

Modelling of climate change impact on forest tree populations

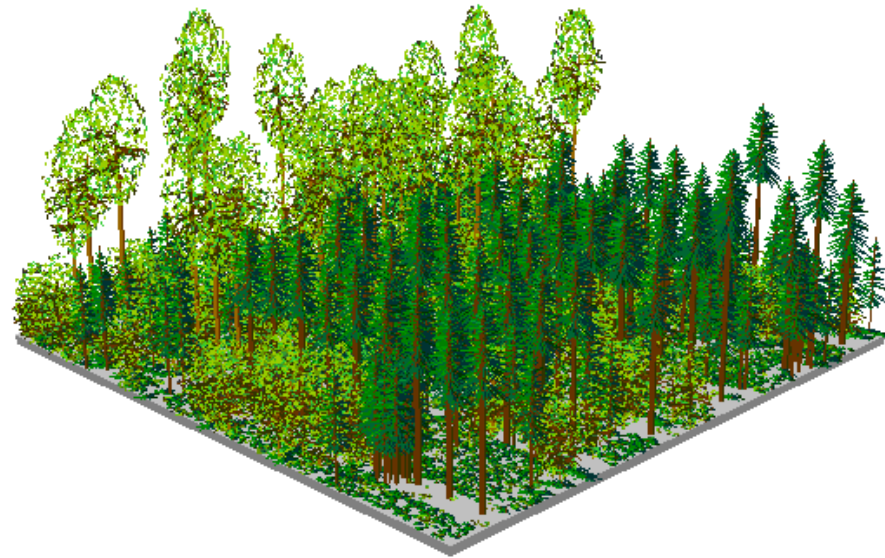
Koen Kramer
Alterra

Evoltree Summer School
Zvolen, September 10-14, 2007



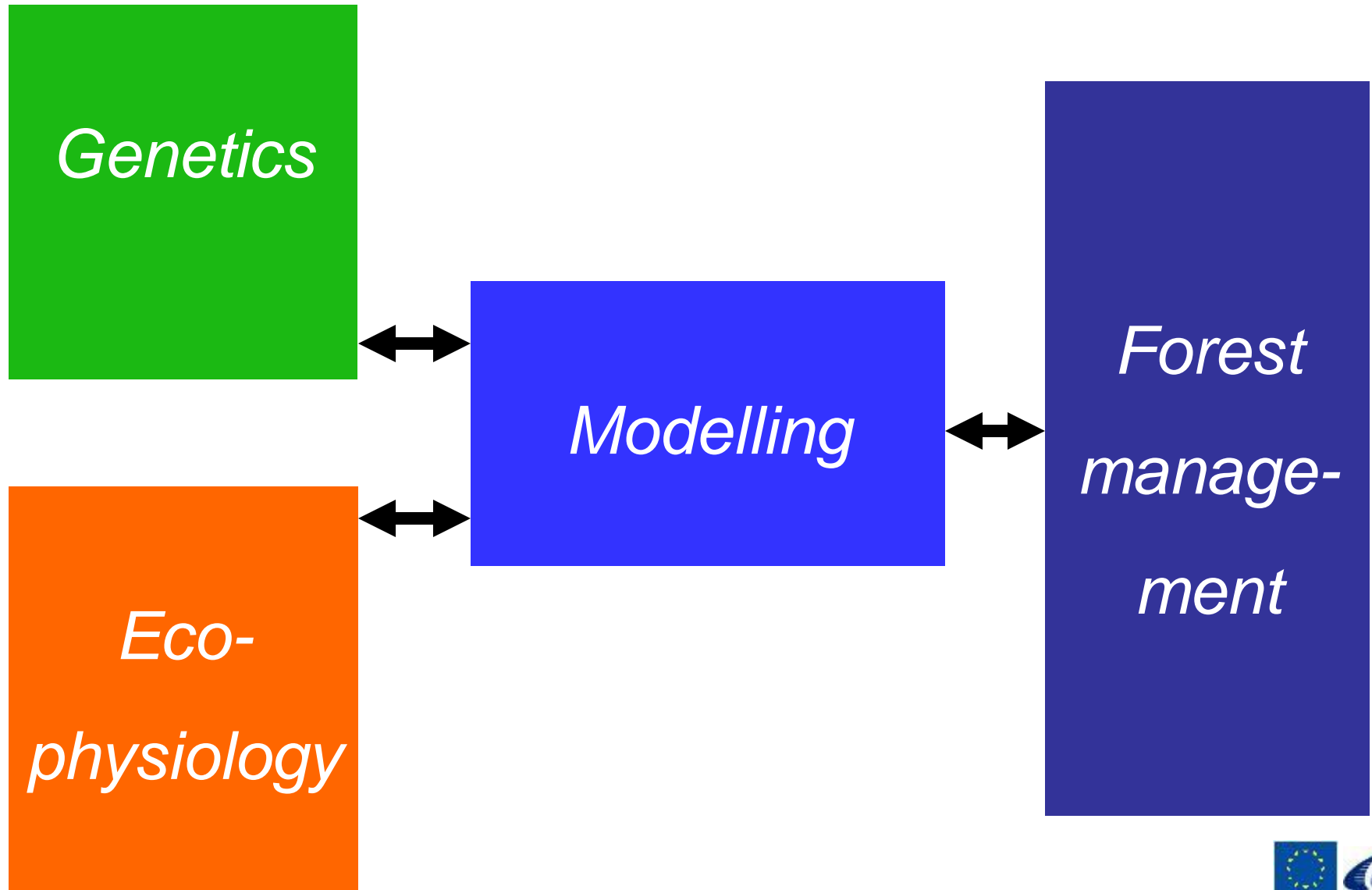
Example: beech and pine

ISMB-ECCB after Time: 50 year



Simulations based on past century climate

Modelling ambition



Structure of the presentation

Modelling principles

The model ForGEM

- genetic components
- eco(physio)logical component
- forest management

Examples: impact of forest management

----- break-----

Modelling the annual cycle

Examples: impact of climate change

Model characteristics

Mathematical model

Simulates 'real world' phenomena

Systems of differential/or difference equations

Deterministic or probabilistic

Event driven

Has a time component: dynamic modelling

Individual based model

- Individual/behavior tracked in time
- Spatially explicit

Defining a model

Important aspects in defining a model

- Elements needed
- Structure and structuring of the data
- Defining the mathematics

Program requirements

- Clear execution flow
- Easy readable and adjustable
- Step size control

The simulated world consists of:

Systems

- One system can contain another system (part of, lies in)
- Relationships between systems are input-output relationships
- Systems differ in state variables and functions
- Differential- or difference equations

Events

- Triggered by state variables and input
- Discrete moment in time

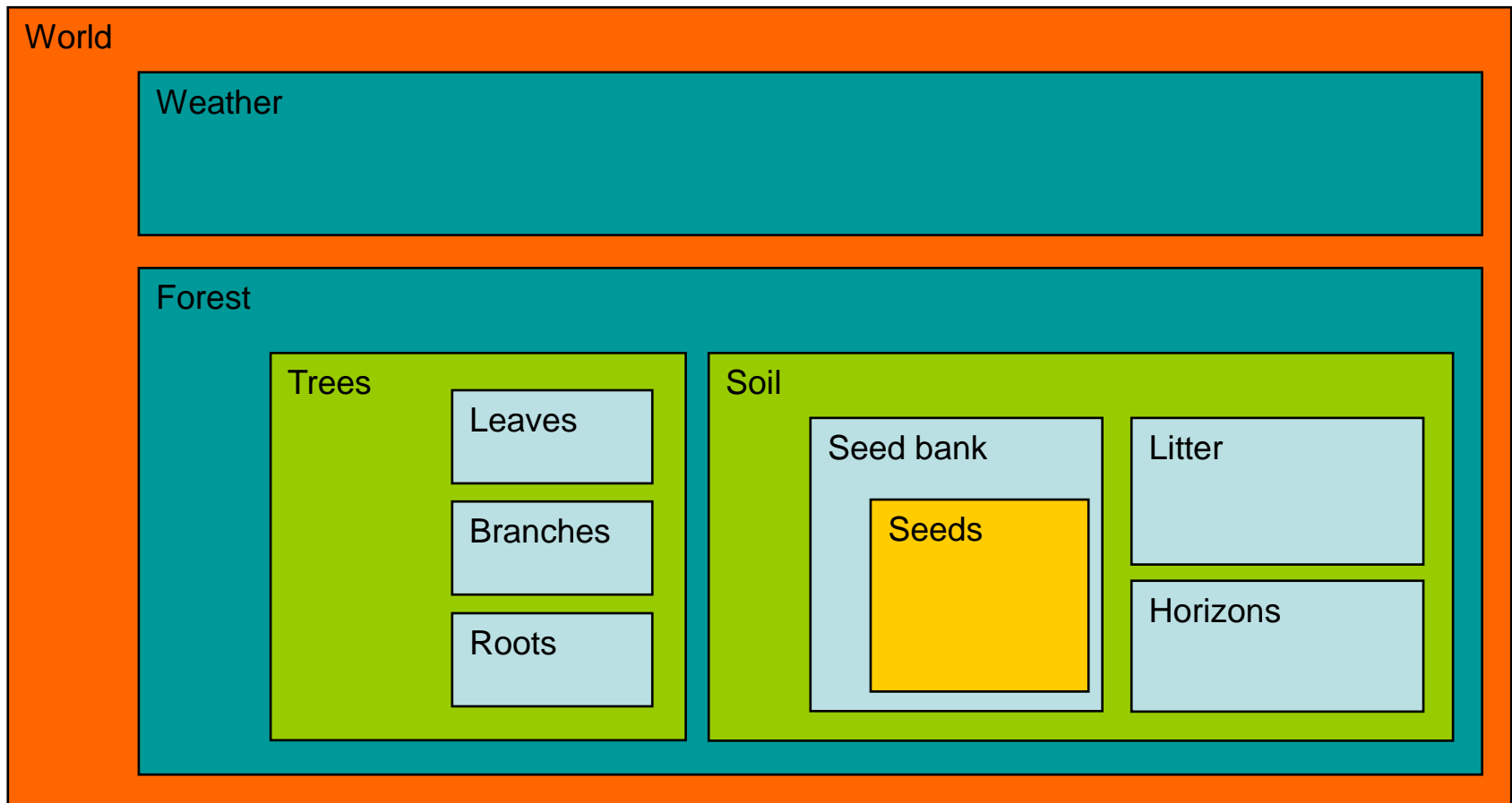
Processes

- Grouped differential-, difference equations across (sub) systems describing a process
- Light interception, Water use, etc.
- Belong to systems (e.g. light interception belongs to forest)

