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SpaDES 4 Dummies

Contents

List of Figures

List of Tables

Preface

This guide will take you through how to make and link your own modules using SpaDES in two examples. Both examples draw on basic uses of statistical models in ecology, notably the relationships between environmental variables and species abundance and presence.

Part 1 is very minimal, and uses only dummy data. It is meant to introduce you to the different components of a SpaDES module. Part 2 uses real and freely available data, and provides a deeper look into several useful aspects of SpaDES, notably caching and spatial data processing.

To install SpaDES, please have a look at SpaDES installation[1].

[1] https://github.com/PredictiveEcology/SpaDES.install/tree/installFromSource#readme

1

Introducing SpaDES with a dummy ecological model

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Let's imagine we want to explore how the relationship between a species' abundance and temperature changes over time. Both the abundance data and the temperature data are being constantly updated by a simulation model, and we want to analyse the relationship between the two iteratively, without needing to manually run a script to account for the newly generated data inputs.

1.1 BEFORE SpaDES...

If we use R to develop our species abundance and temperature simulation models in the 'conventional way', we'll probably have i) (the worst case scenario) several scripts that run simulations and data treatment/analysis separately and have to be executed manually, or ii) a long script where everything happens - the simulations and data analysis -, iii) a main script that sources others that do the simulation and analyses. Option i is more common when different software are used for different parts of the process (e.g., a simulation model in *C++* generates data that is then analysed in R). Option ii is inconvenient because very long scripts make changes and updates to the script - debugging can also be more tiresome. Option iii, is similar to the SpaDES way of thinking. The difference is that SpaDES defines a standard way of writing different components of a model, or of a modelling framework. This makes changing, updating and sharing code - or modules - easier, as well as swapping and adding modules in a modelling framework.

The example below is so minimal that it is unlikely to show the full benefits of using SpaDES - the same could be accomplished with a fairly short script. However, it introduces the different parts of a module and how to link modules.

Part 2 goes a step further and uses real datasets to project species presences across a landscape in Canada. In this example, we introduce SpaDES features that we most commonly use in our work (e.g., caching and spatial data processing) and provide some coding best practices that we use ourselves (e.g., code assertions).

1.1.1 Setup

Load the necessary packages (make sure they are installed first, of course)

```
## please start from a clean R session
library(raster)
library(quickPlot)
library(ggplot2)
library(SpaDES.tools)
```

And now create a raster template:

```
r <- raster(nrows = 100, ncols = 100, xmn = -50, xmx = 50, ymn = -50, ymx
= 50)
```

1.1.2 Species abundance "simulations"

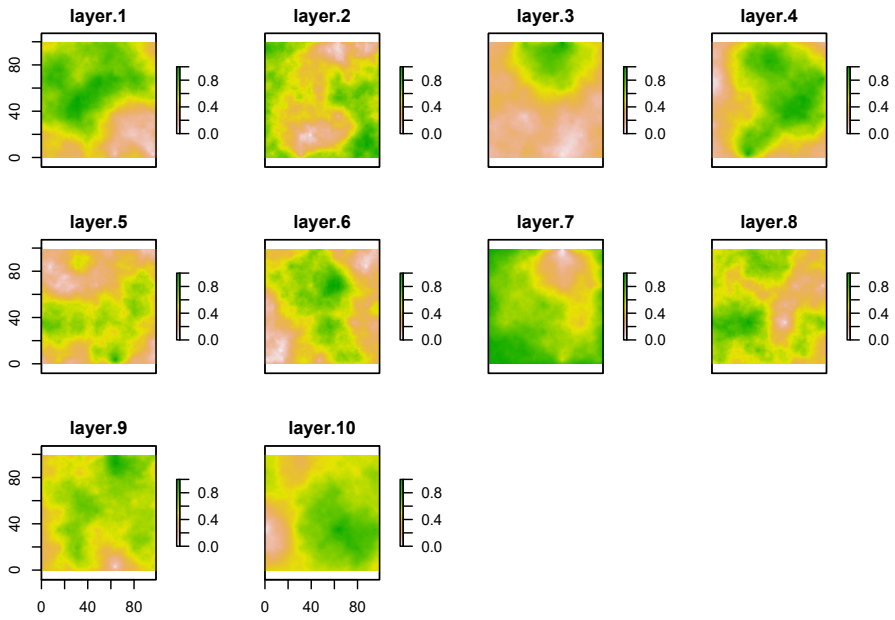
Our VERY simple "simulation" model (in form of a function) generates rasters that follow a Gaussian distribution

```
abundance_model <- function(ras, Time) {
  abund_outputs <- list()
  for (t in 1:Time) {
    # abund_outputs[[t]] <- gaussMap(ras, scale = 100, var = 0.03) ##
    RandomFields no longer available
    abund_outputs[[t]] <- NLMR::nlm_mpd(
      ncol = ncol(ras),
```

```
      nrow = nrow(ras),
      resolution = unique(res(ras)),
      roughness = 0.5, ## TODO: adjust to approximate gaussMap version
      rand_dev = 100,
      rescale = TRUE,
      verbose = FALSE
    )
  }
  return(abund_outputs)
}
```

Set the length of the simulation (or simply the number of model iterations), run it and plot results (all ABUNDANCE plots together):

```
Time <- 10
abundance <- abundance_model(r = r, Time = Time)
dev()
plot(stack(abundance))
```



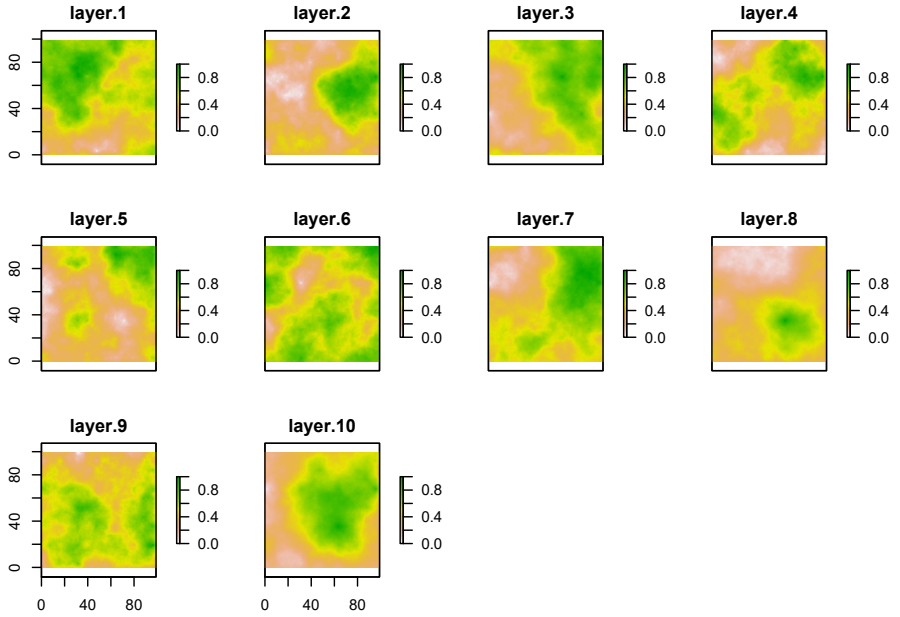
1.1.3 Temperature "simulations"

The temperature simulation model will be similar to the vegetation one - remember this is a dummy example.

```
temp_model <- function(r, Time) {
  temp_outputs <- list()
  for (t in 1:Time) {
    # temp_outputs[[t]] <- gaussMap(r, scale = 100, var = 0.1) ##
    RandomFields no longer available
    temp_outputs[[t]] <- NLMR::nlm_mpd(
      ncol = ncol(r),
      nrow = nrow(r),
      resolution = unique(res(r)),
      roughness = 0.5, ## TODO: adjust to approximate gaussMap version
      rand_dev = 100,
      rescale = TRUE,
      verbose = FALSE
    )
  }
  return(temp_outputs)
}
```

Run the model and plot results (all temperature plots together)

```
temperature <- temp_model(r = r, Time = Time)
plot(stack(temperature))
```



1.1.4 Data analysis

Now we analyse if species abundance and temperature are correlated. First, we create the data analysis function (a simple linear model):

```
stats_analysis <- function(Data) {
  if (all(c("abund", "temp") %in% colnames(Data))) {
    lm1 <- lm(abund ~ temp, data = Data)
    ggplot(Data) +
      geom_point(aes(x = temp, y = abund)) +
      geom_abline(intercept = lm1$coefficients["(Intercept)"],
                  slope = lm1$coefficients["temp"], size = 2, col =
                  "blue") +
      theme_bw() +
      labs(x = "Temp.", y = "Species abundance")

  } else {
    stop("Data must contain 'abund' and 'temp' columns")
  }
}
```

Then we create a loop to analyse each plot of our time-series:

```
for (t in 1:Time) {
  outputdata <- data.frame(abund = abundance[[t]][], temp =
temperature[[t]][])
  stats_analysis(Data = outputdata)
}
```

1.2 AFTER SpaDES...

1.2.1 The control script

Let us now solve the same problem using the SpaDES approach. We start by creating an *.R* script (it can have any name) that sets up and runs the SpaDES model. The control script for this example is located on the root of the *SpaDES4Dummies* GitHub repository under the name `Part1_DummyModel.R`. Note that Markdown (`.Rmd`) scripts can also be used instead of R scripts.

We start by making sure all SpaDES packages and they dependencies are installed and up to date using `SpaDES.install::installSpaDES`.

```
## start again from a clean R session
if (!require("Require")) install.packages("Require")
Require::Require("PredictiveEcology/SpaDES.install@development")
SpaDES.install::installSpaDES(ask = TRUE)

library(SpaDES)  ## should automatically download all packages in the
SpaDES family and their dependencies

## decide where you're working
mainDir <- "."
```

```
setPaths(cachePath = file.path(mainDir, "cache"),
         inputPath = file.path(mainDir, "inputs"),
         modulePath = file.path(mainDir, "modules"),
         outputPath = file.path(mainDir, "outputs"))

getPaths() ## check that this is what you wanted

## Let's create a self-contained module that will simulate the species'
abundance for any given period of time and frequency.
if (!dir.exists(file.path(getPaths()$modulePath, "speciesAbundance"))) {
  newModule(name = "speciesAbundance", path = getPaths()$modulePath)
}
```

We then create modules using `newModule`. `newModule` creates a module folder (*speciesAbundance*) inside `/modules` that contains both the module `.R` script template, as well as the documentation template (the `.Rmd` file). Although we will not be discussing the `.Rmd` file, please bear in mind that this is a **fundamental** part of creating a reproducible and transparent module - check out the Guide to Reproducible Code in Ecology and Evolution[1] from the British Ecological Society). The documentation should contain a the description of the module, its input, parameters and outputs, and potentially a reproducible examples of how the module is executed.

`newModule` also created the folder `/data` where data necessary to the module can be put in, and the folder `/tests` that may contain testing scripts. We will not be using either of them in this example.

/!\ ATTENTION /!

`newModule` should only be run once, otherwise it will replace all edits and contents of the module folder with the templates - this is why it is wrapped in an `if` statement above.

Now go ahead, open the `speciesAbundance.R` script and have a look at it.

[1] http://www.britishecologicalsociety.org/wp-content/uploads/2017/12/guide-to-reproducible-code.pdf

1.2.2 General module structure: *speciesAbundance* module

The module template contains all the essential components of a module, with examples, and may seem overwhelming at first. We'll go through it step by step (although not necessarily following the order of the script). The module script can be divided into 4 parts:

[Defining the Module]: this is where the module is **defined**, i.e., the module's metadata (e.g. module author(s), time units, basic parameters, general inputs and outputs, etc.);

[Events and event functions]: these are the "actions" (or events) executed in the module (i.e. species reproduction, plotting, saving parameters) - simply put, **WHAT** the module does;

[Scheduling Events]: this is how SpaDES schedules when each event is going to happen - in which order (e.g. during the simulation, when will SpaDES plot a graph) - simply put, **WHEN** the module does it;

[Additional module functions]: any additional functions needed (e.g. this is used to keep the coding of your module as clear and straightforward as possible);

The first thing to note is that **the user does not need to manually run** any of the code inside a module's `.R` script. The function `simInit()` will do so when it sets up the simulation. We will see this see this later in detail.

1.2.2.1 Defining the Module

The first section of the script is defines the module's metadata[2]. It allows defining the module's author, keywords, any required packages and module(s) and their versions, but also parameters (and their default values) and input objects that the module requires, and the output objects it creates.

Although this dummy module example requires no true input data, we will define the template raster R as an "input" in the `expectsInput` function, and provide a default object in `.inputObjects` (see below). As for the outputs, it produces a list of abundance rasters (produced during the `abundanceSim` event). So we define it as an output in the`createsOutput` function.

Note that we removed several parameters that come with the template created by the `newModule` function, as they are not needed for this example.

[2] http://data-informed.com/what-is-metadata-a-simple-guide-to-what-everyone-should-know/

To distinguish what input and output objects are in the context of a module, a good rule of thumb is that inputs are all the `sim$...` objects that appear for the first time (in the module events) on the **right-hand side** of a `<-`, whereas output parameters are the `sim$...` objects that appear for the first time to the **left-hand side** of a `<-`. Another way of explaining it for objects is illustrated in Fig. 1.1:

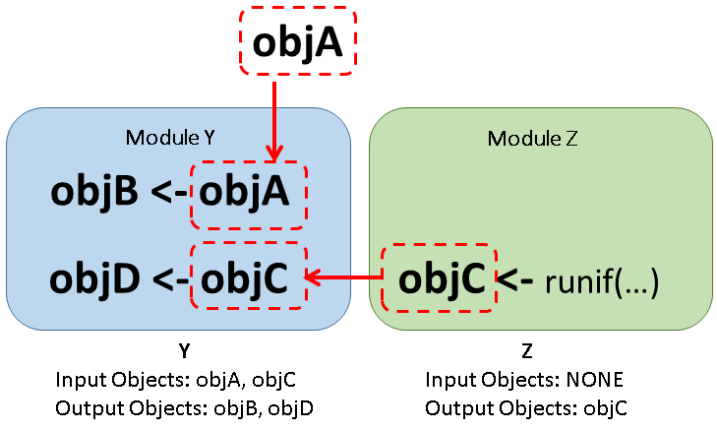


FIGURE 1.1: Inputs and outputs in SpaDES: Object A comes from outside of the module (e.g. from an internet URL, from data you have, or from '.inputObjects'), while Module Z produces object C. Both objects serve as an inputs for Module Y, which in return produce as outputs objects B and D, respectivelly from objects A and C. As Module Z uses a simple function *internally* to create object C, it doesn't have any inputs, such as our dummy example.

The exception to this rule are the default input objects created by the `.inputObjects` function (see [.inputObjects function]) during the `simInit` call.

Here is how we defined the *speciesAbundance* module:

```
defineModule(sim, list(
  name = "speciesAbundance",
  description = "",
  keywords = "",
  authors = person("Me", email = "me@example.com", role = c("aut",
  "cre")),
  childModules = character(0),
  version = list(speciesAbundanceData = "0.0.0.9000"),
```

```
  timeframe = as.POSIXlt(c(NA, NA)),
  timeunit = "year",
  citation = list("citation.bib"),
  documentation = deparse(list("README.txt", "speciesAbundance.Rmd")),
  reqdPkgs = list("PredictiveEcology/SpaDES.core@development
  (>=1.0.10.9000)",
                  "raster", "quickPlot"),
  parameters = bindrows(
    #defineParameter("paramName", "paramClass", value, min, max,
    "parameter description"),
    defineParameter("simulationTimeStep", "numeric", 1, NA, NA,
                    "This describes the simulation time step interval"),
    defineParameter(".plotInitialTime", "numeric", 1, NA, NA,
                    "Describes the simulation time at which the first plot
                    event should occur."),
    defineParameter(".plotInterval", "numeric", 1, NA, NA,
                    "Describes the simulation time interval between plot
                    events.")
  ),
  inputObjects = bindrows(
    # expectsInput("objectName", "objectClass", "input object
    description", sourceURL, ...),
    expectsInput("r", objectClass = "RasterLayer", desc = "Template
    raster")
  ),
  outputObjects = bindrows(
    #createsOutput("objectName", "objectClass", "output object
    description", ...),
    createsOutput("abundRasters", "list", "List of layers of species
    abundance at any given year")
  )
))
```

Note that the package versions that you define will depend on the ones that are installed on your computer. So take care to change them accordingly. The SpaDES package version suggested by the template reflects the version on your computer.

