Settings in control file, TM-R-script, and GUI

General expressions and explanations used in the tables below:

1. **cal. yr**: Calendars year , e.g. 1700-2100 .
2. **sim. yr**: years from start of simulation (1-401)
3. **real coordinates**: coordinates of simulation area in meters
4. **relative coordinates**: grid cell i and j, starting from 1
5. **Control file:** All settings needed to run the TreeMig application/exe are compiled in the control file. This file can also directly be manipulated. But caution: this is error-prone!
6. **Stockability**: whether trees are allowed to grow (1) or prevented (0) by human land use (e.g. settlements, agriculture…), or by abiotic conditions except climate (e.g. water bodies, rocks, glaciers…)
7. **Bioclim file:** Input file containing all yearly bioclimatic input data. Calculated from temperature, precipitation, soil conditions, slope and aspect. Format: x,y,time, DDsum, WiT, DrStr. Located in folder "R".
8. **Other drivers:** Besides Bioclim also a few other drivers can be used: disturbance intensity, drought relevant for germination, browsing pressure and nutrient content. They are either read in, then they are additional columns in the Bioclim file, or they are set to values constant over time and the grid.
9. **Output**: files containing the time, location and values of output variables. Format: x , y, time, values of variable for the species. .txt or netcdf (nc4). Outputs are the states (numbers of trees per species and height class in a grid cell and at a time point) converted to certain variable, e.g. total biomass per species in the grid cell and at a time point, either per patch size (833 m2) or ha.
10. **Statefile**: the entire state of the simulation is written out and stored at defined times. These statefiles can then be read in again in a new simulation, and this simulation is started at exactly this state. Can and should be used for security: in case a long simulation crashes, not only the results up to this time are saved in the output files, but also the exact state at the last time point when the file was written out was, is available for restarting the simulation from then on. The statefile grid and time must match in the grid with the grid and start time of the simulation.
11. **Boolean Constants**: **T** for true or **F** for false
12. **Coordinates of input data**: eventually in m. But TM package and GUI translate them from any coordinate system to m.
13. **Inoculation:** During a given, normally short, time at the start of the simulation a fixed small amount of seeds is distributed in all cells in predefined grid cells, and there is no seed dispersal from seed production. This is done to allow a simulation start from scratch. Without seeds, not trees would grow. After the inoculation, the normal seed production and seed dispersal is switched on and the fixed seed input off.
14. **Spinup:** simulation until start of different simulation experiments. Usually from bare ground, with a short inoculation period, until an equilibrium is reached under standard conditions.
15. **Stochastic (T) or deterministic (F) seed dispersal:** The dispersal kernel can be interpreted as fraction of seeds always landing in a certain cell (determininistic,fast),

or as a probability for a single seed to land there (stochastic, slow). Makes a difference for small seed numbers.

16. **Fast Fourier Transform (FFT) for dispersal:** For large grids and big kernels, brute force evaluation of the dispersal convolution, i.e. determining the seeds reaching each cell from each other cell, can be very time consuming. In these cases, the use of the Fast Fourier Transform for the dispersal is much more efficient (Lehsten et al., 2019).

17. **Seedbank dynamics:** Seed bank dynamics consists of seed input, seed survival and germination, updating the seedbank of the previous year. If seedbank dynamics is not simulated, the seeds arriving at the cell in the current year are killed after germination, so no seeds from the years before are kept.

18. **Seed antagonists**: Optionally, species specific antagonists, e.g. seed predators or seed pathogens, harming the seedbank, can be included. Then, their population dynamics is explicitly calculated, with the following SeedAnta… rates.

19. **Seed carrying capacity**: As an alternative to explicit calculation of seed antagonists, a restriction of seeds (carrying capacity) in the seedbed is included, which is modeled by a logistic model with the parameter carrying capacity as the maximum value of seeds in the seedbed. The restriction acts on each species separately, but the parameter is the same for all species.

