect.txt"*.
14. **Run Simulation** (will take a while).
15. **Plot**, e.g. **Species along Gradient (Latitude)** or **Species Limits**.

H.2 Additional spatio-temporal inputs

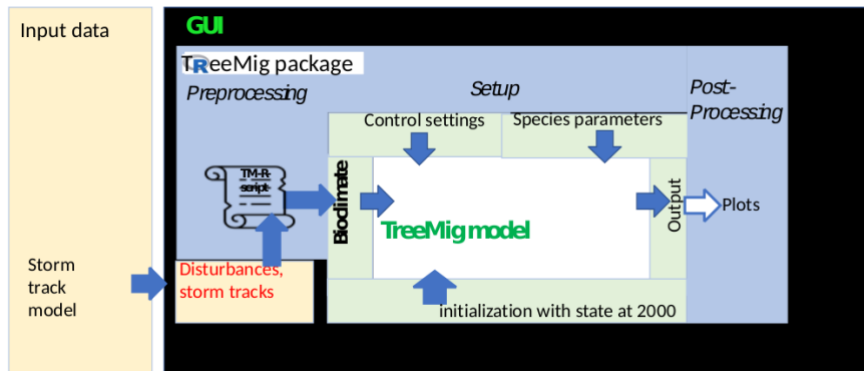
In addition to bioclimate and stockability, you can give the simulation also 4 additional inputs that vary in time and/or space (table 2). However, you must provide these yourself. To do so, add additional columns to the bioclimate file. Rename the bioclimate file and place it into the **E folder** of the new simulation you are about to run. Then use this bioclimate file in your simulations.

Table 2: Other spatio-temporal input data which can be altered in the *"TM-R-script"*.

Input	Column-Name	Range	Unit
(Large-scale) disturbance intensity (prescribed)	Distu	0-1	year ⁻¹
Browsing pressure	browsPress	0-10	-
Drought stress for germination	germDrought	0-1	-
Nutrient availability	nutrients	>0, 300 is very high	t ha ⁻¹

Example for spatio-temporal disturbances: Storm tracks

This is an example for using spatio-temporal disturbances. These could be clearcuts, fires, avalanches, rockfall... To demonstrate how they can be included we give a (very artificial!) example for storms affecting the simulated landscape in tracks of a random length and width, starting at random points and oriented from southwest to northeast.



1. Go to your "standard short" simulation.
2. Get the "TM-R-Script" of this simulation. Run it in a second RStudio session, leaving out the last command `runTreeMig()`. (This is done only to transfer the settings to the StormTracks simulation)
3. Open and run the script "AdditionalRScripts/StormTracks.R", which generates the stormtracks. It consists of a function to create the stormtracks, and the main program where this function is called and the stormtrack results are plotted.
4. You can modify your settings of *maxnumbtrackspereyearandcell*, *maxtracklength*, and *maxtrackwidth* and run the script again.
5. The stormtracks are merged to the bioclimate, which now contains the new column "*Distu*". The new bioclimate file is written to the **E folder** with the extension "*_withDistu*".
6. Run TreeMig
7. You can either do the plots directly in the script ...
8. ...or go back to the GUI and load the environment again. A new simulation with "*_Distu*" should appear. You can do the plots or use it as template for follow up simulations.

I. Some good practices

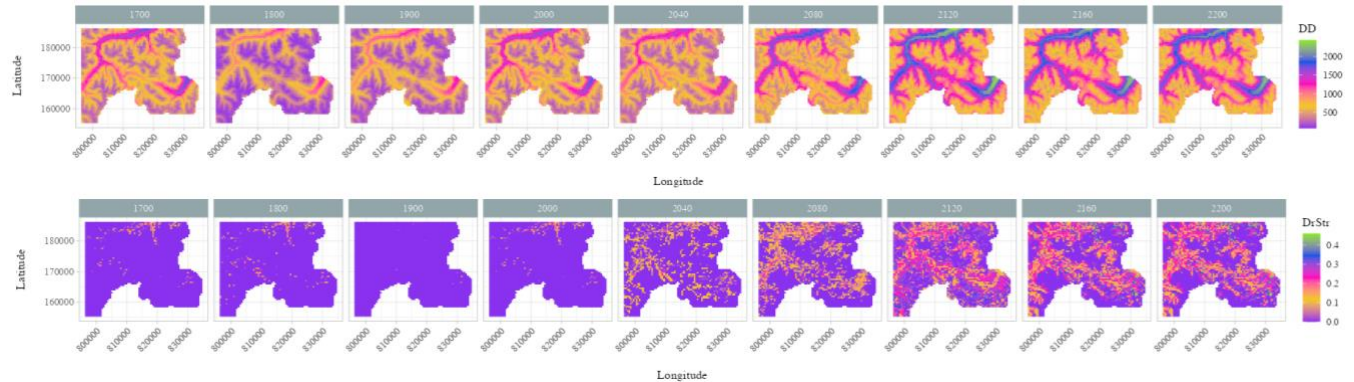
It is convenient that everything you have done is stored in the folders of your **TMEnvironment**, and will be read in the next time you load this TMEnvironment. But this also means that the reading in will take longer and longer the more and the larger simulations with large bioclimates, result files and plots you have. So, try to reduce the amount of information in one TMEnvironment.