Transitions

- Some systems can change into other systems due to events

NSM: Nested Simulation Modelling

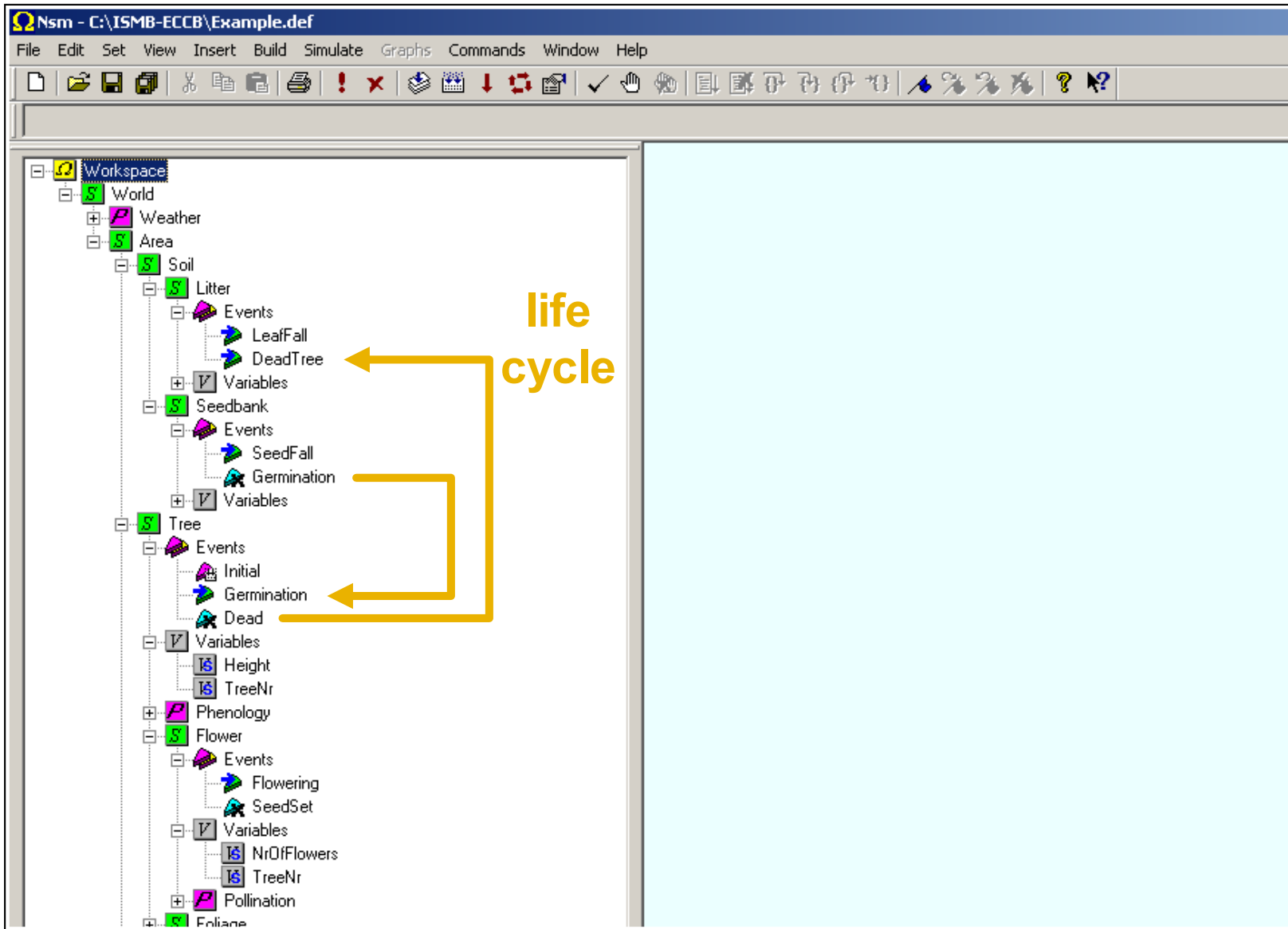


Each system has its own variables and functions and interacts with other systems with input-output relations

Structuring a model

Nsm - C:\ISMB-ECCB\Example.def

File Edit Set View Insert Build Simulate Graphs Commands Window Help



The screenshot displays the Nsm software interface with a hierarchical model structure. The 'Workspace' tree is expanded to show the following components:

- World
 - Weather
 - Area
 - Soil
 - Litter
 - Events
 - LeafFall
 - DeadTree
 - Variables
 - Seedbank
 - Events
 - SeedFall
 - Germination
 - Variables
 - Tree
 - Events
 - Initial
 - Germination
 - Dead
 - Variables
 - Height
 - TreeNr
 - Phenology
 - Flower
 - Events
 - Flowering
 - SeedSet
 - Variables
 - NrOfFlowers
 - TreeNr
 - Pollination
 - Foliage

A yellow arrow labeled "life cycle" indicates a path from the "Germination" event in the "Tree" section, through the "Dead" event, to the "Germination" event in the "Seedbank" section, and finally to the "LeafFall" event in the "Litter" section.

State and Output variables

Nsm - C:\ISMB-ECCB\Example.def

File Edit Set View Insert Build Simulate Graphs Commands Window Help

life cycle

SpeciesName	TreeNr	Height	...
Fagus sylvatica	1	30	.
Fagus sylvatica	2	31	.
Fagus sylvatica	3	28	.
Fagus sylvatica	4	29	.
Quercus robur	5	30	.
Pinus sylvestris	6	32	.
Quercus robur	7	34	.
Pinus sylvestris	8	27	.
Pinus sylvestris	9	22	.

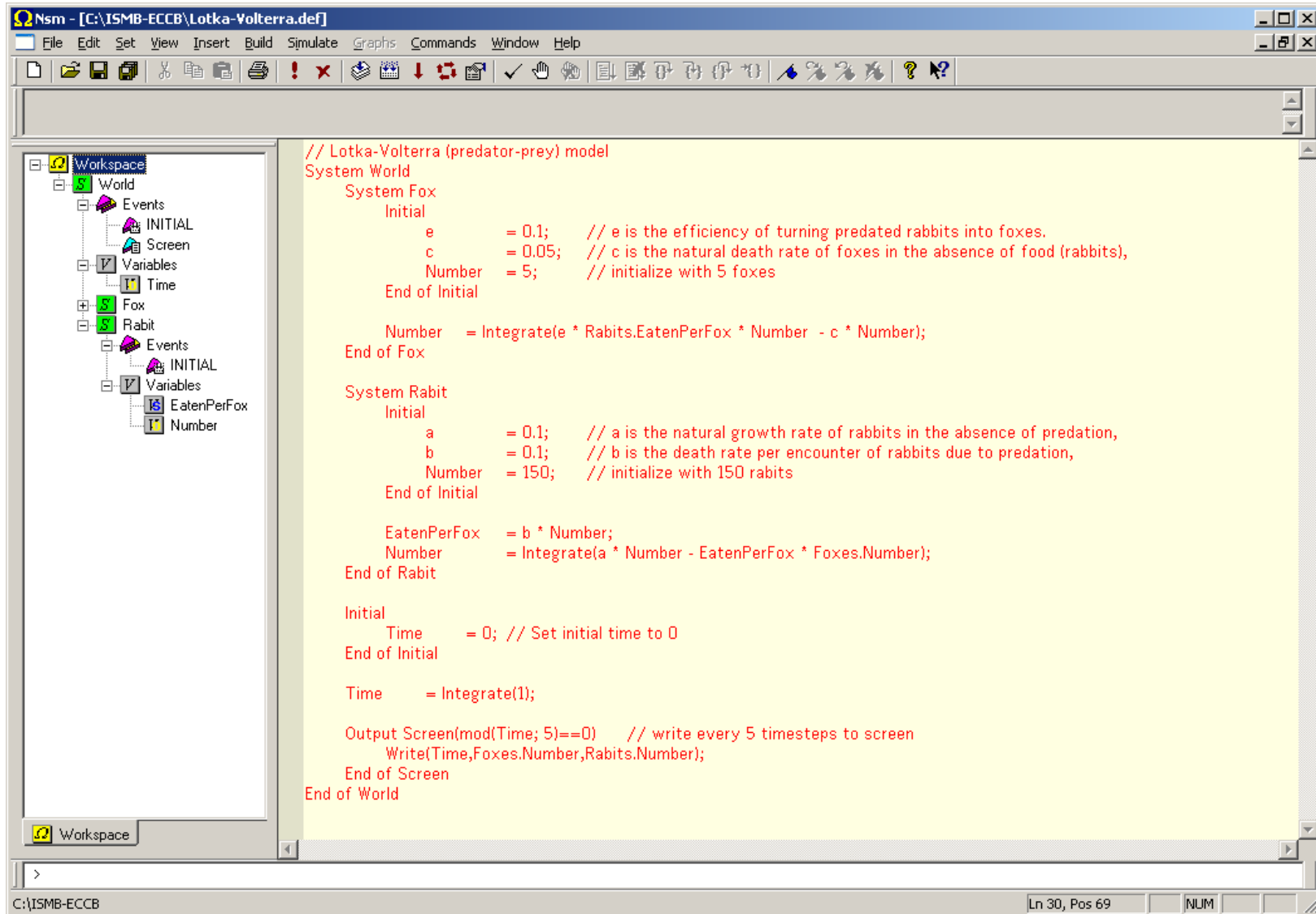
Triggering events

The screenshot shows the Nsm software interface with a hierarchical tree structure. Annotations include:

- annual cycle:** A green arrow pointing to the 'Events' node under 'Tree'.
- life cycle:** A yellow arrow pointing to the 'Events' node under 'Tree'.
- Callout box:** "If any MomentOfBudBurst is true then BudBurst is triggered for that tree". This points to the 'MomentOfBudBurst' variable under 'Phenology'.

SpeciesName	TreeNr	Height	...
Fagus sylvatica	1	30	.
Fagus sylvatica	2	31	.
Fagus sylvatica	3	28	.
Fagus sylvatica	4	29	.
Quercus robur	5	30	.
Pinus sylvestris	6	32	.
Quercus robur	7	34	.
Pinus sylvestris	8	27	.
Pinus sylvestris	9	22	.