20. **Boundary condition of simulation area**: What happens to seeds going over the edge of the simulation area? They can be just lost or enter the simulation area at the opposite side.

21. **Immigration file:** Specifies which species enter the simulation area where in which periods. Format: txt file, in each line one species in seam sequence as in species parameter file. One row: species name, number of immigration events, then for each of the immigration events year, lat, lon, sim.yrs and relative coordinates.

22. **Clumping**: The clumping factor (facvar) for the light frequency describes how narrow the assumed distribution of densities of leaf area is, which goes back to the assumed spatial distribution of trees. The clumping factor thus influences strongly the distribution of light. 1 corresponds to a random spatial distribution of leaf area, i.e. a Poisson distribution of the densities per patch area. Facvar: 0 corresponds to a uniform spatial distribution and values >1 to clumped spatial distributions. Normally set to 1.

In Control file (and GUI)

In the TM-R-script, the settings can be set or changed by ctr$setOption(Variable name in first column in this table, value), e.g. ctr$setOption("startYear", 1700)

Variable in control file, FORTRAN code	Variable in TM-R-script	Field in GUI	Explanation	Example	unit
experimentID	simulationID	Simulation ID	Identifier of simulation experiment. Bioclim and output file names contain this ID.	newsim	-
Time					
numyrs	numYears	Simulation duration numbers of years to be simulated in Control Settings/General	Total number of years to be simulated.		sim. yrs
simustartyear	startYear	Simulation Period	Start year of simulation		cal. yr
reportIntervals	reportIntervals	report intervals in Control Settings/Output	Periodicity of output, either one value for the entire period or different settings for different times (in actual years)	5 or 50 1600 1950 10 1951 2100	cal. yr
inoculationTime	inoculationTime	initial simulation time in Control Settings/General	Length of inoculation time, i.e. period of free seed dispersal	10	sim. yrs
stateOutputDist	stateOutputDist	interval of statefile output for backup in Control Settings/Output	Periodicity of statefile output.	100	sim. yrs
stateOutputYears	stateOutputYears	specific years for statefile output	specific years for statefile output	1950 2000 or empty	cal. yr
readStateVect	readFromStatefile	Read initial state from statefile? in Initial State	Shall the initial state be read from an existing state file?	T F	
		State-file path ? in Initial State	Which statefile shall be used? standard value is "InitialValues.txt" in the current TreeMig directory Not specified in control file.		
Space					

Variable in control file, FORTRAN code	Variable in TM-R-script	Field in GUI	Explanation	Example	unit
pltsiz	patchArea	patch area, area of reference for distrib. In Control Settings/Grid	Patch area, area of reference for internal calculation. Assumed interaction (shading) range of one big tree.	833. (leave it on this value)	m^2
Maxlat, maxlon	numRows, numCols	Calculated from coordinates and resolution	used number of rows in grid	10	-
cellSideLength	gridCellLength		Resolution, side-length of grid cell	500.000	m
unitOfSpatialData	unitOfInputData		one unit of input data (stock, bioclim) corresponds to "unitOfSpatialData" m.	1.0	m
lonRealStart, lonRealEnd, latRealStart, latRealEnd	lonRealStart, lonRealEnd, latRealStart, latRealEnd	in the interactive map	left (west)/right(east)/bottom(south)/top(north) edge in real coordinates	796500.000	m
startlatStart, startlatEnd, startlonStart startlonEnd	startlatStart, startlatEnd, startlonStart startlonEnd	The relative coordinates of the inoculation area can either be directly typed in Control Settings/Grid/initial cell position , or in Select Initial Cell. selected as center etc, or chosen on the grid.	Relative coordinates of "inoculation" area, where seeds are distributed during the inoculation period at start	3,5,7,9	grid cell index
boundaries	boundaries	Boundary conditions Control Settings/Grid	Boundary condition of simulation area. Are they lost (a: absorbing), or do they enter the simulation area the other side (c: cyclic, w: at west or east s: at north or south)?	a	
Environment					

