# Perturbations

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## Testing simulation with perturbations

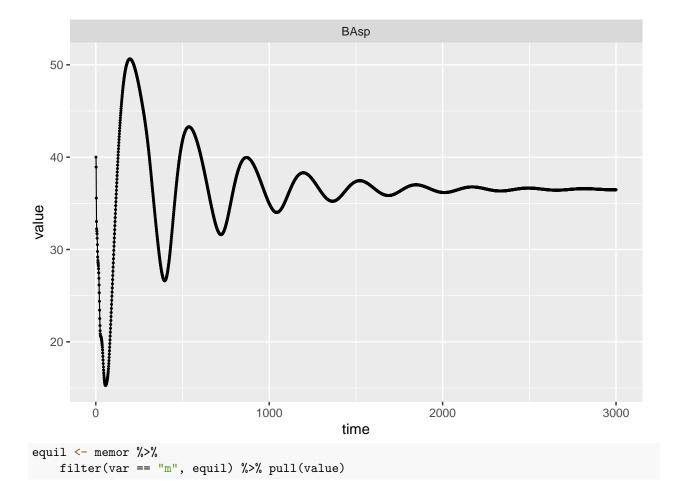
This document show how to simulate a species with perturbation occurring in time. For now, the package is in experimental state and use the branch *tempest*. For this example we will use the species *Picea abies* as an example.

Only the Julien disturbance model is explained in this case.

```
# Libraries
library(ggplot2)
library(dplyr)
##
## Attachement du package : 'dplyr'
## Les objets suivants sont masqués depuis 'package:stats':
##
##
       filter, lag
## L'objet suivant est masqué depuis 'package:testthat':
##
##
       matches
## Les objets suivants sont masqués depuis 'package:base':
##
##
       intersect, setdiff, setequal, union
library(devtools)
# Loading all functions of the package
devtools::load_all()
## i Loading treeforce
species <- "Picea_abies"</pre>
data(list = paste0("fit_", species))
climate <- subset(climate_species, sp == species & N == 2, select = -c(N, sp))</pre>
climate <- drop(as.matrix(climate))</pre>
ipm_Picea <- make_IPM(</pre>
    "Picea_abies", climate, "opt_Picea_clim", fit = fit_Picea_abies,
    mesh = c(m = 700, L = 90, U = get_maxdbh(fit_Picea_abies) * 1.1),
    BA = 0:100, verbose = TRUE
)
## Launching integration loop
## GL integration occur on 32 cells
```

```
## midbin integration occur on 25 cells
## Integration =>----- 3% | ETA: 1mIntegration =>-----
## Time difference of 1.2 mins
Picea_abies <- species(IPM = ipm_Picea, init_pop = def_initBA(40),</pre>
                      harvest_fun = def_harv)
We want to start our simulations with an equilibrium size distribution so we compute here first
forest_ipm <- new_forest(species = list(Picea = Picea_abies))</pre>
time <- 3000
set.seed(42)
memor <- sim_deter_forest.forest(forest_ipm, tlim = time,</pre>
                                     equil_dist = 250, equil_time = time,
                                     verbose = TRUE, correction = "cut") %>%
   tree_format()
## apply a IPM cut correction
## Starting while loop. Maximum t = 3000
## time 500 | BA diff : 21.00
## time 1000 | BA diff : 7.35
## time 1500 | BA diff : 2.35
## time 2000 | BA diff : 0.83
## time 2500 | BA diff : 0.32
## time 3000 | BA diff : 0.12
## Simulation ended after time 3000
## BA stabilized at 36.47 with diff of 0.12 at time 3000
## Time difference of 13.1 secs
memor %>%
   filter(var %in% c("BAsp"), ! equil, value != 0) %>%
   ggplot(aes(x = time, y = value)) +
   facet_wrap(~ var, scales = "free_y") +
   geom_line(size = .4) + geom_point(size = .4) +
```

NULL



# Disturbance

#### Definition of disturbance

We define a disturbance by few parameters used later in the formula.

- I its intensity
- type the class of disturbance. This is often a label in "storm", "fire" and "biotic". This is not used in the formula but to filter species parameters fitted.

We can set all of this in a data frame object. We had a last column named **IsSurv**. It's used to tell the simulation if the survival part of the IPM is needed during a disturbance. In this case, the data do not allow differentiation between disturbance mortality and background mortality. Therefore, we need to deactivate baseline mortality so that it is not double counted.

```
ex_disturb <- data.frame(type = "storm", intensity = 0.5, IsSurv = FALSE)</pre>
```

#### Impact on population

The disturbance impact on the population result from parameters computed by Julien. They compose a function that takes the size distribution, quadratic diameter of the species, intensity (I) and duration (t) of the disturbance. A set of parameters was made for each type of disturbance and species.