- Clean up your simulations from time to time. Erase those you don't need any more by clicking on the "x" of the black simulation panels and activating all options "Simulation results", "Simulation plots" and "Simulation statefiles".
- Clean up your bioclimates in **E**, but carefully. Check first in the simulations or in the corresponding ctrl-files in **C** which bioclimates are still needed, and which not
- If you start a completely new project, make a new TMEnvironment!

J. Annex 1: Interpretation of the plots of the Swiss National Park Simulation

Here some examples how to interpret the plots.

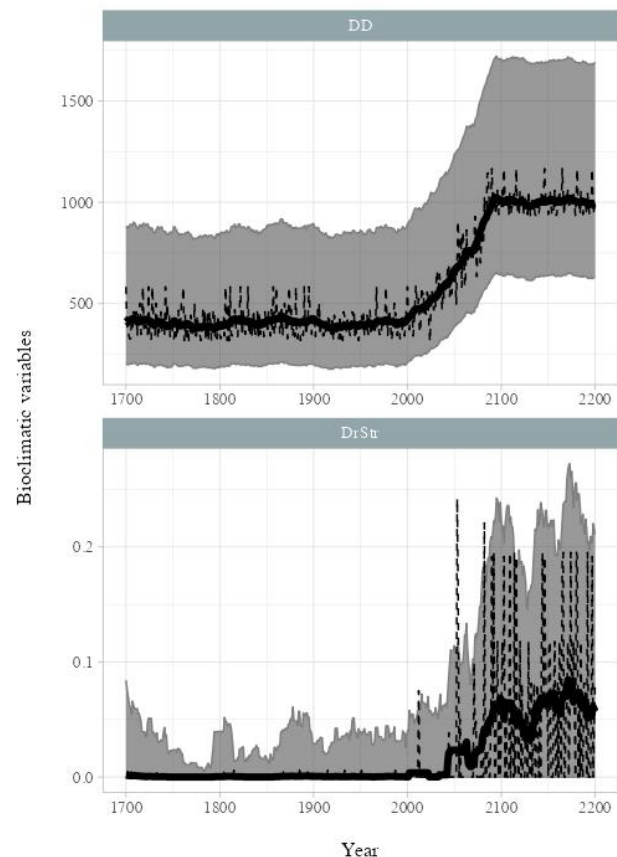
Bioclimate maps



The bioclimatic variables day degree sum (DD, top) and drought stress (DrStr, bottom) over time (columns) and space reflect the altitudes of the simulation area Swiss National Park and surroundings, the inter-annual variability (compare e. g. years 1700 to 1800, 2120 to 2160), and climate change with increasing DD and DrStr between 2000 to 2100.

