1.3 - Model inputs

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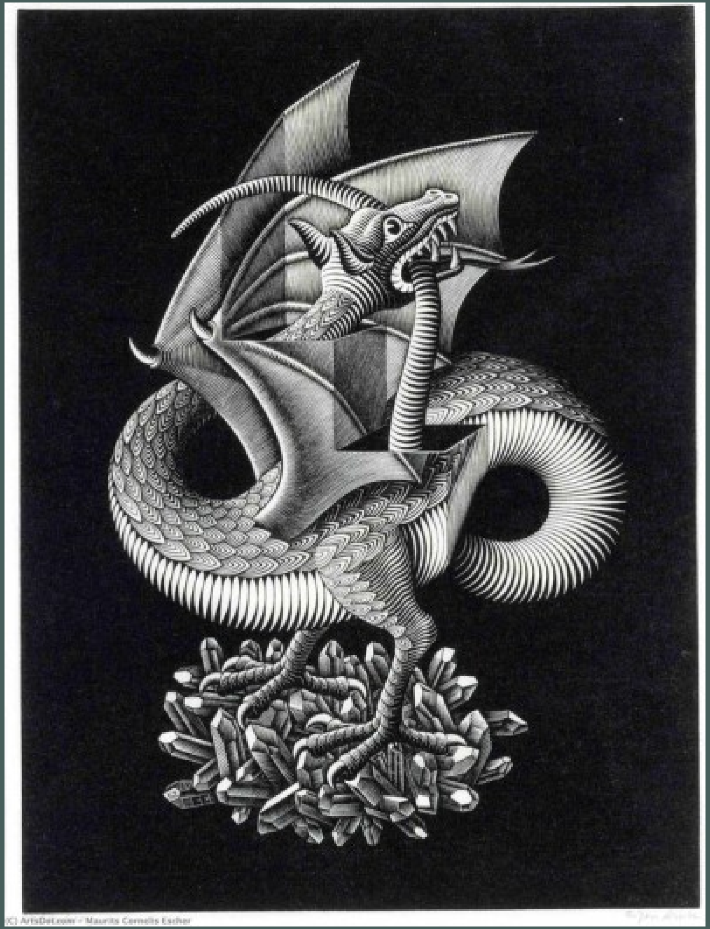

Outline

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

1. Species parameters

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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 6 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 1 2 3 4 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.

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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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```

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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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)
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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*).

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Creating a 'forest' object from forest inventory data

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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
`forest_mapShrubTable()`	Helps filling `shrubData` table
`forest_mapTreeTable()`	Helps filling `treeData` table
`forest_mapWoodyTables()`	Helps filling a `forest` object
`IFN2forestlist()`	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
```

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## 18.604547  6.428755        NA
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```
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```

```
## [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`.

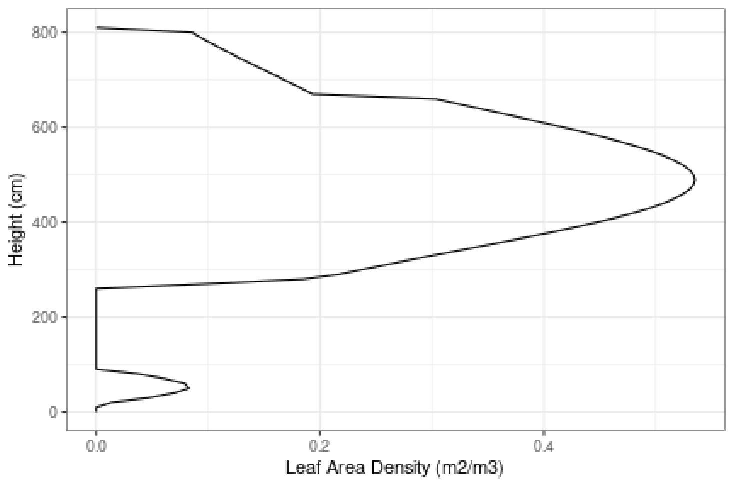
Users will not normally call `forest2aboveground()`, but is important to understand what is going on behind the scenes.

