# Development of a demo-genetic model for SFE and parameter estimation using Approximate Bayesian Computing methods 

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Applibugs - 21/06/2018

Landscape
Ecology \&
Vegetation Science

## Study sites and species



## Collected data

- 15 "isolated" patches of spontaneous forests


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- 15 "isolated" patches of spontaneous forests
- Exhaustive tree mapping (location and size)
- Dendrochronological data
- Genetic data


## Model overview

- Individual based model of tree population
- Spatialized on a grid of 1 m 2 cell
- One year time step


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- Included processes : growth, mortality, fecundity, pollen and seed dispersal, tree establishment, parenthood relationship between trees


## Model overview



## Model overview



## Growth <br> dbh and neighbours

## Model overview



## Growth dbh and neighbours



Pollen fecundity dbh Dispersal

## Model overview



## Growth dbh and neighbours



Pollen fecundity dbh Dispersal


Seed fecundity dbh
Dispersal

## Model overview



## Growth dbh and neighbours



Pollen fecundity dbh Dispersal


Seed and pollen immigration

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## Growth <br> dbh and neighbours



Pollen fecundity dbh Dispersal


Young tree establishment neighbours

Seed and pollen immigration

## Model overview



## Growth <br> dbh and neighbours



Pollen fecundity dbh Dispersal
Parenthood assignation


Young tree establishment neighbours

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## Model overview

Mortality dbh and growth rate


## Growth dbh and neighbours



Pollen fecundity dbh Dispersal
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## Model overview



## Growth

 dbh and neighbours

Mortality dbh and growth rate

# 22 parameters 

Pollen fecundity dbh Dispersal
Parenthood assignation


Young tree establishment neighbours


Seed fecundity dbh
Dispersal
Seed and pollen immigration

## Simulated forest development

Individual location on the grid and size


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Individual location on the grid and size


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## Simulated forest development

## Size trajectories of individuals alive after 70 years



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## Size trajectories of individuals alive after 70 years



## Summary statistics

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- Around 20 different sumstats for now (tree density, mean size, clumping indexes, fit of size according to neigbourhood index, fit of age according to size, etc.)
- Genetic sumstats ? Example: distribution of number of relatives according to size ?
- Choice of the summary statistics ?


## Number of simulations to run





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## Quantification of data information



Parenthood assignation


## Quantification of data information



## General data

## Parenthood assignation



## Quantification of data information



## Spatial data

## General data

## Parenthood assignation



## Quantification of data information



## Dynamics data

Spatial data

## General data

## Parenthood assignation



## Quantification of data information



## Dynamics data

## Genetic data

## Parenthood assignation



## General data

## Spatial data



## Quantification of data information



## Dynamics data

 <br> \section*{Genetic data <br> \section*{Genetic data <br> <br> Parenthood assignation} <br> <br> Parenthood assignation}Recruitment and


## General data

## Spatial data

## Exemple with growth rate parameters



Parenthood assignation


## Exemple with growth rate parameters



## General data

## Parenthood assignation



## Exemple with growth rate parameters



## Parenthood assignation



## Prior densities



## Prior densities

$A B C$ without dynamics data
$A B C$ with dyna nics data


## Prior densities



## Results without dynamics data




$g_{m}$

## Results with dynamics data method 1




$g_{m}$

## Results with dynamics data method 2


$g_{m}$

$x_{0}$


## Future work

- Parameter estimation
- All parameters
- Quantification of information for all types of data
- Prior information
- Effect of patch size


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- Parameter estimation
- All parameters
- Quantification of information for all types of data
- Prior information
- Effect of patch size
- Model changes
- Two size class
- Processes (mortality, masting, etc.)
- Hierarchy on patches ?
- Demo-genetic model ?

Thank you for your attention.

