



## {matreex} R package

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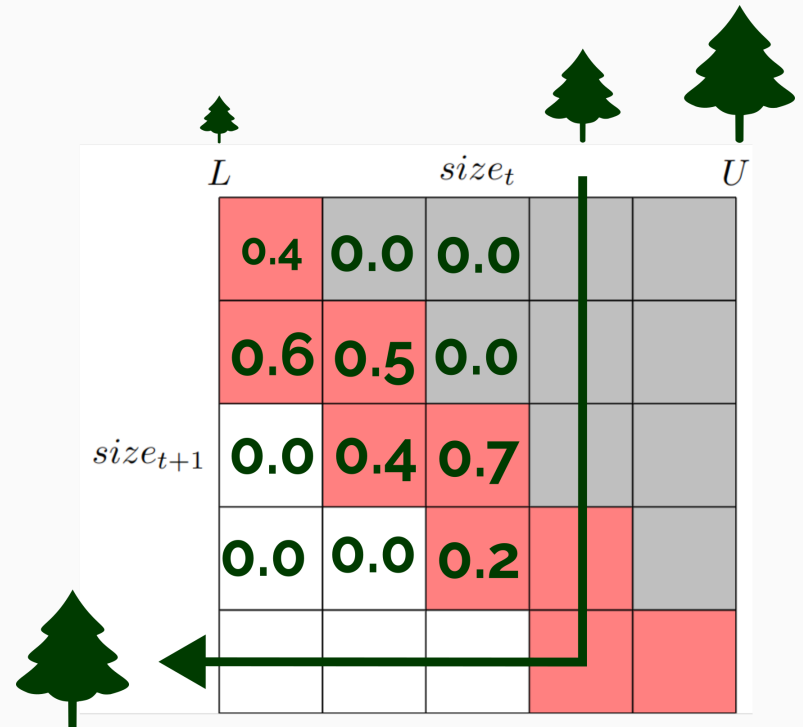
# Vous avez dit matrices ?

Matrices de transitions utilisées en biologie :

Probabilité de passage d'un stade à l'autre. (juvénile -> adulte)

## Problèmes :

- les arbres grandissent *très très* lentement...
- Probabilités difficiles à estimer

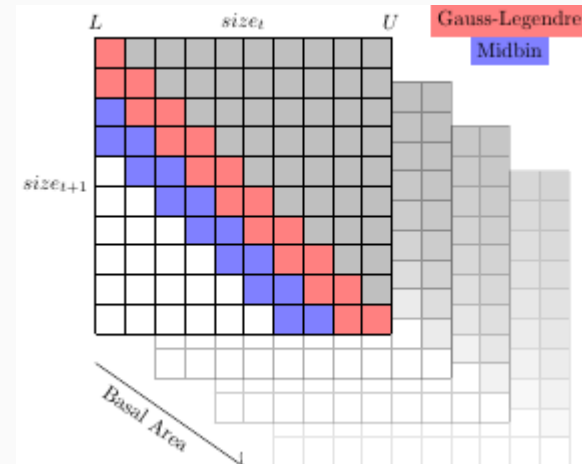


# Integrated Projection Models

Passage de modèles de croissance/survie/reproduction continus à des matrices intégrées.

$$700_x \times 700_y \times 200_{compet} \times 100_{models} \times 27_{espèces}$$

- Objects deviennent complexes à utiliser
- Beaucoup de paramètres pour l'intégration

