twoe (2e): an R package for modelling tropical forest dynamics from permanent sample plot data

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<table>
<thead>
<tr>
<th>1 Introduction</th>
<th>3 Example on MBaiki</th>
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<tbody>
<tr>
<td>- Forest dynamics and PSP</td>
<td>- R code</td>
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<tr>
<td>- Difficulty of analysis</td>
<td>- Tables</td>
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<td>- Objectives</td>
<td>- Graphics</td>
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<td>2 Package description</td>
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<td>- Formatting the data</td>
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<td>- Growth process</td>
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<td>- Recruitment process</td>
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<td>4 Discussion</td>
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<td>- Originality</td>
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<td>- Species treatment</td>
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Studying forest dynamics

What?

- **Ecological knowledge**: Mechanisms determining forest dynamics (e.g. competition for resources, species vulnerability to climate change)

- **Forecasting and forest management**: Thinning strategies and conservation of forest ecosystem services

How?

- **Observing the forest**: In space and time ⇒ PSP

**Paracou tropical forest**

**Capsis platform**
Permanent sample plots

**Measurements**

- **Demographic processes**: Growth, Mortality, Recruitment
- **At the tree level**: species, DBH, position (X,Y)
- **Repeated on the long term**: eg. each year for 10 years

IGBP forest types

MBaiki PSP, Central African Republic
### Raw data

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**Extract of MBaiki data-base**

**twoe R package**
1 Introduction
- Forest dynamics and PSP
- Difficulty of analysis
- Objectives

2 Package description
- Formatting the data
- Growth process
- Mortality process
- Recruitment process

3 Example on MBaiki
- R code
- Tables
- Graphics

4 Discussion
- Originality
- Species treatment
- Applications
- twoe web-site
Difficulties arising from PSP data analysis

Huge amount of data
- MBaiki: 38514 trees, 24 censuses (1982–2009), 924336 measurements!

Imperfect data
- Observation error: negative growth
- Variable time interval
- Several plots
- Missing values
- Growth: Gaussian process, Mortality: Bernoulli process, Recruitment: Poisson process

Unbalanced data
- Many rare species with few individuals
- MBaiki: out of 234 species, only 99 species ≥ 50 individuals (on 40 ha!)

Difficulties
- PSP: complicated data-sets
- Require advanced statistical models

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twoe R package
Objectives of the twoe (2e) R package

- For all the species: modelling growth, mortality and recruitment
- Making the most of the available data (remeasurements)
- Overcoming several difficulties associated to PSP data
- Easy-to-use functions which only require a minimal knowledge of the R software
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entry_data() 

- Transform the raw data into right-format data-sets
- 4 arguments: Data, XY.Plot, R.Comp, L.Cell
- Return 3 data-sets for demographic models: data_growth.txt, data_mortality.txt, data_recruitment.txt

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Growth process: \texttt{entry\_ngrowth\_gibbs()}

Hierarchical Bayesian framework

\textbf{Error process}

\[ G_{ik}^{\text{obs}} \sim \text{Normal}(G_{ik}^{\text{true}}, V_{i}^{\text{err}}) \]
\[ V_{i}^{\text{err}} = (0.927 + 0.0038D_{i})^2 \]

\textbf{Growth process}

\[ \log(G_{ik}^{\text{true}}) \sim \text{Normal}((\beta_{0} + b_{0,k}) + (\beta_{1} + b_{1,k}) \log(D_{i}) + (\beta_{2} + b_{2,k}) \log(C_{i} + 1), V) \]

\textbf{Priors}

\[ [\beta_{0}, \beta_{1}, \beta_{2}] \sim \text{Normal}_3(\mu_{\beta}, V_{\beta}) \]
\[ [b_{0,k}, b_{1,k}, b_{2,k}] \sim \text{Normal}_3(0, V_{b}) \]
\[ V_{b} \sim \text{Inverse-Wishart}(r, rR) \]
\[ V \sim \text{Inverse-Gamma}(\nu, \delta) \]

\( G_{ik} \) is the growth (mm.yr\(^{-1}\)) of tree \( i \) of species \( k \) between census \( c \) and \( c + 1 \)
\( D_{i} \) is the diameter (cm) of tree \( i \) at census \( c \)
\( C_{i} \) is the competition index (m\(^2\).ha\(^{-1}\)) in the neighborhood of tree \( i \) at census \( c \)
\( b_{0,k}, b_{1,k}, b_{2,k} \) are the species random effects
Growth process: `entry_ngrowth_gibbs()`

