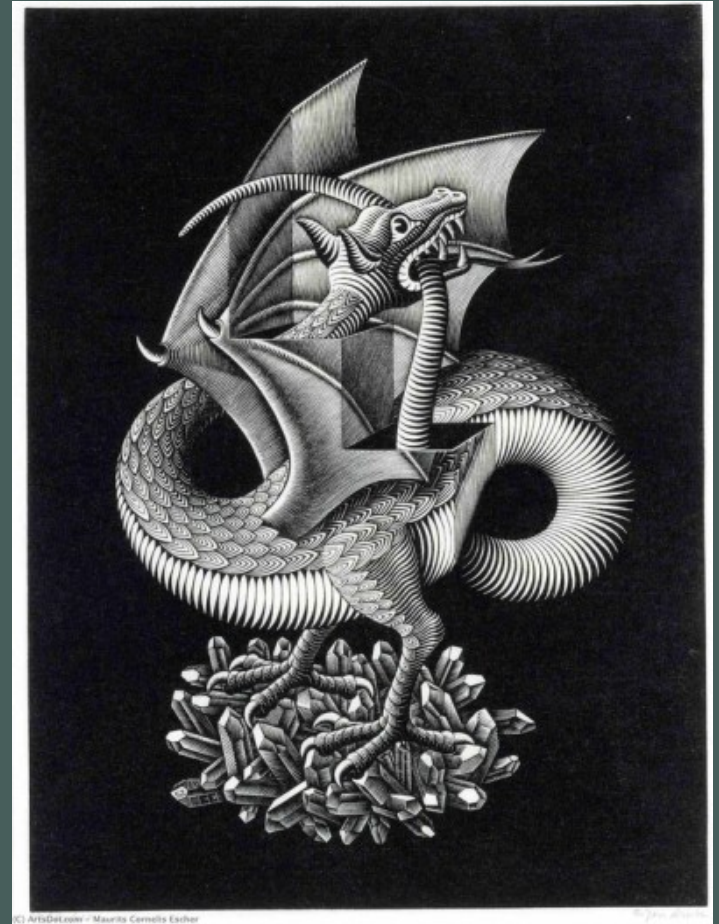


# 1.3 - Model inputs

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2022-06-13



# Outline

1. Species parameters
2. Forest input
3. Vertical profiles
4. Soil input
5. Weather input
6. Simulation control
7. Simulation input object

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```

A large number of parameters (124 columns) can be found in `SpParamsMED`, which may be intimidating.

You can find parameter definitions in table `SpParamsDefinition`:

```
data("SpParamsDefinition")
```

# 1. Species parameters

The following table shows parameter definitions and units:

Show  entries
Search:

	ParameterName	ParameterGroup	Definition	Type	Units
1	Name	Identity	Taxon names (species binomials or genus)	String	
2	IFNcodes	Identity	Codes in the forest inventory, separated by '/'	String	
3	SpIndex	Identity	Species index 0,1,2,♂	Integer	
4	Genus	Taxonomic identity	Taxonomic genus	String	
5	Order	Taxonomic identity	Taxonomical order	String	
6	Family	Taxonomic identity	Taxonomical family	String	

Showing 1 to 6 of 124 entries

Previous
2
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5
...
21
Next

## 2. Forest input

### Forest class

Each *forest plot* is represented in an object of class `forest`, a list that contains several elements.

```
forest <- exampleforestMED
```



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The most important items are two data frames, `treeData` (for trees):

```
forest$treeData
```

```
##   Species    N   DBH Height Z50  Z95
## 1     148 168 37.55    800 100  600
## 2     168 384 14.60    660 300 1000
```

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```
##   Species    N   DBH Height Z50   Z95
## 1      148 168 37.55    800 100   600
## 2      168 384 14.60    660 300 1000
```

and `shrubData` (for shrubs):