Bioclimate Summary

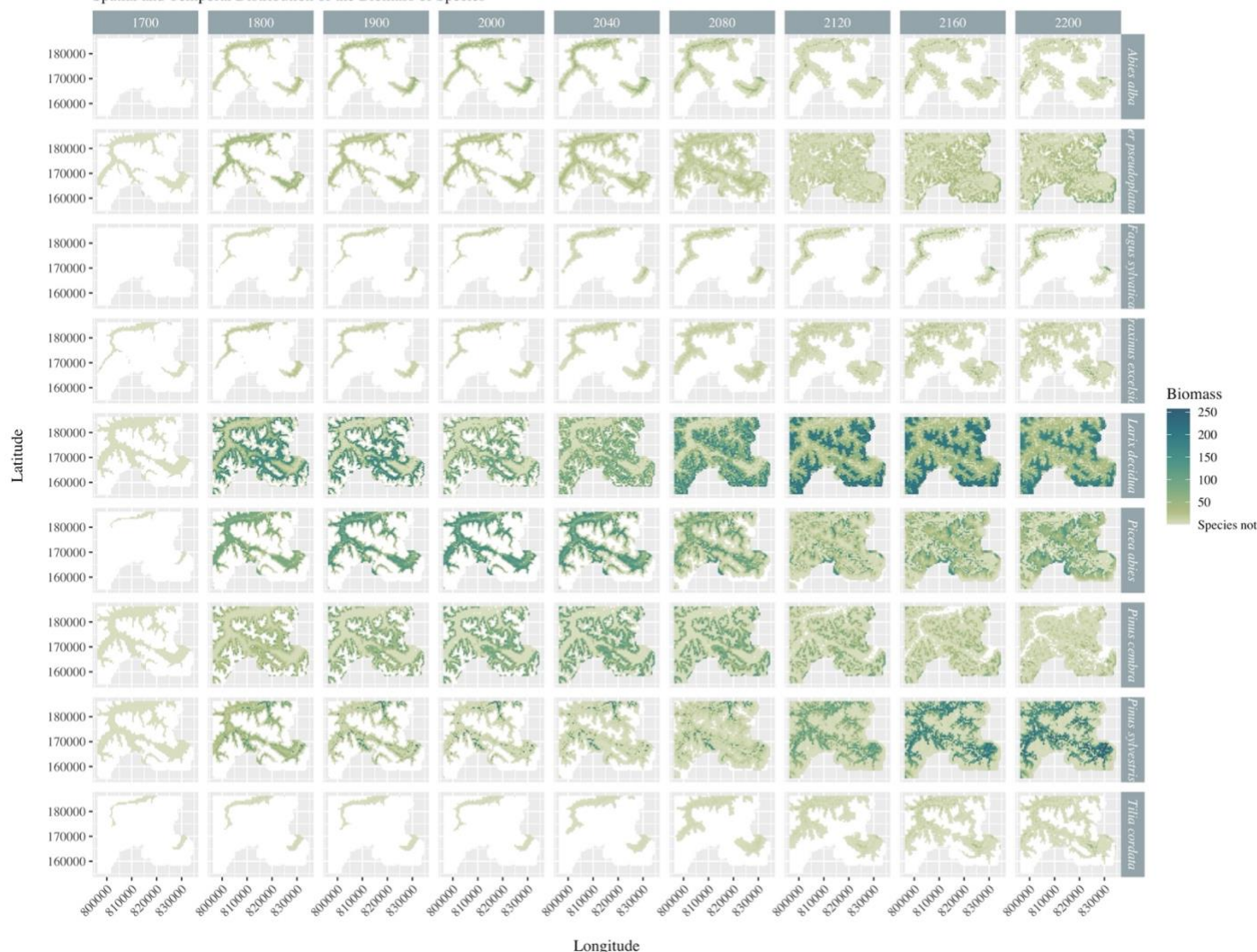
The dashed line is the yearly mean over the entire simulation area, the solid line the 20 years moving average, the grey area is bounded by the 10%-90% quantiles of all grid cells of the simulation area. Day degree sum (DD, top) and Drought stress (DrStr, bottom) increase during climate change 2000-2100. Drought stress under current conditions is mostly zero with only few variability until 2000, then it increases strongly (but to still moderate values) with high inter-annual variability.



