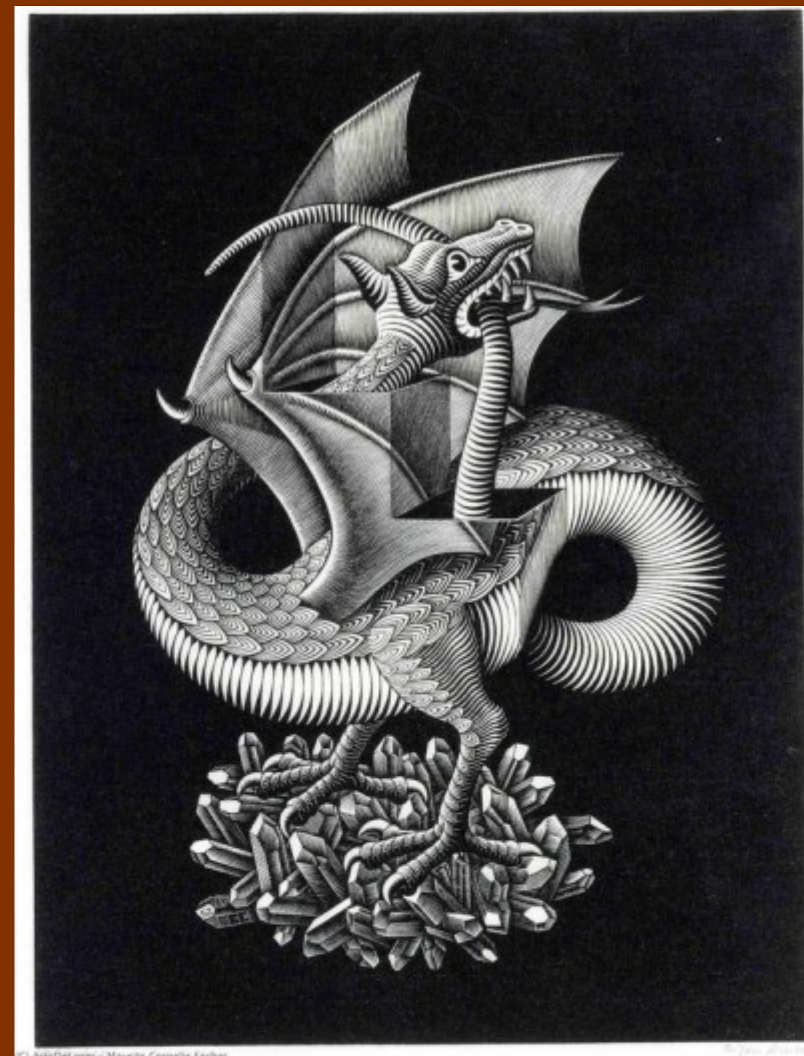
Model inputs

Miquel De Cáceres, Rodrigo Balaguer
Ecosystem Modelling Facility, CREAF

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.

```
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`:

```
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	SpIndex	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 Previous 1 2 3 4 5 … 39 Next

2. Forest input

Forest class

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

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

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

```
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):

```
forest$shrubData
```

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

Important

The distinction between *shrubs* and *trees* is made on the basis of the measured dimensions in forest inventory data (cover vs. density and DBH), disregarding the species growth form.

Forest class

Tree data

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)
`Z95`	Soil depth corresponding to 95% of fine roots (mm)

Shrub data

Variable	Definition
`Species`	Species numerical code (should match `SpIndex` in `SpParams`)
`Cover`	Shrub cover (%)
`Height`	Shrub total height (in cm)
`Z50`	Soil depth corresponding to 50% of fine roots (mm)
`Z95`	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
`forest_mapTreeTable()`	Helps filling `treeData` table
`forest_mapShrubTable()`	Helps filling `shrubData` table
`forest_mapWoodyTables()`	Helps filling both `treeData` and `shrubData` tables

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).