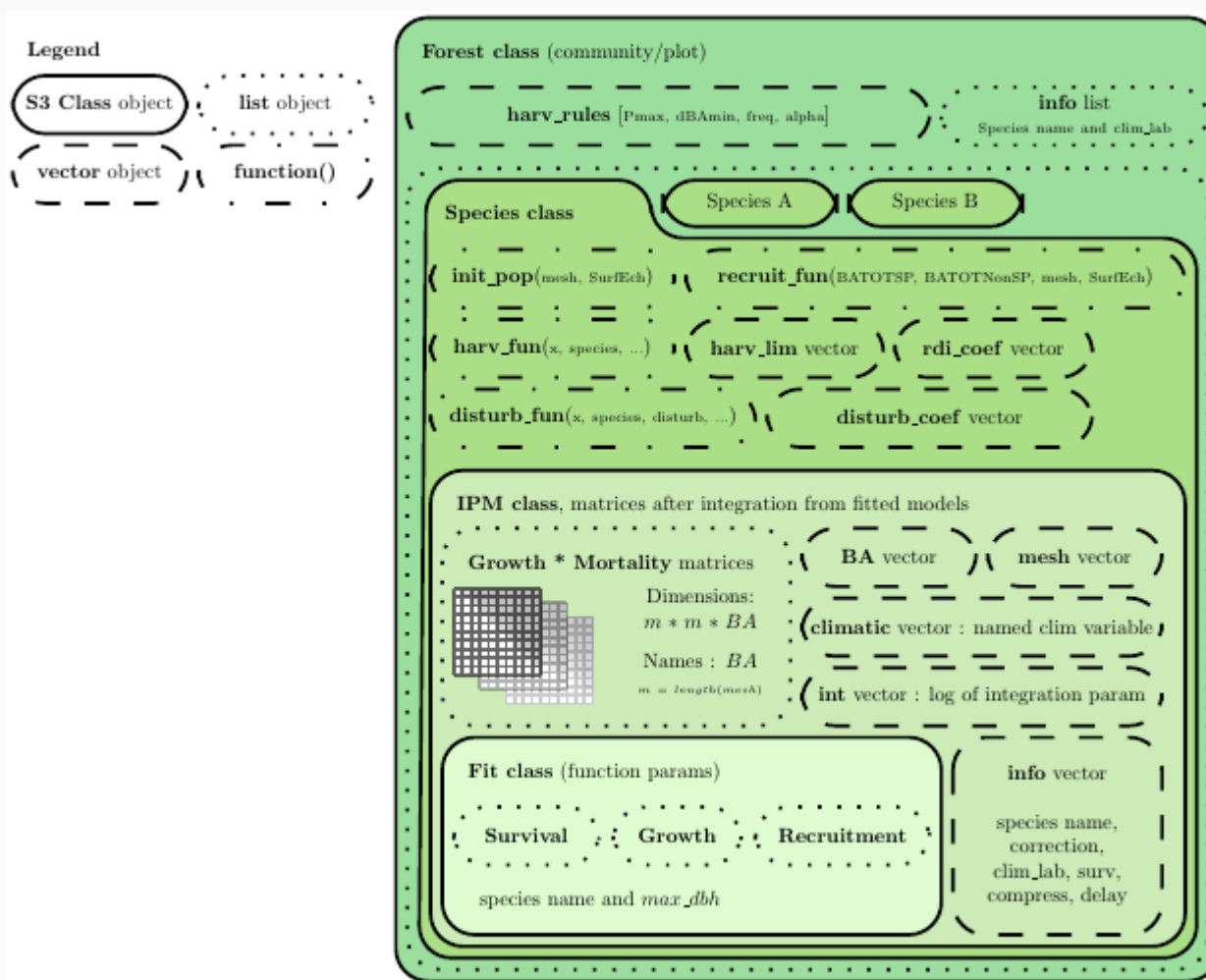


**Creation du package pour simplifier tout cela, documenter et intégrer des datas**

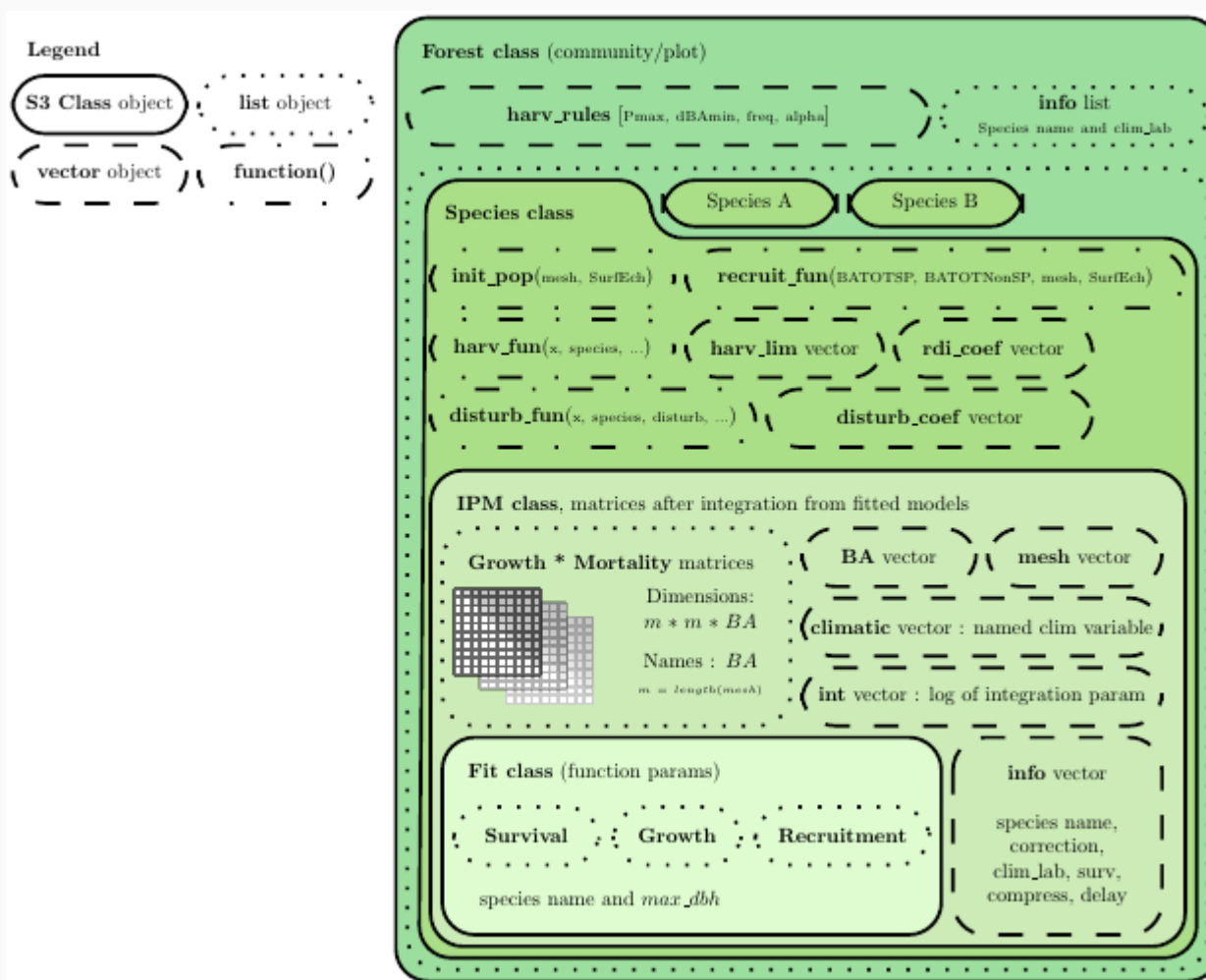
Guyennon et al in: *Global Ecology and Biogeography* (2023)

Kunstler et al in: *Journal of Ecology* (2021)

# Structure des objets R



# Structure des objets R



# Et en code ça donne ?



## Créer une espèce

```
Picea_sp ← species(IPM = Picea_ipm,  
  init_pop = def_init,  
  harvest_fun = def_harv,  
  disturb_fun = def_disturb,  
  harv_lim = c(dth = 175, dha = 575, hmax = 1),  
  rdi_coef = NULL,  
  disturb_coef = NULL  
)
```

## Créer une forêt

```
Picea_for ← forest(species = list(Picea = Picea_sp),  
  harv_rules = c(Pmax = 0.25, dBamin = 3,  
    freq = 1, alpha = 1))
```

# Lancer une simulation



```
set.seed(42) # The seed is here for initial population random functions.
Picea_sim <- sim_deter_forest(
  Picea_for, tlim = 1000, equil_time = 1500, equil_dist = 50, equil_diff = 1
)
```