Example of model code in NSM:



Workspace Tree:

- Workspace
 - World
 - Events
 - INITIAL
 - Screen
 - Variables
 - Time
 - Fox
 - Events
 - INITIAL
 - Variables
 - EatenPerFox
 - Number
 - Rabbit
 - Events
 - INITIAL
 - Variables
 - EatenPerFox
 - Number

Code Editor Content:

```
// Lotka-Volterra (predator-prey) model
System World
  System Fox
    Initial
      e      = 0.1; // e is the efficiency of turning predated rabbits into foxes.
      c      = 0.05; // c is the natural death rate of foxes in the absence of food (rabbits),
      Number = 5; // initialize with 5 foxes
    End of Initial

    Number = Integrate(e * Rabbits.EatenPerFox * Number - c * Number);
  End of Fox

  System Rabbit
    Initial
      a      = 0.1; // a is the natural growth rate of rabbits in the absence of predation,
      b      = 0.1; // b is the death rate per encounter of rabbits due to predation,
      Number = 150; // initialize with 150 rabbits
    End of Initial

    EatenPerFox = b * Number;
    Number      = Integrate(a * Number - EatenPerFox * Foxes.Number);
  End of Rabbit

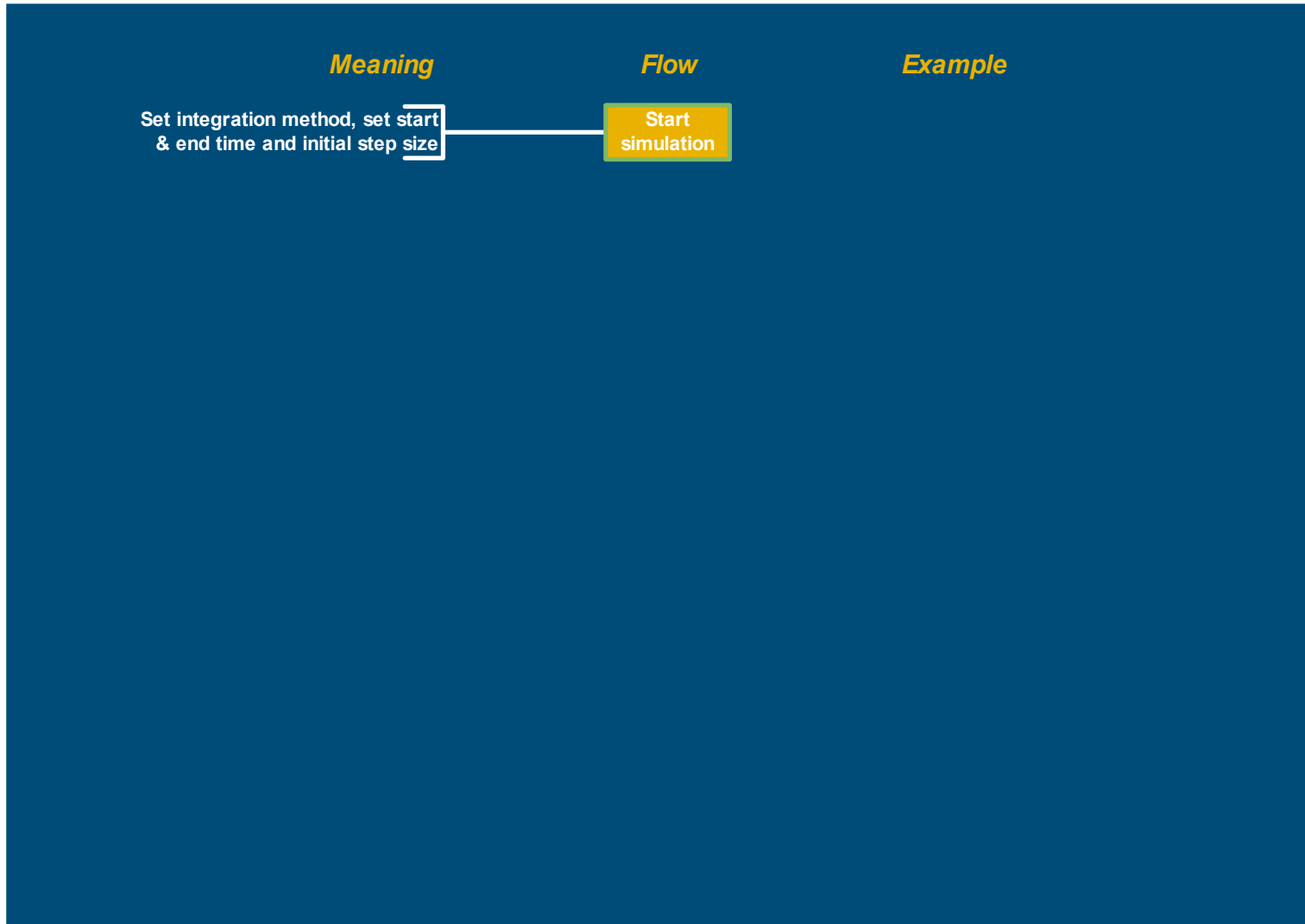
  Initial
    Time = 0; // Set initial time to 0
  End of Initial

  Time = Integrate(1);

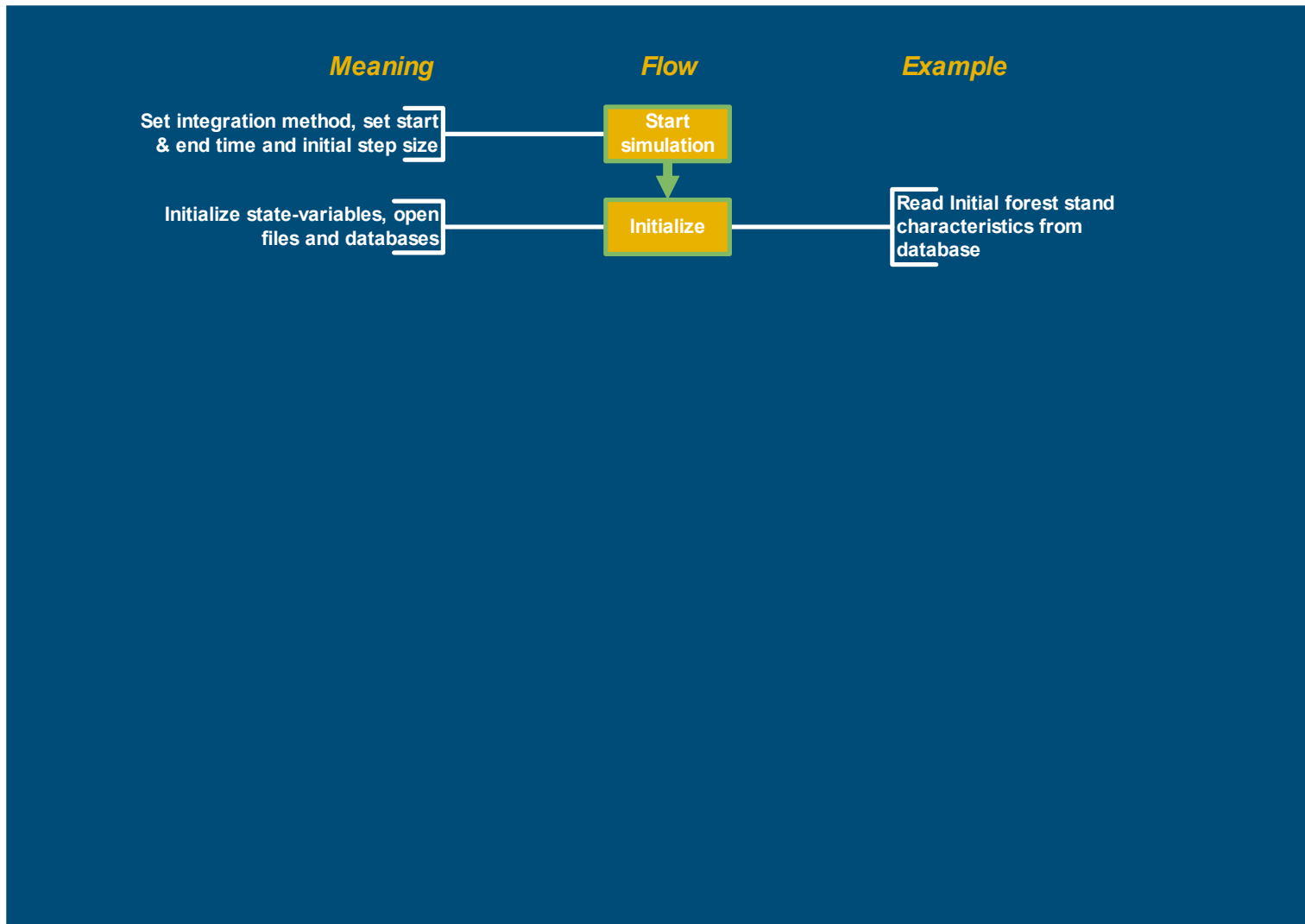
  Output Screen(mod(Time; 5)==0) // write every 5 timesteps to screen
    Write(Time,Foxes.Number,Rabbits.Number);
  End of Screen
End of World
```