Species maps

Biomass per Species per Year

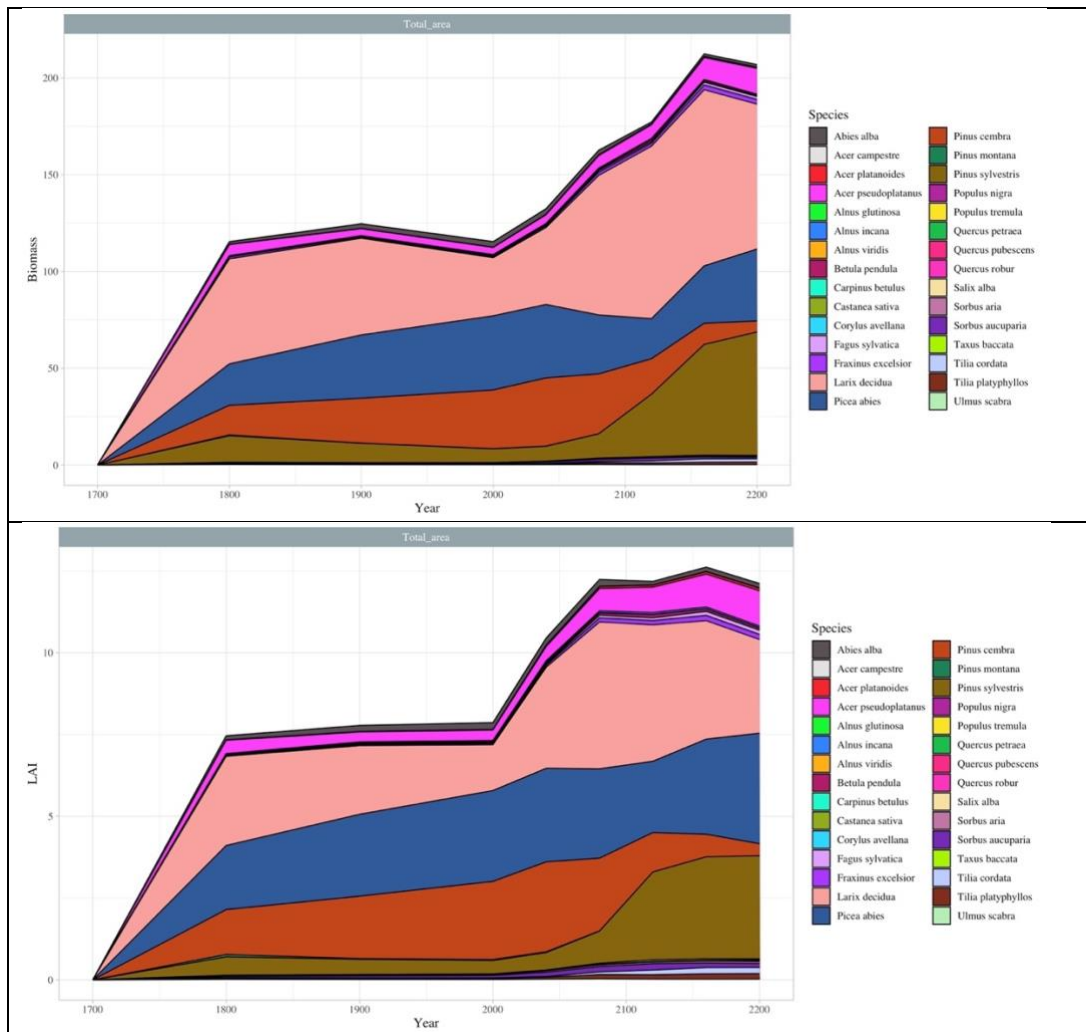
Spatial and Temporal Distribution of the Biomass of Species



Data: WSL Birmensdorf

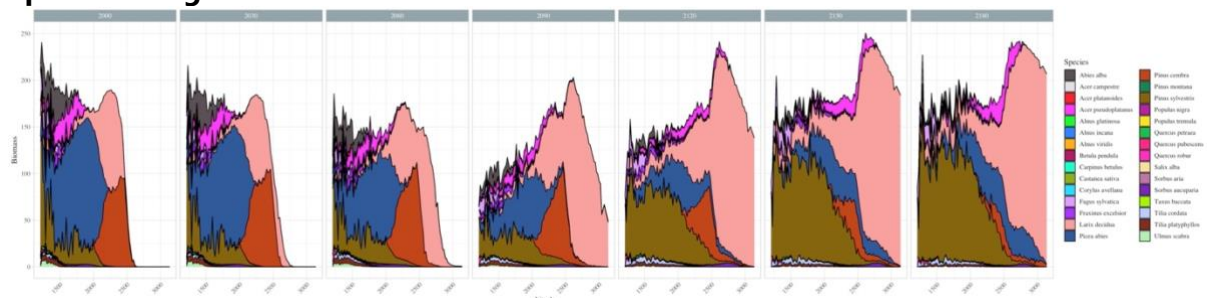
Here shown for the output variable Biomass. Note: only species with maximum biomass > 40 t/ha are shown. Until year 2000 (column 1-4) the climate conditions are constant, and the species on the maps (rows) undergo a succession: the biomass of most species increases, except that of the pioneer *Pinus sylvestris*, which is a bit reduced by competition. The biomasses in the maps reflect the altitudes in the region around the Swiss National Park. They also show the altitudinal belts species due to their bioclimatic niches: in current condition equilibrium, i.e. at year 2000, *Fagus sylvatica*, *Acer pseudoplatanus*, and *Abies alba* are restricted to the valley bottoms, *Picea abies* is also present at the valley slopes, while *Pinus cembra* and *Larix decidua* occur mostly in higher elevations. With climate change (2000-2100), all species expand to and increase biomass in higher elevations. This expansion continues to a certain degree also after 2100 when the climate is constant again. In the lower elevations, the biomass of many species decreases, due to a combination of drought and competition, only the biomass of the drought tolerant *P. sylvestris* increases.