Variable in control file, FORTRAN code	Variable in TM-R-script	Field in GUI	Explanation	Example	unit
ienv	includeEnvInfo	-	Use environment dependence of process functions, if false environmant it always optimal	T F (leave it on T)	
envFromfile	readEnvFromFile		read environmental infos from files?	T F (leave it on T)	
bioclimFile	bioClimFile	Bioclimate/Existing Bioclimate and Write bioclimate to new file	Filename of file with bioclimatic data, supposed to be located in folder "E" in the TMEnvironment	BCNatParkStdMod.txt	
	Default Driver Values				
Distu	defaultDetDistu	default deterministic disturbances Driver Defaults Control Settings	Default values for deterministic disturbance intensity if not present as column in bioclimate file	0	0-1
browsPress	defaultBrowsing	default browsing Driver Defaults Control Settings	default value for browsing if not present as column in bioclimate file	8	0-30
germDrought	defaultDrstr	default drought stress for germination Driver Defaults Control Settings	default drought stress for germination; -1 means "same as DrStr for trees» if not present as column in bioclimate file	-1	0-1
default nutrient availability; nutrients	defaultNutrients	default nutrient availability Driver Defaults Control Settings	default nutrient (N) availability if not present as column in bioclimate file	100	t/ha
Dispersal					
doFFT	doFFT	Dispersal by FFT (T) or brute force (F) Control settings/Seed Dispersal	Dispersal by FFT (T) or brute force (F).	F	
dispersalDifferent	dispDifferent	Dispersal distance different for species? Control settings/Seed Dispersal	Dispersal distance different for species?	T	
kernelType	kernelType	kernelType: 0: circular, 1: single-expon. 2: double-expon. Control settings/Seed Dispersal	Description of the shape of the dispersal kernel: 0: circular, i.e. same value in circular area, 1: single-expon. 2: double-expon.	2	

Variable in control file, FORTRAN code	Variable in TM-R-script	Field in GUI	Explanation	Example	unit
epsKernel	epsKernel	cut-off threshold of kernel (in 1/1000) Control settings/Seed Dispersal	Kernels are not infinitely wide, but cut off at a certain "height", i.e. probability value. cut-off threshold of kernel (in 1/1000)	0.001	
alpha	alphaKernel	Alpha-value of kernel (general)	In the case that all species have the same kernel, i.e. dispersal distance is the same for all species (see above), alpha describes the steepness of the this general kernel Alpha-valuet of kernel (general). It corresponds to the mean dispersal distance.	200	m
active	activeSeedDisp	-	Active or passive seed dispersal. T: active, F passive	active	
doStochSeedDisp	stochSeedDisp	Stochastic (T) or deterministic (F)seed dispersal? Control settings/Seed Dispersal	Stochastic (T) or deterministic (F) seed dispersal? The dispersal kernel can be interpreted as fraction of seeds always landing in a certain cell (determininistic,fast), or as a probability for a single seed to land there (stochastic, slow).	F	
OuterSeeds	numOuterSeeds	No. of seeds/patch coming from outside grid Control settings/Seed Dispersal	Constant amount of seeds for each species that reach the simulation area independent of seed dispersal. Normal seed production and dispersal are also active. No. of seeds/patch coming from outside grid	0	
Seeds					
seedsDifferent	diffSeedProd	-	Seed production different for species? Should be different. If set false, each species gets 10000.0*spec(i)%khmax (its own max. height) /htmax (max. height of all species) seeds.	T	