Status Bar: C:\ISMB-ECCB Ln 30, Pos 69 NUM

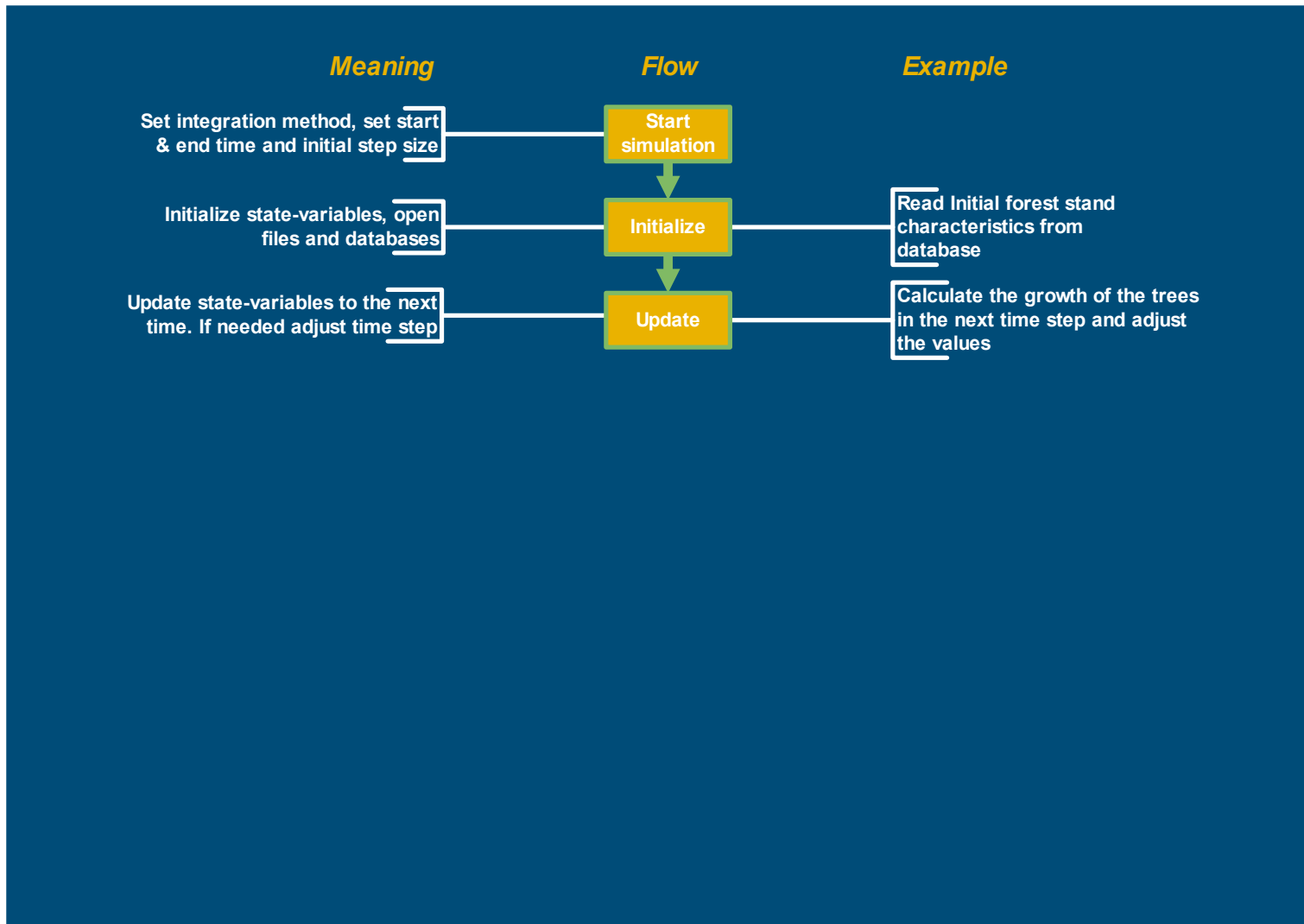
Execution flow



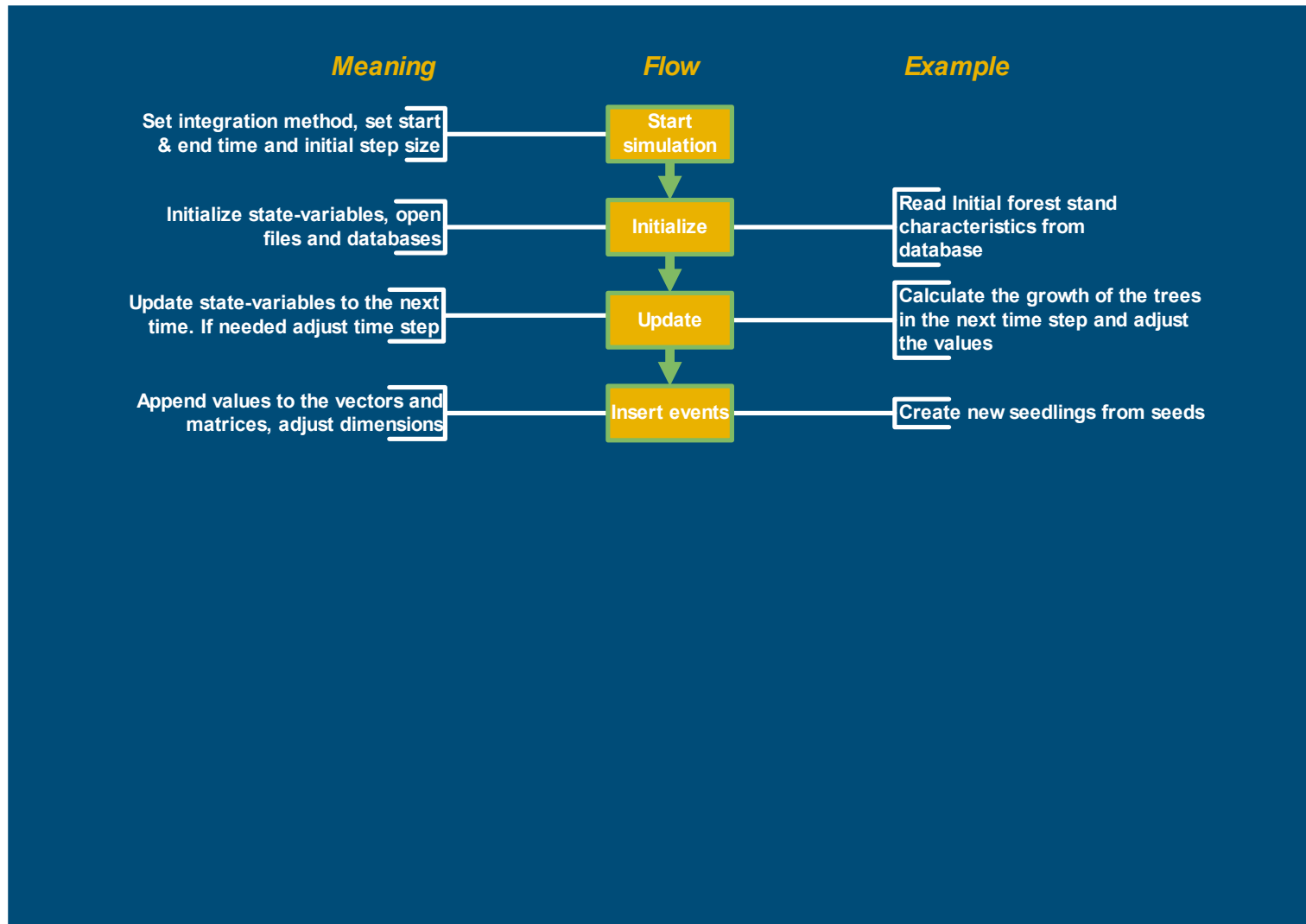
Execution flow



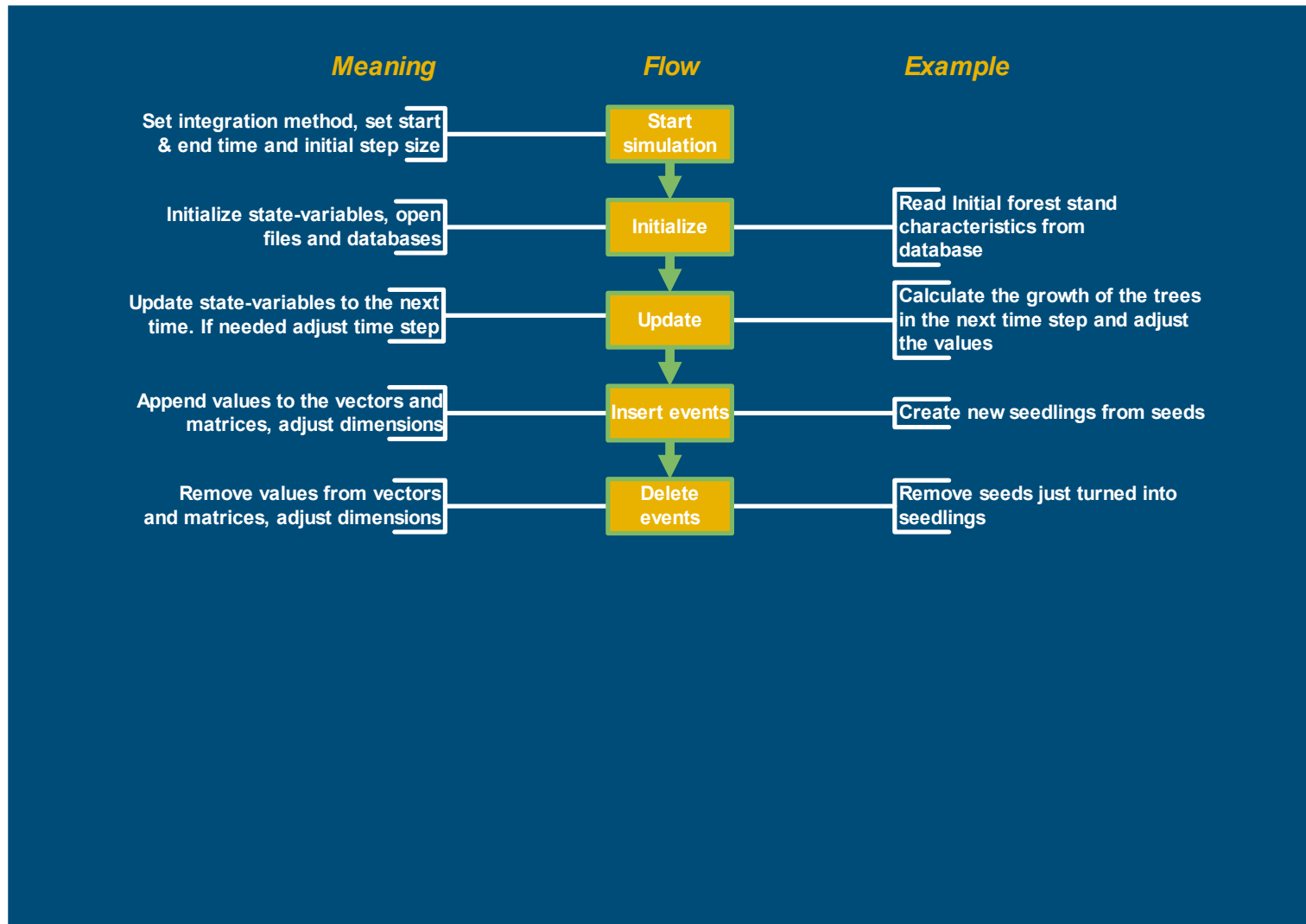
Execution flow



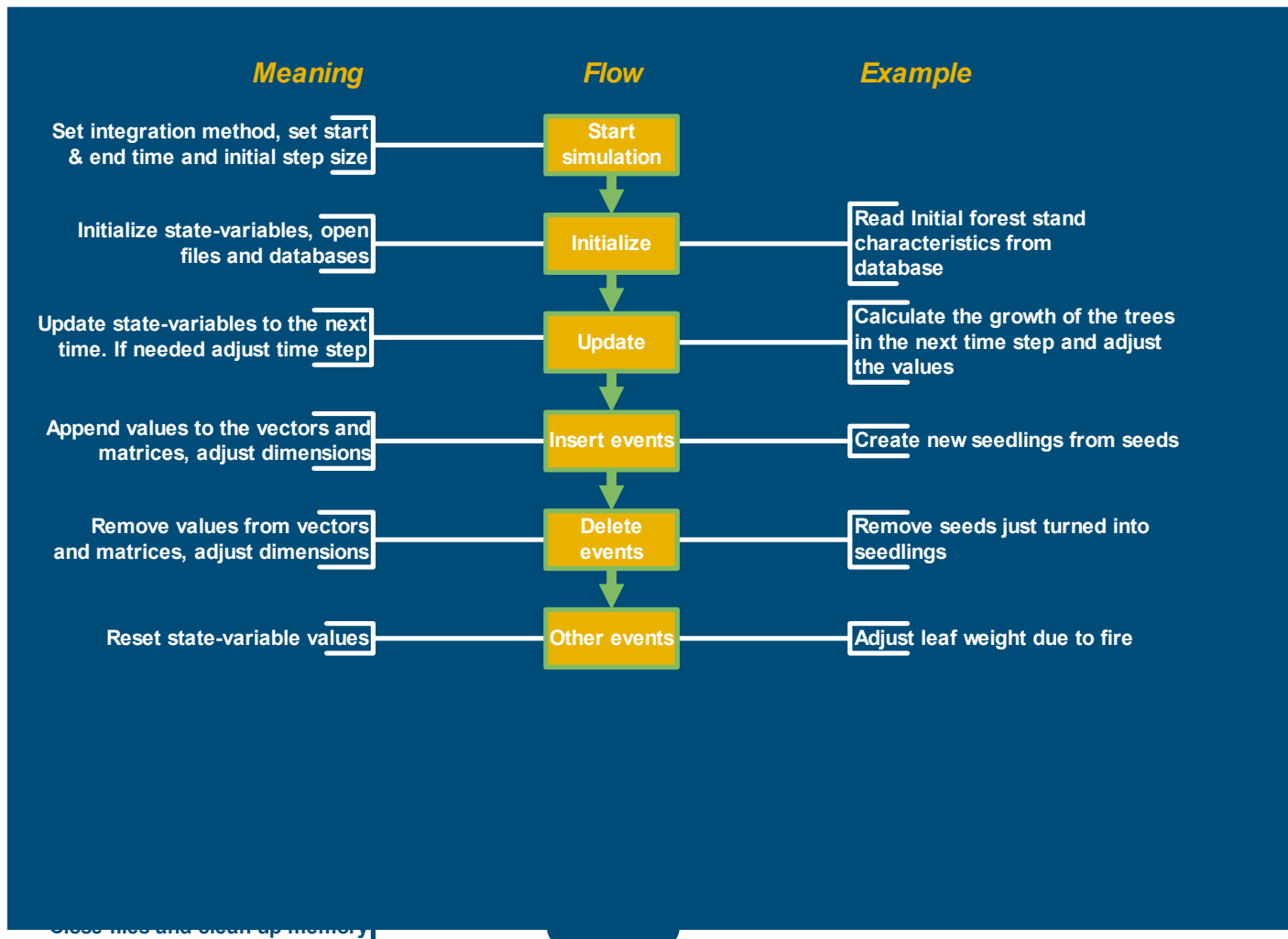
Execution flow



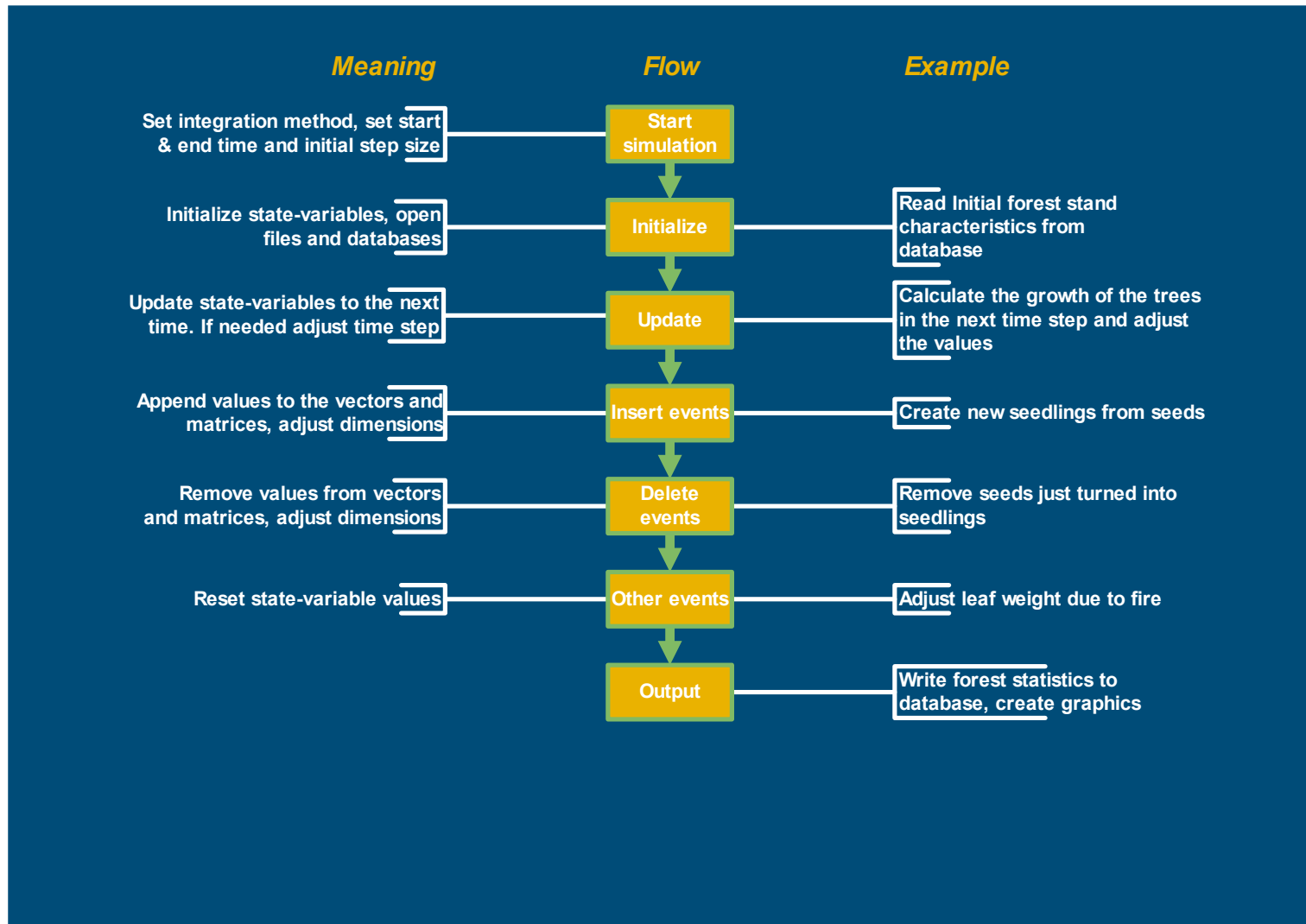
Execution flow



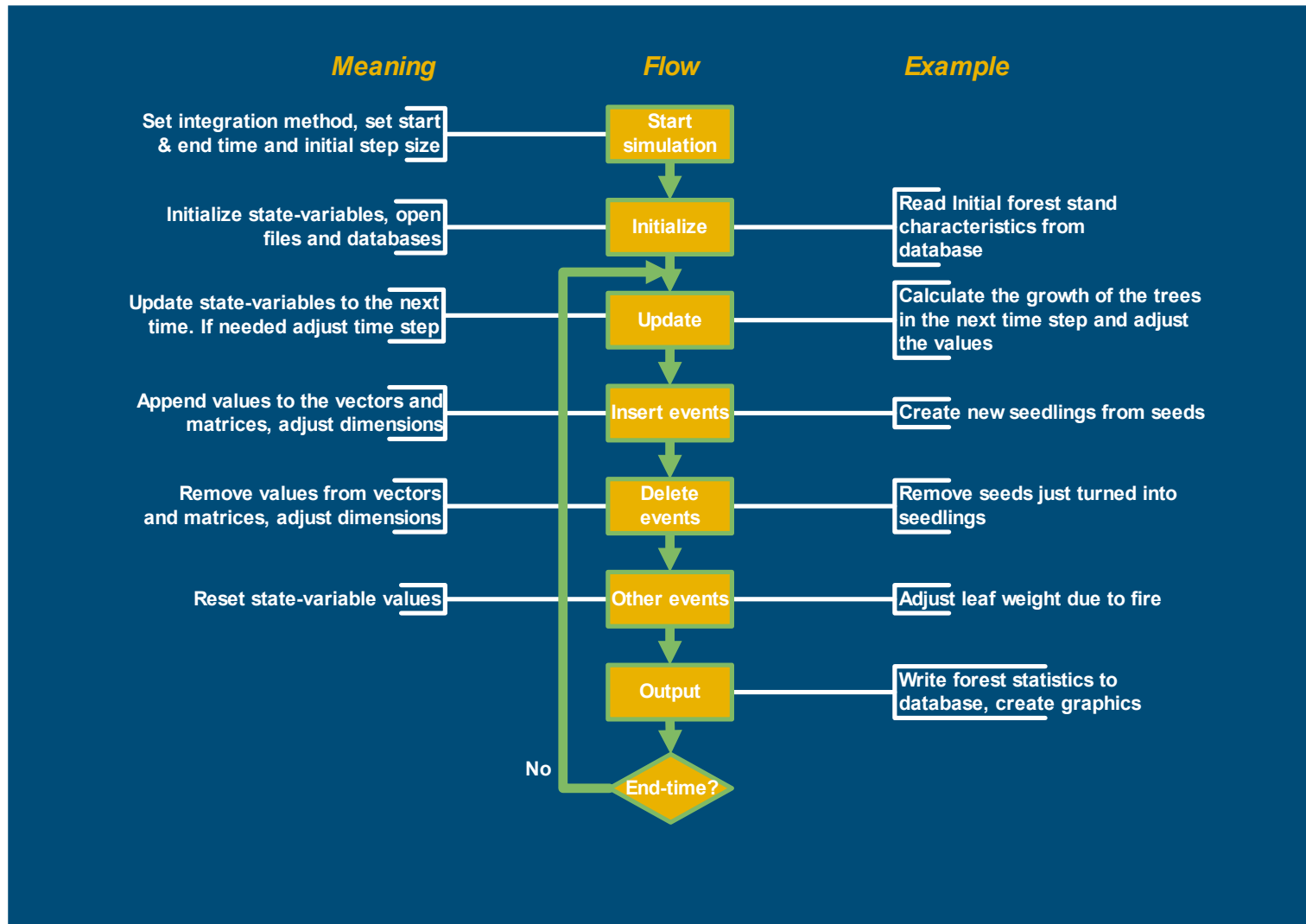
Execution flow