Species Summary



Both biomass [t/ha] and leaf area index (LAI) [m²/m²] averaged over the entire simulation area first increase fast, and stabilize until year 2000. From then on they strongly increase, LAI faster than biomass until they saturate. The strong increase is mostly due to *Pinus sylvestris*.

Species Along Gradients

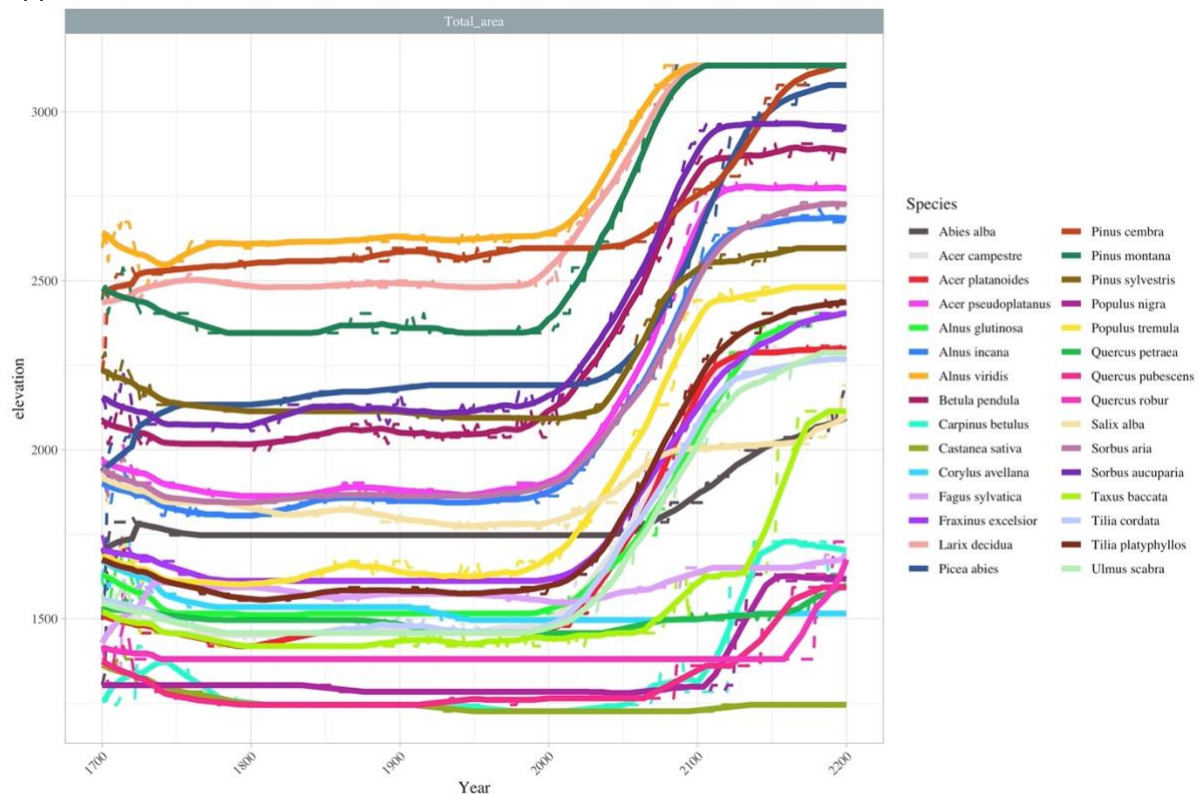


Here a plot of biomass against altitude for different time points, evaluated in 100 altitudinal bins without biomass threshold. Until 2000, the species have formed altitudinal belts, with broad-leaved species, *A. alba* and *P. sylvestris* at low altitudes, *P. abies* at medium altitudes,

and *Pinus cembra* and *L. decidua* forming the timberline. With climate change, all species move upwards, but at different speeds. *P. cembra* is passed and suppressed by *L. decidua* and *P. abies*. The biomass in high elevations increases, mostly due to *L. decidua*. In the lowlands, species get under pressure (probably due to drought) leading to an intermediate biomass decrease, which is later compensated by a strong increase of *P. sylvestris*.