The rest of the script defines the events and their sequences for this mod-

ule - remember SpaDES = Spatial Discrete Event Simulator - and the events themselves.

/!\ ATTENTION /!

defineModule() is not intended to be run directly by the user – it is run internally during a simInit() call (see Simulation setup in a "global" script). In other words, you don't run any part of a module's code directly in your session; you run simInit() with that module listed in the modules argument.

1.2.2.2 Events and event functions

Module events are defined and scheduled in the doEvent.<module name> function (in this example, doEvent.speciesAbundance function; see [Scheduling events]. Since we are only interested in simulating and plotting species abundances, we removed unnecessary events from the script and kept: the initialisation (init), an abundance simulation event (SimulAbund) and a plotting event (abundPlot). Each of these events can execute one or more functions.

Event functions (actual R functions) mustn't be confused with *event names*, which are the names of the events appearing in the doEvent.<module name>.

/!\ ATTENTION /!

Event functions take only one argument, sim (the SpaDES.core::simList object that stores all objects, modules, functions, etc., of a simulation; see ?simList) and event functions always (and only) return sim (using return(invisible(sim))).

1.2.2.2.1 Initialisation event function

The initialisation event function (here, abundanceInit) can be seen as the starting point of the module. Unlike the init event, which must always be present, the function itself does not need to exist (see [Scheduling events]) and can have whatever name we want.

Usually, this function will does pre-simulation steps that are only need to be executed once. In our dummy example, it creates a template raster and a storage list for our species abundance outputs (which will also be rasters). Notice that the only argument to abundanceInit is the sim simList object, which is also its only output.

```
abundanceInit <- function(sim) {
  ## create storage list of species abundance
  sim$abundRasters <- list()

  return(invisible(sim))
}
```

1.2.2.2.2 Abundance simulation event function

The function `abundanceSim` is the core event function of this module, where species abundances are generated via the event. Notice how instead of a *for-loop*, `abundanceSim` runs the `abundance_model` function (which we define separately below) and stores its outputs in the `sim$abundRaster` object. Notice as well that we use `time(sim)` as the identifier of the list slots where outputs are stored (see `?SpaDES.core::time`).

As before, the sole argument and output to this event function is the `sim` object.

```
abundanceSim <- function(sim) {
  ## Generate species abundances - our "simulation"
  sim$abundRasters[[as.character(time(sim))]] <- abundance_model(ras =
sim$r)

  return(invisible(sim))
}
```

The `abundanceSim` function was called `Event1` in the template.

1.2.2.2.3 Plotting event function

Finally, we created the `abundancePlot` event function to plot the species abundance rasters that are produced by the `abundanceSim` event function. Again, the sole argument and output of this function is `sim`.

```
abundancePlot <- function(sim) {
  ## plot abundances
  plotTitle <- paste("Species abundance\nat time",
                     names(sim$abundRasters)[length(sim$abundRasters)])
  abundPlot <- sim$abundRasters[[length(sim$abundRasters)]]
  Plot(abundPlot,
       title = plotTitle,
       new = TRUE, addTo = "abundPlot")

  return(invisible(sim))
}
```

The `abundancePlot` function was called `plotFun` in the template.

1.2.2.3 Scheduling events

The order in which module events are executed is determined by the `doEvent.<module name>` function. This function also defines the events themselves and what happens in them. The `switch` function executes each event (here `init`, `SimulAbund`, and `abundPlot`) and the events schedule themselves. Two things are of particular importance:

1. The `init` event is **mandatory**. This is the only event whose *name* that cannot be changed and that cannot be removed (even if it does not execute any event functions). All other `events` are optional and can be renamed. `SpaDES` searches and executes all modules' `init` events automatically. Note that the names of event functions executed during `init` *can* have any name: here we changed the `Init` function name (suggested by the template) to `abundanceInit`.
2. **Events should only schedule themselves**. The only exception is the `init`, which schedules the first time all other events are executed (even if a particular event only occurs once at the end of the simulation).

It is usually easier to fill the `doEvent.<module name>` function *after* having defined the event functions (as we did above). For instance, we know that plotting should occur after the generation of species abundances, and so the

`abundPlot` will be scheduled to occur after the `SimulAbund` event, by changing event priority (see `?priority`).

This is how we configured our `doEvent.speciesAbundance` function:

```
doEvent.speciesAbundance = function(sim, eventTime, eventType, debug =
FALSE) {
  switch(
    eventType,
    init = {
      ## do stuff for this event
      sim <- abundanceInit(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, eventTime = start(sim), moduleName =
"speciesAbundance",
                           eventType = "SimulAbund")
      sim <- scheduleEvent(sim, eventTime = P(sim)$.plotInitialTime,
                           moduleName = "speciesAbundance", eventType =
                           "abundPlot",
                           eventPriority = .normal()+0.5)
    },
    SimulAbund = {
      ## do stuff for this event
      sim <- abundanceSim(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, eventTime = time(sim) +
P(sim)$simulationTimeStep,
                           moduleName = "speciesAbundance", eventType =
                           "SimulAbund")
    },
    abundPlot = {
      ## do stuff for this event
      sim <- abundancePlot(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, eventTime = time(sim) +
P(sim)$.plotInterval,
```

```
                          moduleName = "speciesAbundance", eventType =
                          "abundPlot",
                          eventPriority = .normal()+0.5)
    },
    warning(paste("Undefined event type: '", current(sim)[1, "eventType",
    with = FALSE],
                  "' in module '", current(sim)[1, "moduleName", with =
                  FALSE], "'", sep = ""))
  )
  return(invisible(sim))
}
```

We suggest having a look at `?base::switch` too fully understand its behaviour. In short, `base::switch` tells R to execute (or switch) different code depending on the value of `EXPR` (here `eventType`). Here, this means that the behaviour of the function `doEvent.speciesAbundance` will change depending on the present `eventType`. So we need to define what behaviour it should have for each the event type defined in the module - namely, which functions will be executed and whether to schedule future events with `scheduleEvent`.

1.2.2.3.1 *init*

The first event is, obviously, `init` - again **its name cannot be changed**.

In `init` we run the initialisation event function (`abundanceInit`) - optional - and schedule the first occurrence of all other events (here, the abundance simulation, `SimulAbund`, and plotting, `abundPlot`, events). Because the `init` is the only event that `SpaDES` always executes at the start of the simulation, if no events are scheduled during `init`, no events will be executed after the `init`. Notice two things:

1. The `SimulAbund` event is scheduled at `start(sim)` (i.e. at the first time step of the simulation), which means that it will run after the `init` event, but still in the same "year".
2. `init` schedules the first plotting event to be executed at the time defined by the `.plotInitialTime` parameter, which is stored in the `sim` object (and obtained using `SpaDES.core::P(sim)`), but with a slightly lower event priority `eventPriority = .normal()+0.5` (see `?priority`).

1.2.2.3.2 ***SimulAbund***

The `SimulAbund` event is defined next. This event used to be called `event1` in the template, and we changed its name to be more informative of what it does. It is the core event of this module, where species abundances are generated via the event function `abundanceSim`.

The even also **schedules itself** to occur at a frequency defined by the `simulationTimeStep` parameter

1.2.2.3.3 ***abundPlot***

Finally, we schedule the plotting event, `abundPlot` (which used to be called `plot` in the template). Similarly to the `SimulAbund` event, it executes an event function (`abundancePlot`) and reschedules itself. An important difference is that it uses the `.plotInterval` parameter, instead of `simulationTimeStep`, when rescheduling itself. This way, future events will occur depending on the time step and plot interval parameters defined in the global script (or their default values defined in the metadata section).

1.2.2.4 `.inputObjects` function

The end of the template `.R` script defines a function called `.inputObjects`. This is where the developer should include code to provide the defaults for any input objects required by the module. This is the ideal place to produce the R template raster, instead of in `abundanceInit`, as it would allow a future user (or module) to provide their own R template (e.g. for another study area). At it is, any R supplied by the user or another module will be overridden by the execution of the `init` event.

Default inputs should be supplied in a way that allows these defaults to be overridden by the user (by supplying a named list of objects via `simInit(objects = ...)`) or by any other modules that produce these objects. For this, we rely on the `SpaDES.core::suppliedElsewhere` function, which detects if a given object has already been supplied by the user or if it will be supplied by another module.

Note that `suppliedElsewhere` does not know whether the module that supplies the object will be executed *before* the present module, as it is blind to module scheduling order. When modules are relatively simple and have an approximately linear flow of interdependencies, `SpaDES` is usually able to tell the order in which modules need to be executed. In more complex cases it is a good

idea to pass a vector of module names to `simInit(loadOrder = ...)` definining the order of module execution.

Here's an example of how to do this (the commented instructions have been deleted):

```
.inputObjects <- function(sim) {
  if (!suppliedElsewhere("r")) {
    ## make template raster if not supplied elsewhere.
    sim$r <- raster(nrows = 100, ncols = 100, xmn = -50, xmx = 50, ymn =
-50, ymx = 50)
  }
  return(invisible(sim))
}
```

If we chose to supply the default R in `.inputObjects`, then we should remove its creation from the `abundanceInit` function and add it to the metadata as an input. We have done this, so that `abundanceInit` only creates a storage list for the outputs:

```
abundanceInit <- function(sim) {
  ## create storage list of species abundance
  sim$abundRasters <- list()

  return(invisible(sim))
}
```

It is good practice to provide default input objects to all remaining modules, so that they can work stand-alone. We have done this below.

/!\ ATTENTION /!

If R becomes an input with defaults it must be ***added to the module metadata*** *inside an* `expectsInput` *call.*

1.2.2.5 Additional module functions

Events can also rely on other functions that can either be sourced from other scripts, or defined at the end of the module script (e.g. usually before `.in-`

`putObjects`, although the order is irrelevant). This is the case for the species abundances generator function, which we coded in a separate script called `abundance_model.R`. Scripts with accessory functions like these go into module's `R/` folder.

Functions should also be accompanied by metadata. Here we provide a description of the function, its parameters, returning value and what other package functions it relies on using the `roxygen2` documentation style (indicated by `#'`).

```
#' Accessory function to speciesAbundance module
#'
#' @param ras a raster layer used as template.
#' @return a fake abundance raster generated as a Gaussian map with scale
= 100 and variance = 0.01
#' @import NLMR nlm_mpd
abundance_model <- function(ras) {
  # abund_ras <- gaussMap(ras, scale = 100, var = 0.01) ## RandomFields
  no longer available
  abund_ras <- NLMR::nlm_mpd(
    ncol = ncol(ras),
    nrow = nrow(ras),
    resolution = unique(res(ras)),
    roughness = 0.5, ## TODO: adjust to approximate gaussMap version
    rand_dev = 100,
    rescale = TRUE,
    verbose = FALSE
  )
  return(abund_ras)
}
```

1.2.3 Creating and adding additional modules: the *temperature* module

The order in which modules are first executed (i.e. their `init` events) can be automatically determined by inter-module dependencies (i.e. module inputs

that are the outputs of other modules). If there are no inter-module dependencies this order is determined by the order in which the modules are listed in the `Part1_DummyModel.R` script, or via the `simInit(loadOrder = ...)` argument.

After the `init` event, the module execution order follows the order of events. This means that a module's events can be scheduled before and after another module's events within the same simulation time step. However, keep in mind that this can make the simulation flow hard to follow, debug and change when additional modules are added.

The second module we created generates yearly temperatures. Apart from different objects and functions names, this module also has the template raster R as required input object. Recall that R is created during the `.inputObjects` of the *speciesAbundance* module. When the two modules are linked, this object will not be created twice because `suppliedElsewhere("r")` will tell the *temperature* module that R will be supplied by another module. This may appear trivial in this example, but it can be extremely useful when inuts are heavy objects that require lengthy computations to be produces.

This is how we set up the `temperature.R` script looks like:

```
# Everything in this file gets sourced during simInit, and all functions
and objects
# are put into the simList.
defineModule(sim, list(
  name = "temperature",
  description = "Temperature simulator",
  keywords = c("temperature", "gaussian", "spatial"),
  authors = person("Me", email = "me@example.com", role = c("aut",
  "cre")),
  childModules = character(0),
  version = list(speciesAbundanceData = "0.0.0.9000"),
  timeframe = as.POSIXlt(c(NA, NA)),
  timeunit = "year",
  citation = list("citation.bib"),
  documentation = list("README.txt", "temperature.Rmd"),
  reqdPkgs = list("PredictiveEcology/SpaDES.core@development
  (>=1.0.10.9000)",
```

```
                "raster", "achubaty/NLMR"),
  parameters = bindrows(
    #defineParameter("paramName", "paramClass", value, min, max,
    "parameter description"),
    defineParameter("simulationTimeStep", "numeric", 1, NA, NA,
                    "This describes the simulation time step interval"),
    defineParameter(".plotInitialTime", "numeric", 1, NA, NA,
                    "This describes the simulation time at which the first
                    plot event should occur"),
    defineParameter(".plotInterval", "numeric", 1, NA, NA,
                    "This describes the simulation time interval between
                    plot events")
  ),
  inputObjects = bindrows(
    #expectsInput("objectName", "objectClass", "input object
    description", sourceURL, ...),
    expectsInput("r", "RasterLayer", "Template raster")
  ),
  outputObjects = bindrows(
    #createsOutput("objectName", "objectClass", "output object
    description", ...),
    createsOutput("tempRasters",  "list", "List of raster layers of
    temperature at any given year")
  )
))

## event types
#   - type `init` is required for initialiazation

doEvent.temperature = function(sim, eventTime, eventType, debug = FALSE)
{
  switch(
    eventType,
    init = {
      ## do stuff for this event
      sim <- Init(sim)

      ## schedule future event(s)
```

```
      sim <- scheduleEvent(sim, eventTime = start(sim), moduleName =
"temperature", eventType = "SimulTemp")
      sim <- scheduleEvent(sim, eventTime = P(sim)$.plotInitialTime,
moduleName = "temperature",
                           eventType = "tempPlot", eventPriority =
                           .normal() + 0.5)
    },
    SimulTemp = {
      ## do stuff for this event
      sim <- update(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, eventTime = time(sim) +
P(sim)$simulationTimeStep, moduleName = "temperature",
                           eventType = "SimulTemp")
    },
    tempPlot = {
      ## do stuff for this event
      sim <- plotting(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, eventTime = time(sim) +
P(sim)$.plotInterval, moduleName = "temperature",
                           eventType = "tempPlot", eventPriority =
                           .normal() + 0.5)
    },
    warning(paste("Undefined event type: '", current(sim)[1, "eventType",
    with = FALSE],
                  "' in module '", current(sim)[1, "moduleName", with =
                  FALSE], "'", sep = ""))
  )
  return(invisible(sim))
}

## This is the 'init' event:
Init <- function(sim) {
  ## create storage list of species temperature
  sim$tempRasters <- list()
```

```
  return(invisible(sim))
}

## This is the temperature simulation event function
update <- function(sim) {
  ## Generate temperature - our "updated data"
  sim$tempRasters[[as.character(time(sim))]] <- temperature_model(ras =
sim$r)

  return(invisible(sim))
}

## This is the plotting event funciton
plotting <- function(sim) {
  ## plot temperature
  plotTitle <- paste("Temperature\nat time",
                     names(sim$tempRasters)[length(sim$tempRasters)])
  tempPlot <- sim$tempRasters[[length(sim$tempRasters)]]
  Plot(tempPlot,
       title = plotTitle,
       new = TRUE, addTo = "tempPlot")

  return(invisible(sim))
}

.inputObjects <- function(sim) {
  if (!suppliedElsewhere("r")) {
    ## make template raster if not supplied elsewhere.
    sim$r <- raster(nrows = 100, ncols = 100, xmn = -50, xmx = 50, ymn =
-50, ymx = 50)
  }
  return(invisible(sim))
}
```

Again, we added an accessory `temperature_model` function in a separate script `R/temperature_model.R`:

```
#' Accessory function to temperature module
#'
#' @param ras a raster layer used as template.
#' @return a fake temperature raster generated as a Gaussian map with
scale = 100 and variance = 0.01
#' @import NLMR nlm_mpd
temperature_model <- function(ras) {
  # temp_ras <- gaussMap(ras, scale = 100, var = 0.01) ## RandomFields no
  longer available
  temp_ras <- NLMR::nlm_mpd(
    ncol = ncol(ras),
    nrow = nrow(ras),
    resolution = unique(res(ras)),
    roughness = 0.5, ## TODO: adjust to approximate gaussMap version
    rand_dev = 100,
    rescale = TRUE,
    verbose = FALSE
  )
  return(temp_ras)
}
```

1.2.4 Modules that depend on other modules: the *speciesTempLM* module

Our third and last module, *speciesTempLM*, will be used to run the statistical analysis at each year, after the abundances and temperatures are generated (**species** and **Temp**erature **L**inear **M**odel). Hence, it will depend on the outputs of the *speciesAbundance* and the *temperature* modules.