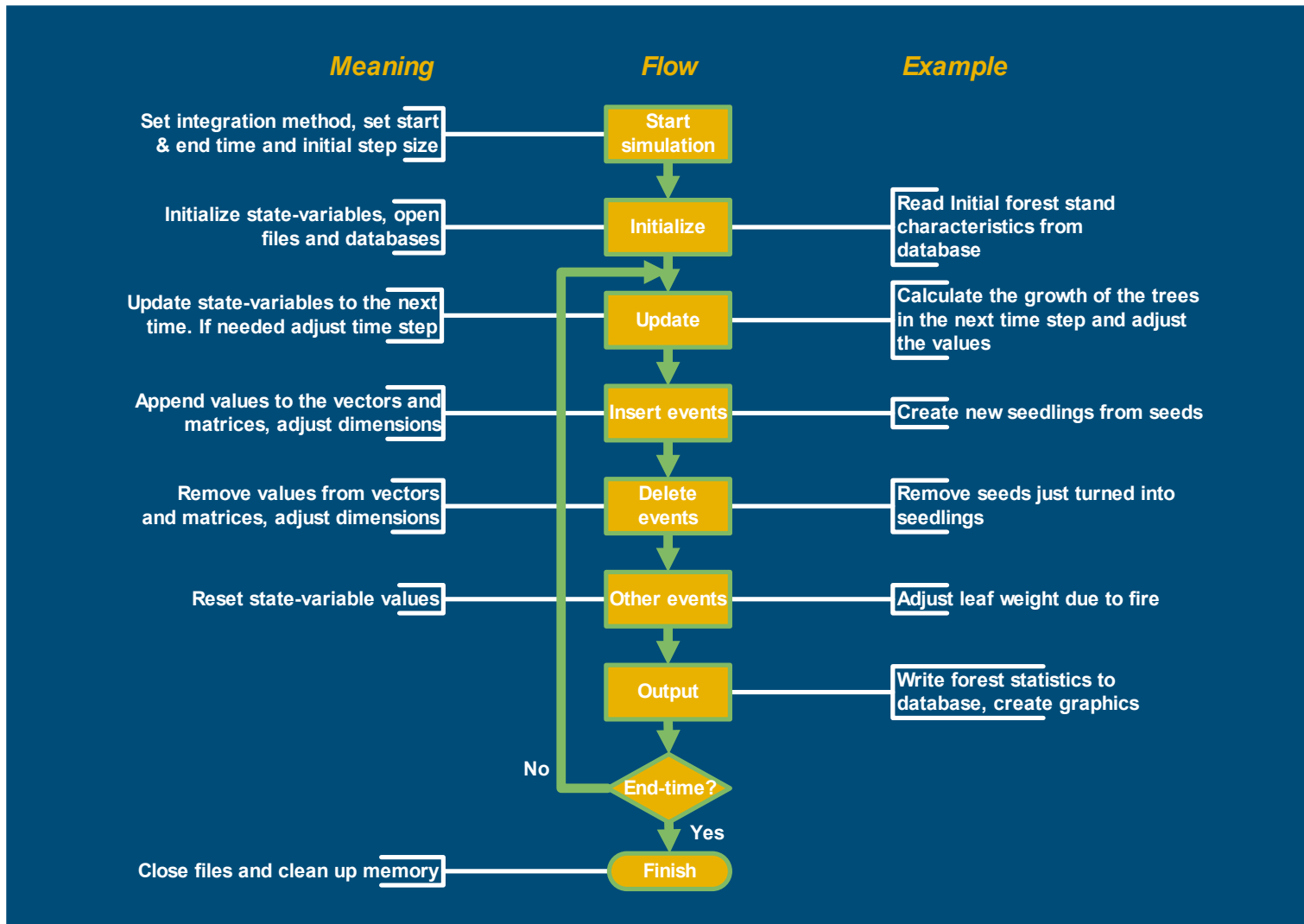
Execution flow



Execution flow



Execution flow



Individual based modeling: advantages

Population does not need to be in equilibrium state

Focus on mechanisms between individuals

Feedback of individuals/population with environmental changes

It's the individual who reacts to changes in the environment

Keeps as close as possible to biological processes