```
forest$shrubData
```

```
##   Species Cover Height Z50   Z95
## 1      165   3.75    80 200 1000
```

## 2. Forest input

### Forest class

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Variable	Definition
Species	Species numerical code (should match SpIndex in SpParams)
N	Density of trees (in individuals per hectare)
DBH	Tree diameter at breast height (in cm)
Height	Tree total height (in cm)
Z50	Soil depth corresponding to 50% of fine roots (mm)
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**Important:** medfate's *naming conventions* for tree cohorts and shrub cohorts uses T or S, the row number and species numerical code (e.g. "T1\_148" for the first tree cohort, corresponding to *Pinus halepensis*).

## 2. Forest input

### Creating a 'forest' object from forest inventory data

Forest inventories can be conducted in different ways, which means that the starting form of forest data is diverse.

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Building forest objects from inventory data will always require some data wrangling, but package **medfateutils** provides functions that may be helpful:



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Building forest objects from inventory data will always require some data wrangling, but package **medfateutils** provides functions that may be helpful:

Function	Description
<code>forest_mapShrubTable()</code>	Helps filling shrubData table
<code>forest_mapTreeTable()</code>	Helps filling treeData table
<code>forest_mapWoodyTables()</code>	Helps filling a forest object
<code>IFN2forestlist()</code>	Creates a list of forest objects from Spanish forest inventory data

## 2. Forest input

### Forest attributes

The **medfate** package includes a number of functions to examine properties of the plants conforming a forest object:

- `plant_*`: Cohort-level information (species name, id, leaf area index, height...).
- `species_*`: Species-level attributes (e.g. basal area, leaf area index).
- `stand_*`: Stand-level attributes (e.g. basal area).

```
plant_basalArea(forest)
```

```
##      T1_148      T2_168      S1_165  
## 18.604547   6.428755          NA
```

```
stand_basalArea(forest)
```

```
## [1] 25.0333
```

## 2. Forest input

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##      T1_148      T2_168      S1_165
## 18.604547   6.428755         NA
```

```
stand_basalArea(forest)
```

```
## [1] 25.0333
```

```
plant_LAI(forest, SpParamsMED)
```

```
##      T1_148      T2_168      S1_165
## 0.96734365 0.86167321 0.03928201
```

```
stand_LAI(forest, SpParamsMED)
```

```
## [1] 1.868299
```

## 2. Forest input

### Aboveground data

An important information for simulation model is the estimation of initial **leaf area index** and **crown dimensions** for each plant cohort, which is normally done using *allometries*.

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We can illustrate this step using function `forest2aboveground()`:

```
above <- forest2aboveground(forest, SpParamsMED)
above
```

##	SP	N	DBH	Cover	H	CR	LAI_live	LAI_expanded	LAI_dead
## T1_148	148	168.0000	37.55	NA	800	0.6605196	0.96734365	0.96734365	0
## T2_168	168	384.0000	14.60	NA	660	0.6055642	0.86167321	0.86167321	0
## S1_165	165	749.4923	NA	3.75	80	0.8032817	0.03928201	0.03928201	0

where species-specific allometric coefficients are taken from `SpParamsMED`.

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where species-specific allometric coefficients are taken from `SpParamsMED`.

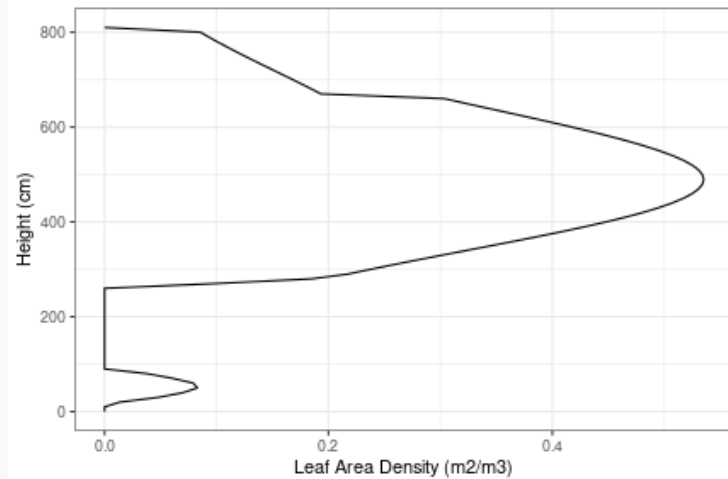
Users will not normally call `forest2aboveground()`, but is important to understand what is going on behind the scenes.