The interest of keeping the statistical analysis in a separate module lies on the fact that it allows us to easily swap and compare different statistical models to analyse our data if we want to.

It also allows for greater flexibility when it comes to **when** the statistical model is supposed to run. For example, we may want to fit it at every 5 years, instead of every year, using the previous 5 years of data. By having the statistical analysis contained in its own module, we don't need to change other module scripts in order to make these changes.

Finally, we draw your attention to a few differences in this module's script before we see it:

- The **frequency** of the statistical analysis (and correspondent plots) will be determined by the parameter `statsTimestep`. This parameter also determines the number of data years to be used to fit the linear model. If `statsTimestep = 5`, the statistical analysis will use the precedent 5 years of data including the year in which the event is running (a total of 6 years of data);
- This module **requires inputs** that have no defaults in `.inputObjects`. They are specified in `inputObjects` part of `defineModule` - notice how I've respected the names, classes and description of the objects that come from the *speciesAbundance* and the *temperature* modules;
- We have **two additional functions** in a separate script (`R/linear_model_functions.R`): the function fitting the linear model and a plotting function.

Below is the full module script. Notice how the future events where scheduled to `P(sim)$statsTimestep + 0.1`, to force the statistical analyses to occur **after** the abundance and temperature rasters are ready.

```
# Everything in this file gets sourced during simInit, and all functions
and objects
# are put into the simList.
defineModule(sim, list(
  name = "speciesTempLM",
  description = "Statistical analysis of species ~ temperature
  relationships using LM",
  keywords = c("linear model"),
  authors = person("Me", email = "me@example.com", role = c("aut",
  "cre")),
  childModules = character(0),
  version = list(speciesAbundanceData = "0.0.0.9000"),
  timeframe = as.POSIXlt(c(NA, NA)),
  timeunit = "year",
  citation = list("citation.bib"),
```

```
  documentation = list("README.txt", "speciesTempLM.Rmd"),
  reqdPkgs = list("PredictiveEcology/SpaDES.core@development
  (>=1.0.10.9000)",
                  "raster", "ggplot2", "data.table", "reshape2"),
   parameters = bindrows(
    #defineParameter("paramName", "paramClass", value, min, max,
    "parameter description"),
    defineParameter("statsTimestep", "numeric", 1, NA, NA, "This
    describes the how often the statitiscal analysis will be done")
  ),
  inputObjects = bindrows(
    #expectsInput("objectName", "objectClass", "input object
    description", sourceURL, ...),
    expectsInput("abundRasters", "list", "List of raster layers of
    species abundance at any given year"),
    expectsInput("tempRasters", "list", "List of raster layers of
    temperature at any given year")
  ),
  outputObjects = bindrows(
    #createsOutput("objectName", "objectClass", "output object
    description", ...),
    createsOutput("outputdata", "list", "List of dataframes containing
    species abundances and temperature values per pixel"),
    createsOutput("outputLM", "list", "List of output yearly LMs
    (abundance ~ temperature)"),
    createsOutput("yrs", "numeric", "Vector of years used for statistical
    analysis")
  )
))

## event types
#   - type `init` is required for initialiazation

doEvent.speciesTempLM = function(sim, eventTime, eventType, debug =
FALSE) {
  switch(
    eventType,
    init = {
```

```
      ## do stuff for this event
      sim <- statsInit(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, P(sim)$statsTimestep, "speciesTempLM",
                           "stats", eventPriority = .normal() + 2)
      sim <- scheduleEvent(sim, P(sim)$statsTimestep, "speciesTempLM",
                           "statsPlot", eventPriority = .normal() + 2.5)
    },
    stats = {
      ## do stuff for this event
      sim <- statsAnalysis(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, time(sim) + P(sim)$statsTimestep,
"speciesTempLM",
                           "stats", eventPriority = .normal() + 2)
    },
    statsPlot = {
      ## do stuff for this event
      sim <- statsPlot(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, time(sim) + P(sim)$statsTimestep,
"speciesTempLM",
                           "statsPlot", eventPriority = .normal() + 2.5)
    },
    warning(paste("Undefined event type: '", current(sim)[1, "eventType",
    with = FALSE],
                  "' in module '", current(sim)[1, "moduleName", with =
                  FALSE], "'", sep = ""))
  )
  return(invisible(sim))
}

## template initialization
statsInit <- function(sim) {
  ## create outputs storage lists
```

```
  sim$outputLM <- list()

  return(invisible(sim))
}

## Statistical analysis event
statsAnalysis <- function(sim) {
  ## get all species abundances data available
  abundData <- data.table(getValues(stack(sim$abundRasters)))
  abundData[, pixID := 1:nrow(abundData)]
  abundData <- melt.data.table(abundData, id.var = "pixID",
                               variable.name = "year", value.name = "abund")
  abundData[, year := as.numeric(sub("X", "", year))]

  ## get all temperature data available
  tempData <- data.table(getValues(stack(sim$tempRasters)))
  tempData[, pixID := 1:nrow(tempData)]
  tempData <- melt.data.table(tempData, id.var = "pixID",
                              variable.name = "year", value.name = "temp")
  tempData[, year := as.numeric(sub("X", "", year))]

  ## merge per year
  setkey(abundData, pixID, year)
  setkey(tempData, pixID, year)
  sim$outputdata <- abundData[tempData]

  sim$outputLM[[as.character(time(sim))]] <- linearModel(Data =
sim$outputdata)
  return(invisible(sim))
}

## Plotting event
statsPlot <- function(sim) {
  model <- sim$outputLM[[as.character(time(sim))]]

  modelPlot <- ggplot(sim$outputdata) +
    geom_point(aes(x = temp, y = abund)) +
    geom_abline(intercept = model$coefficients["(Intercept)"],
```

```
                slope = model$coefficients["temp"], size = 2, col =
                "blue") +
    theme_bw() +
    labs(x = "Temp.", y = "Species abundance")

  plotTitle <- paste("abundance ~ temperature\n",
                     "years", range(sim$outputdata$year)[1],
                     "to", range(sim$outputdata$year)[2])
  Plot(modelPlot,
       title = plotTitle,
       new = TRUE, addTo = "modelPlot")

  return(invisible(sim))
}

.inputObjects <- function(sim) {
  # Any code written here will be run during the simInit for the purpose
  of creating
  # any objects required by this module and identified in the
  inputObjects element of defineModule.
  # This is useful if there is something required before simulation to
  produce the module
  # object dependencies, including such things as downloading default
  datasets, e.g.,
  # downloadData("LCC2005", modulePath(sim)).
  # Nothing should be created here that does not create a named object in
  inputObjects.
  # Any other initiation procedures should be put in "init" eventType of
  the doEvent function.
  # Note: the module developer can check if an object is
  'suppliedElsewhere' to
  # selectively skip unnecessary steps because the user has provided
  those inputObjects in the
  # simInit call, or another module will supply or has supplied it. e.g.,
  # if (!suppliedElsewhere('defaultColor', sim)) {
  #   sim$map <- Cache(prepInputs, extractURL('map')) # download,
  extract, load file from url in sourceURL
  # }
```

```
  #cacheTags <- c(currentModule(sim), "function:.inputObjects") ##
  uncomment this if Cache is being used
  dPath <- asPath(getOption("reproducible.destinationPath",
dataPath(sim)), 1)
  message(currentModule(sim), ": using dataPath '", dPath, "'.")

  # ! ----- EDIT BELOW ----- ! #

  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}
```

And the script with the accessory functions:

```
## Accessory functions to speciesTempLM module

#' Accessory function to speciesTempLM module that calculates a
#'  linear regression between species abundances and temperature
#'
#' @param Data a data.frame or data.table that contains an \code{abund}
#'   column and a \code{temp} column with abundance and temperature
values
#'   in each location, respectively.
#' @return a linear model (\code{lm}) object fitted with the formula:
#'  \code{abund ~ temp}

linearModel <- function(Data){
  lm1 <- lm(abund ~ temp, data = Data)
  return(lm1)
}
```

1.2.5 Simulation

1.2.5.1 Simulation setup in a "global" script

We can now go back to our `Part1_DummyModel.R` script and set the simulation up.

The function `simInit` needs a few arguments listing simulation folder directories, parameters, simulation times, modules and, optionally, input objects supplied by the user. `simInit` will prepare a simulation object that can later be run by the `spades` function:

- The first list, `modules`, contains modules we want to activate.
- `times` is a named list containing the start and end times of the simulation and what time units we're working with (with "start" and "end" being the list `names`. It thus defines the length of the simulation. It is important that the start and ending times are defined in decimals, because `SpaDES` allows decomposing time units into smaller fractions.
- `parameters` is a named list of named lists, containing parameters values passed to each module. Note that because the module metadata will (or should) contain default parameter values, here we pass only parameters which we want to change with respect to their defaults. For instance, `.plotInterval` is used and defined in the *speciesAbundance* and *temperature* modules, but not passed to the `simInit` function because we want to use the default value. As a developer providing a reproducible example, we may also chose to list important and useful parameters, even if the value is the same as the default. Here we chose to list `.plotInitialTime` (a parameter used and defined in the *speciesAbundance* and *temperature* modules), but provide the default value (we experimenting with it by changing its value in the `Part1_DummyModel.R`).
- `paths` contains the folder directory paths that we set earlier.

```
## list the modules to use
simModules <- list("speciesAbundance", "temperature", "speciesTempLM")

## Set simulation and module parameters
```

```
simTimes <- list(start = 1, end = 10, timeunit = "year")
simParams <- list(
  speciesAbundance = list(simulationTimeStep = 1,
                          .plotInitialTime = 1),
  temperature = list(simulationTimeStep = 1,
                     .plotInitialTime = 1),
  speciesTempLM = list(statsTimestep = 5)
)

## make a list of directory paths
simPaths <- getPaths()

## Simulation setup
mySim <- simInit(times = simTimes, params = simParams,
                 modules = simModules, paths = simPaths)
```

Finally, we highlight that `simInit` also executes all `.inputObjects` functions, and schedules the `init` events, but does not execute them:

```
events(mySim)
```

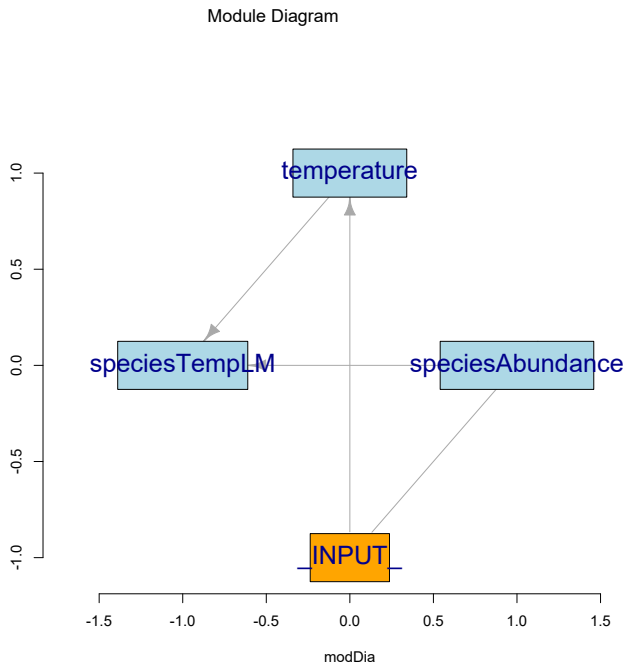
1.2.5.2 Checking the simulation setup

Before starting the simulations we should check if the modules were linked correctly.

Module diagram

`moduleDiagram` is a useful function that shows module inter-dependencies as a network diagram. The direction of the arrows indicates an output to input flow. You can see that *speciesAbundance* and *temperature* inputs (specifically our R raster) are supplied by an external source ("*INPUT*") - the user or `.inputObjects`. Whereas the inputs to the *speciesTempLM* module are outputs of the *speciesAbundance* and *temperature* modules.

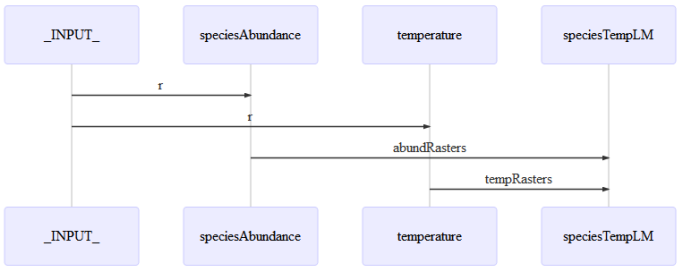
```
moduleDiagram(mySim)
```



Object diagram

`objectDiagram` provides another way of checking module linkages. It explicitly shows module inter-dependencies by depicting the objects that establish links between modules.

```
objectDiagram(mySim)
```



1.2.5.3 Running SpaDES

We run the simulation using the `spades` function, which takes the output of the `simInit`, executes the already scheduled `init` events, which schedule the remainder of the events. We passed `debug = TRUE` so that `spades` prints the events as they are being executed. In case something fails, this helps diagnosing where the issue occurred.

```
## run simulation
dev() # on Windows and Mac, this opens external device if using Rstudio,
it is faster
clearPlot()
mySim2 <- spades(mySim, debug = TRUE)
```

We suggest experimenting with changing parameter values and trying to create and add other modules to further explore all the SpaDES flexibility. The more complex the project gets, the more advantageous it is to use SpaDES to turn modules *on* or *off*, swapping modules to run, e.g., different statistical analyses, or to include different data.

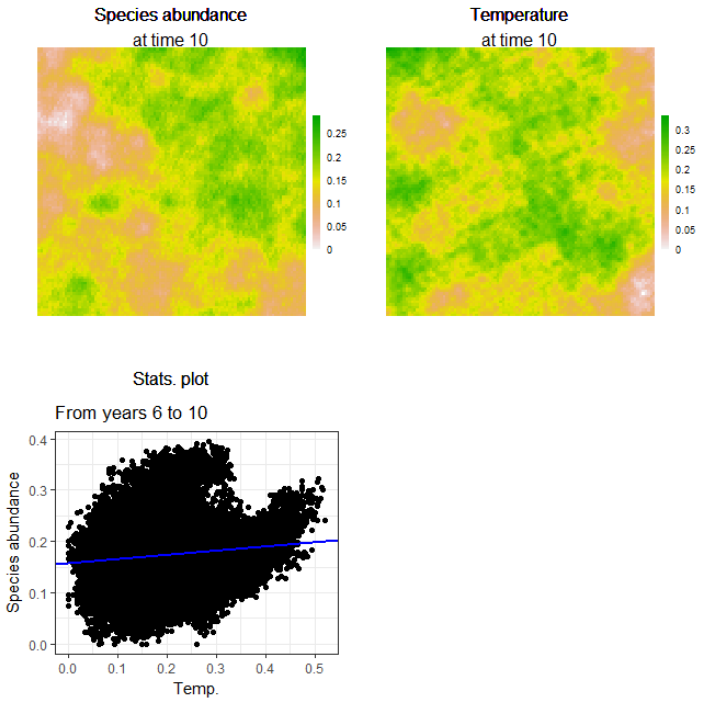


FIGURE 1.2: Simulation plots: Final plot of the simulation

1.2.6 Additional notes

SpaDES is an extremely powerful package, whose potential goes well beyond what has been discussed in this dummy example. If you want to explore it further, we recommend following Part 2 for a more realistic (but still simple) SpaDES application.