R function

```
entry_ngrowth_gibbs()
```

- Such hierarchical model cannot be fitted with classical tools (`nlme()`, `lme4` in R)
- `twoe` R package includes an easy-to-use function to fit the model
- Model can include various covariate types: climatic covariates at the plot level, species functional trait, etc.

```
entry_ngrowth_gibbs(fixed, random, group, diameter, data, burnin=1000, mcmc=10000, thin=10, verbose=1, seed=NA, beta.start=NA, sigma2.start=NA, Vb.start=NA, mubeta=0, Vbeta=1.0E6, r, R, nu=0.001, delta=0.001, ...)
```
Algorithms

- **Gibbs sampler** to obtain Markov Chain Monte Carlo for each parameter
- **adaptive Metropolis-Hastings** algorithm for latent variables (acceptance rate \(~44\%\))
- **Chib and Carlin block-sampling** for random effects \(\rightarrow\) convergence
- **Woodbury matrix identity** for large matrix computation
- **C++** code with the **Scythe** statistical library \(\rightarrow\) speed
1 Introduction
- Forest dynamics and PSP
- Difficulty of analysis
- Objectives

2 Package description
- Formatting the data
- Growth process
- Mortality process
- Recruitment process

3 Example on MBaiki
- R code
- Tables
- Graphics

4 Discussion
- Originality
- Species treatment
- Applications
twoe web-site
Mortality process: entry_mortality_gibbs()

Hierarchical Bayesian framework

Mortality process
\[ S_{ik} \sim \text{Bernoulli}(\theta'_{ik}) \]
\[ \theta'_{ik} = 1 - (1 - \theta_{ik})^{Y_i} \]
\[ \text{logit}(\theta_{ik}) = (\beta_0 + b_{0,k}) + (\beta_1 + b_{1,k})(D_i - 20) + (\beta_2 + b_{2,k})(C_i - 20) + \epsilon_i \]

Priors
\[ \epsilon_i \sim \text{Normal}(0, V = 1) \]
\[ [\beta_0, \beta_1, \beta_2] \sim \text{Normal}_3(\mu_\beta, V_\beta) \]
\[ [b_{0,k}, b_{1,k}, b_{2,k}] \sim \text{Normal}_3(0, V_b) \]
\[ V_b \sim \text{Inverse-Wishart}(r, rR) \]

\( S_{ik} \) is the status (0=alive, 1=dead) of tree \( i \) of species \( k \) between census \( c \) and \( c + 1 \)
\( Y_i \) is the time interval (yr) between census \( c \) and \( c + 1 \)
\( \theta'_{ik} \) is the mortality rate for time interval \( Y_i \)
\( \theta_{ik} \) is the annual mortality rate
\( D_i \) is the diameter (cm) of tree \( i \) at census \( c \)
\( C_i \) is the competition index \( (m^2.ha^{-1}) \) in the neighborhood of tree \( i \) at census \( c \)
\( b_{0,k}, b_{1,k}, b_{2,k} \) are the species random effects

twoe R package
Mortality process: `entry_mortality_gibbs()`

**R function**

```
entry_mortality_gibbs(fixed, random, group, interval=1, data,
burnin=5000, mcmc=10000, thin=10, verbose=1, seed=NA, beta.start=NA,
sigma2.start=NA, Vb.start=NA, mubeta=0, Vbeta=1.0E6, r, R, nu=0.001,
delta=0.001, FixOD=0, ...)  
```
Introduction
- Forest dynamics and PSP
- Difficulty of analysis
- Objectives

Package description
- Formatting the data
- Growth process
- Mortality process
- Recruitment process

Example on MBaiki
- R code
- Tables
- Graphics

Discussion
- Originality
- Species treatment
- Applications
- twoe web-site
Recruitment process: \texttt{entry_recruitment_gibbs()}

Hierarchical Bayesian framework

Recruitment process

\[
R_{jk} \sim \text{Poisson}(\lambda'_{jk})
\]

\[
\lambda'_{jk} = \lambda_{jk} Y_j A_j
\]

\[
\log(\lambda_{jk}) = (\beta_0 + b_{0,k}) + (\beta_1 + b_{1,k})(BA_{jk} - 0.5) + (\beta_2 + b_{2,k})(C_j - 20) + \epsilon_j
\]

Priors

\[
\epsilon_j \sim \text{Normal}(0, V = 1)
\]

\[
[\beta_0, \beta_1, \beta_2] \sim \text{Normal}_3(\mu_\beta, V_\beta)
\]

\[
[b_{0,k}, b_{1,k}, b_{2,k}] \sim \text{Normal}_3(0, V_b)
\]

\[
V_b \sim \text{Inverse-Wishart}(r, rR)
\]

\(R_{jk}\) is the number of recruits of quadrat \(j\) for species \(k\) between census \(c\) and \(c + 1\)