# 3. Vertical profiles

## Leaf distribution

Vertical leaf area distribution (at the cohort-, species- or stand-level) can be examined using:

```
vprofile_leafAreaDensity(forest, SpParamsMED)
```

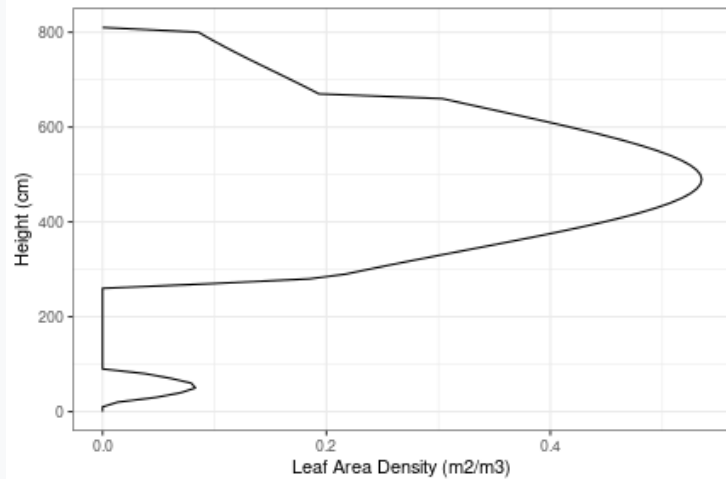


### 3. Vertical profiles

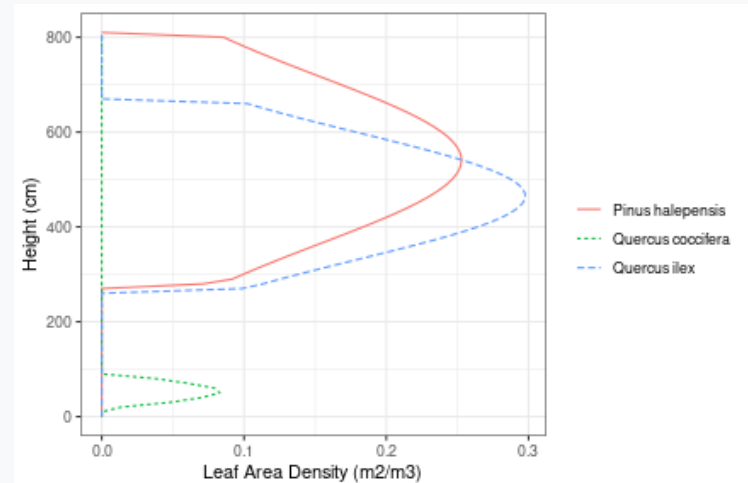
#### Leaf distribution

Vertical leaf area distribution (at the cohort-, species- or stand-level) can be examined using:

```
vprofile_leafAreaDensity(forest, SpParamsMED)
```



```
vprofile_leafAreaDensity(forest, SpParamsMED,  
  byCohorts = TRUE, bySpecies = TRUE)
```



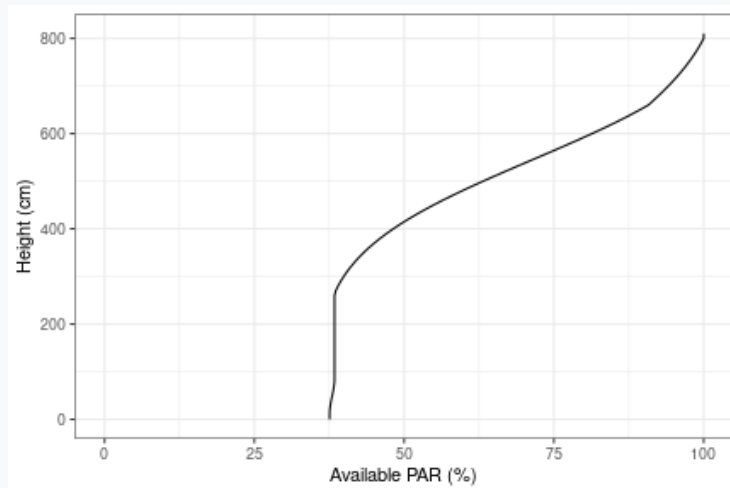


### 3. Vertical profiles

#### Radiation extinction

Radiation extinction (PAR or SWR) profile across the vertical axis can also be examined:

```
vprofile_PARExtinction(forest, SpParamsMED)
```