## Résultats

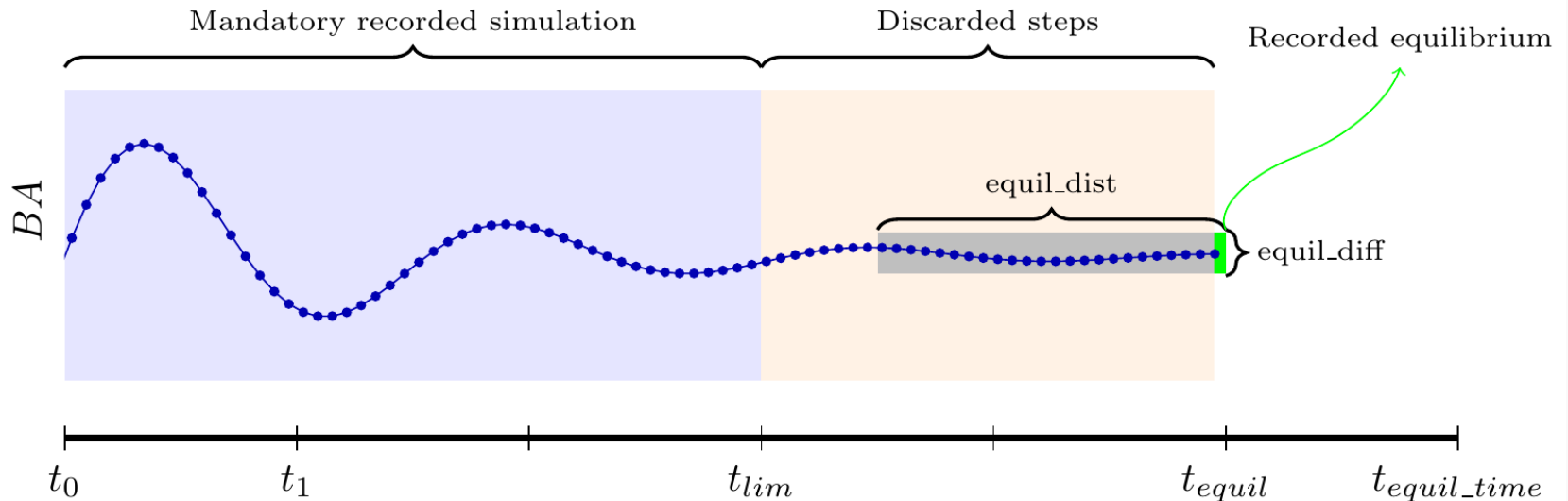
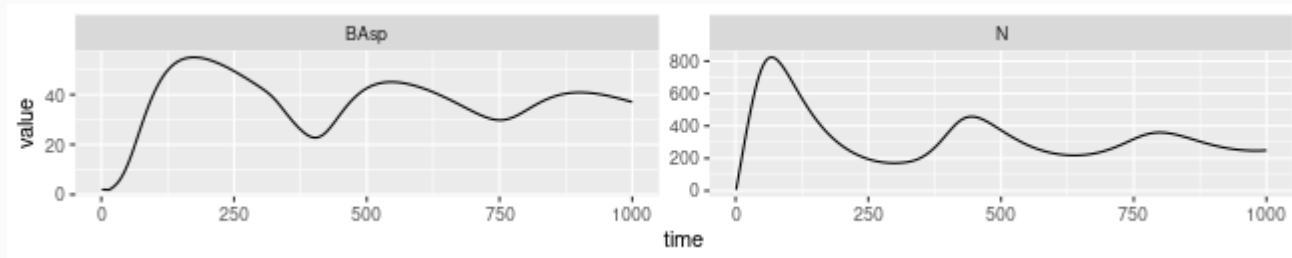
Format de sortie de type long prévu pour les plots avec `{ggplot2}` et des filtres `{dplyr}`

```
Picea_sim %>%
  dplyr::filter(var = "BAsp", ! equil) %>% head()
```

```
## # A tibble: 6 × 7
##   species      var    time  mesh  size equil value
##   <chr>      <chr> <dbl> <dbl> <dbl> <lgl> <dbl>
## 1 Picea_abies BAsp      1    NA    NA FALSE  1.96
## 2 Picea_abies BAsp      2    NA    NA FALSE  1.95
## 3 Picea_abies BAsp      3    NA    NA FALSE  1.95
## 4 Picea_abies BAsp      4    NA    NA FALSE  1.95
## 5 Picea_abies BAsp      5    NA    NA FALSE  1.95
## 6 Picea_abies BAsp      6    NA    NA FALSE  1.94
```