```r
plant_basalArea(forest, SpParamsMED)
```

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

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

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

```r
stand_basalArea(forest)
```

```
[1] 25.0333
```

```r
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()`:

```
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 0.84874773   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`.

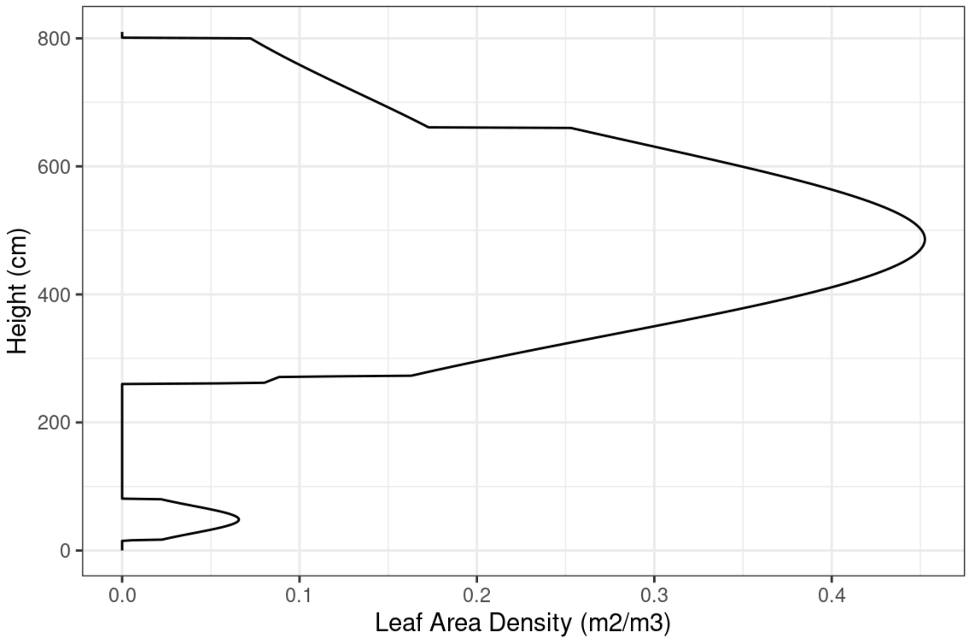
Users will not normally call `forest2aboveground()`, but is important to understand what is going on behind the scenes.

3. Vertical profiles

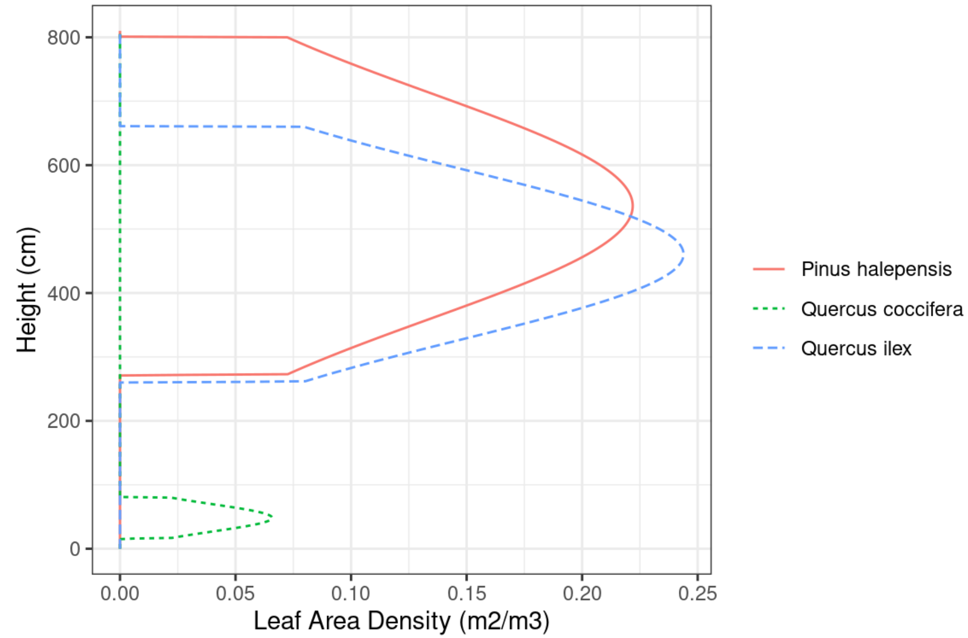
Leaf distribution

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

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



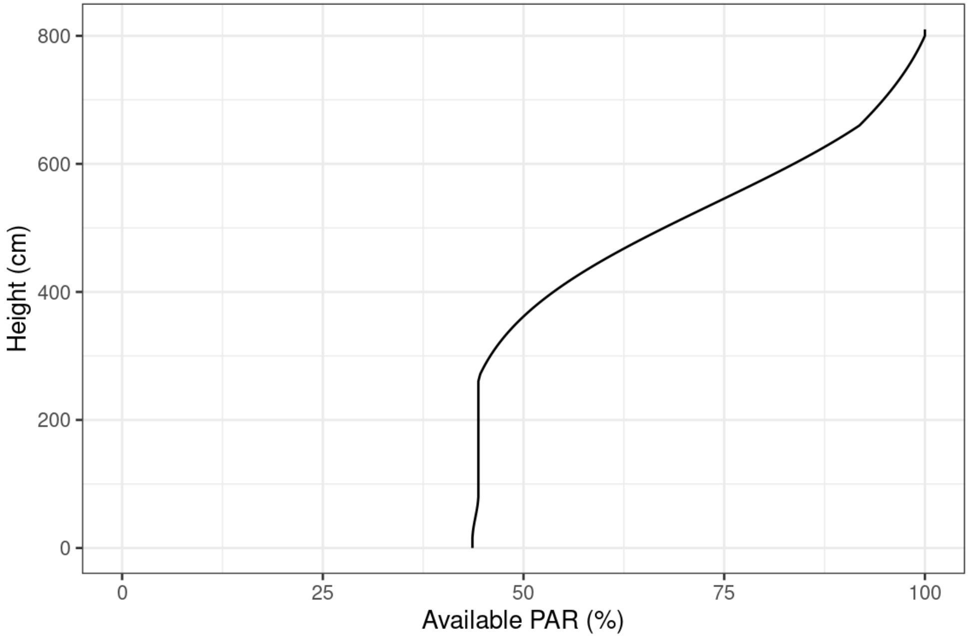