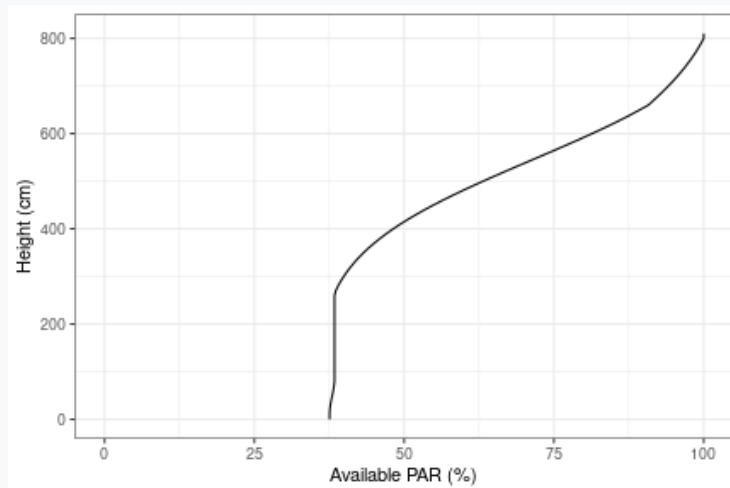


# 3. Vertical profiles

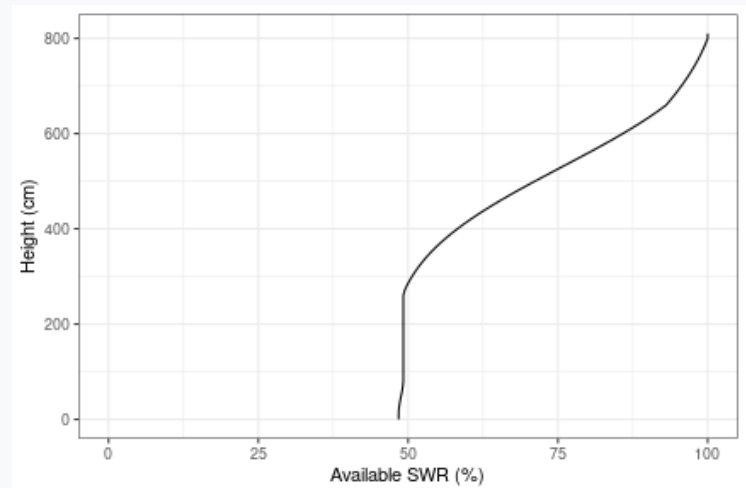
## Radiation extinction

Radiation extinction (PAR or SWR) profile across the vertical axis can also be examined:

```
vprofile_PARExtinction(forest, SpParamsMED)
```



```
vprofile_SWRExtinction(forest, SpParamsMED)
```

