

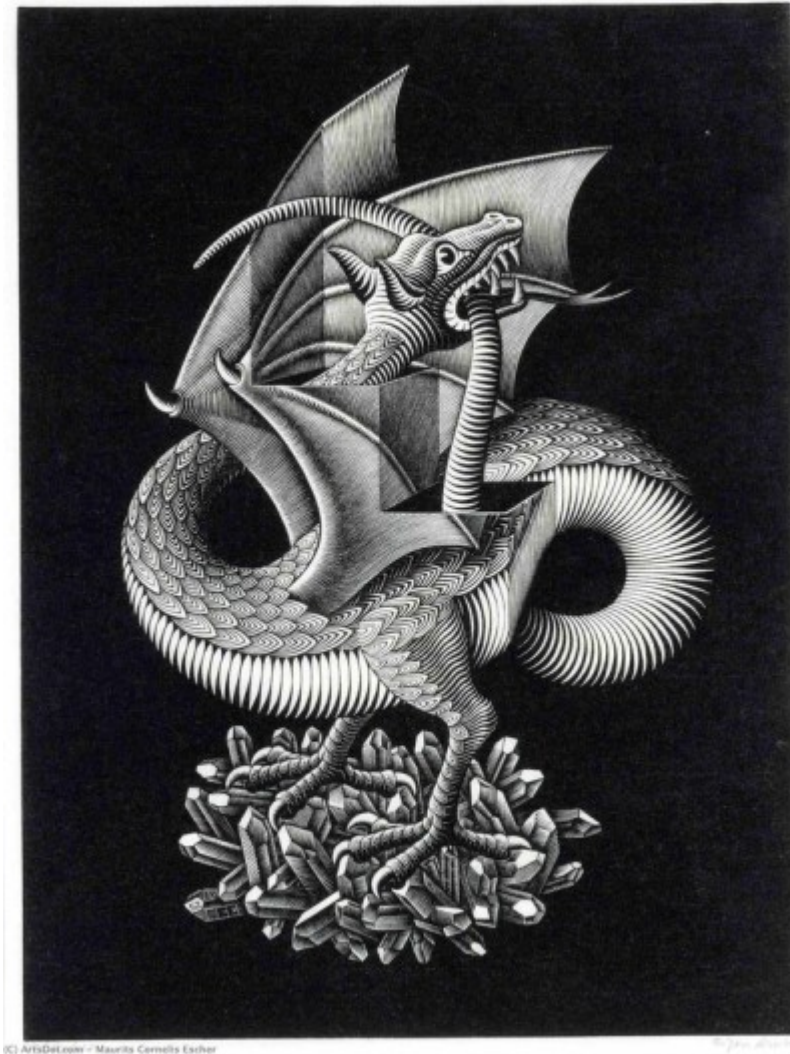
# Model inputs

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# Outline

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

M.C. Escher - Dragon, 1952



# 1. Species parameters

# Species parameter table

Simulation models in **medfate** require a `data.frame` with species parameter values.

The package includes a default data set of parameter values for 217 Mediterranean taxa.

```
1 data("SpParamsMED")
```

A large number of parameters (157 columns) can be found in `SpParamsMED`, which may be intimidating.

You can find parameter definitions in table `SpParamsDefinition`:

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

# Species parameter table

The following table shows parameter definitions and units:

Show 

4

 entries

Search:

	ParameterName	ParameterGroup	Definition	Type	Units	Strict
1	Name	Identity	Plant names (species binomials, genus or other) used in vegetation data	String		true
2	SplIndex	Identity	Internal species codification (0,1,2,)	Integer		true
3	AcceptedName	Taxonomic identity	Accepted scientific name of a taxon (genus, species, subspecies or variety) used for parameterization	String		false
4	Species	Taxonomic identity	Taxonomic species of accepted name	String		false

Showing 1 to 4 of 156 entries

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## 2. Forest input

# Forest class

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

```
1 forest <- medfate::exampleforest
```