Also, do go to the SpaDES webpage[3] to find further information about the platform, as well as upcoming workshops and publications and to the Predictive Ecology Github repository[4] to see all the SpaDES modules and SpaDES-related packages that we maintain.

Happy SpaDESing!

[3] http://predictiveecology.org/
[4] http://https://github.com/PredictiveEcology/

2

A more realistic example of SpaDES

Authors: Ceres Barros, Alex M. Chubaty

In Part 1 of this guide, we described how to create new SpaDES modules, their different components, how to link different modules and how to set up and run a simulation.

Here, we assume that you are familiar with these steps, but go further in showing important SpaDES features that facilitate many of the steps common to most ecological modelling exercises. For the sake of simplicity, we focus our example on projecting a species' distribution as a function of climate covariates. Yet, the true power of SpaDES is more evident when using complex dynamic simulation models parametrised using large datasets and ran across large spatial areas.

This example is broken into four main parts: 1) Module creation and coding; 2) Running the model; 3) Caching; and 4) Best practices. By no mean does it cover caching or best practices in full, as each of these topics is very extensive, but it highlights some of their essentials in SpaDES and from our own experience.

2.1 The example: projecting species distribution shifts under climate change

Species distribution models (SDMs) have been widely used in ecology to predict how species presences and absences across a landscape may change under changing environmental conditions. As a result, there are several R packages that have been built with this in mind (e.g. `dismo` Hijmans et al. 2021; `biomod2` Thuiller et al. 2021) and many ecologists do these analyses exclusively in R.

Often, these analyses are run only once for a given set of species, baseline

and projected environmental conditions, and researchers will have a few R scripts (or maybe just one longer script) that load the data into R, do any necessary pre-processing steps, fit the models and run species distribution projections. The usefulness of SpaDES comes when we want an automated and standardized workflow that can be easily updated with new data and adapted with new algorithms. SpaDES provides a common standard and a modular approach to modelling that facilitates expanding, debugging and sharing code, but also various tools that bring many well-known best practices from computer- and data-science workflows (including reproducible, modular workflows, and caching), to the realm of ecological modelling, so that they can be used by non-computer-scientists with minimal learning. In an SDM project this means that updating data and algorithms, and automating iterative forecasting become easier and less prone to errors. When SpaDES modules are open and shared, this also expands a potential pool of users who can themselves help improve the code.

2.2 Module creation and coding

With the above in mind, in this example we created three modules that source and pre-process data ('data modules') and a module that fits an SDM and iteratively forecasts species distributions (we call it a 'simulation module', although the simulation only involves predicting from a statistical model). The idea is that we could, for instance, provide different data sources to one of the data modules and only update the parts of the simulation that are affected by this change (i.e. presumably the other data module steps with not be affected). Or, we could develop a second simulation module using a different SDM approach and swap the two modules to inspect which provides better predictions.

Our data modules are *speciesAbundanceData* and *climateData*. The simulation module is *projectSpeciesDist*. We start by creating an `.R` script to set up and control the simulation. In this example this script is called `Part2_SDMs.R`. The script begins with a few lines of code that ensure necessary packages are installed and loaded (see Reproducible package installation). It then defines

the necessary folder directories for the simulation and creates the modules in the `modules/` folder:

```
## Get necessary R packages, but don't load any
if (!require("Require")) install.packages("Require")
Require::Require("PredictiveEcology/SpaDES.install@development", require
= FALSE)
Require::Require("PredictiveEcology/SpaDES.experiment@development",
require = FALSE)
SpaDES.install::installSpaDES(ask = TRUE)

## decide where you're working
mainDir <- "."

# mainDir <- getwd()
SpaDES.core::setPaths(cachePath = file.path(mainDir, "cache"),
                      inputPath = file.path(mainDir, "inputs"),
                      modulePath = file.path(mainDir, "modules"),
                      outputPath = file.path(mainDir, "outputs"))

simPaths <- SpaDES.core::getPaths() ## check that this is what you wanted

## Let's create a self-contained module that will simulate the species'
abundance for any given period of time and frequency.
if (!dir.exists(file.path(simPaths$modulePath, "speciesAbundanceData"))){
  SpaDES.core::newModule(name = "speciesAbundanceData", path =
simPaths$modulePath)
}

if (!dir.exists(file.path(simPaths$modulePath, "climateData"))){
  SpaDES.core::newModule(name = "climateData", path =
simPaths$modulePath)
}

if (!dir.exists(file.path(simPaths$modulePath, "projectSpeciesDist"))){
  SpaDES.core::newModule(name = "projectSpeciesDist", path =
simPaths$modulePath)
}
```

Notice how we protect the `newModule` call with an `if` statement that first detects whether the module directory exists already. This is necessary to prevent overwriting existing modules should this script be run a second time in the same location (see Protect yourself and others from common mistakes/problems).

`setPaths` will create the project folder directories in case they do not exist (no overwriting occurs in case they do).

Finally, note that we do not load any R packages yet, as we will later use `Require` to make sure all module dependencies are installed before running the simulation (see Reproducible package installation). Because `Require` may attempt to install missing packages and because installing packages should be done in a clean R session, we will only load any packages after all the installation steps are complete.

2.2.1 Data modules

The next two sections show our two data modules `.R` scripts. We assume you are already familiar with the different parts of a module `.R` script; if not, see Part 1. We do not discuss the module `.Rmd` files, which should document each module in detail (see [Module documentation – module .Rmd]).

2.2.1.1 *speciesAbundanceData* module:

This module downloads freely available spatial layers of *Picea glauca* percent cover (% cover) across Canada and pre-processes them to match a user-supplied study area raster. We use the new `terra` package throughout this example, since the `raster` package will soon be discontinued.

The `prepInputs` function downloads the % cover layer from the Canadian National Forest Inventory data server using the URL supplied by `sppAbundURL` and processes it to match the study area raster (`studyAreaRas`) supplied by the user. The module then outputs *Picea glauca* % cover as a raster (`sppAbundanceRas`) and as a `data.table` (`sppAbundanceDT`). The `data.table` contains added information about the year of the simulation during which the data should be used (here, only the first year when SDM fitting happens).

We export species % cover in two formats (a raster and a table) for demonstrational purposes, but also because we could envision that this model (i.e. group of modules) could save the species distribution projections for

several points in time in a more compact format of a `data.table` – large raster layers can consume a considerable amount of disk space (see Coding for the future).

```
## Everything in this file and any files in the R directory are sourced
during `simInit()`;
## all functions and objects are put into the `simList`.
## To use objects, use `sim$xxx` (they are globally available to all
modules).
## Functions can be used inside any function that was sourced in this
module;
## they are namespaced to the module, just like functions in R packages.
## If exact location is required, functions will be:
`sim$.mods$<moduleName>$FunctionName`.
defineModule(sim, list(
  name = "speciesAbundanceData",
  description = paste("Data module to prepare tree species cover data for
  species distribution modelling.",
                      "Defaults to using Canadian National Forest
                      Inventory data."),
  keywords = c("minimal SpaDES example", "species distribution model"),
  authors = structure(list(list(given = c("Ceres"), family = "Barros",
  role = c("aut", "cre"), email = "ceres.barros@ubc.ca", comment =
  NULL)), class = "person"),
  childModules = character(0),
  version = list(speciesAbundanceData = "0.0.0.9000"),
  timeframe = as.POSIXlt(c(NA, NA)),
  timeunit = "year",
  citation = list("citation.bib"),
  documentation = list("README.md", "speciesAbundanceData.Rmd"), ## same
  file
  reqdPkgs = list("PredictiveEcology/SpaDES.core@development
  (>=1.0.10.9000)",
                  "terra", "ggplot2", "rasterVis"),
  parameters = bindrows(
    #defineParameter("paramName", "paramClass", value, min, max,
    "parameter description"),
    defineParameter("sppAbundURL", "character",
```

```
                  paste0(
                  "https://ftp.maps.canada.ca/pub/nrcan_rncan/Forests_Foret/"
                  ,
                 "canada-forests-attributes_attributs-forests-canada/",

                                      "2001-attributes_attributs-
                        2001/NFI_MODIS250m_2001_kNN_Species_Pice_Gla_v1.tif"
                        ), NA,
                        NA,
                  paste("URL where the first RasterLayer of species
                  abundance resides.",
                       "This will be the abundance data used to fit the
                        species ditribution model.",
                       "Defaults to *Picea glauca* percent cover across
                        Canada, in 2001",
                       "(from Canadian National Forest Inventory forest
                        attributes)")),
  defineParameter(".plots", "character", "screen", NA, NA,
                  "Used by Plots function, which can be optionally used
                  here"),
  defineParameter(".plotInitialTime", "numeric", start(sim), NA, NA,
                 "Describes the simulation time at which the first plot
                  event should occur."),
  defineParameter(".plotInterval", "numeric", NA, NA, NA,
                  "Describes the simulation time interval between plot
                  events."),
  defineParameter(".saveInitialTime", "numeric", NA, NA, NA,
                 "Describes the simulation time at which the first save
                  event should occur."),
  defineParameter(".saveInterval", "numeric", NA, NA, NA,
                  "This describes the simulation time interval between
                  save events."),
  defineParameter(".studyAreaName", "character", NA, NA, NA,
                 "Human-readable name for the study area used. If NA, a
                  hash of studyArea will be used."),
  ## .seed is optional: `list('init' = 123)` will `set.seed(123)` for
  the `init` event only.
  defineParameter(".seed", "list", list(), NA, NA,
```

```
                  "Named list of seeds to use for each event (names)."),
    defineParameter(".useCache", "logical", FALSE, NA, NA,
                    "Should caching of events or module be used?")
  ),
  inputObjects = bindrows(
    #expectsInput("objectName", "objectClass", "input object
    description", sourceURL, ...),
    expectsInput("studyAreaRas", objectClass = "RasterLayer",
                 desc = "A binary raster of the study area")
  ),
  outputObjects = bindrows(
    #createsOutput("objectName", "objectClass", "output object
    description", ...),
    createsOutput("sppAbundanceDT", "data.table",
                  desc = paste("Species abundance data from
                  `sppAbundanceRas`, with columns 'cell',",
                               "'x', 'y', 'sppAbund' and 'year' (an
                               integer matching the number in",
                               "names(`sppAbundanceRas`)." )),
    createsOutput("sppAbundanceRas", "SpatRaster",
                  desc = paste("A species abundance layer used to fit a
                  species distribution model",
                               "at the start of the simulation. Layers
                               named as:",
                               "paste('year', start(sim):end(sim), sep =
                               '_')). Data obtained from",
                               "P(sim)$sppAbundURL"))
  )
))

## event types
#   - type `init` is required for initialization

doEvent.speciesAbundanceData = function(sim, eventTime, eventType, debug
= FALSE) {
  switch(
    eventType,
    init = {
```

```
      ## do stuff for this event
      sim <- abundanceInit(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, eventTime = P(sim)$.plotInitialTime,
                           moduleName = "speciesAbundanceData", eventType
                           = "abundPlot",
                           eventPriority = .normal())
    },
    abundPlot = {
      ## do stuff for this event
      sim <- abundancePlot(sim)
    },
    warning(paste("Undefined event type: '", current(sim)[1, "eventType",
    with = FALSE],
                  "' in module '", current(sim)[1, "moduleName", with =
                  FALSE], "'", sep = ""))
  )
  return(invisible(sim))
}

## event functions
#   - keep event functions short and clean, modularize by calling
subroutines from section below.

## Initialisation Event function
abundanceInit <- function(sim) {
  ## download data - prepInputs does all the heavy-lifting of dowloading
  and pre-processing the layer and caches.
  ## there seems to be an issue masking this particular raster with
  `terra` and `GDAL`, so we'll not use them here.
  opts <- options("reproducible.useTerra" = FALSE,
                  "reproducible.useGDAL" = FALSE)
  on.exit(options(opts), add = TRUE)
  sppAbundanceRas <- prepInputs(targetFile =
"NFI_MODIS250m_2001_kNN_Species_Pice_Gla_v1.tif",
                                url = P(sim)$sppAbundURL,
                                # fun = "terra::rast",
```

```
                                # projectTo = sim$studyAreaRas,
                                # cropTo = sim$studyAreaRas,
                                # maskTo = sim$studyAreaRas,
                                rasterToMatch =
                                raster::raster(sim$studyAreaRas),
                                maskWithRTM = TRUE,
                                overwrite = TRUE,
                                cacheRepo = cachePath(sim))
  options(opts)
  if (is(sppAbundanceRas, "RasterLayer")) {
    sppAbundanceRas <- terra::rast(sppAbundanceRas)
  }

  names(sppAbundanceRas) <- paste("year", time(sim), sep = "_")
  sppAbundanceDT <- as.data.table(as.data.frame(sppAbundanceRas, xy =
TRUE, cells = TRUE))
  sppAbundanceDT[, year := as.integer(sub("year_", "",
names(sppAbundanceRas)))]
  setnames(sppAbundanceDT, "year_1", "sppAbund")

  ## export to sim
  sim$sppAbundanceRas <- sppAbundanceRas
  sim$sppAbundanceDT <- sppAbundanceDT

  return(invisible(sim))
}

## Plotting event function
abundancePlot <- function(sim) {
  ## plot species abundance
  Plots(sim$sppAbundanceRas, fn = plotSpatRaster, types = P(sim)$.plots,
        usePlot = TRUE, filename = file.path(outputPath(sim), "figures",
        "speciesAbundance"),
        plotTitle = "Species abundance data", xlab = "Longitude", ylab =
        "Latitude")

  return(invisible(sim))
}
```

```
.inputObjects <- function(sim) {

  #cacheTags <- c(currentModule(sim), "function:.inputObjects") ##
  uncomment this if Cache is being used
  dPath <- asPath(getOption("reproducible.destinationPath",
dataPath(sim)), 1)
  message(currentModule(sim), ": using dataPath '", dPath, "'.")

  # ! ----- EDIT BELOW ----- ! #

  if (!suppliedElsewhere(sim$studyAreaRas)) {
    ## code check: did the user supply a study area?
    stop("Please supply a 'studyAreaRas' SpatRaster")
  }

  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}
```

2.2.1.2 *climateData* module:

This module downloads and processes freely available spatial layers of four bioclimatic variables used to fit the SDM of *Picea glauca* in the study area.

The module uses a different way to download data. It relies on two input `data.tables` that contain the URLs for each climate covariate, one for baseline conditions, the other for projected climate conditions, both containing information about when each layer should be used during the simulation (the "year"column).

We have only supplied one set of data sources for default baseline climate conditions (`baselineClimateURLs`) and for climate projections (`projClimateURLs`), all of which are downloaded from WorldClim at 2.5 minutes resolution. The baseline climate data correspond to the 1970-2000 period Fick and Hijmans (2017), which aligns well with the species % cover data year (2001). The climate projections were obtained for 2021-2040, 2041-2060, 2061-2080 and 2081-2100, from CMIP6 downscaled future

projections using the CanESM5 model (Swart et al. 2019) under the SSP 585 climate scenario.

We encourage providing different (or additional) URLs referring to projections for other climate periods, other climate models and other climate scenarios (see WorldClim[1] for a list of climate projections).

If providing other URLs to obtain different climate data, pay special attention to the "year" column of `projClimateURLs` – the URLs need to correspond to the simulation year during which they will be used (not necessarily the actual climate year, unless the simulation years follow the same numbering).