3. Vertical profiles

Leaf distribution

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

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



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```
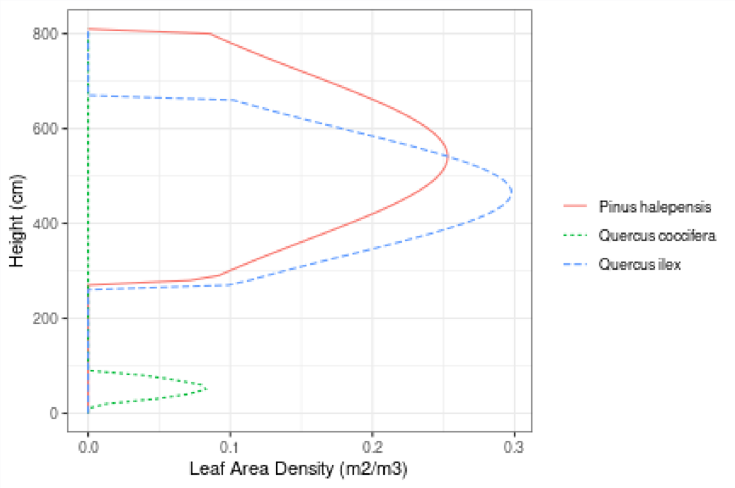

```
vprofile_leafAreaDensity(forest, SpParamsMED,
    byCohorts = TRUE, bySpecies = TRUE)
```

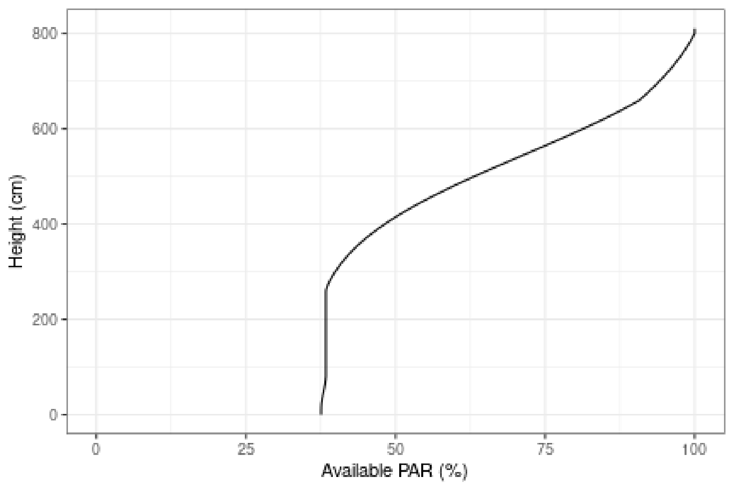


3. Vertical profiles

Radiation extinction

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

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



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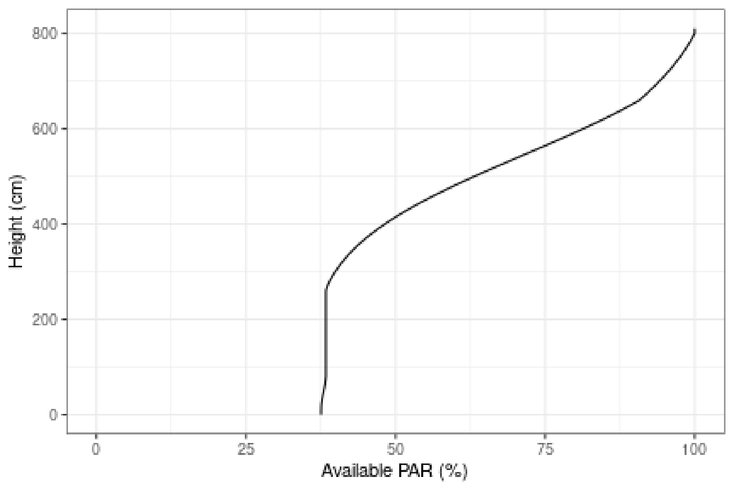
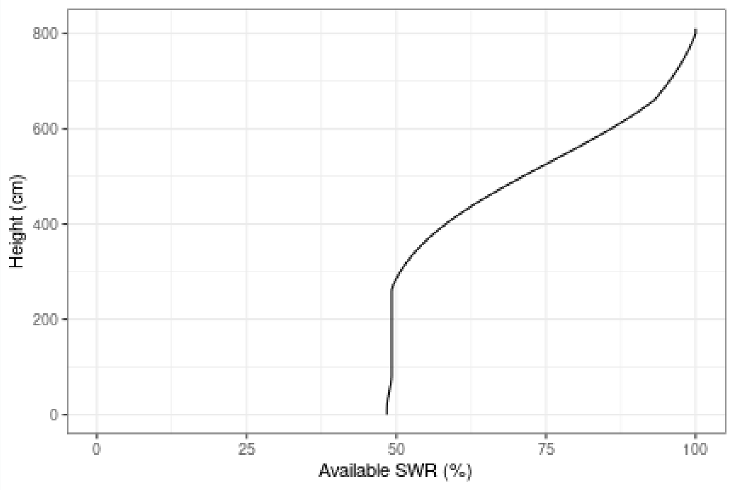


```
vprofile_SWRExtinction(forest, SpParamsMED)
```