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

```
1 forest$treeData
```

	Species	N	DBH	Height	Z50	Z95
1	Pinus halepensis	168	37.55	800	100	600
2	Quercus ilex	384	14.60	660	300	1000

and `shrubData` (for shrubs):

```
1 forest$shrubData
```

	Species	Cover	Height	Z50	Z95
1	Quercus coccifera	3.75	80	200	1000

# Forest class

## Tree data

Variable	Definition
<a href="#">Species</a>	Species numerical code (should match <a href="#">SpIndex</a> in <a href="#">SpParams</a> )
<a href="#">N</a>	Density of trees (in individuals per hectare)
<a href="#">DBH</a>	Tree diameter at breast height (in cm)
<a href="#">Height</a>	Tree total height (in cm)
<a href="#">Z50</a>	Soil depth corresponding to 50% of fine roots (mm)
<a href="#">Z95</a>	Soil depth corresponding to 95% of fine roots (mm)

## Shrub data

Variable	Definition
<a href="#">Species</a>	Species numerical code (should match <a href="#">SpIndex</a> in <a href="#">SpParams</a> )
<a href="#">Cover</a>	Shrub cover (%)
<a href="#">Height</a>	Shrub total height (in cm)
<a href="#">Z50</a>	Soil depth corresponding to 50% of fine roots (mm)
<a href="#">Z95</a>	Soil depth corresponding to 95% of fine roots (mm)

### 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*).



# Creating a ‘forest’ from forest inventory data

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

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

Function	Description
<code>forest_mapShrubTable()</code>	Helps filling <code>shrubData</code> table
<code>forest_mapTreeTable()</code>	Helps filling <code>treeData</code> table
<code>forest_mapWoodyTables()</code>	Helps filling a <code>forest</code> object

# 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).

```
1 plant_basalArea(forest, SpParamsMED)
```

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

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

```
      T1_148      T2_168      S1_165
0.84874773 0.70557382 0.03062604
```

```
1 stand_basalArea(forest)
```

```
[1] 25.0333
```

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

```
[1] 1.758585
```

# 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*.

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

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

	SP	N	DBH	Cover	H	CR	LAI_live	LAI_expanded	LAI_dead
T1_148	148	168.0000	37.55	NA	800	0.6605196	0.84874773	0.84874773	0
T2_168	168	384.0000	14.60	NA	660	0.6055642	0.70557382	0.70557382	0
S1_165	165	749.4923	NA	3.75	80	0.8032817	0.03062604	0.03062604	0
	LAI_nocomp	ObsID							
T1_148	1.29720268	<NA>							
T2_168	1.01943205	<NA>							
S1_165	0.04412896	<NA>							

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

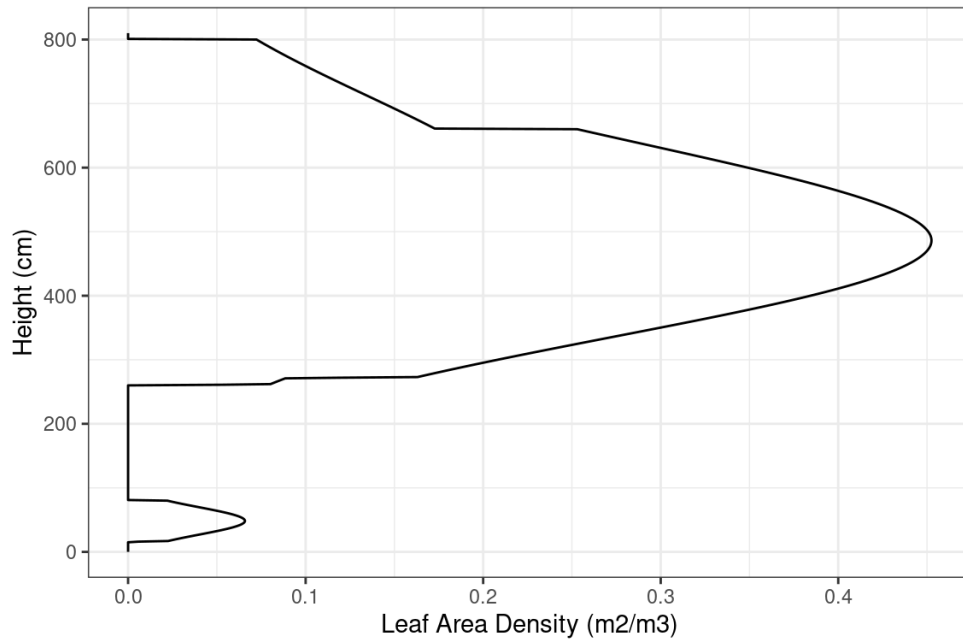
Users will not normally call `forest2aboveground()`, but is important to understand what is going on behind the scenes.