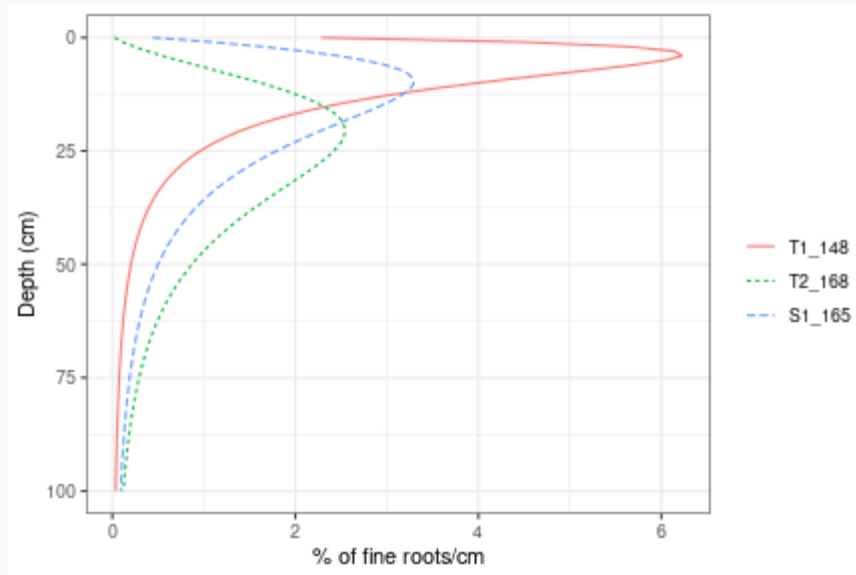


### 3. Vertical profiles

#### Belowground root distribution

Users can visually inspect the distribution of fine roots of forest objects by calling function `vprofile_rootDistribution()`:

```
vprofile_rootDistribution(forest, SpParamsMED)
```



## 3. Vertical profiles

### Interactive forest inspection

Function `shinyplot()` is a more convenient way to display properties and profiles of forest objects:

```
shinyplot(forest, SpParamsMED)
```

## 4. Soil input

### Soil physical description

Soil physical characteristics are specified using a **data.frame** with soil layers in rows and attributes in columns:

- `widths` - layer widths, in mm.
- `clay` - Percentage of clay (within volume of soil particles).
- `sand` - Percentage of sand (within volume of soil particles).
- `om` - Percentage of organic matter per dry weight (within volume of soil particles).
- `bd` - Bulk density (g/cm<sup>3</sup>)
- `r fc` - Rock fragment content (in whole-soil volume).

## 4. Soil input

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- `bd` - Bulk density (g/cm<sup>3</sup>)
- `rfc` - Rock fragment content (in whole-soil volume).

They can be initialized to default values using function `defaultSoilParams()`:

```
spar <- defaultSoilParams(2)
print(spar)
```

```
##   widths clay sand om   bd rfc
## 1    300   25   25 NA  1.5  25
## 2    700   25   25 NA  1.5  45
```

... and then you should modify default values according to available soil information.

## 4. Soil input

### Drawing soil physical attributes from *SoilGrids*

*SoilGrids* is a global database of soil properties:

*Hengl T, Mendes de Jesus J, Heuvelink GBM, Ruiperez Gonzalez M, Kilibarda M, Blagotic A, et al. (2017) SoilGrids250m: Global gridded soil information based on machine learning. PLoS ONE 12(2): e0169748. doi:10.1371/journal.pone.0169748.*

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Package **medfateutils** allows retrieving Soilgrids data by connecting with the SoilGrids **REST API**



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Package **medfateutils** allows retrieving Soilgrids data by connecting with the SoilGrids **REST API**

To start with, we need a spatial object of class `sf` or `sfc` (from package **sf**) containing the geographic coordinates of our target forest stand:

```
cc <- c(1.32, 42.20)
coords_sf <- sf::st_sfc(sf::st_point(cc), crs=4326)
```

## 4. Soil input

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```
cc <- c(1.32, 42.20)
coords_sf <- sf::st_sfc(sf::st_point(cc), crs=4326)
```

We then call `soilgridsParams()` along with a desired vertical width (in mm) of soil layers:

```
soilgridsParams(coords_sf, widths = c(300, 700, 1000))
```

## 4. Soil input

### Soil input object

Soil input for simulations is an object of class `soil` (a list) that is created from physical description using a function with the same name:

```
examplesoil <- soil(spar)  
class(examplesoil)
```

```
## [1] "soil" "list"
```

## 4. Soil input

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examplesoil <- soil(spar)
class(examplesoil)
```

```
## [1] "soil" "list"
```