\(Y_j\) is the time interval (yr) between census \(c\) and \(c + 1\)

\(A_j\) is the area (m\(^2\)) of quadrat \(j\)

\(\lambda'_{jk}\) is the mean number of recruits for time interval \(Y_j\) and area \(A_j\)

\(\lambda_{jk}\) is the mean number of recruits (.yr\(^{-1}\).m\(^{-2}\))

\(BA_{jk}\) is the basal area of conspecific trees (m\(^2\).ha\(^{-1}\)) for sp. \(k\) in the quadrat \(j\) at census \(c\)

\(C_j\) is the competition index (m\(^2\).ha\(^{-1}\)) in the quadrat \(j\) at census \(c\)

\(b_{0,k}, b_{1,k}, b_{2,k}\) are the species random effects
Recruitment process: `entry_recruitment_gibbs()`

R function

`entry_recruitment_gibbs()`

- GLM with unclassical link function (variable time interval $Y_i$ and quadrat area $A_j$)
- Such hierarchical model cannot be fitted with classical tools (`glm()`, `lme4` in R)
- `twoe` R package includes an easy-to-use function to fit the model
- Model can include various covariate types: climatic covariates at the plot level, species functional trait, etc.
- Model allows integrating overdispersion in the data (common)

`entry_recruitment_gibbs(fixed, random, group, interval=1, area=1, data, burnin=5000, mcmc=10000, thin=10, verbose=1, seed=NA, beta.start=NA, sigma2.start=NA, Vb.start=NA, mubeta=0, Vbeta=1.0E6, r, R, nu=0.001, delta=0.001, FixOD=0, ...)`

`twoe` R package
1 Introduction
   - Forest dynamics and PSP
   - Difficulty of analysis
   - Objectives

2 Package description
   - Formatting the data
   - Growth process
   - Mortality process
   - Recruitment process

3 Example on MBaiki
   - R code
   - Tables
   - Graphics

4 Discussion
   - Originality
   - Species treatment
   - Applications
   - twoe web-site
Example on MBaiki

R code

- MBaiki: 38514 trees, 24 censuses, 234 species
- ~15 lines of R code
- entry_growth, entry_mortality, entry_recruitment

```
library(twoe)
# Creating data-sets
# Importing permanent-plot data-set
Data <- read.table(file="TreeFile", sep="\t", header=TRUE)
XY.Plot <- read.table(file="PlotFile", sep="\t", header=TRUE)
# Creating the entry data-set
entry_data(Data, XY.Plot, R_COMP=15, L_Cell=20)

# Growth
# Importing growth data
data_growth <- read.table(file="data_growth.txt", header=TRUE, sep="\t")
# Calling entry_growth
ten_growth(data_growth, burnin=1000, mcmc=1000, thin=1, quantiles=5)

# Mortality
# Importing mortality data
data_mortality <- read.table(file="data_mortality.txt", header=TRUE, sep="\t")
# Calling entry_mortality
ten_mortality(data_mortality, burnin=1000, mcmc=1000, thin=1, quantiles=5)

# Recruitment
# Importing recruitment data
data_recruitment <- read.table(file="data_recruitment.txt", header=TRUE, sep="\t")
# Calling entry_recruitment
ten_recruitment(data_recruitment, burnin=1000, mcmc=1000, thin=1, quantiles=5)

# Simulations
# Calling exit_simu
exit_simu(Data, XY.Plot, R.Recruitment=10, R.Comp=15, L.Cell=20, Plot.Sim="ALL", Year.Sim=10, Step.Sim=1)
```

Outputs

- Tables: MCMC, parameter values and significance
- Graphics: MCMC, posterior distributions, model predictions by species, forest dynamics

twoe R package
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- Mortality process
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3 **Example on MBaiki**
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- Tables
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4 **Discussion**
- Originality
- Species treatment
- Applications
- twoe web-site

twoe R package
### MCMC samples

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Can be analysed further with the coda package or R twoe R package
Parameter values and significance

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</tr>
</tbody>
</table>
Introduction
- Forest dynamics and PSP
- Difficulty of analysis
- Objectives

Package description
- Formatting the data
- Growth process
- Mortality process
- Recruitment process

Example on MBaiki
- R code
- Tables
- Graphics

Discussion
- Originality
- Species treatment
- Applications
- twoe web-site
MCMC and posterior distributions

Trace of beta0

Density of beta0

Trace of beta1

Density of beta1

Trace of beta2

Density of beta2

N = 1000  Bandwidth = 0.03273

N = 1000  Bandwidth = 0.006606

twoe R package
Model predictions by species

Sp162 = *Musanga cecropioides* R.Br. & Tedlie
Model predictions by species

Sp160

\[ D \text{ mean} = 16 \text{ cm} \]