```r
vprofile_leafAreaDensity(forest, SpParamsMED,
    byCohorts = TRUE, bySpecies = TRUE)
```



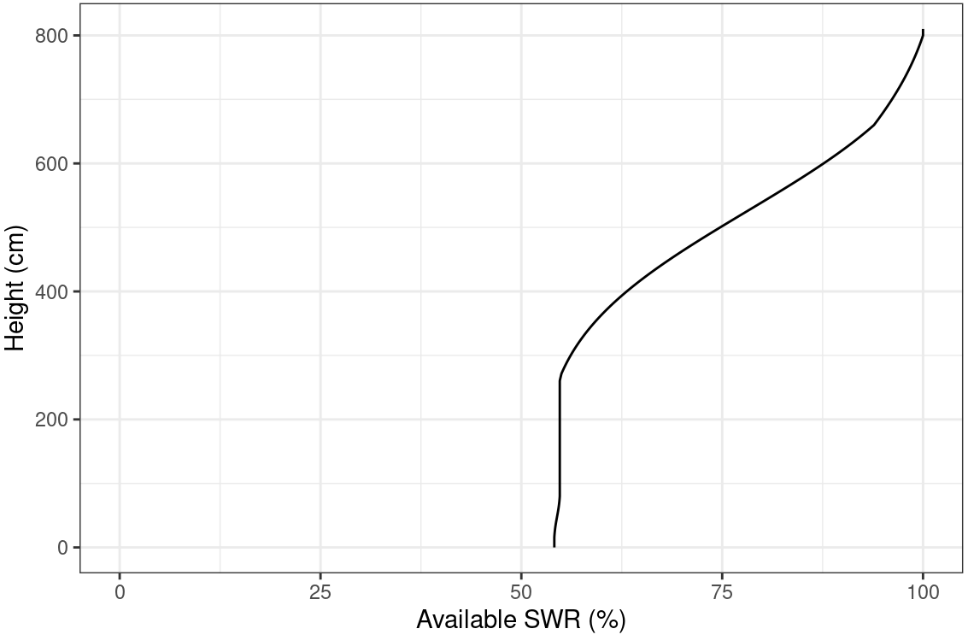
Radiation extinction

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

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



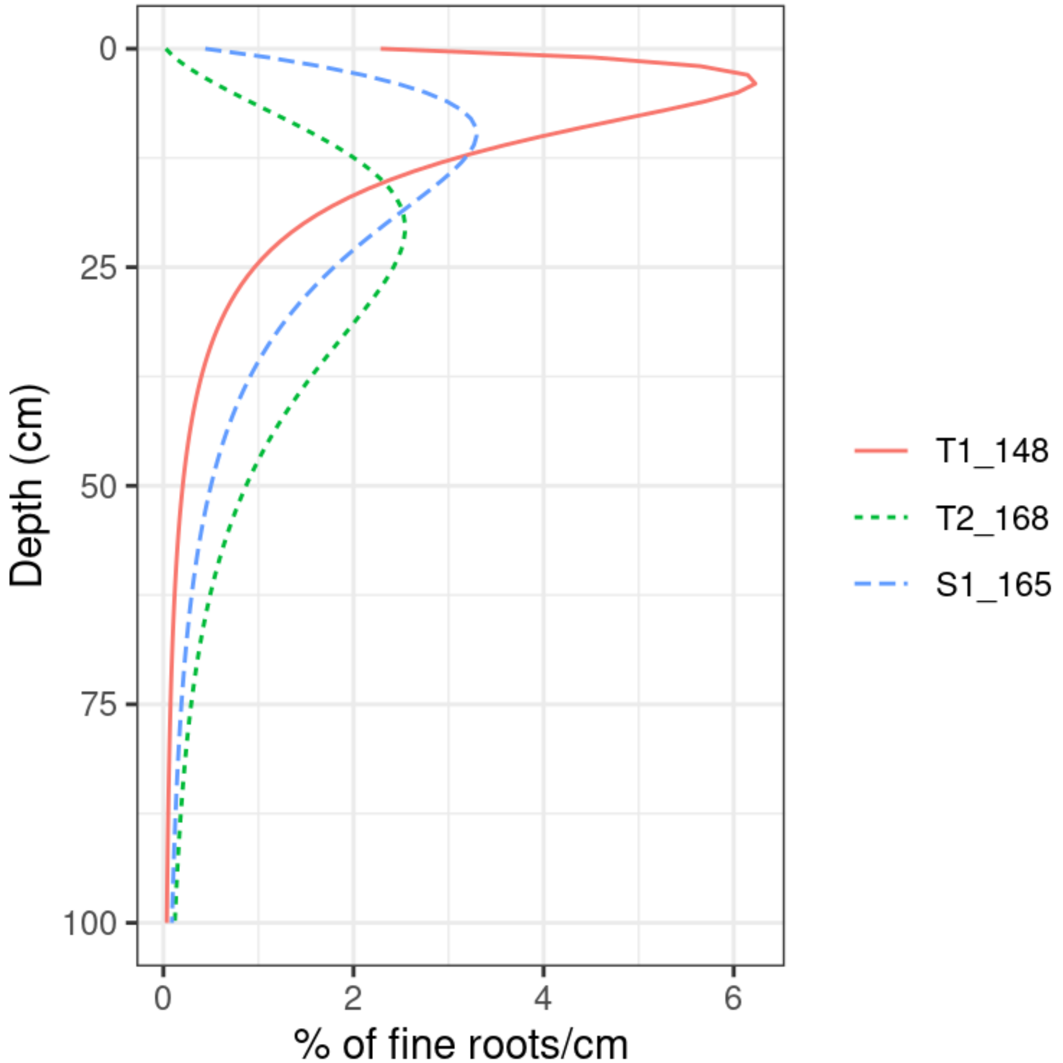