A `print()` function has been defined for objects of class `soil`, that displays several soil parameters and properties.

```
examplesoil
```

```
## Soil depth (mm): 1000
##
## Layer 1 [ 0 to 300 mm ]
##   clay (%): 25 silt (%): 50 sand (%): 25 organic matter (%): NA [ Silt loam ]
##   Rock fragment content (%): 25 Macroporosity (%): 5
##   Theta WP (%): 14 Theta FC (%): 30 Theta SAT (%): 49 Theta current (%) 30
##   Vol. WP (mm): 32 Vol. FC (mm): 68 Vol. SAT (mm): 111 Vol. current (mm): 68
##   Temperature (Celsius): NA
##
## Layer 2 [ 300 to 1000 mm ]
##   clay (%): 25 silt (%): 50 sand (%): 25 organic matter (%): NA [ Silt loam ]
##   Rock fragment content (%): 45 Macroporosity (%): 5
##   Theta WP (%): 14 Theta FC (%): 30 Theta SAT (%): 49 Theta current (%) 30
##   Vol. WP (mm): 55 Vol. FC (mm): 117 Vol. SAT (mm): 190 Vol. current (mm): 117
##   Temperature (Celsius): NA
##
```

## 4. Soil input

### Water retention curves

The **water retention curve** is used to represent the relationship between soil water content (  $\theta$  ; %) and soil water potential (  $\Psi$  ; MPa).

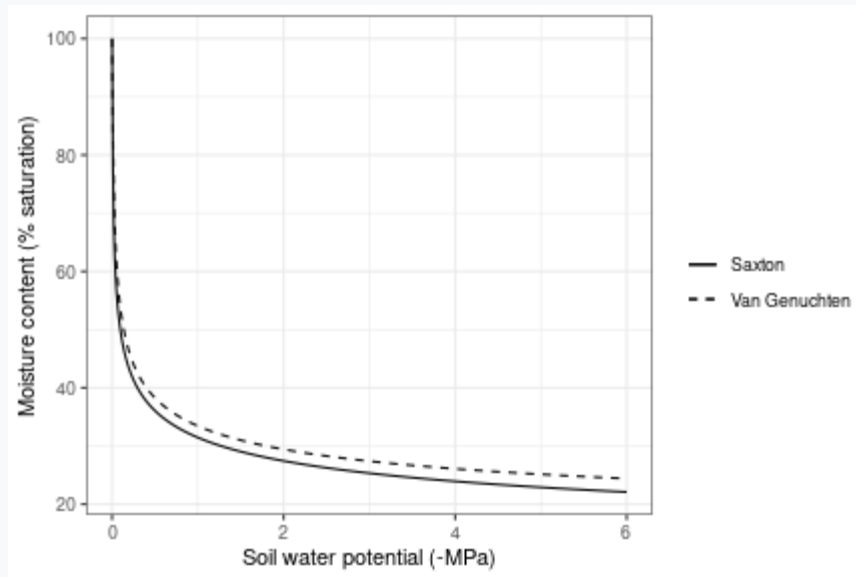
## 4. Soil input

### Water retention curves

The **water retention curve** is used to represent the relationship between soil water content ( $\theta$ ; %) and soil water potential ( $\Psi$ ; MPa).

The following code calls function `soil_retentionCurvePlot()` to illustrate the difference between the two water retention models in this soil:

```
soil_retentionCurvePlot(examplesoil, model="both")
```



## 5. Weather input

All simulations in the package require **daily weather** inputs in form of a `data.frame` with dates as `row.names`.

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Variables	Units
Mean/maximum/minimum temperature	$^{\circ}C$
Precipitation and potential evapo-transpiration (PET)	$l \cdot m^{-2} \cdot day^{-1}$
Mean/maximum/minimum relative humidity	%
Radiation	$MJ \cdot m^{-2} \cdot day^{-1}$
Wind speed	$m \cdot s^{-1}$



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Wind speed	$m \cdot s^{-1}$

An example of daily weather data frame:

```
data(examplemeteo)
head(examplemeteo, 2)
```

```
##           MinTemperature MaxTemperature Precipitation MinRelativeHumidity MaxRelativeHumidity
## 2001-01-01      -0.5934215       6.287950      4.869109           65.15411           100.0000
## 2001-01-02      -2.3662458       4.569737      2.498292           57.43761           94.7178
##
##           Radiation WindSpeed
## 2001-01-01    12.89251    2.000000
## 2001-01-02    13.03079    7.662544
```

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##
##           Radiation WindSpeed
## 2001-01-01    12.89251    2.000000
## 2001-01-02    13.03079    7.662544
```

Simulation functions have been designed to accept data frames generated using package **meteoland**.

## 6. Simulation control

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The default parameterization is obtained using function `defaultControl()`:

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control <- defaultControl()
```

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The default parameterization is obtained using function `defaultControl()`:

```
control <- defaultControl()
```

A large number of control parameters exist:

```
names(control)
```

Control parameters should be left to their **default values** until their effect on simulations is fully understood!