# 3. Vertical profiles

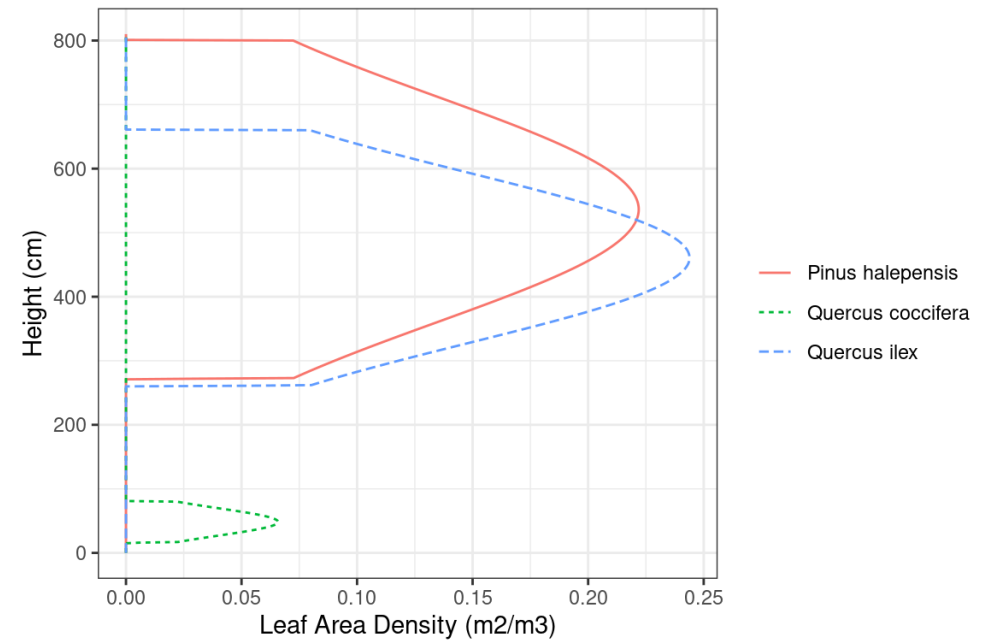
# Leaf distribution

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

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



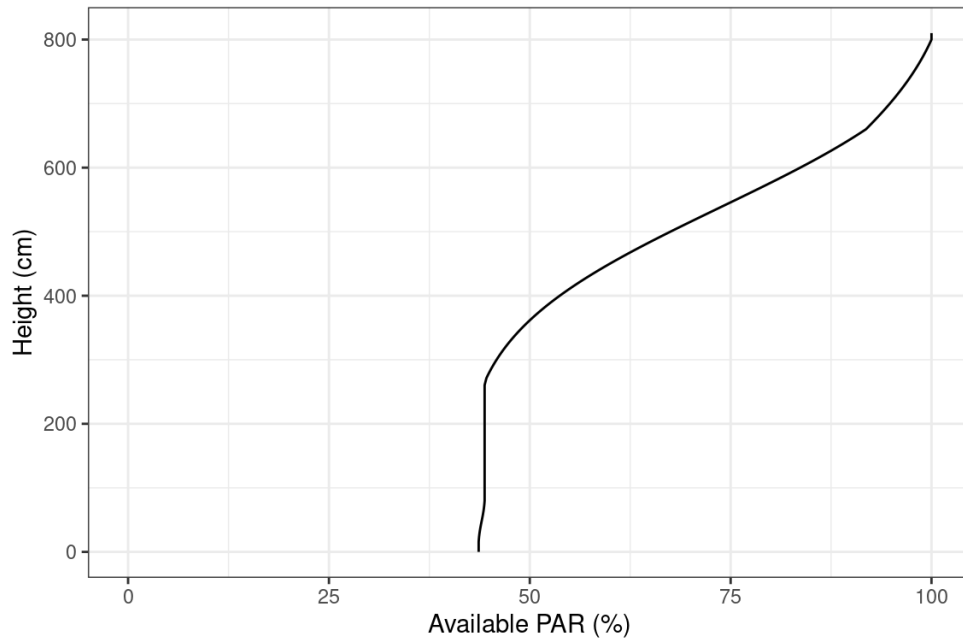
```
1 vprofile_leafAreaDensity(forest, SpParamsMED,
2   byCohorts = TRUE, bySpecies = TRUE)
```