# Des sorties graphiques

```
Picea_sim %>% dplyr::filter(var %in% c("BAsp", "N"), ! equil) %>%  
  ggplot(aes(x = time, y = value)) +  
  geom_line() + facet_wrap(~var, scales = "free_y")
```





# Reproductibilité



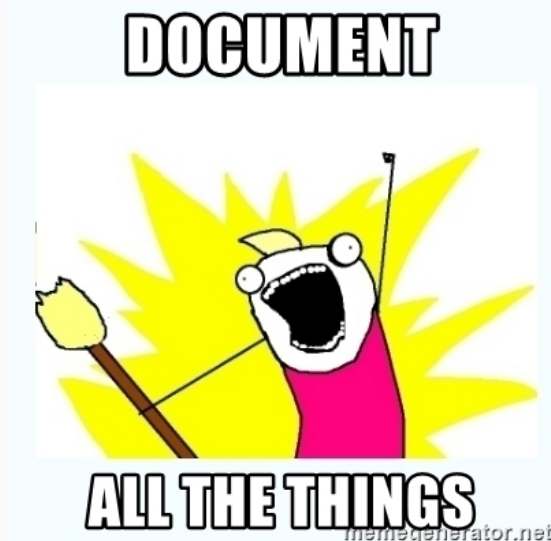
Résultats reproductibles par autrui

Code accessible (installation, lecture)

Possibilité de remonter des problèmes

Développement en commun dans l'équipe

Documentation accessible, exemples, tests



Site {pkgdown}

matreex 0.3.0 Get started Reference Articles • Changelog INRAE LESSEM

Search for

## {matreex}

The goal of this package is to run integrated projection models of tree species in single or multi-specific density dependence context. The simulations return the size distribution dynamics along time. These models can be completed with different harvest and disturbance models and be runned untill equilibrium.

Main methods have been developed for [Kunstler et al \(2020\)](#) and [Guyennon et al 2023](#) as well as european tree species growth/survival/recruitment models.

### Installation

#### Dependencies

This package relies on very few packages listed below, that you can install with the following code.

```
deps <- c('checkmate', 'Matrix', 'here', 'dplyr',
          'rlang', 'tidyr', 'purrr', 'cli',
          'statmod')
for (i in deps ){
  if(!require(i, character.only = TRUE))
    install.packages(i)
}
```

#### Stable version

You can install the '{matreex}' package from [gitlab](#) with:

```
# install.packages("remotes")
remotes::install_gitlab("gowachin/matreex")
```

*Github repository is only a mirror from gitlab. If you are added in the github repo, the code below will do it!*

```
# install.packages("remotes")
remotes::install_github("gowachin/matreex")
```

#### Development version

You can install the development version of '{matreex}' from gitlab with:

```
# install.packages("remotes")
remotes::install_gitlab("gowachin/matreex", ref = "dev")
# or
remotes::install_github("gowachin/matreex", ref = "dev")
```

#### Links

[Browse source code](#)

#### License

[Full license](#)  
[MIT](#) + [File LICENSE](#)

#### Citation

[Citing matreex](#)

#### Developers

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#### Dev status

[Check status](#) [Status](#)  
[Package status](#) [Status](#)  
[Repo status](#) [Status](#)  
[Dev status](#) [Status](#)

# Envie de faire pousser des forêts ?

 [gowachin/matreex](https://github.com/gowachin/matreex)

Slides created via the R package [xaringan](#).