Like in the `speciesAbundanceData` module, the `prepInputs` function processes the cliamte layers to match the study area raster (`studyAreaRas`) and compiles all climate data in the `climateDT` object and as raster layer objects (`baselineClimateRas` and `projClimateRas`) – the module's outputs.

```
## Everything in this file and any files in the R directory are sourced
during `simInit()`;
## all functions and objects are put into the `simList`.
## To use objects, use `sim$xxx` (they are globally available to all
modules).
## Functions can be used inside any function that was sourced in this
module;
## they are namespaced to the module, just like functions in R packages.
## If exact location is required, functions will be:
`sim$.mods$<moduleName>$FunctionName`.
defineModule(sim, list(
  name = "climateData",
  description = paste("Data module to prepare climate data for species
  distribution modelling.",
                      "Defaults to using bioclimatic variables from
                      Worldclim."),
  keywords = c("minimal SpaDES example", "species distribution model"),
  authors = structure(list(list(given = c("Ceres"), family = "Barros",
  role = c("aut", "cre"), email = "ceres.barros@ubc.ca", comment =
  NULL)), class = "person"),
  childModules = character(0),
```

[1] https://www.worldclim.org/data/cmip6/cmip6climate.html

```
  version = list(climateData = "0.0.0.9000"),
  timeframe = as.POSIXlt(c(NA, NA)),
  timeunit = "year",
  citation = list("citation.bib"),
  documentation = list("README.md", "climateData.Rmd"), ## same file
  reqdPkgs = list("PredictiveEcology/SpaDES.core@development
  (>=1.0.10.9000)",
                  "ggplot2", "rasterVis", "terra", "data.table"),
  parameters = bindrows(
    #defineParameter("paramName", "paramClass", value, min, max,
    "parameter description"),
    defineParameter(".plots", "character", "screen", NA, NA,
                    "Used by Plots function, which can be optionally used
                    here"),
    defineParameter(".plotInitialTime", "numeric", start(sim), NA, NA,
                    "Describes the simulation time at which the first plot
                    event should occur."),
    defineParameter(".plotInterval", "numeric", NA, NA, NA,
                    "Describes the simulation time interval between plot
                    events."),
    defineParameter(".saveInitialTime", "numeric", NA, NA, NA,
                    "Describes the simulation time at which the first save
                    event should occur."),
    defineParameter(".saveInterval", "numeric", NA, NA, NA,
                    "This describes the simulation time interval between
                    save events."),
    defineParameter(".studyAreaName", "character", NA, NA, NA,
                    "Human-readable name for the study area used. If NA, a
                    hash of studyArea will be used."),
    ## .seed is optional: `list('init' = 123)` will `set.seed(123)` for
    the `init` event only.
    defineParameter(".seed", "list", list(), NA, NA,
                    "Named list of seeds to use for each event (names)."),
    defineParameter(".useCache", "logical", FALSE, NA, NA,
                    "Should caching of events or module be used?")
  ),
  inputObjects = bindrows(
    #expectsInput("objectName", "objectClass", "input object
    description", sourceURL, ...),
```

```
    expectsInput("baselineClimateURLs", "data.table",
                 desc = paste("A table with columns 'vars', 'URL',
                 'targetFile' and 'year', containing",
                              "variable names, URLs and raster file names
                              of each climate covariate",
                              "used in the species distribution models.
                              Year is the first year of the",
                              "simulation (not the reference climate
                              period). Defaults to Worldclim's",
                              "'bio1', 'bio4', 'bio12' and 'bio15'
                              bioclimatic variables for the 1970-2000",
                              "climate period, at 2.5 minutes.")),
    expectsInput("projClimateURLs", "data.table",
                 desc = paste("Same as `baselineClimateURLs` but refering
                 to projected climate layers.",
                              "Variable names in 'vars' need to the same as
                              in `baselineClimateURLs`",
                              "and P(sim)$projClimateURLs. Years should
                              correspond to simulation years.",
                              "Defaults to 2081-2100 projections using the
                              CanESM5 climate model and the",
                              "SSP 585 climate scenario, at 2.5 minutes,
                              obtained from Worldclim.")),
    expectsInput("studyAreaRas", objectClass = "SpatRaster",
                 desc = "A binary raster of the study area")
  ),
  outputObjects = bindrows(
    #createsOutput("objectName", "objectClass", "output object
    description", ...),
    createsOutput("climateDT", "data.table",
                  desc = paste("A data.table with as many columns as the
                  climate covariates",
                               "used in the species distribution model and
                               'year' column describing",
                               "the simulation year to which the data
                               corresponds.")),
    createsOutput("baselineClimateRas", "SpatRaster",
                  desc = paste("Baseline climate layers obtained from
                  `baselineClimateURLs`")),
```

```
    createsOutput("projClimateRas", "SpatRaster",
                  desc = paste("Baseline climate layers obtained from
                  `projClimateURLs`"))
  )
))

## event types
#   - type `init` is required for initialization

doEvent.climateData = function(sim, eventTime, eventType, debug = FALSE)
{
  switch(
    eventType,
    init = {
      ## do stuff for this event
      sim <- climateInit(sim)

      ## schedule future event(s)
      sim <- scheduleEvent(sim, eventTime = P(sim)$.plotInitialTime,
                           moduleName = "climateData", eventType =
                           "climPlot",
                           eventPriority = .normal())
    },
    climPlot = {
      ## do stuff for this event
      sim <- climatePlot(sim)
    },
    warning(paste("Undefined event type: '", current(sim)[1, "eventType",
    with = FALSE],
                  "' in module '", current(sim)[1, "moduleName", with =
                  FALSE], "'", sep = ""))
  )
  return(invisible(sim))
}

## event functions
#   - keep event functions short and clean, modularize by calling
subroutines from section below.
```

```
## Initialisation Event function
climateInit <- function(sim) {
  ## GET BASELINE DATA
  ## make a vector of archive (zip) file names if the url points to one.
  archiveFiles <- sapply(sim$baselineClimateURLs$URL, function(URL) {
    if (grepl("\\.zip$", basename(URL))) {
      basename(URL)
    } else {
      NULL
    }
  }, USE.NAMES = FALSE)

  ## check that baseline climate data only has one year value
  if (length(unique(sim$baselineClimateURLs$year)) != 1) {
    stop(paste("'baselineClimateURLs' should all have the same 'year'
    value,",
               "corresponding to the first year of the simulation"))
  }
  ## download data - prepInputs does all the heavy-lifting of dowloading
  and pre-processing the layer and caches.
  baselineClimateRas <- Cache(Map,
                              f = prepInputs,
                              url = sim$baselineClimateURLs$URL,
                              targetFile =
                              sim$baselineClimateURLs$targetFile,
                              archive = archiveFiles,
                              MoreArgs = list(
                                fun = "terra::rast",
                                overwrite = TRUE,
                                projectTo = sim$studyAreaRas,
                                cropTo = sim$studyAreaRas,
                                maskTo = sim$studyAreaRas,
                                rasterToMatch = sim$studyAreaRas,
                                cacheRepo = cachePath(sim)),
                              cacheRepo = cachePath(sim))

  names(baselineClimateRas) <- paste0(sim$baselineClimateURLs$vars,
  "_year", sim$baselineClimateURLs$year)
```

```
  ## make a stack
  baselineClimateRas <- rast(baselineClimateRas)

  ## make a data.table
  baselineClimateData <- as.data.table(as.data.frame(baselineClimateRas,
xy = TRUE, cells = TRUE))
  setnames(baselineClimateData, sub("_year.*", "",
  names(baselineClimateData))) ## don't need year in names here
  baselineClimateData[, year := unique(sim$baselineClimateURLs$year)]

  ## GET PROJECTED DATA
  ## make a vector of archive (zip) file names if the url points to one.
  archiveFiles <- lapply(sim$projClimateURLs$URL, function(URL) {
    if (grepl("\\.zip$", basename(URL))) {
      basename(URL)
    } else {
      NULL
    }
  })

  ## download data - prepInputs does all the heavy-lifting of dowloading
  and pre-processing the layer and caches.
  ## workaround Mar 30th 2022 cache issue with terra.
  projClimateRas <- Cache(Map,
                          f = prepInputs,
                          url = sim$projClimateURLs$URL,
                          targetFile = sim$projClimateURLs$targetFile,
                          archive = archiveFiles,
                          MoreArgs = list(
                            overwrite = TRUE,
                            fun = "raster::stack",
                            projectTo = sim$studyAreaRas,
                            cropTo = sim$studyAreaRas,
                            maskTo = sim$studyAreaRas,
                            rasterToMatch = sim$studyAreaRas,
                            cacheRepo = cachePath(sim)),
                          cacheRepo = cachePath(sim))
```

```
  if (any(sapply(projClimateRas, function(x) is(x, "RasterLayer") | is(x,
  "RasterStack")))){
    projClimateRas <- lapply(projClimateRas, terra::rast)
  }

  ## these rasters are different. The tif file contains all the variables
  in different layers
  ## so, for each variable, we need to keep only the layer of interest
  projClimateRas <- mapply(function(stk, var) {
    lyr <- which(sub(".*_", "BIO", names(projClimateRas[[1]])) == var)
    return(stk[[lyr]])
  }, stk = projClimateRas, var = sim$projClimateURLs$vars)
  names(projClimateRas) <- paste0(sim$projClimateURLs$vars, "_year",
  sim$projClimateURLs$year)

  ## make a stack
  projClimateRas <- rast(projClimateRas)

  ## make a data.table
  projClimateData <- as.data.table(as.data.frame(projClimateRas, xy =
TRUE, cells = TRUE))

  ## melt so that year is in a column
  projClimateDataMolten <- lapply(unique(sim$projClimateURLs$vars),
function(var, projClimateData) {
    cols <- grep(paste0(var, "_year"), names(projClimateData), value =
TRUE)
    idCols <- names(projClimateData)[!grepl("_year",
names(projClimateData))]

    moltenDT <-  melt(projClimateData, id.vars = idCols, measure.vars =
cols,
                      variable.name = "year", value.name = var)
    moltenDT[, year := sub(paste0(var, "_year"), "", year)]
    moltenDT[, year := as.integer(year)]
    return(moltenDT)
  }, projClimateData = projClimateData)
```

```
  idCols <- c(names(projClimateData)[!grepl("_year",
names(projClimateData))], "year")
  ## set keys for merge
  projClimateDataMolten <- lapply(projClimateDataMolten, function(DT,
cols) {
    setkeyv(DT, cols = cols)
    return(DT)
  }, cols = idCols)

  projClimateData <- Reduce(merge, projClimateDataMolten)

  ## bind the two data.tables
  if (!identical(sort(names(baselineClimateData)),
  sort(names(projClimateData)))) {
    stop("Variable names in `projClimateURLs` differ from those in
    `baselineClimateURLs`")
  }

  ## check
  if (!compareGeom(baselineClimateRas, projClimateRas, res = TRUE,
  stopOnError = FALSE)) {
    stop("`baselineClimateRas` and `projClimateRas` do not have the same
    raster properties")
  }

  ## export to sim
  sim$baselineClimateRas <- baselineClimateRas
  sim$projClimateRas <- projClimateRas
  sim$climateDT <- rbindlist(list(baselineClimateData, projClimateData),
use.names = TRUE)

  return(invisible(sim))
}

## Plotting event function
climatePlot <- function(sim) {
  ## plot climate rasters
  allRasters <- rast(list(sim$baselineClimateRas, sim$projClimateRas))
```

```
  lapply(sim$baselineClimateURLs$vars, function(var, allRasters) {
    lrs <- grep(paste0(var, "_"), names(allRasters))
    file_name <- paste0("climateRas_", var)
    Plots(allRasters[[lrs]],
          fn = plotSpatRasterStk, types = P(sim)$.plots,
          usePlot = FALSE,
          filename = file.path(outputPath(sim), "figures", file_name),
          xlab = "Longitude", ylab = "Latitude")
  }, allRasters = allRasters)

  return(invisible(sim))
}


.inputObjects <- function(sim) {
  #cacheTags <- c(currentModule(sim), "function:.inputObjects") ##
  uncomment this if Cache is being used
  dPath <- asPath(getOption("reproducible.destinationPath",
dataPath(sim)), 1)
  message(currentModule(sim), ": using dataPath '", dPath, "'.")

  # ! ----- EDIT BELOW ----- ! #

  if (!suppliedElsewhere(sim$studyAreaRas)) {
    ## code check: did the user supply a study area?
    stop("Please supply a 'studyAreaRas' SpatRaster")
  }

  if (!is(sim$studyAreaRas, "SpatRaster")) {
    sim$studyAreaRas <- rast(sim$studyAreaRas)
  }

  if (!suppliedElsewhere(sim$baselineClimateURLs)) {
    sim$baselineClimateURLs <- data.table(vars = c("BIO1", "BIO4",
"BIO12", "BIO15"),

                                                                  URL = c(
                                          "https://biogeo.ucdavis.edu/data/worldclim/v2.1/base/wc2.1_2
                                          ,
```

```
                                                    "https://biogeo.ucdavis.edu/data/worldclim/v2.1/base
                                                    ,
                                                    "https://biogeo.ucdavis.edu/data/worldclim/v2.1/base
                                                    ,
                                                    "https://biogeo.ucdavis.edu/data/worldclim/v2.1/base
                                                    ),
                                          targetFile =
                                          c("wc2.1_2.5m_bio_1.tif",
                                          "wc2.1_2.5m_bio_4.tif",
                                          "wc2.1_2.5m_bio_12.tif",
                                          "wc2.1_2.5m_bio_15.tif"),
                                          year = rep(1L, 4))
  }

  if (!suppliedElsewhere(sim$projClimateURLs)) {
    sim$projClimateURLs <- data.table(vars = rep(c("BIO1", "BIO4",
"BIO12", "BIO15"), times = 4),
                                                        URL = rep(c(
                                    "https://geodata.ucdavis.edu/cmip6/2.5m/CanESM5/ssp585/wc2.1_2.5
                                    2040.tif",
                                                    "https://geodata.ucdavis.edu/cmip6/2.5m/CanESM5/ssp5
                                                    2060.tif",
                                                    "https://geodata.ucdavis.edu/cmip6/2.5m/CanESM5/ssp5
                                                    2080.tif",
                                                    "https://geodata.ucdavis.edu/cmip6/2.5m/CanESM5/ssp5
                                                    2100.tif"),
```

```
                                        each = 4),

                                    targetFile = rep(c(
                                "wc2.1_2.5m_bioc_CanESM5_ssp585_2021-
                                2040.tif",

                                                        "wc2.1_2.5m_bioc_CanESM5_ssp585_2041-
                                                        2060.tif",

                                                        "wc2.1_2.5m_bioc_CanESM5_ssp585_2061-
                                                        2080.tif",

                                                        "wc2.1_2.5m_bioc_CanESM5_ssp585_2081-
                                                        2100.tif"),
                                                    each = 4),
                                year = rep(2L:5L, each = 4))
  }

  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}
```

We draw your attention to a few particular aspects of the data modules:

- How we took care to define the data classes of parameters, expected inputs and module outputs in their respective metadata sections;
- How we added additional R packages necessary to run the module to the metadata;
- How we added default values for parameters and inputs explicitly used by the modules (others like `.plotInterval` were left as `NA`). The exception was the `studyAreaRas` input object for which we do not provide a default. However, we added a code check in `.inputObject` that stops interrupts R if this object is not in `sim` (see Protect yourself and others from common mistakes/problems)

- How we use the function `prepInputs` to do most of the heavy-lifting of downloading data and spatial pre-processing. This function is able to recognize whether the data has already been downloaded, and can cache all spatial processing tasks (see Caching). In some cases, we wrapped `prepInputs` in a `Map` call to loop through several URLs and download and pre-process many data layers. This `Map` call can also be cached with `Cache`.
- How we use the function `Plots` to control plotting to the screen device and/or save to image files depending on the `P(sim)$.plots` argument. Note that `Plots` works best with functions that output `ggplot` objects, or that are compatible with `quickPlot::Plot`.
- The fact that neither module depends on the other. This is not a required feature of data modules, but just so happens to be the case in this example. In fact, in more complex modelling frameworks, like the LandR model (Barros et al. n.d.), we often have several data modules that depend on each other (e.g., LandR *Biomass_speciesData*[2] sources and processes tree species percent cover data that is used by LandR *Biomass_borealDataPrep*[3] to estimate several parameters for the forest landscape simulation model LandR *Biomass_core*[4]).
- How we export objects created within the module functions to `sim`. Without doing so, these objects are lost after the function is executed.