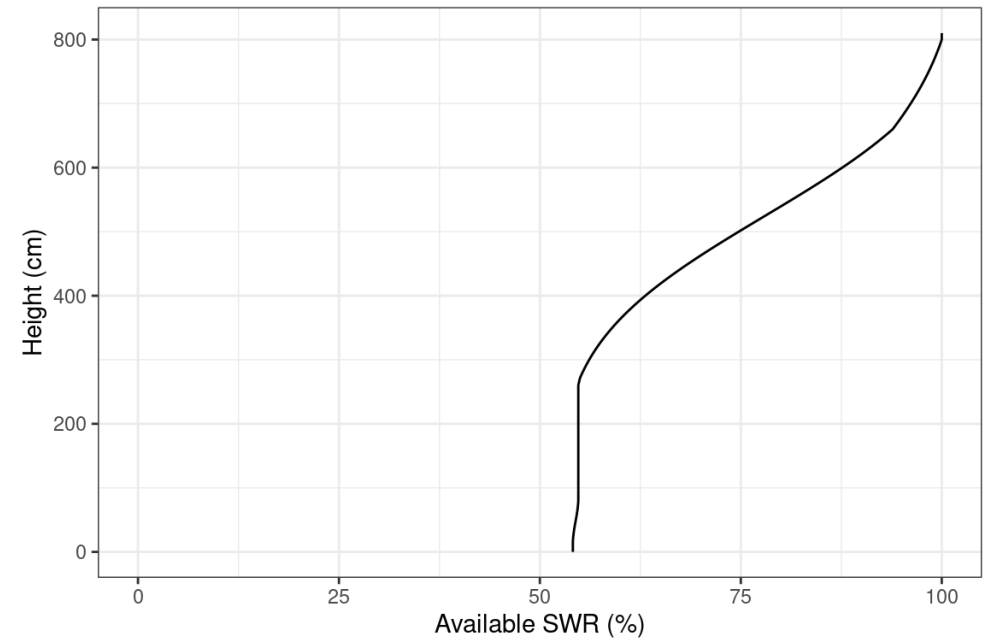
# Radiation extinction

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

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



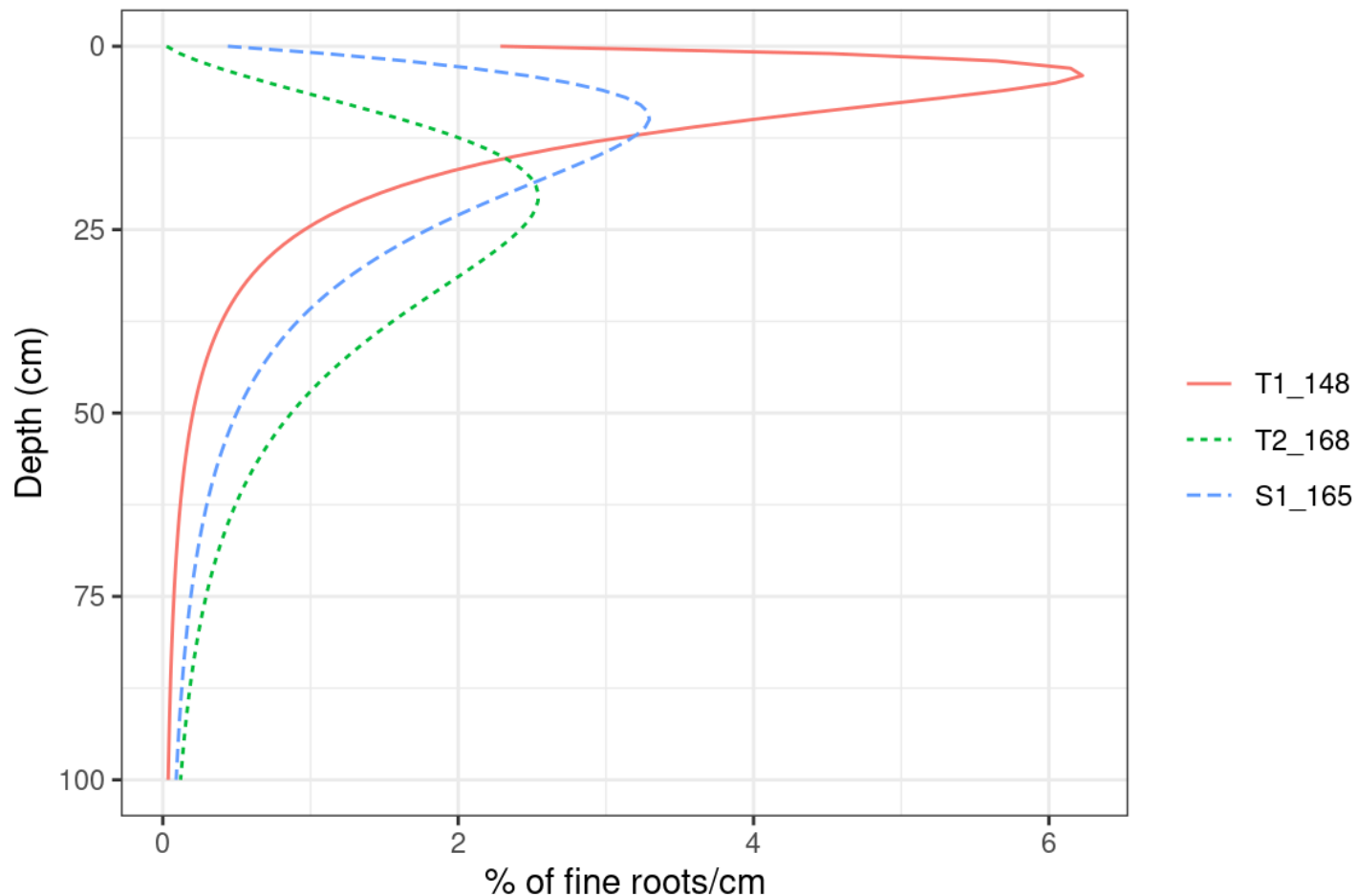
```
1 vprofile_SWRExtinction(forest, SpParamsMED)
```



# Belowground root distribution

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

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



# Interactive forest inspection

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

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



## 4. Soil input

# Soil physical description

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

Attribute	Description
<code>widths</code>	Layer widths, in mm.
<code>clay</code>	Percentage of clay (within volume of soil particles).
<code>sand</code>	Percentage of sand (within volume of soil particles).
<code>om</code>	Percentage of organic matter per dry weight (within volume of soil particles).
<code>nitrogen</code>	Total nitrogen (g/kg). Not used at present.
<code>bd</code>	Bulk density (g/cm <sup>3</sup> )
<code>rfc</code>	Rock fragment content (in whole-soil volume).

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

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

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

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

# 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.*

Package **medfateland** 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:

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

# Initialized soil

The soil initialized for simulations is a data frame of class `soil` that is created from physical description using a function with the same name:

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

```
[1] "soil"      "data.frame"
```

The initialised soil data frame contains additional columns with soil hydraulic parameters and state variables for moisture (`w`) and temperature (`Temp`):

```
1 examplesoil
```

```
widths sand clay      usda om nitrogen  bd rfc  macro      Ksat VG_alpha
1    300   25   25 Silt loam NA         NA 1.5  25 0.0485 5401.471 89.16112
2    700   25   25 Silt loam NA         NA 1.5  45 0.0485 5401.471 89.16112
      VG_n VG_theta_res VG_theta_sat W Temp
1 1.303861      0.041      0.423715 1  NA
2 1.303861      0.041      0.423715 1  NA
```