Interactions are too complex to model at higher level of aggregation

Statistics at population level (up scaling to higher level) can always be computed

Individual based modeling: disadvantages

Lower speed of simulation due to high number of computations

Smaller spatial scale due to memory limitations

Needs a lot of parameters

BUT:

Can be used as a basis for models at an aggregated scale

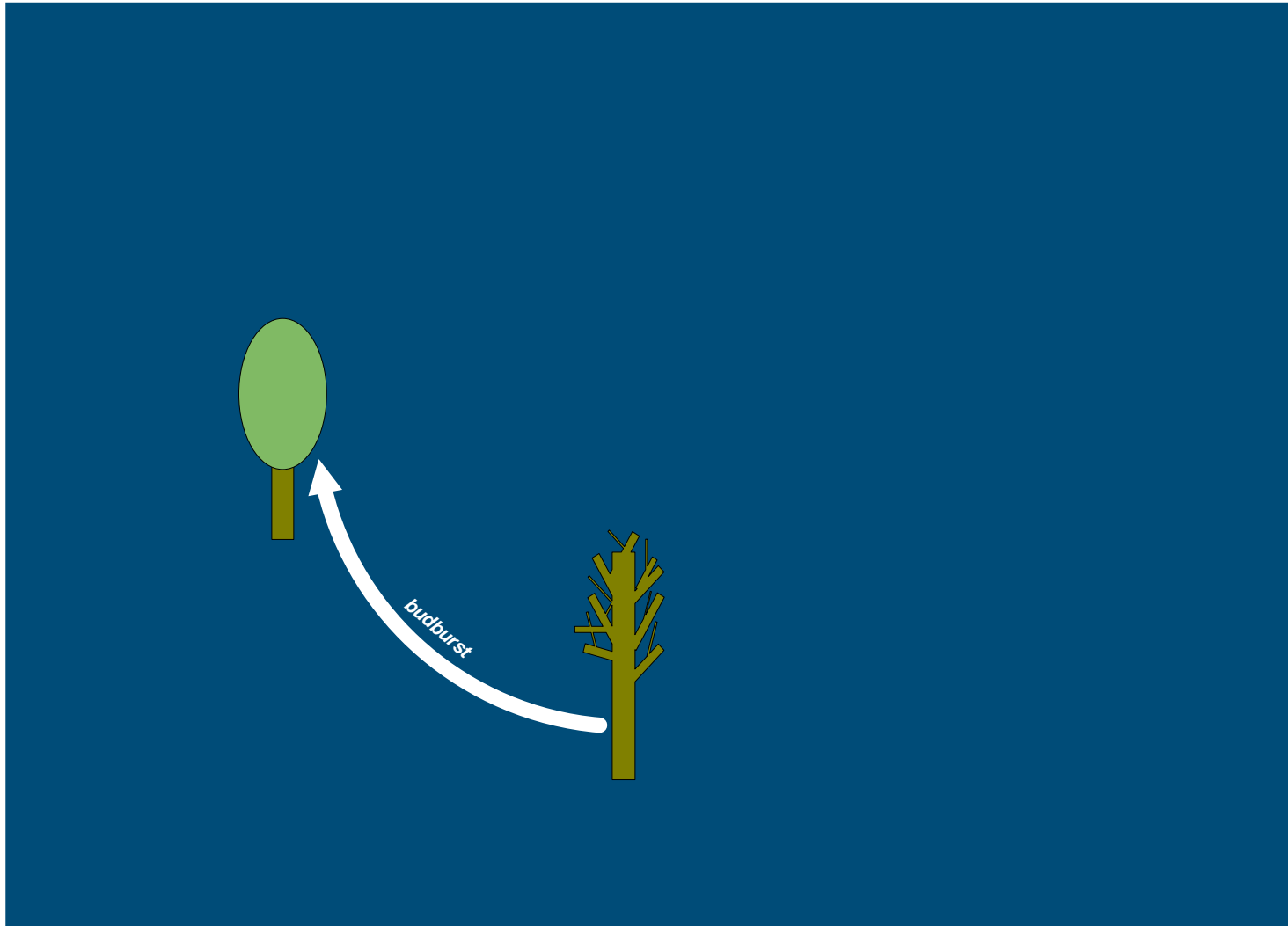
AND:

A population based model is a special case of individual based model

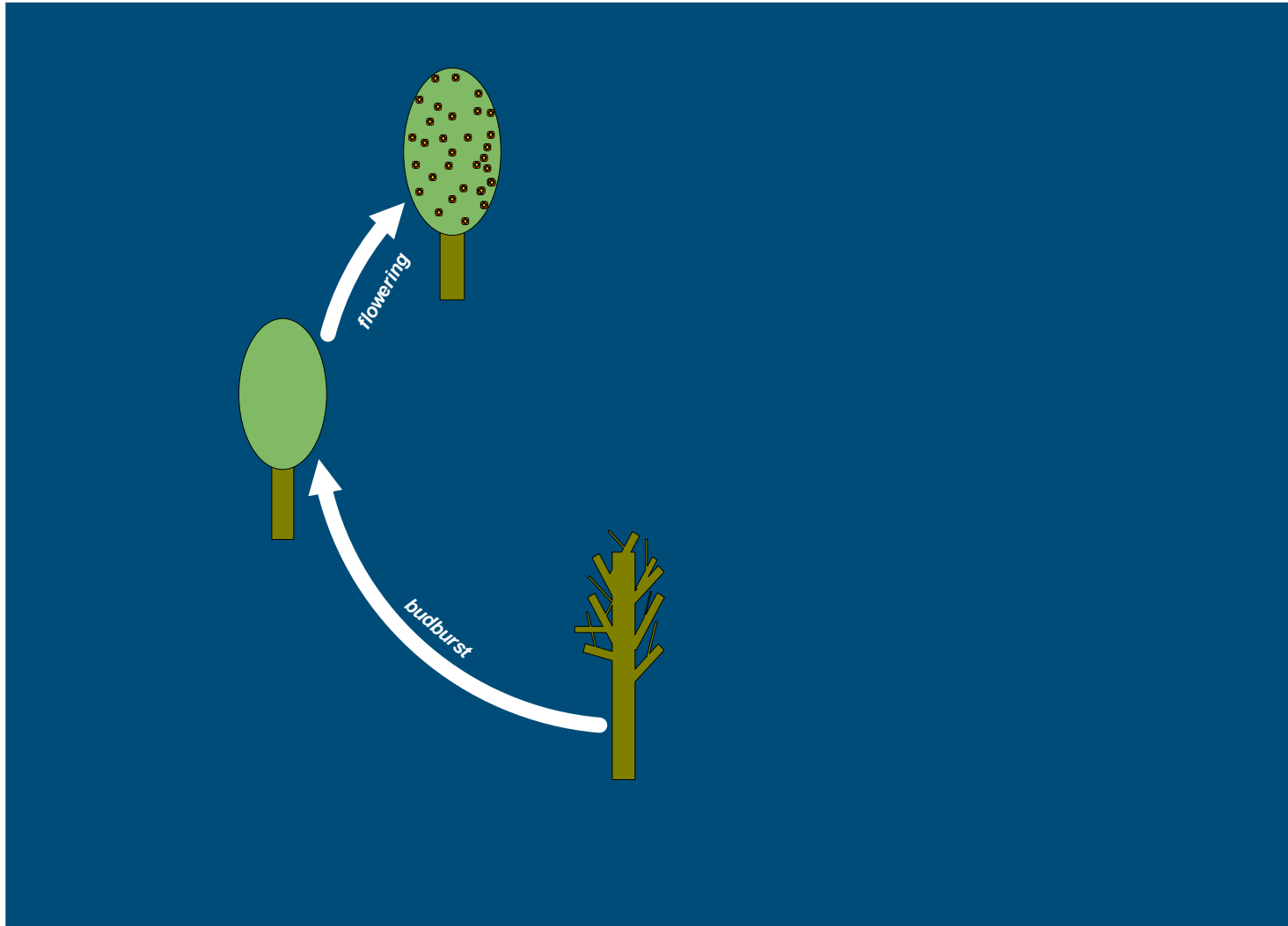
Life and annual cycle



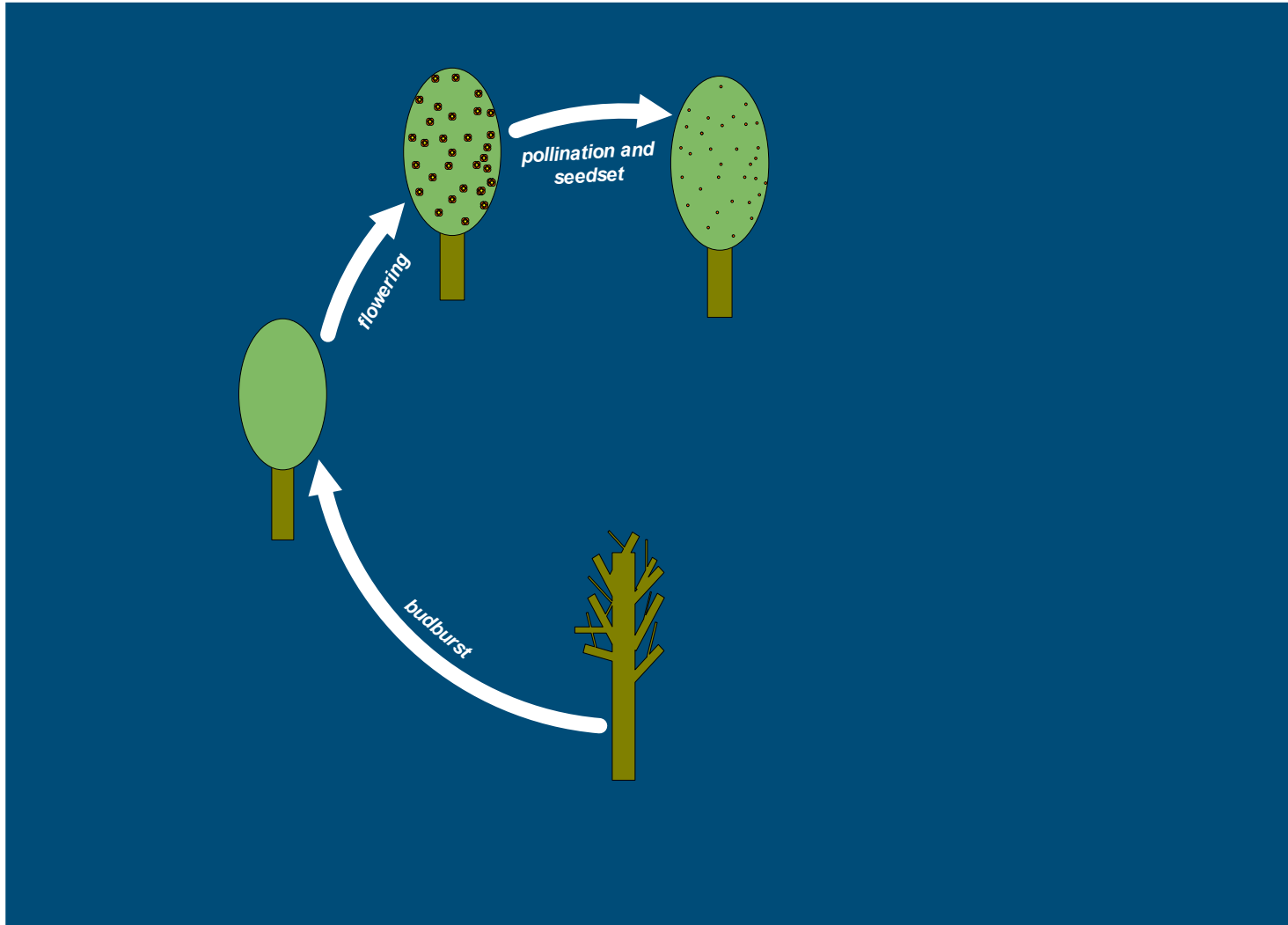
Life and annual cycle



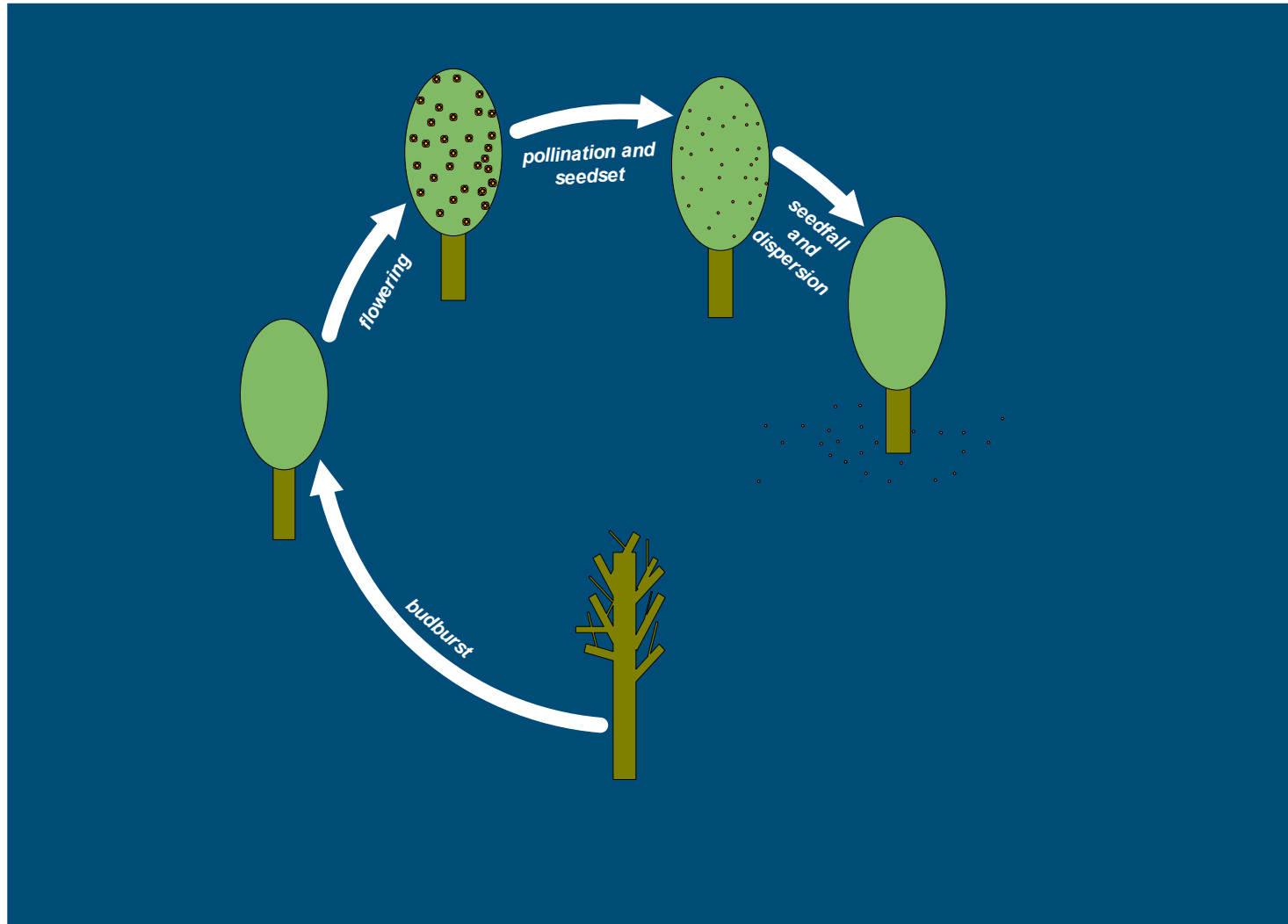