Sp162

\[ D \text{ mean} = 29 \text{ cm} \]

Sp165

\[ D \text{ mean} = 24 \text{ cm} \]

Sp166

\[ D \text{ mean} = 13 \text{ cm} \]

Sp162 = *Musanga cecropioides* R.Br. & Tedlie
Forest dynamics

Plot P22

- Observations
- Predictions

Fast growing species:
- Sp162, Sp109
- Sp17, Sp16, Sp306

R code

twoe R package
Introduction
- Forest dynamics and PSP
- Difficulty of analysis
- Objectives

Package description
- Formatting the data
- Growth process
- Mortality process
- Recruitment process

Example on MBaiki
- R code
- Tables
- Graphics

Discussion
- Originality
- Species treatment
- Applications
- twoe web-site
## Originality compared to existing forest simulators

### twoe R package
- Software is focused on **parameter inference**
- **General framework** adapted to tropical forests world-wide
- **Advanced statistical models** are available for non-statisticians

### Tropical forest dynamics simulators

<table>
<thead>
<tr>
<th>Simulator</th>
<th>Country</th>
<th>Author</th>
</tr>
</thead>
<tbody>
<tr>
<td>FORMIND</td>
<td>Malaysia</td>
<td>Huth</td>
</tr>
<tr>
<td>CAFOGROM</td>
<td>Brazil</td>
<td>Alder</td>
</tr>
<tr>
<td>GMNQR</td>
<td>Australia</td>
<td>Vanclay</td>
</tr>
<tr>
<td>SELVA</td>
<td>Fr. Guiana</td>
<td>Gourlet-F.</td>
</tr>
<tr>
<td>SYMFOR</td>
<td>Indonesia</td>
<td>Phillips</td>
</tr>
<tr>
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<td>...</td>
<td>...</td>
</tr>
</tbody>
</table>
1 Introduction
   - Forest dynamics and PSP
   - Difficulty of analysis
   - Objectives

2 Package description
   - Formatting the data
   - Growth process
   - Mortality process
   - Recruitment process

3 Example on MBaiki
   - R code
   - Tables
   - Graphics

4 Discussion
   - Originality
   - Species treatment
   - Applications
   - twoe web-site
Species diversity and functional groups

Twoe R package

- **No a priori** regarding functional groups
- Each species: unique set of demographic parameters
- Demographic models can capture diversity

Tropical forest dynamics simulators

- Species are grouped **a priori** regarding some “key” functional traits
- Tree maximal height, seed size, wood-density, SLA, etc.
- 5 to 22 groups

Introduction
- Forest dynamics and PSP
- Difficulty of analysis
- Objectives

Package description
- Formatting the data
- Growth process
- Mortality process
- Recruitment process

Example on MBaiki
- R code
- Tables
- Graphics

Discussion
- Originality
- Species treatment
- Applications
- twoe web-site
Applications

Ecological knowledge
- Do species have significantly different demographic rates?
- Relationship between demography and species functional traits/phylogeny?
- Species vulnerability to climate change.

Forest management
- Test of sylvicultural scenarios
- Conservation of forest ecosystem services: biodiversity, carbon and wood production
Applications

Do species have significantly different demographic rates?

Hubbell, 2001, neutral theory
Relationship between demography and species functional traits/phylogeny?
Test of sylvicultural scenarios for conservation of ecosystem services.

Capsis platform: [http://capsis.cirad.fr](http://capsis.cirad.fr)
1 Introduction
   ● Forest dynamics and PSP
   ● Difficulty of analysis
   ● Objectives

2 Package description
   ● Formatting the data
   ● Growth process
   ● Mortality process
   ● Recruitment process

3 Example on MBaiki
   ● R code
   ● Tables
   ● Graphics

4 Discussion
   ● Originality
   ● Species treatment
   ● Applications
   ● twoe web-site
twoe web-site

http://twoe.sourceforge.net

- On SourceForge
- source code
- manual
- slides

twoe version 1.0
Published on 16 juillet 2011 in Mon dossier: Closed

twoe (2e) is a software which aims first, at estimating the demographic parameters of tropical tree species from permanent forest plot data (through an R package) and second, at simulating forest dynamics (through a Capsis module). Authors: Ghislain Vieilledent, François de Coligny.

R package

- Package source: twoe_1.0.tar.gz
- Windows binary (R 2.15.2): twoe_1.0.zip
- Reference manual: twoe.pdf
- Slides: slides_twoe.pdf
Thank you for attention...