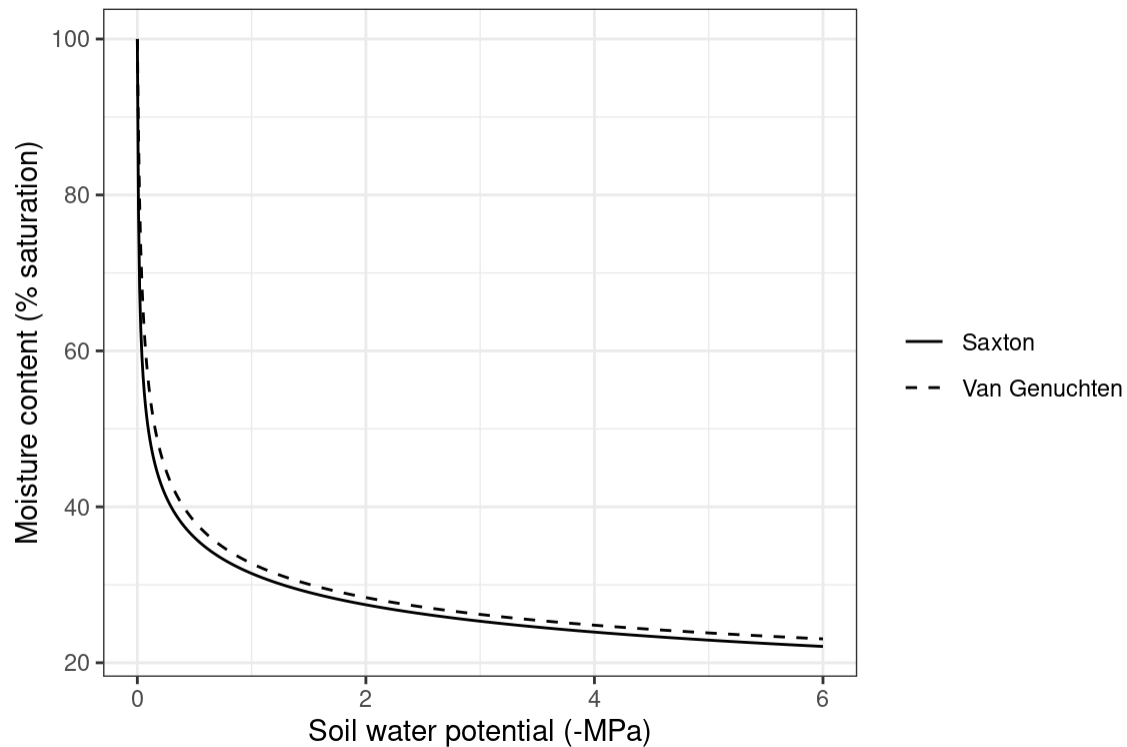
We can skip calling function `soil()` in our scripts to run simulations, but again is good to know what is behind the scenes.

# 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 two (Saxton and Van Genuchten) water retention models in this soil:

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



# 5. Simulation control

# Simulation control list

The behaviour of simulation models can be controlled using a set of **global parameters**.

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

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

A large number of control parameters exist:

```
1 names(control)
```

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

## 6. Simulation input object



# Simulation input object

## Functions `spwb()` and `growth()`

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

The combination can be done via functions `spwbInput()` and `growthInput()`:

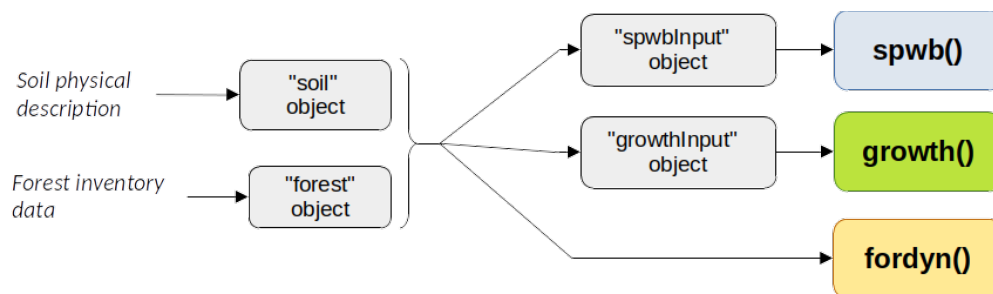
```
1 x <- spwbInput(forest, examplesoil, SpParamsMED, control)
```

## Function `fordyn()`

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

## Summary

The following workflow summarises the initialisation for the three functions:



# 7. Weather forcing

# Weather data frame

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

Variables	Units
Maximum/minimum temperature	$^{\circ}\text{C}$
Precipitation	$\text{l} \cdot \text{m}^{-2} \cdot \text{day}^{-1}$
Maximum/minimum relative humidity	%
Radiation	$\text{MJ} \cdot \text{m}^{-2} \cdot \text{day}^{-1}$
Wind speed	$\text{m} \cdot \text{s}^{-1}$