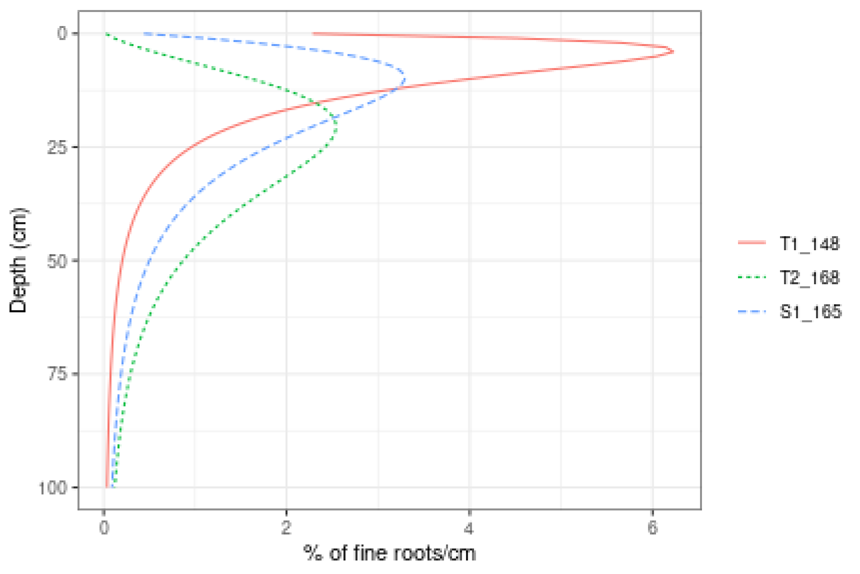


3. Vertical profiles

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/cm3)
- `rfc` - Rock fragment content (in whole-soil volume).

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- `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

To start with, we need an object of class `SpatialPoints` (from package **sp**) containing the geographic coordinates of our target forest stand:

```
cc <- matrix(c(1.32, 42.20), nrow=1)
sp <- SpatialPoints(cc, proj4string = CRS(SRS_string = "EPSG:4326"))
```

4. Soil input

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```
cc <- matrix(c(1.32, 42.20), nrow=1)
sp <- SpatialPoints(cc, proj4string = CRS(SRS_string = "EPSG:4326"))
```

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