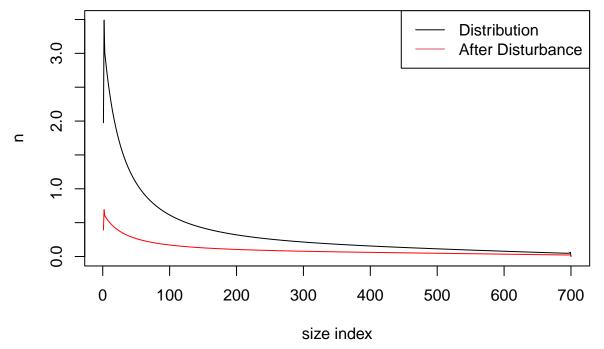
```
dqm = \sqrt{\frac{\sum_{i=1}^{m} size_{i}^{2} \times value_{i}}{\sum_{i=1}^{m} value_{i}}} logratio = log(\frac{size}{dqm}) dbh.scaled = dbh.intercept + size \times dbh.slopelogratio.scaled = logratio.intercept + size \times dbh.slopelogratio.scaled = logratio.scaled = lograti
```

The parameters are estimated with Bayesian computations. The mean of all estimations are stored inside the package for each combination of species and disturbance type.

```
(coefs <- filter(treeforce::disturb_coef, species == "Picea_abies"))</pre>
##
     disturbance
                      species
                                      a0
                                                 a1
## 1
          biotic Picea_abies -5.645296  0.0000000  5.831757 -0.079284149
## 2
           storm Picea_abies -4.568872 -0.1489534 5.359453 0.003335358
                      dbh.slope logratio.intercept logratio.slope
     dbh.intercept
## 1
        -0.7868063 0.007928421
                                          0.4682191
                                                           2.923733
## 2
        -0.7197517 0.007261211
                                          0.1725871
                                                           2.722508
Picea_abies$disturb_coef <- coefs</pre>
```

Linked with this set of parameters, we need to provide a disturbance function to the species we want to simulate. The species is initiated with an empty function that will throw warnings.

```
#' Disturbance function
#'
#' @param x population state distribution at time t
#' @param species The species class object of interest to get mesh and RDIcoef
#' values from. RDIcoef is a one line dataframe with RDI coefficient for one
#' species.
#' @param disturb Disturbance parameters. Highly depend on the disturbance
#' impact parameters given to the species.
#' @param ... Not used in this case.
#' \describe{
#' \item{qmd}{Forest Quadratic Mean Diameter}
#' }
#'
disturb_fun <- function(x, species, disturb = NULL, ...){</pre>
    dots <- list(...)</pre>
    qmd <- dots$qmd
    size <- species$IPM$mesh</pre>
    coef <- species$disturb_coef</pre>
    if(any(disturb$type %in% coef$disturbance)){
        coef <- subset(coef, disturbance == disturb$type)</pre>
    } else {
        stop(sprintf("The species %s miss this disturbance type (%s) parameters",
                      sp_name(species), disturb$type))
    }
    logratio <- log(size / qmd)</pre>
    dbh.scaled = coef$dbh.intercept + size * coef$dbh.slope
    logratio.scaled = coef$logratio.intercept + logratio * coef$logratio.slope
    Pkill <- plogis(coef$a0 + coef$a1 * logratio.scaled +
                         coef$b * disturb$intensity ^(coef$c * dbh.scaled))
    return(x* Pkill) # always return the mortality distribution
}
```



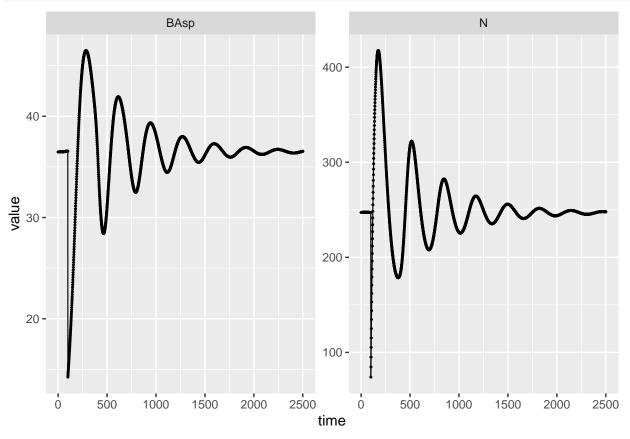
#### **Simulations**

Running a simulation takes the same parameters as usual, with an added data.frame with disturbance along time. We need to think about a clean way to build this table...