Variable in control file, FORTRAN code	Variable in TM-R-script	Field in GUI	Explanation	Example	unit
mathgtDifferent	diffMaturHeight	-	maturation heigth different for species? Should be different. If set false the height of maturity is set to about 0.8 times species height.	T	
mastSeeding	mastSeeding	-	Periodic seed production ? If set true (recommended) the seeds are produced according to a sine wave with read-in period over the years, otherwise constantly.	T	
seedBank	seedBank	-	Seedbank dynamics? Shall the seed bank dynamics be calculated? If not, the seeds arriving at the cell in the current year are killed after germination.	T	
Density					
seedlcrowndiamInCm	seedlingCrownDia	Diameter of seedling crowns (cm) Control settings/Density	Diameter of seedling crowns (cm) . Is used to estimate how many seedlings fit on a given area, and to restrict the number of seedlings of all species (by a saturation function) to this number.	20.	cm
withSeedAntagonists	includeSeedAnta	-	Seed antagonists included ? If TRUE, the population dynamics of seed antagonists is explicitly calculated with the following SeedAnta… rates Normally FALSE.	F	
seedAntaGraz	seedAntaGraz	-	grazing rate of seed antagonists		
seedAntaEff	seedAntaEff	-	efficiency of grazing of seed antagonists		
seedAntaMort	seedAntaMort	-	mortality of seed antagonists		
seedAntaRain	seedAntaRain	-	constant influx of seed antagonists		
withSeedCarrCap	inclCarryCapa	-	Carrying capacity for seeds included?	T	

Variable in control file, FORTRAN code	Variable in TM-R-script	Field in GUI	Explanation	Example	unit
seedCarrCap	seedCarryCapa	Control settings/Density	carrying capacity of seeds /833 m^2(of each species)		
Immigration			Immigration of given species in given cells at given times		
immigration	immigration	-	immigration included? Shall the immigration be simulated? If yes, immigration happens for the species in the times and locations specified in the immigration file.	F	
immifilename	immigrationFile	-	File with species immigration.	IMMIGRATIONFILE.txt	
Disturbances		These are the small scale disturbances which act on all cells independently and are not species specific. Larger scale disturbances can be added via the bioclim file.			
disturbances	disturbances	Disturbances included? Control settings/Disturbances	disturbances included ?	T	
disturbProb	disturbProb		disturbance probability per cell and year = 1/return interval	0.001	
disturbIntensity	disturbIntens		proportion of trees which die by disturb.	0.8	
Clumping					
fcvarInit	facVarInit	-	Clumping factor for light freq. initial. ; facvar in the inoculation phase . Normally set to 1.	1.	
fcvarDyn	facVarDyn	-	Clumping factor for light freq. spatial; facvar in the spatial dynamics phase. Normally set to 1.	1.	
	Light dependence				

Variable in control file, FORTRAN code	Variable in TM-R-script	Field in GUI	Explanation	Example	unit
estabEqHC0	estabEqHC0	-	light dep. of establ. for seedl. or germination Is the establishment and germination simulated as light dependent? Is the light dependence of the growth and survival of the 0th height class (< 1.37m, saplings) taken from the original ForClim light dependence of establishment? Otherwise, the growth and survival light dependences of the first height class are used. Normally set to true.	T	
contLightDepGerm	contLightDepG	-	light dep. of establ. continuous. Applying a smoothed step function instead of a maximum function for the light response function of germination. Should be set to true	T	
Species Parameters		Species Selection. Based on the defined species parameter file, the selected species, and potential changes Edit Species Parameters the Wrapper constructs a new species parameter file in folder P.	For meaning of parameters see SpecParsMeanings.xlsx		
specfilename	speciesParsFile	-	File with species parameters. Text file, must be in folder P.	TreePars2.txt	
Output			Various output variables are possible		
writeOutput%netcdf	outputNetcdf		Write output as netcdf (T) or txt (F)	F	