```
soilgridsParams(sp, 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"
```

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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 (θ ; %) and soil water potential (Ψ ; MPa).

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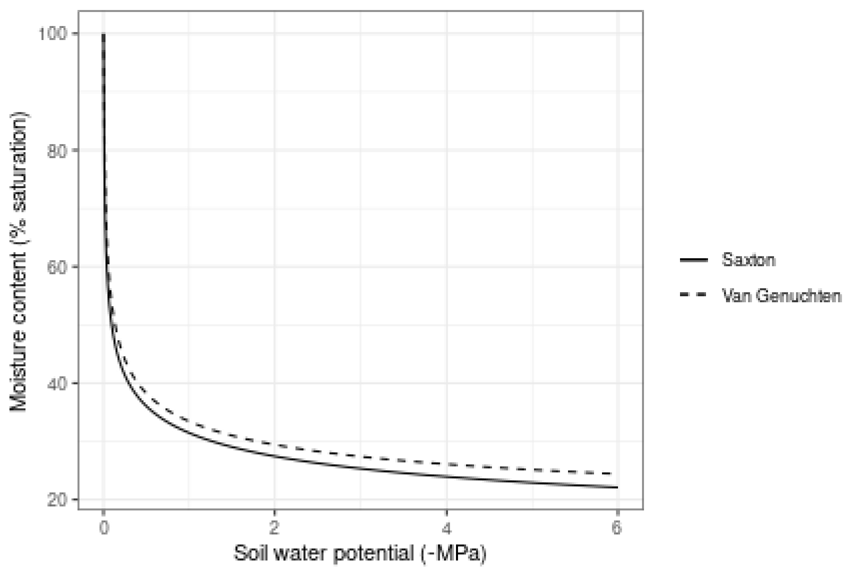
The **water retention curve** is used to represent the relationship between soil water content (θ ; %) and soil water potential (Ψ ; MPa).

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")
```



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Variables	Units
Mean/maximum/minimum temperature	ºC
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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```

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

6. Simulation control

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```
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```

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)
```

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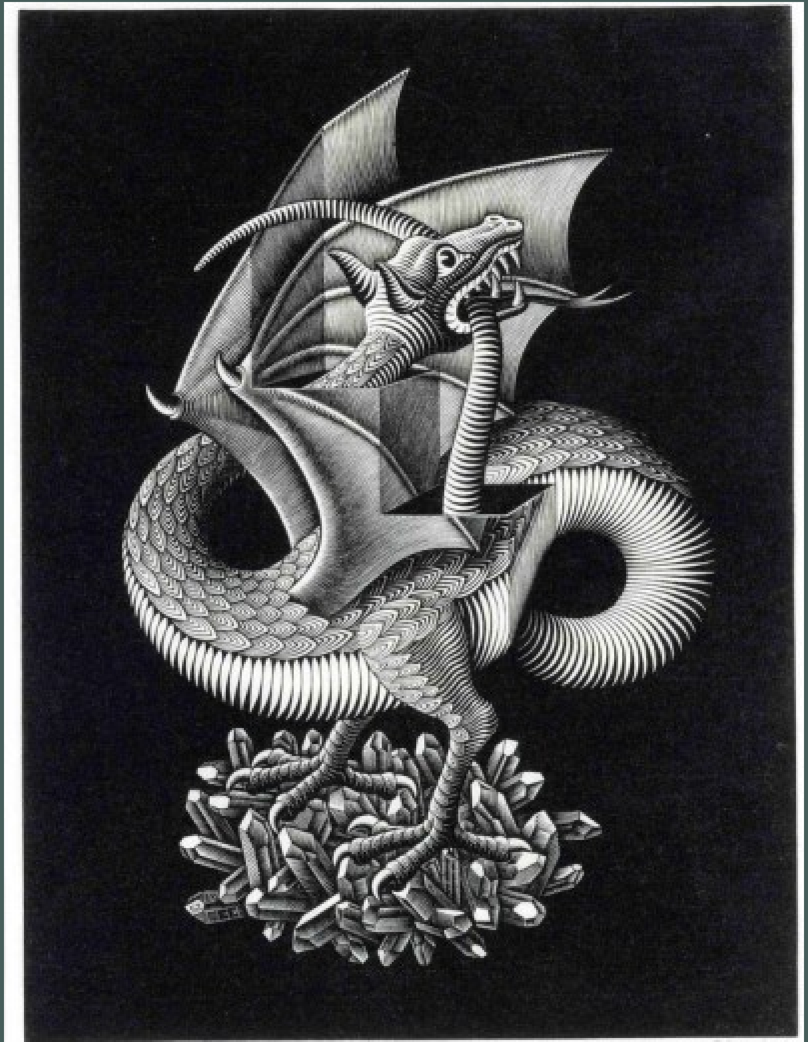
Function `fordyn()` is different from the other two models: the user enters forest, soil, weather, species parameters and simulation control inputs *directly* into the simulation function.

M.C. Escher - Dragon, 1952



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