Species Limits

Upper treelines



Here the leading edge of the species in terms of elevation (treeline) is plotted against time for all species in the gradient plot. A species' leading edge is defined as the location in the gradient (here elevation) below which the biomass is larger than a given fraction, here 5%, of the species' maximum biomass.

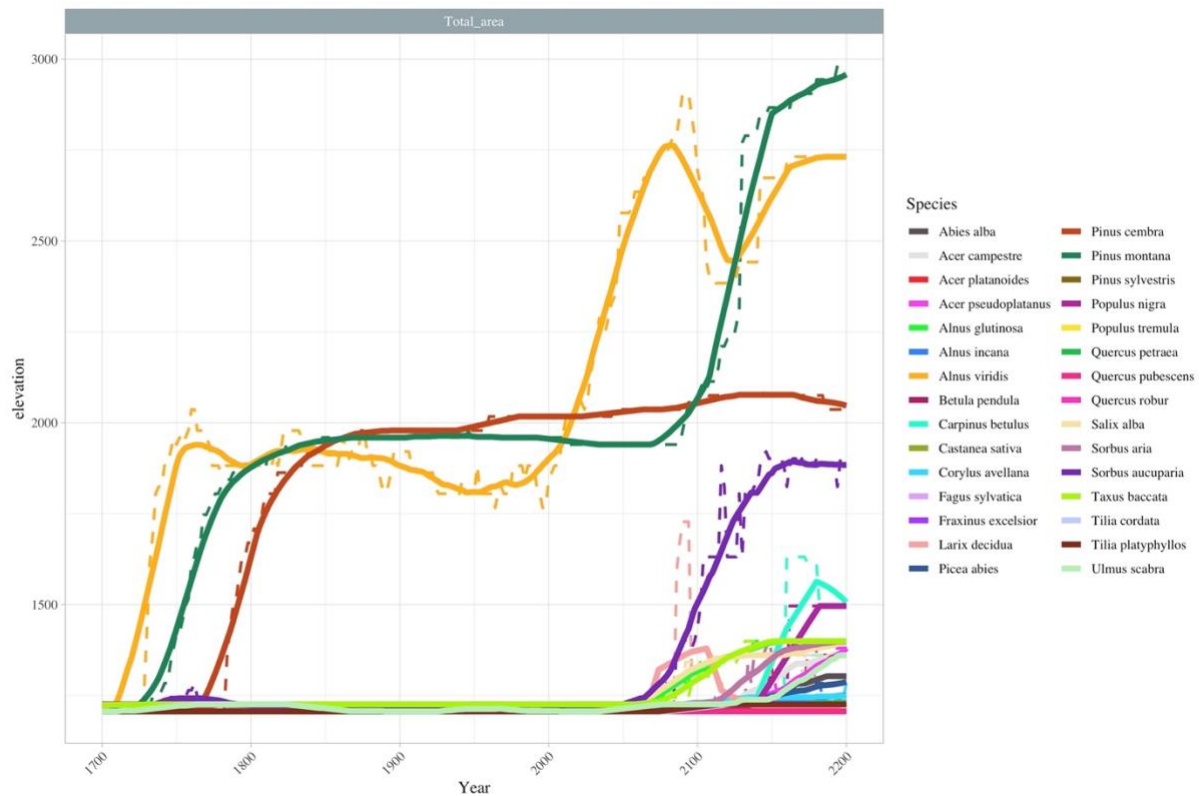
At the beginning (1700-1800), many species' treelines move rapidly upwards (see in the dashed lines) and then move downwards again. This is not due to a real movement of the species, but to biomass changes by the typical overshooting behaviour of forest patch-type models in the first decades of a succession.

Before 2000, nearly all species have a $\pm$ stable treeline, reflecting their temperature requirements. *Alnus viridis*, *Pinus cembra*, *Pinus montana*, and *Larix decidua* form the total upper treeline.