Variable in control file, FORTRAN code	Variable in TM-R-script	Field in GUI	Explanation	Example	unit
writeOutput%biomass	writeBiomass		Write total species biomasses	T	t/ha
writeOutput%number	writeNumbers		Write total species numbers	F	n/ha
writeOutput%hstruct	writecHStruct		write species height structures	F	n/patch and height class
writeOutput%seeds	writeSeeds		write species seeds	F	n/patch size
writeOutput%antagonists	writeSeedAnta		write species seed antagonists	F	n/patch size
writeOutput%pollen	writePollen		write species pollen percent	F	%
writeOutput%LAI	writeLAI		write species LAI ; double sided leaf area index	T	m^2/m^2
writeOutput%basalArea	writeBasalArea		write species basal area	F	m^2/ha
writeOutput%NPP	writeNPP		write species NPP; roughly estimated as difference of biomass between years	F	t/ha
writeOutput%ingrowth	writeSpecIngrowth		write species ingrowth above 1.37 m	F	n/patch size
writeOutput%biodiv	writeBiodiv		write biodiversities; calculated according to Shannon-Weaver	F	0-1
writeOutput%light	writeLightDistr		write light distributions; Fractions in light classes in each height class	F	
tabsepOutput	outputWithTabs		output with tabs (T) or commas (F)	T	

Only in GUI:

Section in GUI	Field in GUI	Explanation
	Write bioclimate to new file	The bioclimate that is maybe extended Extend Bioclimate or masked out by land use Stockability over Time/ Add Stockability is stored under this name.
Input Data		
	Input Data	Here is the place where you can define all your input data. Input data can later be used for bioclimate calculation and stockfile. Required are data for temperature, precipitation, slope, aspect, water holding capacity, stockability. You can add several of these files.
	Directories	Where your input data are stored
Simulation		
Define Study Area	Round coordinates	To "smooth" the coordinates given by the selection on the map
Bioclimate		
	New Bioclimate /From File	Chose here from the files defined in Input Data the ones to be used
Extend Bioclimate		If the bioclimate years don't cover all the simulation years, we can extend the bioclimate to match the simulation years. This is done by using the bioclimate data of years, which are random sampled from Sample years.
Stockability over Time	New Stock File	Here, one or several files can be added that contain the stockability over a certain time period. The Filter refers to the classes of the Swiss Areal Statistics NOASO4. The meaning of the classes can be looked up in View NOASO4 Classes. Alternatively, a stockability file of cells and times can be given as CSV. This stockability file or the one derived from the aerial statistics is then used to mask out the non-stockable cells in the bioclimate file.
Species selection	Select Species	The simulation will run only for the selected species, which are interacting with each other. From the selection and the edited species parameters a new species parameter file with the experiment id is constructed.
	Edit Species Parameterrs	Here you can change parameters. Will also stored in the new species parameter file.
Initial State	State-file path	Here you have to indicate your statefile. It must match the dimensions and the start time of your simulation.

Plots		
Species Output Variables Maps	plotSpeciesOutputMaps	Maps of biomass of selected simulated species for different time points
	simulationID	ID/name of the simulation to load
	output.variable	Select which of the simulated output variables should be plotted.
	species	Select which simulated species shall be plotted
	years	Add a sequence of years, 'all_years' or specific years (custom) for the plots
	species.comparison	If true then all species maps are plotted in one figure, otherwise separately for each species.
	animated	Make a movie from the single plots
	color.option	Different color styles
	output.threshold	Select only species that are over the specified threshold of the output variable
	filename	Custom name for output figures. Otherwise it will be generate by the function based on the selected parameters
	ggplot.args	Arguments determining the technical characteristics of the plot, like size, resolution, for movies the duration
Bioclimate Summary	plotBioclimateSummary	Bioclimate over time, averaged over whole area or within subareas
	simulationID	ID/name of the simulation to load
	years	Add a sequence of years, 'all_years' or specific years (custom) for the plots
	bioclim.var	What shall be plotted? Choose DD (day degree sum), WiT (mean temperature of coldest month), DrStr (drought stress) or 'all'
	sub.area	Defines only a subarea of the simulated study area. This can either be a data.frame for points by providing lat and lon or a shapefile with multiple polygons.
	averaging.intervall	Time-span used to create the smoothed mean over time.
	quant.boundries	Upper and lower quantiles to show the confidence intervals over the entire time. 0.5 e.g. will give the median.
	filename	Custom name for output figures. Otherwise it will be generate by the function based on the selected parameters
	ggplot.args	Arguments determining the technical characteristics of the plot, like size, resolution, for movies the duration
Bioclimate Maps	plotBioClimateMaps	Maps of bioclimate at different time points
	simulationID	ID/name of the simulation to load