2.2.1.3 Prediction module

We show below the `.R` script for the *projectSpeciesDist* module. This module depends entirely on the other two, as we did not provide any default input objects in the `.inputObjects` function. This is, of course, not good practice, but again we warn the user early on (in the `.inputObjects` function) if the module cannot find the necessary inputs.

This module fits a machine learning SDM using the MaxEnt algorithm implemented in the `dismo` package. We recommend having a look at this guide[5] to learn about fitting SDMs with `dismo` and more. Before fitting the SDM, the module converts any non-binary species data into presences and absences.

The main outputs are species distribution projections in the form of plots and a stacked raster layer (`sppDistProj`) and the fitted SDM object.

[2] https://github.com/PredictiveEcology/Biomass_speciesData
[3] https://github.com/PredictiveEcology/Biomass_borealDataPrep
[4] https://github.com/PredictiveEcology/Biomass_core
[5] https://rspatial.org/raster/sdm/index.html

```
## Everything in this file and any files in the R directory are sourced
during `simInit()`;
## all functions and objects are put into the `simList`.
## To use objects, use `sim$xxx` (they are globally available to all
modules).
## Functions can be used inside any function that was sourced in this
module;
## they are namespaced to the module, just like functions in R packages.
## If exact location is required, functions will be:
`sim$.mods$<moduleName>$FunctionName`.
defineModule(sim, list(
  name = "projectSpeciesDist",
  description = "",
  keywords = "",
  authors = structure(list(list(given = c("Ceres"), family = "Barros",
  role = c("aut", "cre"), email = "ceres.barros@ubc.ca", comment =
  NULL)), class = "person"),
  childModules = character(0),
  version = list(projectSpeciesDist = "0.0.0.9000"),
  timeframe = as.POSIXlt(c(NA, NA)),
  timeunit = "year",
  citation = list("citation.bib"),
  documentation = list("README.md", "projectSpeciesDist.Rmd"), ## same
  file
  reqdPkgs = list("PredictiveEcology/SpaDES.core@development
  (>=1.0.10.9000)", "ggplot2",
                  "data.table", "dismo"),
  parameters = bindrows(
    #defineParameter("paramName", "paramClass", value, min, max,
    "parameter description"),
    defineParameter("predVars", "character", c("BIO1", "BIO4", "BIO12",
    "BIO15"), NA, NA,
                    "Predictors used in statistical model."),
    defineParameter("statModel", "character", "MaxEnt", NA, NA,
                    paste("What statitical algorith to use. Currently only
                     'MaxEnt' and 'GLM' are",
                          "supported. 'MaxEnt will fit a MaxEnt model
                          using dismo::maxent; 'GLM'",
```

```
                        "will fit a generalised linear model with a
                        logit link using",
                        "glm(..., family = 'binomial'). In both cases
                        all predictor variables are used,",
                        "and for GLM only additive effects are
                        considered." )),
    defineParameter(".plots", "character", "screen", NA, NA,
                    "Used by Plots function, which can be optionally used
                    here"),
    defineParameter(".plotInitialTime", "numeric", start(sim), NA, NA,
                    "Describes the simulation time at which the first plot
                    event should occur."),
    ## .seed is optional: `list('init' = 123)` will `set.seed(123)` for
    the `init` event only.
    defineParameter(".seed", "list", list(), NA, NA,
                    "Named list of seeds to use for each event (names)."),
    defineParameter(".useCache", "logical", FALSE, NA, NA,
                    "Should caching of events or module be used?")
  ),
  inputObjects = bindrows(
    #expectsInput("objectName", "objectClass", "input object
    description", sourceURL, ...),
    expectsInput("climateDT", "data.table",
                 desc = paste("A data.table with as many columns as the
                 climate covariates",
                              "used in the species distribution model and
                              'year' column describing",
                              "the simulation year to which the data
                              corresponds.")),
    expectsInput("sppAbundanceDT", "data.table",
                 desc = paste("A species abundance data. Converted to
                 presence/absence data, if not binary")),
    expectsInput("studyAreaRas", objectClass = "RasterLayer",
                 desc = "A binary raster of the study area")
  ),
  outputObjects = bindrows(
    #createsOutput("objectName", "objectClass", "output object
    description", ...),
```

```
    createsOutput(objectName = "sppDistProj", objectClass = "SpatRaster",
                  desc = paste("Species distribution projections - raw
                  predictions.",
                               "Each layer corresponds to a prediciton
                               year")),
    createsOutput(objectName = "evalOut", objectClass =
    "ModelEvaluation",
                  desc = paste("`sdmOut` model evaluation statistics.
                  Model evaluated on the 20% of",
                               "the data. See `?dismo::evaluation`.")),
    createsOutput(objectName = "sdmData", objectClass = "data.table",
                  desc = "Input data used to fit `sdmOut`."),
    createsOutput(objectName = "sdmOut", objectClass = c("MaxEnt", "glm"),
                  desc = paste("Fitted species distribution model. Model
                  fitted on 80%",
                               "of `sdmData`, with remaining 20% used for
                               evaluation.")),
    createsOutput(objectName = "thresh", objectClass = "numeric",
                  desc = paste("Threshold of presence that maximises the
                  sum of the sensitivity",
                              "(true positive rate) and specificity (true
                               negative rate).",
                               "See `dismo::threshold(..., stat =
                               'spec_sens')`."))
  )
))

## event types
#   - type `init` is required for initialization

doEvent.projectSpeciesDist = function(sim, eventTime, eventType) {
  switch(
    eventType,
    init = {
      ### check for more detailed object dependencies:
      ### (use `checkObject` or similar)

      # do stuff for this event
```

```
      sim <- SDMInit(sim)

      # schedule future event(s)
      sim <- scheduleEvent(sim, start(sim), "projectSpeciesDist",
"fitSDM")
      sim <- scheduleEvent(sim, start(sim), "projectSpeciesDist",
"evalSDM",
                           eventPriority = .normal() + 1)
      sim <- scheduleEvent(sim, start(sim), "projectSpeciesDist",
"projSDM",
                           eventPriority = .normal() + 2)
      sim <- scheduleEvent(sim, P(sim)$.plotInitialTime,
"projectSpeciesDist", "plotProjSDM",
                           eventPriority = .normal() + 3)

    },
    fitSDM = {
      # ! ----- EDIT BELOW ----- ! #
      sim <- fitSDMEvent(sim)
      # ! ----- STOP EDITING ----- ! #
    },
    evalSDM = {
      # ! ----- EDIT BELOW ----- ! #
      sim <- evalSDMEvent(sim)
      # ! ----- STOP EDITING ----- ! #
    },
    projSDM = {
      # ! ----- EDIT BELOW ----- ! #
      sim <- projSDMEvent(sim)

      sim <- scheduleEvent(sim, time(sim) + 1L, "projectSpeciesDist",
"projSDM")
      # ! ----- STOP EDITING ----- ! #
    },
    plotProjSDM = {
      # ! ----- EDIT BELOW ----- ! #
      plotProjEvent(sim)
```

```
      sim <- scheduleEvent(sim, time(sim) + 1L, "projectSpeciesDist",
"plotProjSDM",
                           eventPriority = .normal() + 1)

      # ! ----- STOP EDITING ----- ! #
    },
    warning(paste("Undefined event type: \'", current(sim)[1,
    "eventType", with = FALSE],
                  "\' in module \'", current(sim)[1, "moduleName", with =
                  FALSE], "\'", sep = ""))
  )
  return(invisible(sim))
}

## event functions
#   - keep event functions short and clean, modularize by calling
subroutines from section below.

### template initialization
SDMInit <- function(sim) {
  # # ! ----- EDIT BELOW ----- ! #
  ## at this point we can only have the following columns
  if (!identical(sort(names(sim$sppAbundanceDT)), sort(c("cell", "x",
  "y", "sppAbund", "year")))) {
    stop(paste("sim$sppAbundanceDT can only have the following columns at
    the start of year 1:\n",
               paste(c("cell", "x", "y", "sppAbund", "year"), collapse =
               ", ")))
  }

  if (length(setdiff(sim$climateDT$cell, sim$sppAbundanceDT$cell)) > 0 ||
      length(setdiff(sim$sppAbundanceDT$cell, sim$climateDT$cell)) > 0) {
    stop("'cell' columns in `climateDT` and `sppAbundanceDT` have
    different values")
  }

  if (!P(sim)$statModel %in% c("MaxEnt", "GLM")) {
    stop("'statModel' parameter must be 'MaxEnt' or 'GLM'")
```

```
  }

  ## a few data cleaning steps to make sure we have presences and
  absences:
  sppAbundanceDT <- copy(sim$sppAbundanceDT)
  if (min(range(sppAbundanceDT$sppAbund)) < 0) {
    sppAbundanceDT[sppAbund < 0, sppAbund := 0]
  }

  if (max(range(sppAbundanceDT$sppAbund)) > 1) {
    message("Species data is > 1. Converting to presence/absence")
    sppAbundanceDT[sppAbund > 0, sppAbund := 1]
  }

  ## join the two datasets - note that there are no input species
  abundances beyond year 1
  sim$sdmData <- merge(sim$climateDT, sppAbundanceDT[, .(cell, sppAbund,
year)],
                       by = c("cell", "year"), all = TRUE)
  setnames(sim$sdmData, "sppAbund", "presAbs")

  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}

fitSDMEvent <- function(sim) {
  # ! ----- EDIT BELOW ----- ! #
  ## break data into training and testing subsets
  dataForFitting <- sim$sdmData[year == time(sim)]

  if (nrow(dataForFitting) == 0) {
    stop(paste("No data for year", time(sim), "provided to fit the
    model"))
  }

  group <- kfold(dataForFitting, 5)
  ## save the the split datasets as internal objects to this module
  mod$trainData <- dataForFitting[group != 1, ]
```

```
  mod$testData <-  dataForFitting[group == 1, ]

  predVars <- P(sim)$predVars
  if (P(sim)$statModel == "MaxEnt") {
    sim$sdmOut <- maxent(x = as.data.frame(mod$trainData[, ..predVars]),
                         p = mod$trainData$presAbs)
  } else {
    ## make an additive model with all predictors - avoid using
    as.formula, which drags the whole environment
    form <- enquote(paste("presAbs ~", paste(predVars, collapse = "+")))
    sim$sdmOut <- glm(formula = eval(expr = parse(text = form)),
                      family = "binomial", data = mod$trainData)
  }
  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}

evalSDMEvent <- function(sim) {
  # ! ----- EDIT BELOW ----- ! #
  ## validate model
  predVars <- P(sim)$predVars
  sim$evalOut <- evaluate(p = mod$testData[presAbs == 1, ..predVars],
                          a = mod$testData[presAbs == 0, ..predVars],
                          model = sim$sdmOut)
  ## save the threshold of presence/absence in an internal object to this
  module
  sim$thresh <- threshold(sim$evalOut, 'spec_sens')

  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}

projSDMEvent <- function(sim) {
  # ! ----- EDIT BELOW ----- ! #
  ## predict across the full data and make a map
  dataForPredicting <- sim$sdmData[year == time(sim)]

  if (nrow(dataForPredicting) == 0) {
```

```
    stop(paste("No data for year", time(sim), "provided to calculate
    predictions"))
  }

  predVars <- P(sim)$predVars
  preds <- predict(sim$sdmOut, as.data.frame(dataForPredicting[,
..predVars]),
                   progress = '')
  sppDistProj <- replace(sim$studyAreaRas,
which(!is.na(sim$studyAreaRas[])), preds)
  names(sppDistProj) <- paste0("year", time(sim))

  if (is.null(sim$sppDistProj)) {
    sim$sppDistProj <- sppDistProj
  } else {
    sim$sppDistProj <- rast(list(sim$sppDistProj, sppDistProj))
  }

  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}

plotProjEvent <- function(sim) {
  # ! ----- EDIT BELOW ----- ! #
  checkPath(file.path(outputPath(sim), "figures"), create = TRUE)

  if (any(!is.na(P(sim)$.plots))) {

    ## response plot
    ## we can't use Plots to plot and save SDM predictions with dismo.
    ## these are only saved to disk
    fileSuffix <- paste0(P(sim)$statModel, ".png")

      notScreen <- setdiff(P(sim)$.plots, "screen")
    if (any(notScreen != "png")) {
      warning(paste(currentModule(sim), "only saves to PNG at the
      moment."))
    }
```

```
    png(file.path(outputPath(sim), "figures", paste0("SDMresponsePlot_",
    fileSuffix)))
    response(sim$sdmOut)
    dev.off()

    ## species projections
    fileSuffix <- paste0(P(sim)$statModel, "_Year", time(sim))
    clearPlot()
    rawValsPlot <- sim$sppDistProj[[paste0("year", time(sim))]]
    Plots(rawValsPlot, fn = plotSpatRaster, types = P(sim)$.plots,
          usePlot = TRUE, filename = file.path(outputPath(sim),
          "figures", paste0("projRawVals_", fileSuffix)),
          plotTitle = paste("Projected raw values -", "year", time(sim)),
          xlab = "Longitude", ylab = "Latitude")
    PAsPlot <- sim$sppDistProj[[paste0("year", time(sim))]] > sim$thresh
    Plots(PAsPlot, fn = plotSpatRaster, types = P(sim)$.plots,
          usePlot = TRUE, filename = file.path(outputPath(sim),
          "figures", paste0("projPA_", fileSuffix)),
          plotTitle = paste("Projected presence/absence -", "year",
          time(sim)),
          xlab = "Longitude", ylab = "Latitude")
  }

  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}

.inputObjects <- function(sim) {
  #cacheTags <- c(currentModule(sim), "function:.inputObjects") ##
  uncomment this if Cache is being used
  dPath <- asPath(getOption("reproducible.destinationPath",
dataPath(sim)), 1)
  message(currentModule(sim), ": using dataPath '", dPath, "'.")

  # ! ----- EDIT BELOW ----- ! #
  ## check that necessary objects are in the simList or WILL BE supplied
  by another module
  if (!suppliedElsewhere("climateDT") |
  !suppliedElsewhere("sppAbundanceDT") ) {
```

```
    stop("Please provide `climateDT` and `sppAbundanceDT`")
  }

  # ! ----- STOP EDITING ----- ! #
  return(invisible(sim))
}
```

We draw your attention to:

- As we said earlier, we could have added yearly projected values to the `sppAbundanceDT` table. In this case we probably would have changed this object's name, since MaxEnt is not modelling species abundance, but probability of occurrence. We suggest this as an exercise to do on your own
- How links with the data modules are established by declaring data modules' output objects as expected inputs for this module.
- How the `fitSDM` event does not schedule itself (the SDM only needs to be fitted once).
- How, unlike `fitSDM`, the `projSDM` event schedules itself so that model projections are executed for each year of the simulation, provided that there is corresponding environmental data – notice how the functions `fitSDMEvent` and `projSDMEvent` both check that there is data for the current year of the simulation (`time(sim)`).
- How the fitted model object (`sdmOut`) and it's evaluation (`evalOut`) are both module outputs. This way these objects can not only be used by other events, but also inspected by the user after the simulation is finished (see Transparent models).

You will notice that this module performs model fitting (i.e., calibration), predictions and model validation. These three components could be broken into three separate modules. As an exercise, we recommend trying to do so on your own.

2.3 Running the model

2.3.1 Ensuring all packages are installed

After the modules are created, we go back to the `Part2_SDMs.R` script to set up and run the simulation. The first line of code ensures that all module dependencies (and their dependencies and so on) are installed in `.libPaths()`. If not it will attempt to install missing packages. Only then do we load `SpaDES` (necessary to run the simulation).

```
## this line can be used to make sure all packages are installed
SpaDES.install::makeSureAllPackagesInstalled(simPaths$modulePath)

## you should restart R again if any packages were installed

## load necessary packages now
library(SpaDES)
library(SpaDES.experiment)
```

/!\ ATTENTION /!

`makeSureAllPackagesInstalled` may fail to install if other packages have been loaded already, so we recommend running this line from a clean R session. We also recommend restarting the R session after `makeSureAllPackagesInstalled` installs packages.