After 2000, the treelines shift upwards, but with different speeds, and stabilise between 2100 and 2200. For example, *Pinus cembra* shifts up much slower than the other treeline forming species. Also many lower elevation species show a slower and delayed upward shift of their leading edges. This is probably because dominating species, e.g. *Picea abies*, are still present in the lower locations, shown also by their trailing edges in the plot below, i.e. lower

distribution limits remaining at low elevations. This can be due either to still favorable, not too dry conditions at the lower elevations or to long survival despite unfavorable conditions (extinction debt).

Lower treelines



K. Annex 2: Example data

The forest-landscape model [TreeMig](#) requires high-resolution input data on climate, slope and aspect, soil and land use. Here we describe the data sources and how the example data sets in the folder **TMInputData** were created from them.

Climate data

The [CH2018 Climate Scenarios for Switzerland](#)[1][2] provide daily time series at individual Swiss stations and on a regular 2km grid ([DAILY-LOCAL and DAILY-GRIDDED](#))[3]. Both data sets include data of 68 [EURO-CORDEX](#) simulations for the scenarios RCP2.6, RCP4.5 and RCP8.5. All data are available under the Creative Commons license [CC BY 4.0](#).

Since a higher resolution of 200m was required for a sample data set, we used a 200m digital elevation model (see below) and the interpolation software *Daymet* by [Thornton, et al. \(1997\)](#)[4] to interpolate the DAILY-LOCAL data from the [individual Swiss stations](#) of the simulation CLMCOM_CCLM4_MPIESM_EUR11_RCP85.

The new 200m daily gridded data were converted to NetCDF format and subsequently aggregated to monthly means (temperatures) and sums (precipitation) using the Climate Data Operators [CDO](#).

Digital elevation model, slope and aspect

The digital elevation model [DHM25/200](#) [5] by the [Federal Office of Topography swisstopo](#) was first reprojected to the current *Official Swiss reference system* [CH1903+](#). Elevations have been rounded to whole meters. The resulting DEM was then cut out along a 1km buffer outside the Swiss border and exported to GeoTIFF format. Aspect and slope were derived from the DEM using ESRI's ArcGIS software.

Soil data

To derive the bucket size required in TreeMig, absolute values of the properties water storage "WASSERSPEI" and water logging "VERNASS" of the [Swiss Soil Suitability Map](#) [6] [7] were used

$$\text{in bucket size} = \begin{cases} 0.78 + 5.43 * \text{WASSERSPEI} & \text{if } \text{VERNASS} < 4 \\ 0.78 + 5.43 * 6 & \text{else} \end{cases} .$$

Land use/cover data for Switzerland

TreeMig uses a stockability input to mask out grid cells which cannot be forested, e.g. because they are under another land use. This stockability can be derived for Switzerland from land use/land cover data in the Swiss areal statistics [NOAS04, 72 categories](#) [8].

References of example input data

- [1] CH2018 (2018), CH2018 – Climate Scenarios for Switzerland, Technical Report, National Centre for Climate Services, Zurich, 271 pp. ISBN: 978-3-9525031-4-0.
- [2] CH2018 Project Team (2018): CH2018 - Climate Scenarios for Switzerland. National Centre for Climate Services. doi: 10.18751/Climate/Scenarios/CH2018/1.0

- [3] Kotlarski S., Rajczak J. (2018): CH2018 - Climate Scenarios for Switzerland, Documentation of the localized CH2018 datasets - Transient daily time series at the local scale: DAILY-LOCAL, DAILY-GRIDDED.
- [4] Thornton, P.E., Running, S.W., White, M.A. (1997): Generating surfaces of daily meteorological variables over large regions of complex terrain. J. Hydrol. 190: 214-251. [https://doi.org/10.1016/S0022-1694\(96\)03128-9](https://doi.org/10.1016/S0022-1694(96)03128-9).
- [5] © Federal Office of Topography swisstopo.
- [6] © Bundesamt für Statistik (BFS), GEOSTAT, 2020, Bodeneignungskarte der Schweiz, Geodaten.
- [7] Frei, E., U. Voegt, R. Flueckiger, H. Brunner, F. Schai, and R. Haeberli. 1980. Bodeneignungskarte der Schweiz. Eidg. Forschungsanstalt für landwirtschaftlichen Pflanzenbau, Eidg. Forschungsanstalt für Wald, Schnee und Landschaft (WSL), Bern.
- [8] © BFS 1992/1997 Arealstatistik der Schweiz. Bundesamt für Statistik, editor, CH-Neuchatel.