## apply a IPM cut correction

```
## Starting while loop. Maximum t = 2500
## time 100 | Disturbance : storm I = 0.20
## time 500 | BA diff : 18.08
## time 1000 | BA diff : 6.86
## time 1500 | BA diff : 2.54
## time 2000 | BA diff : 0.96
## time 2500 | BA diff : 0.36
## Simulation ended after time 2500
## BA stabilized at 36.54 with diff of 0.36 at time 2500
## Time difference of 10.8 secs
```

```
memor %>%
  filter(var %in% c("BAsp", "N"), ! equil, value != 0) %>%
  ggplot(aes(x = time, y = value)) +
  facet_wrap(~ var, scales = "free_y") +
  geom_line(size = .4) + geom_point(size = .4) +
  NULL
```



## Multispecific simulations

What happens when we add other species?

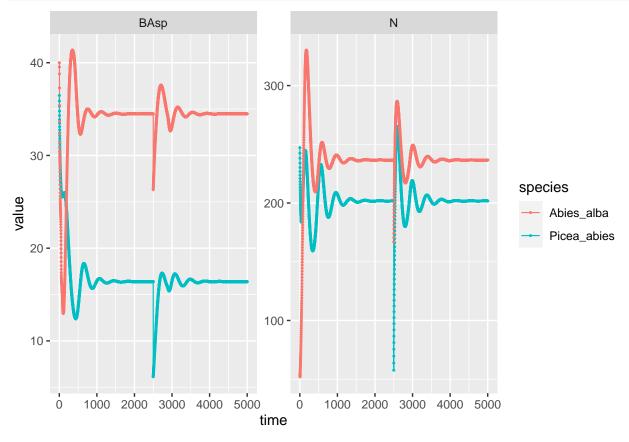
```
species <- "Abies_alba"
data(list = paste0("fit_", species))</pre>
```

```
ipm_Abies <- make_IPM(</pre>
    species, climate, "opt_Picea_clim", fit = fit_Abies_alba,
   mesh = c(m = 700, L = 90, U = get_maxdbh(fit_Picea_abies) * 1.1),
   BA = 0:100, verbose = TRUE
)
## Launching integration loop
## GL integration occur on 32 cells
## midbin integration occur on 25 cells
## Integration =>----- 5% | ETA: 40sIntegration ==>-----
## Time difference of 55.4 secs
Abies_alba <- species(
   IPM = ipm_Abies, init_pop = def_initBA(40),
   harvest_fun = def_harv, disturb_fun = disturb_fun,
   disturb_coef = filter(treeforce::disturb_coef, species == "Abies_alba")
)
time \leftarrow 5000
(disturb <- data.frame(type = "storm", intensity = 0.2,</pre>
                       IsSurv = FALSE, t = 2500)
##
      type intensity IsSurv
                 0.2 FALSE 2500
forest_nsp <- new_forest(species = list(Picea = Picea_abies, Abies = Abies_alba))</pre>
set.seed(42)
memor_nsp <- sim_deter_forest.forest(forest_nsp, tlim = time,</pre>
                                 equil_dist = 250, equil_time = time,
                                 disturbance = disturb,
                                 verbose = TRUE, correction = "cut") %>%
   tree_format()
## apply a IPM cut correction
## Starting while loop. Maximum t = 5000
## time 500 | BA diff : 9.43
## time 1000 | BA diff : 2.16
## time 1500 | BA diff : 0.42
## time 2000 | BA diff : 0.07
## time 2500 | Disturbance : storm I = 0.20
## time 2500 | BA diff : 18.45
## time 3000 | BA diff : 6.19
## time 3500 | BA diff : 1.02
## time 4000 | BA diff : 0.26
## time 4500 | BA diff : 0.05
## time 5000 | BA diff : 0.01
## Simulation ended after time 5000
```

## BA stabilized at 50.88 with diff of 0.01 at time 5000

## Time difference of 40.2 secs

```
memor_nsp %%
filter(var %in% c("BAsp", "N"), ! equil) %>%
ggplot(aes(x = time, y = value, color = species)) +
facet_wrap(~ var, scales = "free_y") +
geom_line(size = .4) + geom_point(size = .4) +
NULL
```



## **Targets**

• Delay is taken into account ?