	years	Add a sequence of years, 'all_years' or specific years (custom) for the plots
	bioclim.var	What shall be plotted? Choose DD (day degree sum), WiT (mean temperature of coldest month), DrStr (drought stress) or 'all'
	single figure	Maps for several bioclimate variables in the same picture?
	animated	Make a movie from the single plots
	color.option	Different color styles
	filename	Custom name for output figures. Otherwise it will be generate by the function based on the selected parameters
	ggplot.args	Arguments determining the technical characteristics of the plot, like size, resolution, for movies the duration
Output Variable Stats	plotOutputVariableStats	Output variable over time, averaged over whole area or within subareas
	simulationID	ID/name of the simulation to load
	species	Select which simulated species shall be plotted
	years	Add a sequence of years, 'all_years' or specific years (custom) for the plots
	output.variable	Select which of the simulated output variables should be plotted.
	plot.type	Lines or stacked area
	output.threshold	Select only species that are over the specified threshold of the output variable
	sub.area	Defines only a subarea of the simulated study area. This can either be a data.frame for points by providing lat and lon or a shapefile with multiple polygons.
	Grid arrange	Produce one plot for different output variables?
	quant.boundries	Upper and lower quantiles to show the confidence intervals over the entire time. 0.5 e.g. will give the median.
	filename	Custom name for output figures. Otherwise it will be generate by the function based on the selected parameters
	ggplot.args	Arguments determining the technical characteristics of the plot, like size, resolution, for movies the duration

Variable along gradients	plotVariableAlongGradient	Output variable vs. another reference variable (e.g. elevation) at different time points
	simulationID	ID/name of the simulation to load
	species	Select which simulated species shall be plotted

	years	Add a sequence of years, 'all_years' or specific years (custom) for the plots	
	output.variable	Select which of the simulated output variables should be plotted.	
	plot.type	Lines or stacked area	
	gradient	Data for the reference variable in the simulation area, will be adapted to the simulation area.	
	custom.raster	Raster data of reference variable, e.g. of a digital elevation model. But can be anything, e.g. density of deers	
	custom.name	Name of the reference variable in the plots	
	se	Should the standard error be plotted	
	bins	Number of bins used to divide the reference variable	
	output.threshold	Select only species that are over the specified threshold of the output variable	
	sub.area	Defines only a subarea of the simulated study area. This can either be a data.frame for points by providing lat and lon or a shapefile with multiple polygons.	
	animated	Make a movie from the single plots	
	filename	Custom name for output figures. Otherwise it will be generate by the function based on the selected parameters	
	ggplot.args	Arguments determining the technical characteristics of the plot, like size, resolution, for movies the duration	
Treeline	plotTreeline	The upper or lower distribution limit (with respect to a reference variable) of the species over time. Settings analogous to "Variable along gradients»	
	simulationID	ID/name of the simulation to load	
	species	Select which simulated species shall be plotted	
	years	Add a sequence of years, 'all_years' or specific years (custom) for the plots	
	threshold.lines	Should there be an "upper", "lower" or "both" limits drawn based on the th.value?	
	th.value	Threshold for the cutoff for the treeline	
	gradient	Data for the reference variable in the simulation area, will be adapted to the simulation area.	
	custom.raster	Raster data of reference variable, e.g. of a digital elevation model. But can be anything, e.g. density of deers	
	custom.name	Name of the reference variable in the plots	
	bins	Number of bins used to divide the reference variable	
	bm.threshold	Select only species that have more than the specified threshold of biomass	

	sub.area	Defines only a subarea of the simulated study area. This can either be a data.frame for points by providing lat and lon or a shapefile with multiple polygons.
	ggplot.args	Arguments determining the technical characteristics of the plot, like size, resolution, for movies the duration