Windows can present problems when many packages are installed and further package installations fail. If you see errors like this after restarting R:

```
   Installing: glue Detaching is fraught with many potential problems; you may have to restart your session
      These will not be unloaded: ellipsis, vctrs Unloading package bit64 --
Installing glue -- (1 of 1. Estimated time left: ...; est. finish: ...calculating) Installing package into
library/4.0' (as 'lib' is unspecified) trying URL '<https://cran.rstudio.com/bin/windows/contrib/4.0/glue

   package 'glue' successfully unpacked and MD5 sums checked Error in unpackPkgZip(foundpkgs[okp, 2L], foun
library\\4.0' for modifying Try removing '\~\R\win-library\\4.0/00LOCK'
```

If you encounter this error, delete the problematic file/folder and try again.

Sometimes `Require` *may still unable to automatically install a package and a manual installation from a clean session is the only solution. In the error above,* `Require` *only detected that* `glue` *was missing during the* `simInit` *call, which meant that other packages had been loaded already causing failure when* `Require` *attempted the installation. This problem persisted even after we avoided loading* `terra` *before running* `simInit` *(we make the study area objects prefixing functions with* `terra::`*), so* `glue` *had to be manually installed.*

2.3.2 Simulation set-up

The simulation folder directories were already set up before creating the modules (see above), but it is still necessary to create a few lists that will be passed to the `simInit` function, which initializes the simulation. These lists define the modules used in the simulation (`simModules`), the start and end of the simulation (`simTimes`), the parameters passed to each module (`simParams`) and external input objects (`simObjects`) like the study area (`studyAreaRas`).

The `studyAreaRas` is created from a random polygon drawn in SW Alberta, Canada, using `SpaDES.tools::randomStudyArea`. (Fig. 2.1).

We also define a few useful global options:

- `reproducible.cachePath` and `reproducible.destinationPath` define the cache directory and the directory where downloaded and processed data will be stored;
- `reproducible.useCache` and `reproducible.useTerra`, which will activate caching and the use of the `terra` package across all `Cache` and `prepInputs` function calls.

```
## a few important options:
options(reproducible.useCache = TRUE,
        reproducible.cachePath = simPaths$cachePath,
        reproducible.destinationPath = simPaths$inputPath, ## all
        downloaded and pre-processed layers go here
        reproducible.useTerra = TRUE)  ## we want to use the terra R
        package
```

```
## list the modules to use
simModules <- list("speciesAbundanceData", "climateData",
"projectSpeciesDist")

## Set simulation and module parameters
simTimes <- list(start = 1, end = 5, timeunit = "year")

## we create two lists of parameters, one using the default MaxEnt
## the other a GLM
simParamsMaxEnt <- list(
  "speciesAbundanceData" = list(
    ".plots" = c("screen", "png"),
    # ".useCache" = c(".inputObjects", "init")
    ".useCache" = FALSE
  ),
  "climateData" = list(
    ".plots" = c("screen", "png"),
    # ".useCache" = c(".inputObjects", "init")
    ".useCache" = FALSE
  ),
  "projectSpeciesDist" = list(
    "statModel" = "MaxEnt",
    ".plots" = c("screen", "png"),
    # ".useCache" = c(".inputObjects", "init")
    ".useCache" = FALSE
  )
)

simParamsGLM <- simParamsMaxEnt
simParamsGLM$projectSpeciesDist$statModel <- "GLM"

## make a random study area.
##  Here use seed to make sure the same study area is always generated
studyArea <- terra::vect(SpaDES.tools::randomStudyArea(size = 1e10, seed
= 123))
studyAreaRas <- terra::rasterize(studyArea,
                                 terra::rast(extent = terra::ext(studyArea),
                                             crs = terra::crs(studyArea,
                                             proj = TRUE),
```

```
                                          resolution = 1000))
simObjects <- list(
  "studyAreaRas" = studyAreaRas
)

## Simulation setup - create two simulations, one for MaxEnt another for
GLM
## SpaDES.experiment::experiment2, will take care of subdirectories to
store outputs
mySimMaxEnt <- simInit(times = simTimes, params = simParamsMaxEnt,
                       modules = simModules, objects = simObjects,
                       paths = simPaths)
mySimGLM <- simInit(times = simTimes, params = simParamsGLM,
                    modules = simModules, objects = simObjects,
                    paths = simPaths)
```

```
## Warning in raster::getData("GADM", country = "CAN", level = 1, path = simPaths$inputPath): getData will
## . Please use the geodata package instead
```

Before running the simulation we look at the module linkage diagrams produced by `moduleDiagram` (Fig. 2.2) and `objectDiagram` (Fig. 2.3) to assess whether modules are linked as expected.

```
moduleDiagram(mySimMaxEnt)
objectDiagram(mySimMaxEnt)
```

2.3.3 Simulation runs

To run the simulation, we can call `spades` on the output `simLists` (called `mySimMaxEnt` and `mySimMaxGLM` here) generated by `simInit`, or use `experiment2` from the `SpaDES.experiment` package. `experiment2` will run as many simulations as `simLists` and organise outputs into sub-folders within the `simPaths$outputs` directory. It can also repeat simulations (`rep` argument) and parallelise across replicates using `future`. See `?experiment2` for examples.

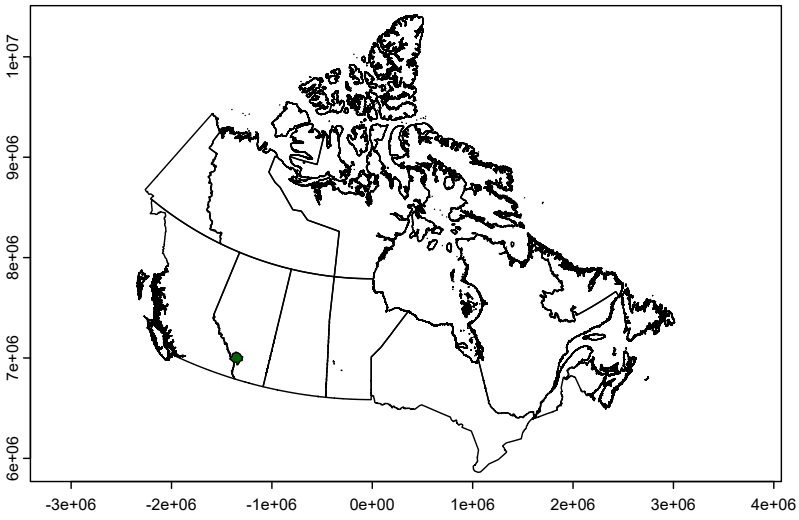


FIGURE 2.1: Study area within Canada.

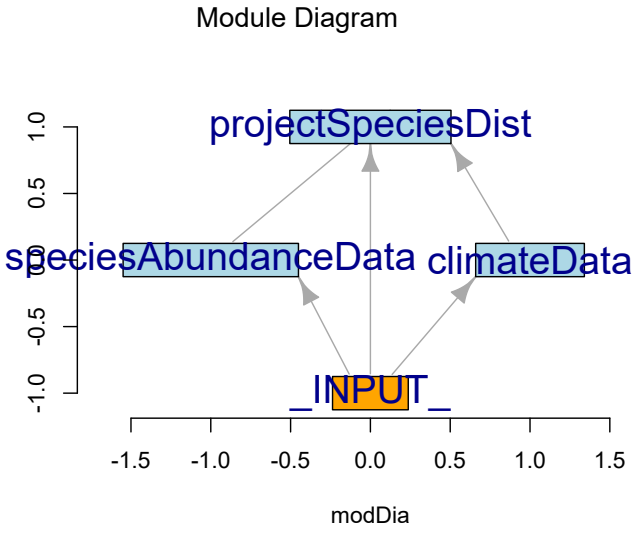


FIGURE 2.2: Module network diagram.

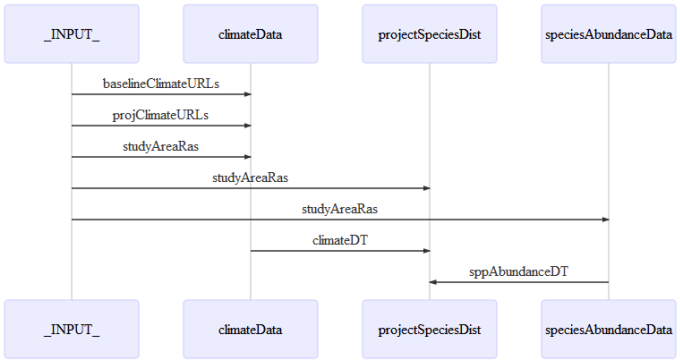


FIGURE 2.3: Module diagram showing module inter-dependencies with object names.

We advise using `spades` when running the model for the first time. Passing the argument `debug = TRUE` will print the progress of the simulation in detail. This helps diagnosing problems when the simulation fails, but also seeing which events are being executed and when particular cache calls are activated.

```
## run simulation
clearPlot(force = TRUE)   ## this forces wiping the graphics device and
opening a new window

## This runs one simulation and stores outputs in the main 'outputs'
folder
## - not what we want, but good for testing
# mySimOut <- spades(mySimMaxEnt, debug = TRUE)

## Better to use when spades runs error-free on the simLists
myExperiment <- experiment2(MaxEnt = mySimMaxEnt,
                            GLM = mySimGLM,
                            debug = TRUE,
                            replicates = 1,
```

```
                          clearSimEnv = FALSE)   ## prevent removing
                          objects from the simLists at the end
## save outputs
qs::qsave(myExperiment, file.path(simPaths$outputPath,
paste0("myExperiment", ".qs")))
```

Try to execute the `spades` call twice to see how much faster it runs after many of the operations have been cached. Notice also, how the `init` events are retrieved from the cache thanks to the `.useCache` parameters passed to the modules (see also Caching).

By default the data modules (*speciesAbundanceData* and *climateData*) save figures of the input species and climate layers (Figs. 2.4 and 2.5, respectively).

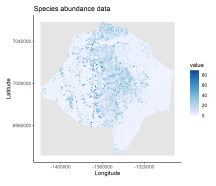


FIGURE 2.4: Prediction plots. Input *Picea glauca* percent cover across the landscape. Note that values are converted to presence/absence.

The prediction module also outputs the projections for each climate period automatically (Figs. 2.6 and 2.7).

The projected layers can also be accessed and plotted via the `simList` object, as can the model validation results.

From the results we can see that the MaxEnt and GLM predictions do not seem to agree, indicating a potential problem. We may be missing important covariates, interactions, or simply more appropriate algorithms.

Peruse each model's estimated coefficients and residuals, and validation results will be a good first step to diagnosing the problem.

```
myExperiment$MaxEnt_rep1$sdmOut   ## this links to an html page

sets <- par(mfrow = c(2,2))
```

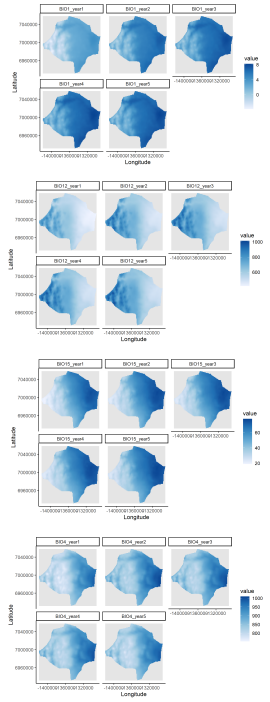


FIGURE 2.5: Prediction plots. Bioclimatic variables under baseline (year 1) and future conditions.

```
plot(myExperiment$GLM_rep1$sdmOut)
par(sets)

## check validation results for the two models
myExperiment$MaxEnt_rep1$evalOut
myExperiment$GLM_rep1$evalOut
```

2.3.3.1 Adding a new climate scenario

Because data were linked to the modules (and the forecasting) via the modules' metadata and inputs, adding a new climate scenario and re-running forecasts is easy.

To do so, we need only to change the URLs for the climate layers, by passing a custom `projClimateURLs data.table` to the *climateData* module. `SpaDES`

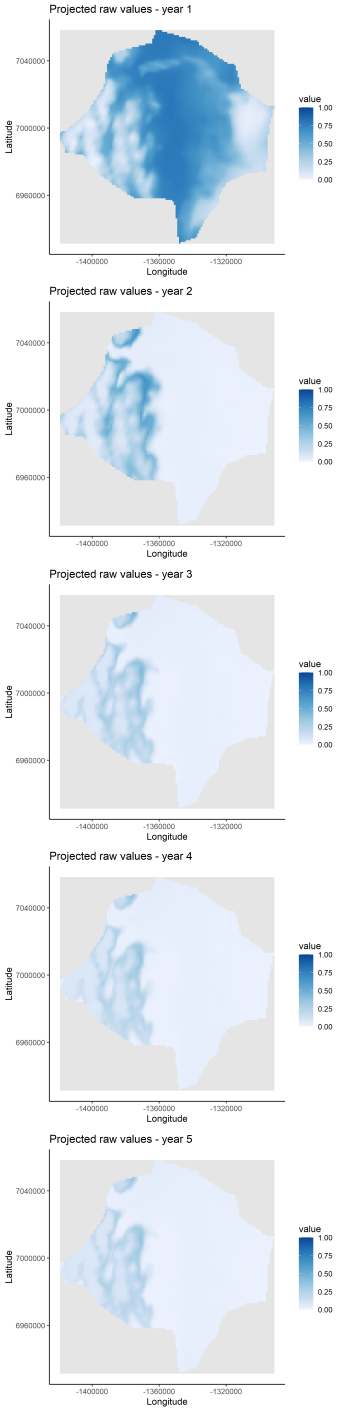


FIGURE 2.6: Prediction plots: Raw predicted values of species probability of occurence under (left to right) baseline climate conditions (first year of simulation), 2021-2040, 2041-2060, 2061-2080 and 2081-2100 climate conditions (second to fifth years of simulation) - using MaxEnt.

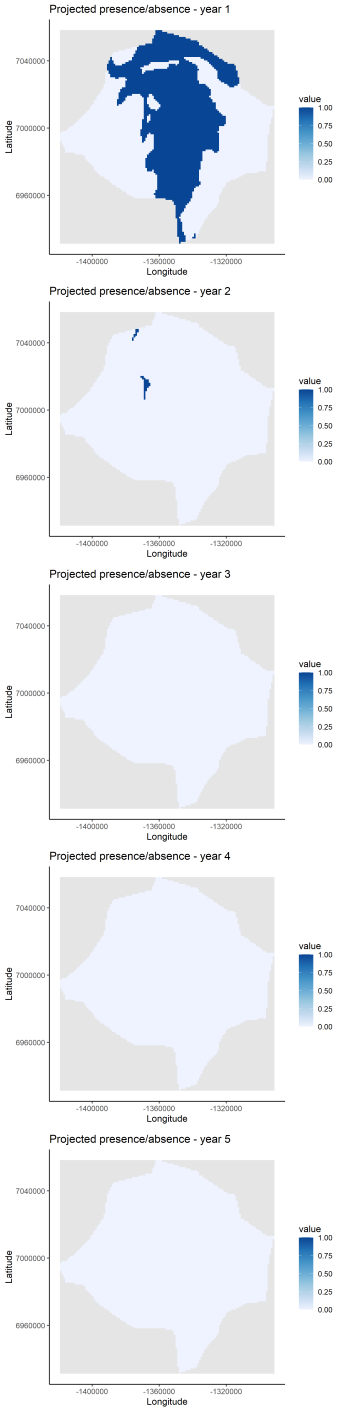


FIGURE 2.7: Prediction plots: Predictions of *Picea glauca* presence/absence under (left to right) baseline climate conditions (first year of simulation), 2021-2040, 2041-2060, 2061-2080 and 2081-2100 climate conditions (second to fifth years of simulation) - using MaxEnt.

will take care of downloading and processing the new layers, as well as forecasting. Model fitting will also be repeated, even if the baseline data did not change, because the `kfold` function we use to partition the data into the training and testing subsets randomly assigns cases to each group. If this was not desired, we could set a random seed before running the fitting event (`fitSDM`) by passing the `.seed` parameter to the *projectSpeciesDist* module (e.g., `.seed = list("fitSDM" = 123)`).

```
## Run with another climate scenario - the most contrasting scenario to
SSP 585
## get the original table from one of the simulations and replace the
climate scenario
projClimateURLs <- myExperiment$MaxEnt_rep1$projClimateURLs
projClimateURLs[, `:=`(URL = sub("ssp585", "ssp126", URL),
                       targetFile = sub("ssp585", "ssp126", targetFile))]

## this time we pass the new table or URLs to the modules, so that
climate layers are changed
simObjects2 <- list(
  "studyAreaRas" = studyAreaRas,
  "projClimateURLs" = projClimateURLs
)

mySimMaxEnt2 <- simInit(times = simTimes, params = simParamsMaxEnt,
                        modules = simModules, objects = simObjects2,
                        paths = simPaths)
mySimGLM2 <- simInit(times = simTimes, params = simParamsGLM,
                     modules = simModules, objects = simObjects2,
                     paths = simPaths)

myExperiment2 <- experiment2(MaxEnt = mySimMaxEnt2,
                             GLM = mySimGLM2,
                             debug = TRUE,
                             replicates = 1,
                             clearSimEnv = FALSE)
## save outputs
qs::qsave(myExperiment2, file.path(simPaths$outputPath,
paste0("myExperiment2", ".qs")))
```

2.3.3.2 Proposed exercises

1. try changing the climate layers (e.g., use different climate scenarios or General Circulation models) and rerunning predictions;
2. try adding other statistical algorithms;
3. try breaking up the prediction module into three modules: a calibration module, a prediction module and a validation module.