```r
vprofile_SWRExtinction(forest, SpParamsMED)
```



Belowground root distribution

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

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



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

Attribute	Description
`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).
`nitrogen`	Total nitrogen (g/kg). Not used at present.
`bd`	Bulk density (g/cm3)
`rfc`	Rock fragment content (in whole-soil volume).

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

```
spar <- defaultSoilParams(2)
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:

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

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

The initialised soil data frame contains additional columns with *hydraulic parameters* (e.g. `Ksat`) and *state variables* for moisture (`W`) and temperature (`Temp`):

```
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
```

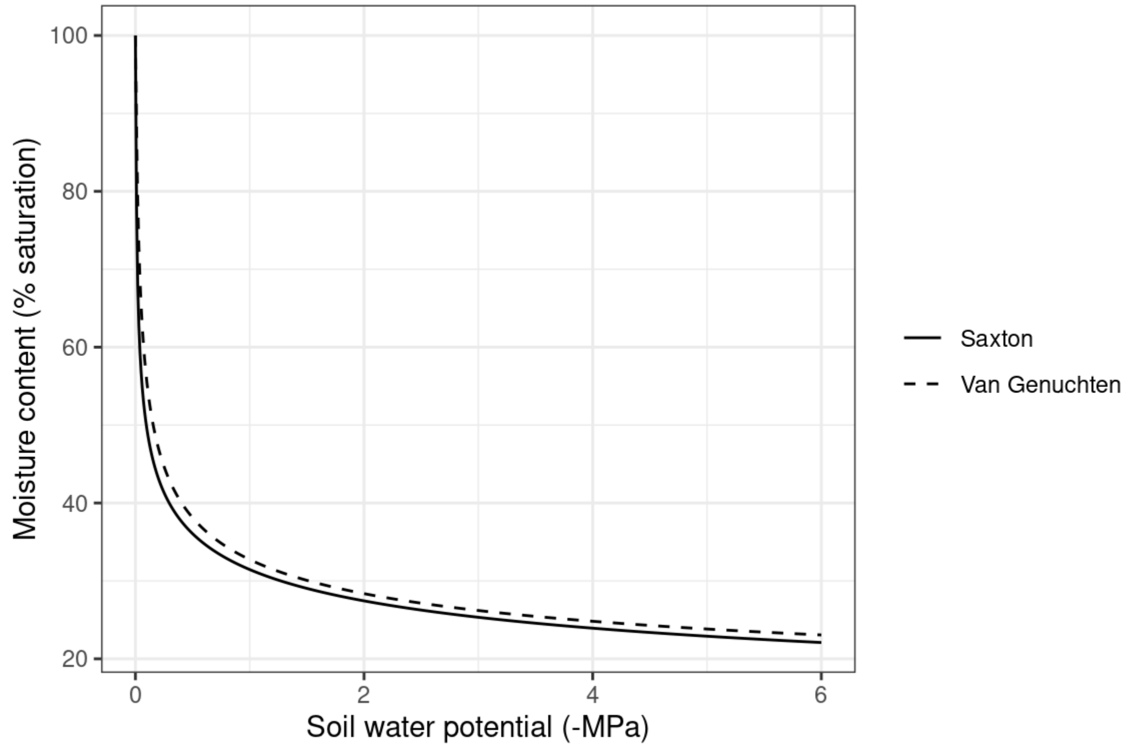
We can skip calling function `soil()` in our scripts to run simulations, but again is good to know what is behind the scenes.

Water retention curves

The **water retention curve** is used to represent the relationship between soil water content (θ; %) and water potential (Ψ; MPa).

The following code calls function `soil_retentionCurvePlot()` to illustrate two water retention curves in this soil:

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



Important

Van Genuchten's model is the default for simulations (see `soilFunctions` in `?defaultControl`), but its parameters may be difficult to estimate correctly.

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()`:

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

A large number of control parameters exist:

```
names(control)
```

Important

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()`:

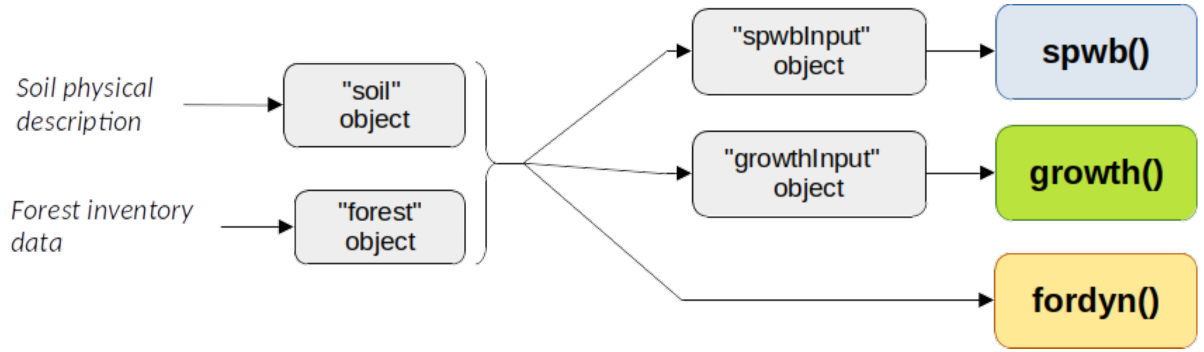
```
x <- spwbInput(forest, examplesoil, SpParamsMED, control)
```

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	^oC
Precipitation	$l \cdot m^{-2} \cdot day^{-1}$
Maximum/minimum relative humidity	%
Radiation	$MJ \cdot m^{-2} \cdot day^{-1}$
Wind speed	$m \cdot s^{-1}$