L. Annex 3: Species names

Latin	English	Deutsch	Francais
<i>Abies alba</i>	Silver fir	Tanne, Weisstanne	Sapin blanc
<i>Larix decidua</i>	European Larch	Europäische Lärche	Mélèze d'Europe
<i>Picea abies</i>	Norway spruce	Fichte, Rottanne	Épicéa commun
<i>Pinus cembra</i>	Swiss stone pine, Arolla pine	Arve, Zirbe	Pin cembro, Arolle
<i>Pinus montana</i>	Mountain pine	Bergföhre, Bergkiefer	Pin de montagne
<i>Pinus sylvestris</i>	Scots pine	Waldföhre, Waldkiefer	Pin sylvestre
<i>Taxus baccata</i>	Common yew	Eibe	If commun
<i>Acer campestre</i>	Field maple	Feldahorn	Érable champêtre
<i>Acer platanoides</i>	Norway maple	Spitzahorn	Érable plane
<i>Acer pseudoplatanus</i>	Sycamore	Bergahorn	Érable sycomore
<i>Alnus glutinosa</i>	Common Alder	Schwarzerle	Aulne glutineux, l'aulne noir
<i>Alnus incana</i>	Grey alder	Grauerle	Aulne blanc
<i>Alnus viridis</i>	Green alder	Grünerle	Aulne vert ou Aulne des Alpes
<i>Betula pendula</i>	Silver birch	Hängebirke	Bouleau blanc
<i>Carpinus betulus</i>	Common Hornbeam	Hagebuche, Hainbuche	Charme commun
<i>Castanea sativa</i>	Sweet Chestnut	Edelkastanie	Châtaignier commun
<i>Corylus avellana</i>	Common Hazel	Gemeine Hasel	Noisetier
<i>Fagus sylvatica</i>	Common Beech	Rotbuche	Hêtre commun
<i>Fraxinus excelsior</i>	Common Ash	Gemeine Esche	Frêne commun
<i>Populus nigra</i>	Black Poplar	Schwarzpappel	Peuplier noir
<i>Populus tremula</i>	Aspen	Zitterpappel, Espe	Tremble
<i>Quercus petraea</i>	Sessile oak	Traubeneiche	Chêne rouvre
<i>Quercus pubescens</i>	Downy oak	Flaumeiche	Chêne pubescent
<i>Quercus robur</i>	Pedunculate oak	Stieleiche	Chêne pédonculé
<i>Salix alba</i>	White willow	Silberweide	Saule blanc
<i>Sorbus aria</i>	Whitebeam	Echte Mehlbeere	Alisier blanc
<i>Sorbus aucuparia</i>	Rowan	Eberesche, Vogelbeere	Sorbier des oiseaux
<i>Tilia cordata</i>	small-leaved lime / linden	Winterlinde	Tilleul à petites feuilles
<i>Tilia platyphyllos</i>	large-leaved lime / linden	Sommerlinde	Tilleul à grandes feuilles
<i>Ulmus glabra</i>	Scots Elm	Bergulme	Orme de montagne

M. Annex 4: Technical requirements and performance of the framework

The *TreeMig*-R package requires R $\geq 4.3.2$, the packages listed above and R packages these depend on. These dependencies are automatically resolved when installing *TreeMig*-R. If these packages are not available as binaries for the OS, they are automatically compiled from

source, which might require additional system libraries to be installed by the user. For the GUI, the used web browser must be compatible with Shiny and have JavaScript enabled. Binaries of the *TreeMig* model (with all needed libraries statically linked) are provided for the latest Windows, macOS, and Ubuntu versions on AMD64, additionally macOS on ARM processors. To compile and link the *TreeMig* source code for other OS (versions) and processors requires a Fortran 95 compiler, the netCDF-fortran library and all libraries it depends on. For access to the *TreeMig* source code (under CC-BY-NC-SA 4.0 license), please contact the authors.

The amount of memory *mem* (in GB) required depends on the number of simulated grid cells (n_c) with the approximate function:

- $\text{mem} = 3.1 + 0.0001 n_c$.

The approximate computing time (in seconds) depends on n_c and on the number of simulated years (n_y) and species (n_s). On an Apple M2 Max processor the computing time is approximately for the

- preprocessing: $152 + 5.7 \cdot 10^{-4} n_c (1 + 0.0124 n_y)$.
- simulation: $-8.3 + 21.4 \cdot 10^{-6} n_c n_y (1 + 0.244 n_s)$.