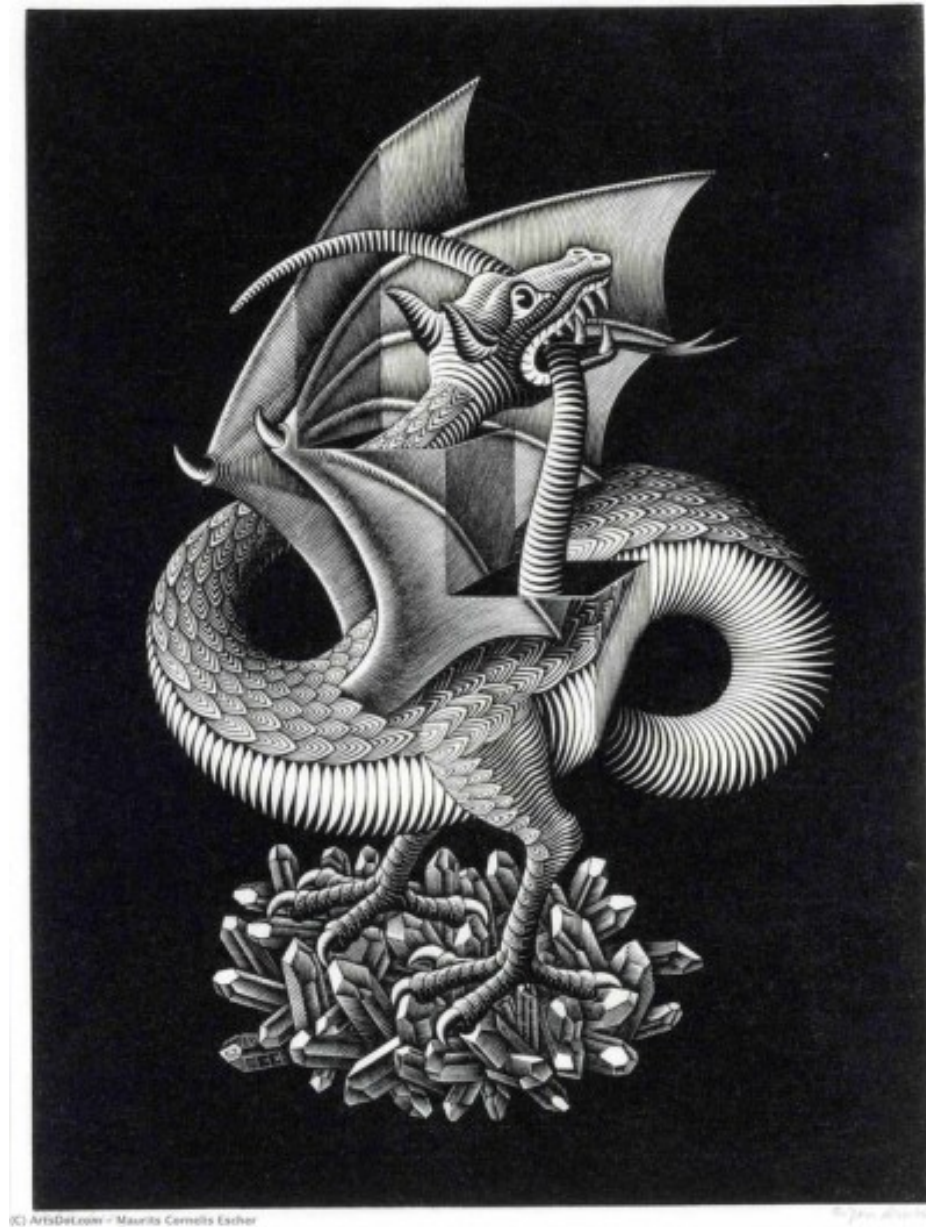
An example of daily weather data frame is included in package **medfate**:

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

```
      dates MinTemperature MaxTemperature Precipitation MinRelativeHumidity
1 2001-01-01    -0.5934215      6.287950      4.869109      65.15411
2 2001-01-02    -2.3662458      4.569737      2.498292      57.43761
  MaxRelativeHumidity Radiation WindSpeed
1          100.0000    12.89251    2.000000
2           94.7178    13.03079    7.662544
```

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

## M.C. Escher - Dragon, 1952



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