## 7. Simulation input object

Simulation functions `spwb()` and `growth()` require combining forest, soil, species-parameter and simulation control inputs into a *single input object*.

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The combination can be done via functions `forest2spwbInput()` and `forest2growthInput()`:

```
x <- forest2spwbInput(forest, examplesoil, SpParamsMED, control)
```

## 7. Simulation input object

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Having this additional step allows *modifying the value* of specific parameters or state variables before calling the simulation functions.



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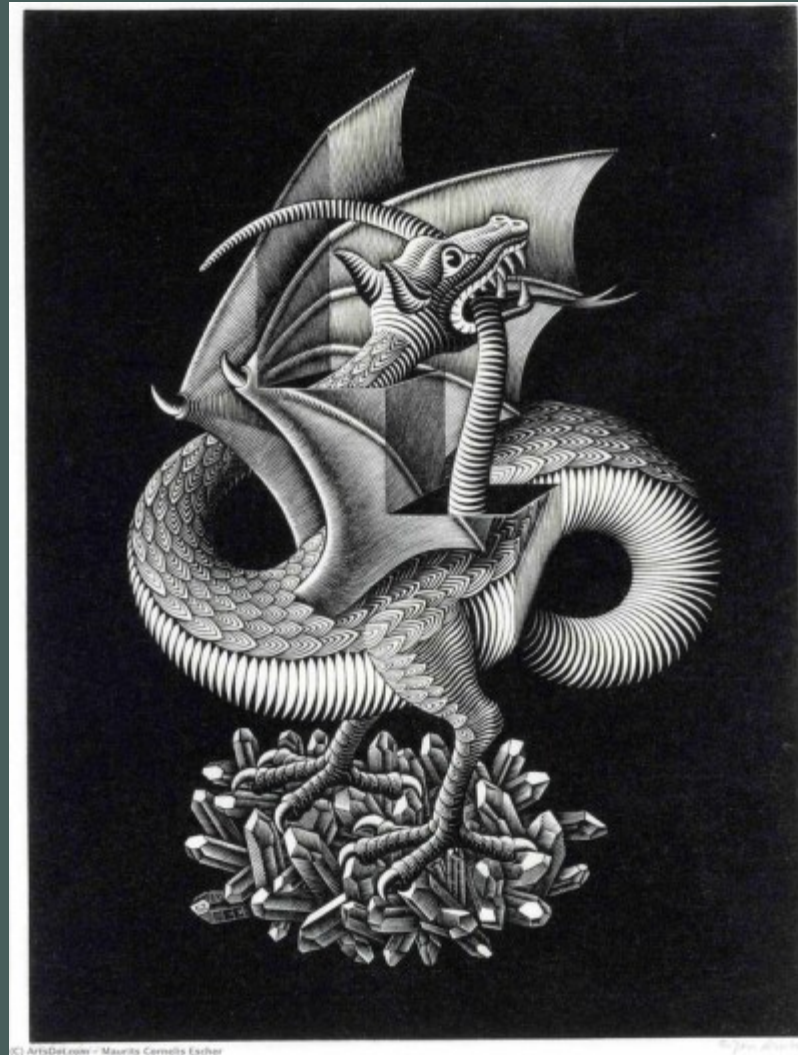
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```
x <- forest2spwbInput(forest, examplesoil, SpParamsMED, control)
```

Having this additional step allows *modifying the value* of specific parameters or state variables before calling the simulation functions.

Function `fordyn()` is different from the other two models: the user enters forest, soil, weather, species parameters and simulation control inputs *directly* into the simulation function.

## M.C. Escher - Dragon, 1952



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