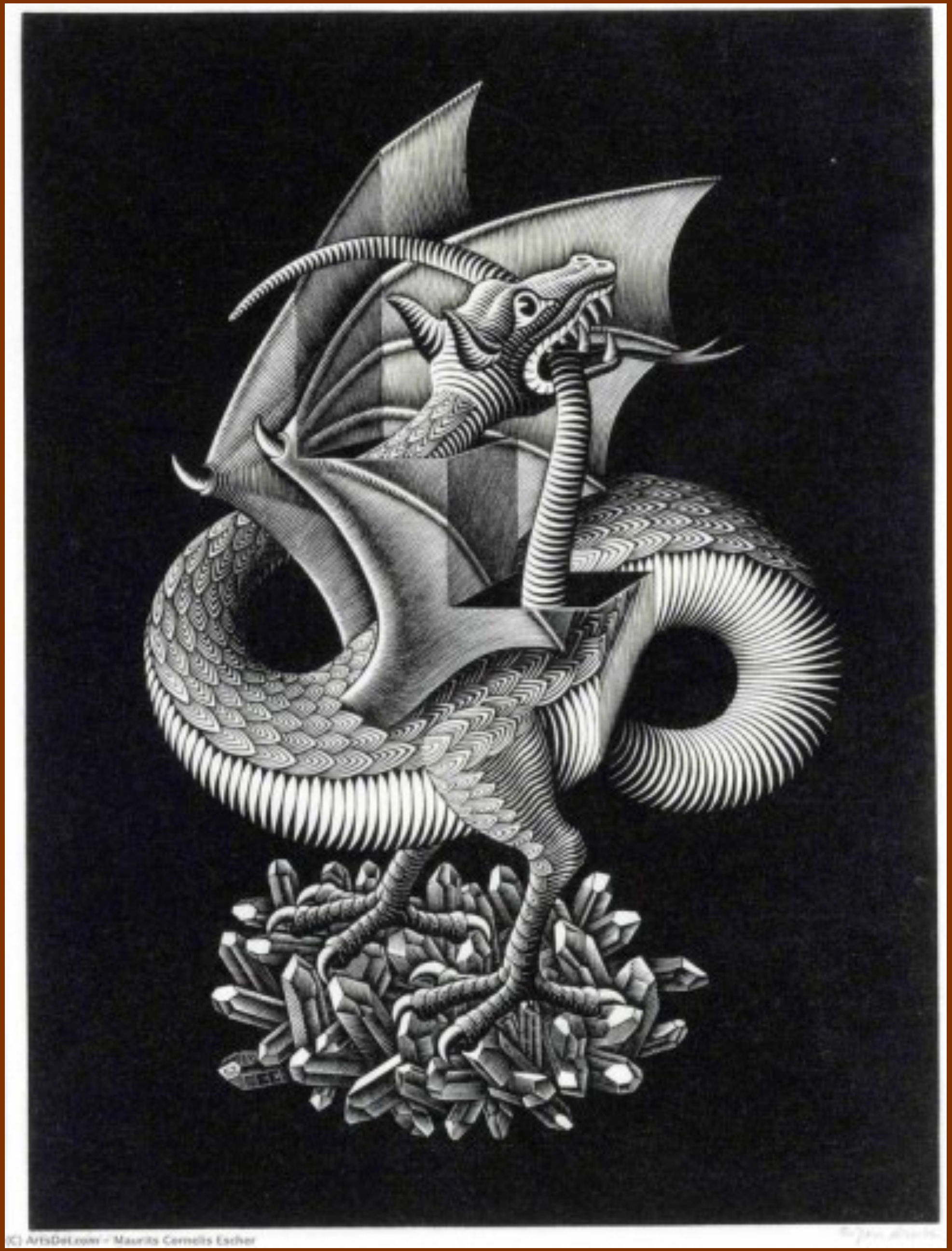
An example of daily weather data frame is included in package **medfate**:

```
data(examplemeteo)
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
```

Tip

- Simulation functions have been designed to accept data frames generated using package meteoland.
- The package will try to fill missing values of some variables with estimates (e.g. for radiation or relative humidity).
- Additional variables (atmospheric pressure or CO2 concentration) are optional.



M.C. Escher - Dragon, 1952