Have fun!

2.3.3.3 Making use of `simList` for reporting

Another advantage of having all simulation parameters, inputs and outputs centralised in one object, is that we can easily inspect and manipulated them afterwards, without the need to load separate objects back into R.

Here we show how we capitalize on this SpaDES feature to create figures of the outputs (Fig. 2.8.

```
## MaxEnt predictions across time and for each climate scenario
--------------
## combine plots from two distinct simulations in a single figure
## (the same can be done to compare MaxEnt and GLM, or plot all
projections)

## fetch the internal plotting function instead of repeating code here
plotFun <-
myExperiment$GLM_rep1@.envir$.mods$climateData$plotSpatRasterStk

## raw predictions exported by the module
sppDistProjMaxEnt <- myExperiment$MaxEnt_rep1$sppDistProj
sppDistProjMaxEnt2 <- myExperiment2$MaxEnt_rep1$sppDistProj

## we convert the raw predictions into presence absence
## using exported threshold
sppDistProjMaxEnt_PA <- myExperiment$MaxEnt_rep1$sppDistProj >
myExperiment$MaxEnt_rep1$thresh
sppDistProjMaxEnt2_PA <- myExperiment2$MaxEnt_rep1$sppDistProj >
myExperiment2$MaxEnt_rep1$thresh
```

```
## rename layers from plotting
names(sppDistProjMaxEnt) <- names(sppDistProjMaxEnt2) <- c("2001",
"2021-2040", "2041-2060", "2061-2080", "2081-2100")
names(sppDistProjMaxEnt_PA) <- names(sppDistProjMaxEnt2_PA) <- c("2001",
"2021-2040", "2041-2060", "2061-2080", "2081-2100")

## for a simpler plot choose only years 2001, 2041-2060 and 2081-2100
yrs <- c("2001", "2041-2060", "2081-2100")
plotMaxEnt <- plotFun(sppDistProjMaxEnt[[yrs]],
                      xlab = "Longitude", y = "Latitude",
                      plotTitle = "MaxEnt raw predictions - SSP 585") +
  scale_fill_viridis_c(na.value = "grey90", limits = c(0,1), begin = 0.25)
plotMaxEnt2 <- plotFun(sppDistProjMaxEnt2[[yrs]],
                       xlab = "Longitude", y = "Latitude",
                       plotTitle = "MaxEnt raw predictions - SSP 126") +
  scale_fill_viridis_c(na.value = "grey90", limits = c(0,1), begin = 0.25)
plotMaxEnt_PA <- plotFun(sppDistProjMaxEnt_PA[[yrs]],
                         xlab = "Longitude", y = "Latitude",
                         plotTitle = "MaxEnt presence/absence - SSP 585") +
  scale_fill_viridis_c(na.value = "grey90", limits = c(0,1), begin = 0.25)
plotMaxEnt2_PA <- plotFun(sppDistProjMaxEnt2_PA[[yrs]],
                          xlab = "Longitude", y = "Latitude",
                          plotTitle = "MaxEnt presence/absence - SSP 126") +
  scale_fill_viridis_c(na.value = "grey90", limits = c(0,1), begin = 0.25)

## organise the plots with mildest scenario first
## It is clear that MaxEnt and GLM do not agree in their prediction
plotAll <- ggarrange(plotMaxEnt2 + labs(title = expression(bold("Scenario
- SSP 126")),
                                        y = expression(atop(bold("Raw
                                        predictions"), "Latitude"))) +
                       theme(legend.title = element_blank(),
                       legend.key.height = unit(3, "lines"),
                             plot.title = element_text(hjust = 0.5),
                             plot.margin = margin(0,0,0,0)),
                     plotMaxEnt + labs(title = expression(bold("Scenario -
SSP 585")),
```

```
                                  y = expression(atop(bold(""), ""))) +
    theme(plot.title = element_text(hjust = 0.5),
    plot.margin = margin(0,0,0,0)),
plotMaxEnt2_PA + labs(title = expression(bold("")),
                                   y = expression(atop(bold(
                                   "Presence/absence"),
                                   "Latitude"))) +
    theme(plot.margin = margin(0,0,0,0)),
plotMaxEnt_PA + labs(title = expression(bold("")),
                                  y = expression(atop(bold(""),
                                  ""))) +
    theme(plot.margin = margin(0,0,0,0)),
legend = "right", common.legend = TRUE, labels =
c("a)", "b)", "c)", "d)"))

## save figure:
figDir <- checkPath(file.path(simPaths$outputPath, "generalFigures"),
create = TRUE)
ggsave(file.path(figDir, "MaxEntPredictions.tiff"), width = 13.5, height
= 5.5, units = "in", dpi = 300)
```

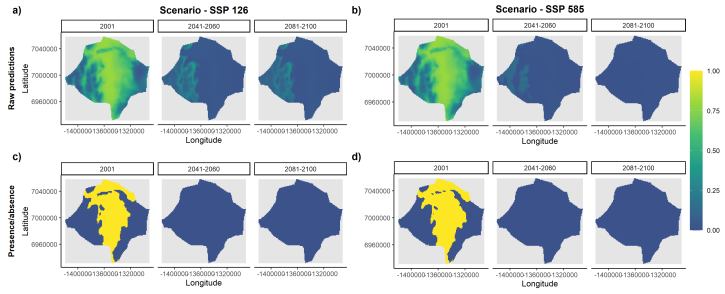


FIGURE 2.8: Adding a new scenario: Predictions of *Picea glauca* probabilities of presences and presence/absence under (left to right) baseline climate conditions, 2041-2060, and 2081-2100 climate projections under two emission scenarios (SSP 136 and SSP 585, the default) – showing MaxEnt forecasts only.

2.4 Caching

In this example, we relied on caching to avoid having to repeat computationally intensive operations. Running the `simInit` and `spades` calls a second time (even after restarting R session) was faster and `SpaDES` informed us of instances where cached objects were being retrieved:

(...) Mar05 19:56:53 clmtDt 1 climateData init 1
Mar05 19:56:53 clmtDt ...(Object to retrieve (a7816e2d0deb3b29.rds)) Mar05 19:56:53 clmtDt loaded cached result from previous Map call (...)

Caching in `SpaDES` is managed by the `reproducible` package, and can be generally broken down into two types: explicitly coded by the module developer, or internal to `SpaDES` functions.

2.4.1 Explicitly caching operations

Throughout the data modules we explicitly cached several data preparation operations using the functions `Cache` and `prepInputs` from the `reproducible` package.

In brief, `Cache` searches for a stored (i.e. cached) output of a given function call; if it does not find it, `Cache` executes the function call, saves its output and saves information about the function inputs and the function's code. If it does find it, `Cache` compares the present inputs and function code against their cached counterparts. In case of a mismatch, the function call is executed again and re-cached.

`prepInputs` calls `Cache` internally at several points, notably to cache spatial processing tasks (e.g. projecting and cropping spatial layers to a study area raster). Another great feature of `prepInputs` is that when it has a source URL for the target file (as when we used `prepInputs` to download species % cover and climate layers), it first checks whether the data have already been downloaded (and potentially extracted from an archive folder – `.zip` file). This is not the same thing as caching, but also avoids unnecessary downloads that can be time consuming.

Note that caching operations involving stochasticity should be avoided, as it will prevent new random outputs from being generated.

We recommend exploring the examples available in the `Cache` and `prepInputs`

R documentation to learn more about their capabilities. In particular, read about `showCache`, `clearCache` and the argument `userTags`, which allow consulting and deleting cached files.

/!\ ATTENTION /!

`Cache` does not deal well with the `apply` family of functions, which is why we used `Map` (instead of `mapply`) to iteratively apply `prepInputs` to several climate layer URLs.

2.4.2 Implicit caching of events

`SpaDES` offers implicit caching of events via the global parameter `.useCache`, which comes in the template modules generated by `newModule`. We call this "implicit" caching, because the developer does not need to add any caching mechanisms to the module code. `SpaDES` automatically reads the value of the `.useCache` parameter and activates caching in the module accordingly.

This parameter can be used to cache (or not) all or some module events (in their entirety). In our example, we cached data preparation events across all modules (the `.inputObjects` and `init` events in this example), but not the events that fitted the SDM and generated projections. In truth, because none of the modules simulate any stochastic processes, we could have cached all events. Loading cached events produced a slightly different message from loading of other cached operations (see above):

```
Mar05 19:58:34 spcsbn 1 speciesAbundanceData init 1\
Mar05 19:58:34 spcsbn ...(Object to retrieve (bffbc48cc055c846.rds)) Mar05 19:58:35 spcsbn loaded cached c
```

2.4.3 Controlling caching without changing module code

In addition to the , which controls caching at the module level.

The user can turn caching on/off without caching module code via three different mechanisms:

- via the `.useCache` parameter – as explained above (Implicit caching of events), setting this parameter controls event caching inside a module;
- via `options("reproducible.useCache")` – setting this option to `TRUE` or `FALSE` in the global environment (`.GlobalEnv`) will affect *all* caching (inside and outside `SpaDES` modules and the simulation);

- via the argument `spades(.useCache = ...)` – this argument behaves in the same way as the `.useCache` module parameter, but supersedes it across *all* modules (i.e. if `spades(..., .useCache = FALSE)`, caching will be turned off even if a module's `.useCache` is `TRUE`).

2.5 Best practices

2.5.1 Reproducible package installation

When sharing code, it is good practice to provide other users with a list of necessary packages (e.g. by listing the sequence of `library` calls at the start of a script). We go a step further and advise users to provide code that automatically installs all necessary packages at the start of their controller script. In addition all modules should contain a full list of packages that they depend on, and any particular versions necessary. If `options("spades.useRequire")` is set to `TRUE` (the default), `SpaDES` will automatically attempt to install any packages listed across all modules if they are not installed in `.libPaths()`, or if the installed version (or branch if installing from GitHub) does not correspond to what is listed in the module `.R` script. Users can also use `Require::pkgSnapshot()` to save a list of installed packages that can be used later by `Require` to install all necessary packages in another machine (see example below).

Please beware that package installation should be done as much as possible from a clean R session especially in the context of a `SpaDES`-based project, where each module can potentially have many different dependencies, which have dependencies of their own (see, for instance, how we delayed package loading until after all modules were in place and had their dependencies checked in `Part2_SDMs.R`)

```
Require::pkgSnapshot("pkgsnapshot.txt")

## on another machine:
Require::Require(packageVersionFile = "pkgsnapshot.txt")
```

```
## See ?Require::pkgSnapshot() for more examples.
```

2.5.2 Protect yourself and others from common mistakes/problems

A developer should put in place code checks, warnings and messages that protect and warn the user against common mistakes or issues. Some of these fall in the category of *code assertions* – small tests that verify a snippet of code. More complex tests that assess whether the module (or a group of modules) is producing expected results for, e.g., an ecological point of view fall in the category of *integration tests*. Here, we only talk about code assertions.

A common assertion is to verify that input format and class conform to what the function expects. If this is not the case, the developer may add a mechanism to correct the faulty inputs (potentially with a warning or message telling the user it did so) or simply stop the computations with a meaningful error. We provide two examples in the `climateData` module, where the `climateInit` function checks whether the bioclimatic variable names are consistent between the baseline and projected climate data, and whether their raster layers match.

Other assertions can prevent undesirable function behaviours, such as the `if` statement protecting the `newModule` call in `Part2_SDMs.R`, or warn the user that something is missing early on, such as the check for `studyAreaRas` existence in the `.inputObjects` of the data modules).

Bear in mind that these are just examples assertions and integration tests are as diverse as the code they test.

2.5.3 Readable code

There are several guides on how to write reader-friendly code. Even if the developer is forever the sole reader of their own code, there are benefits to writing readable code. First, working on it is less tiresome. Second, we quickly forget why we wrote code in a certain away. Code that is well documented and readable is easier to "come back to" and adapt.

We follow many of the recommendations by Hadley Wickham[6], and highlight below those that we find particularly important:

- spacing around operators;
- spacing before left parenthesis, except in a function call;
- adding curly braces after `if`, `else`, `for` and `function`, unless they are very short statements;
- thoroughly commenting the code;
- naming functions meaningfully and avoiding to re-use function names (e.g. avoid `c <- function (...) {}`, as `c` is already a `base` function).

You can automatically cleanup and format your code using the `styler` package. This package provides an Rstudio addin to easily style a block of selected code, or an entire file.

2.5.4 Module documentation – module `.Rmd`

When modules are created using `newModule`, this function provides a template module `.Rmd` file that is meant to document the module. The template suggests a few key sections that should be part of any module's documentation. Notably, an overview of the module and of its inputs, parameters, outputs and general event flow, together with more in-depth descriptions of each of these sections.

The documentation may also contain reproducible examples of how a module can be used, although this is not always relevant. For instance, data modules are often meaningless without downstream modules that use their outputs.

We invite the reader to see the manual of our forest landscape simulation model LandR *Biomass_core*[7], as an example of how we document some of our `SpaDES` modules.

[6] http://adv-r.had.co.nz/Style.html
[7] https://htmlpreview.github.io/?https://github.com/PredictiveEcology/Biomass_core/blob/development/Biomass_core.html

2.5.5 Coding for the future

We often make coding decisions that we regret a few months down the line. This is why as module developers, it is a good idea to think about other possible applications of a module or potential expansion avenues. For instance, trying to imagine if the module can be scaled up or transferred to different study areas, may influence the format of expected inputs and of outputs. In our example, we exported the same type of information (species % cover and climate data) as raster layers and as tables, because we could foresee that the tables could be used to store several projections in a more compact format.

2.5.6 Transparent models

Model transparency is not only about using open source code and making it available. Providing easy access to model data, parameters and outputs is also important. For instance, in our example we deliberately exported the fitted statistical model `sdmOut`, data (`sdmData`) and evaluation statistics (`evalOut`) so that they can be more easily inspected by the user, without needing to "dive in" the code.

`SpaDES` also offers the ability to save any objects that are exported to the `simList` object *without having to change module code*. To do so, the user passes a `data.frame` of object names and (potentially) the simulation times when they should be saved to the `simInit(outputs = ...)` argument. Because objects are saved as `.rds` files by default, any object class can be saved to disk (see `?outputs` for more information).

2.5.7 Additional notes

`SpaDES` is an extremely powerful family of R packages, whose potential goes well beyond what has been discussed here. We recommend going to the `SpaDES` webpage[8] to find out more about the `SpaDES` R modelling platform, upcoming workshops and publications. See also the Predictive Ecology Github repository[9] for a list of all available `SpaDES` modules and `SpaDES`-related packages that we maintain.

[8] http://predictiveecology.org/
[9] http://https://github.com/PredictiveEcology/

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Happy SpaDESing!

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