Life and annual cycle



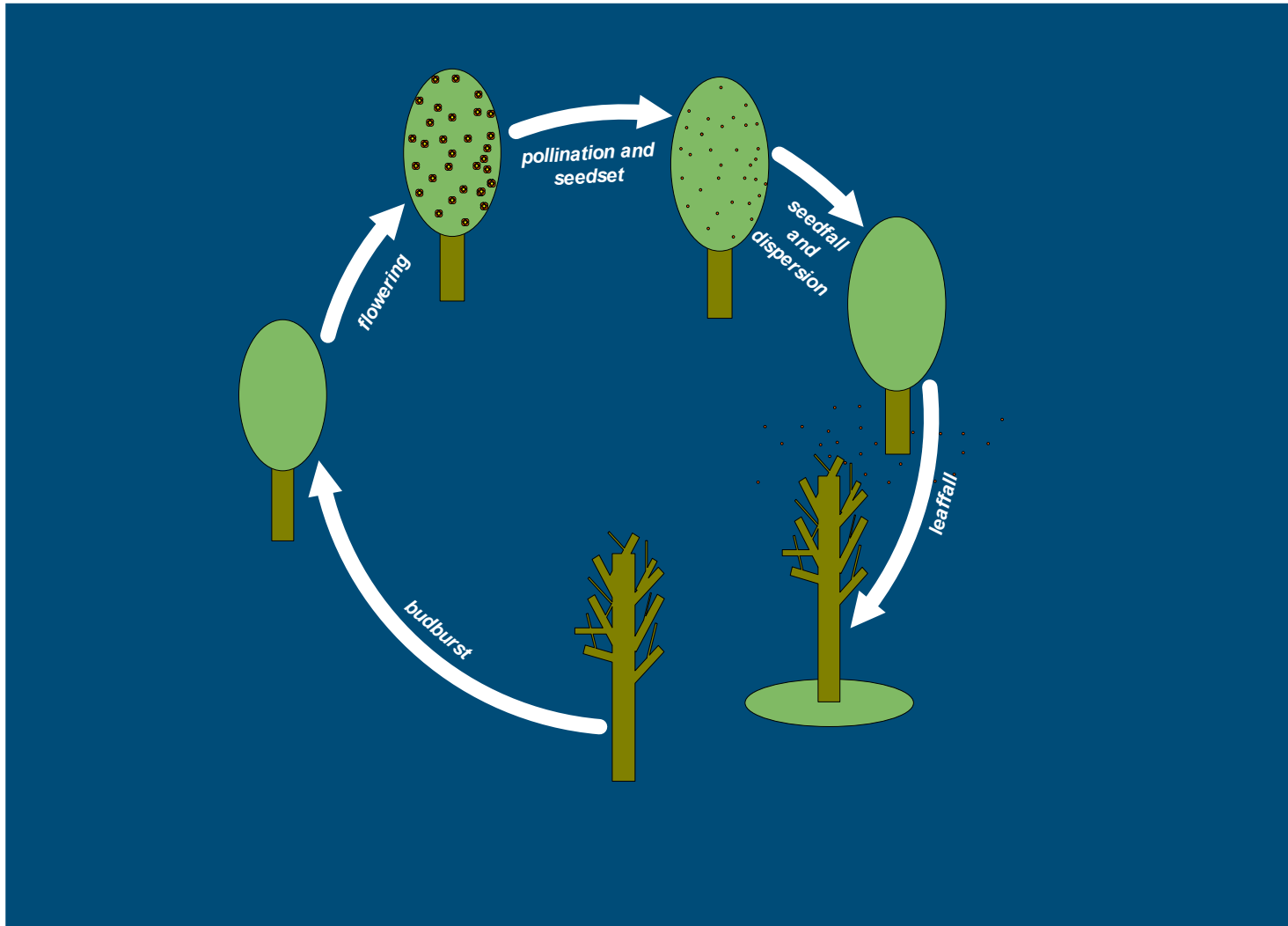
Life and annual cycle



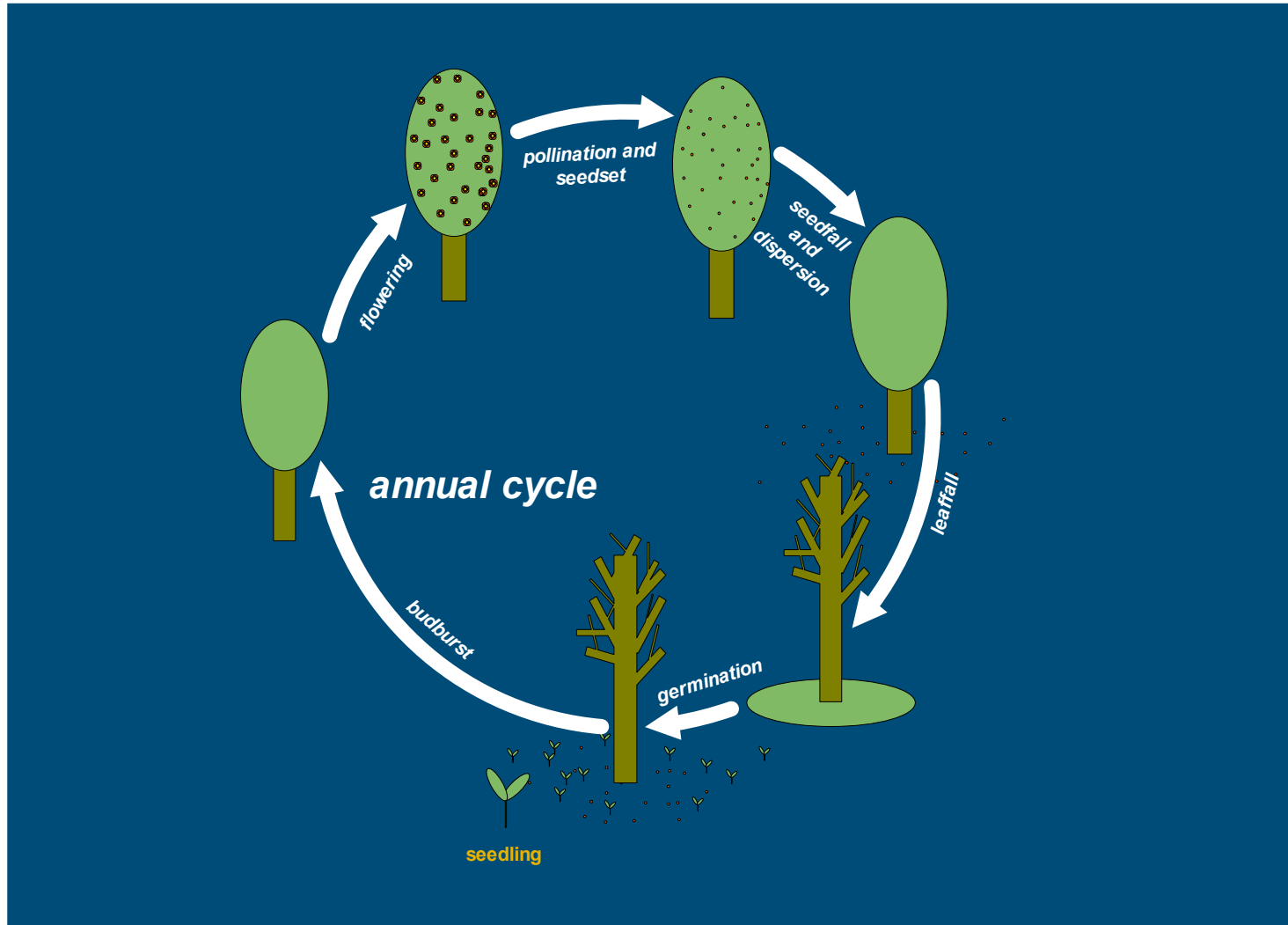
Life and annual cycle



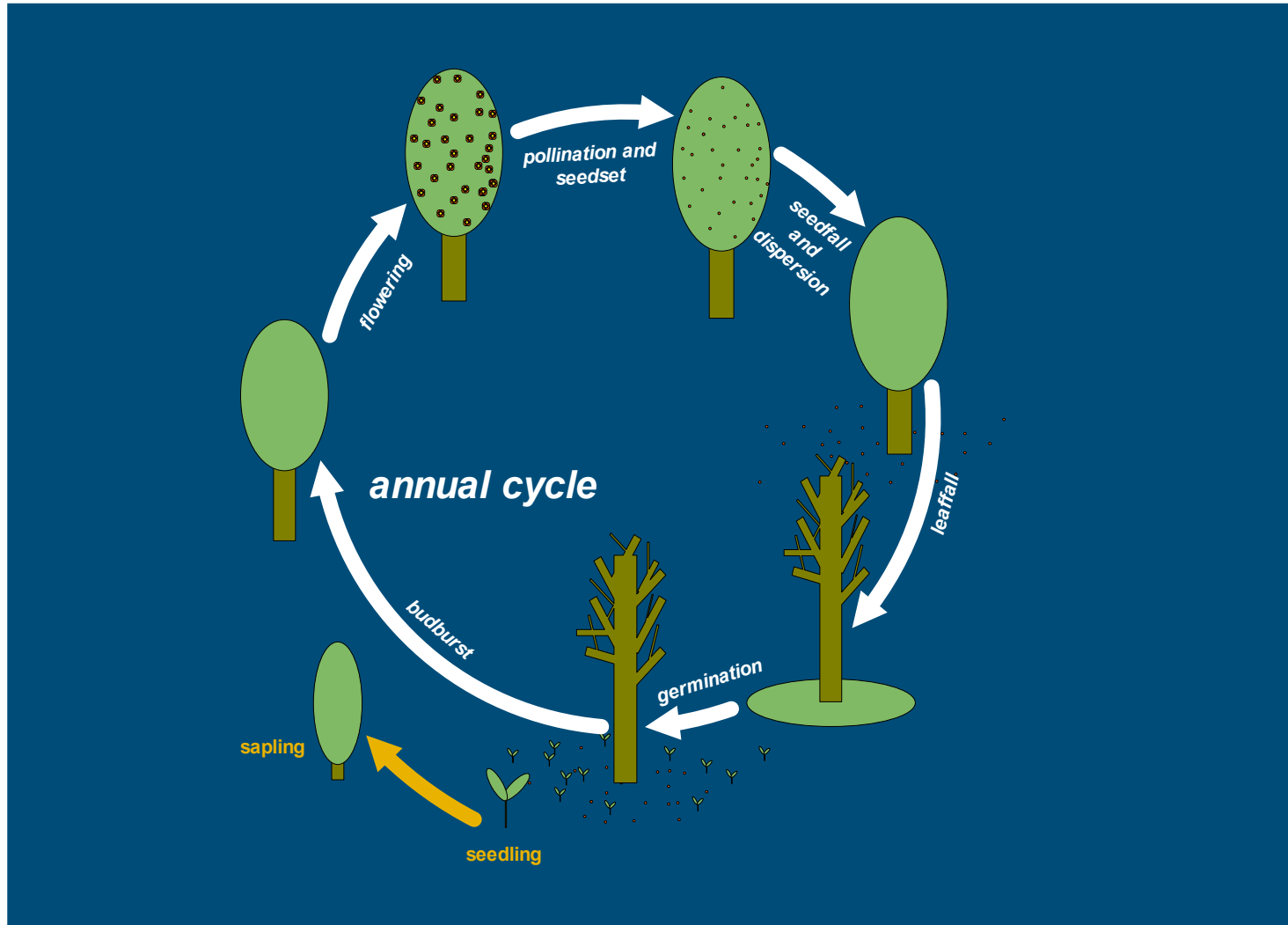
Life and annual cycle



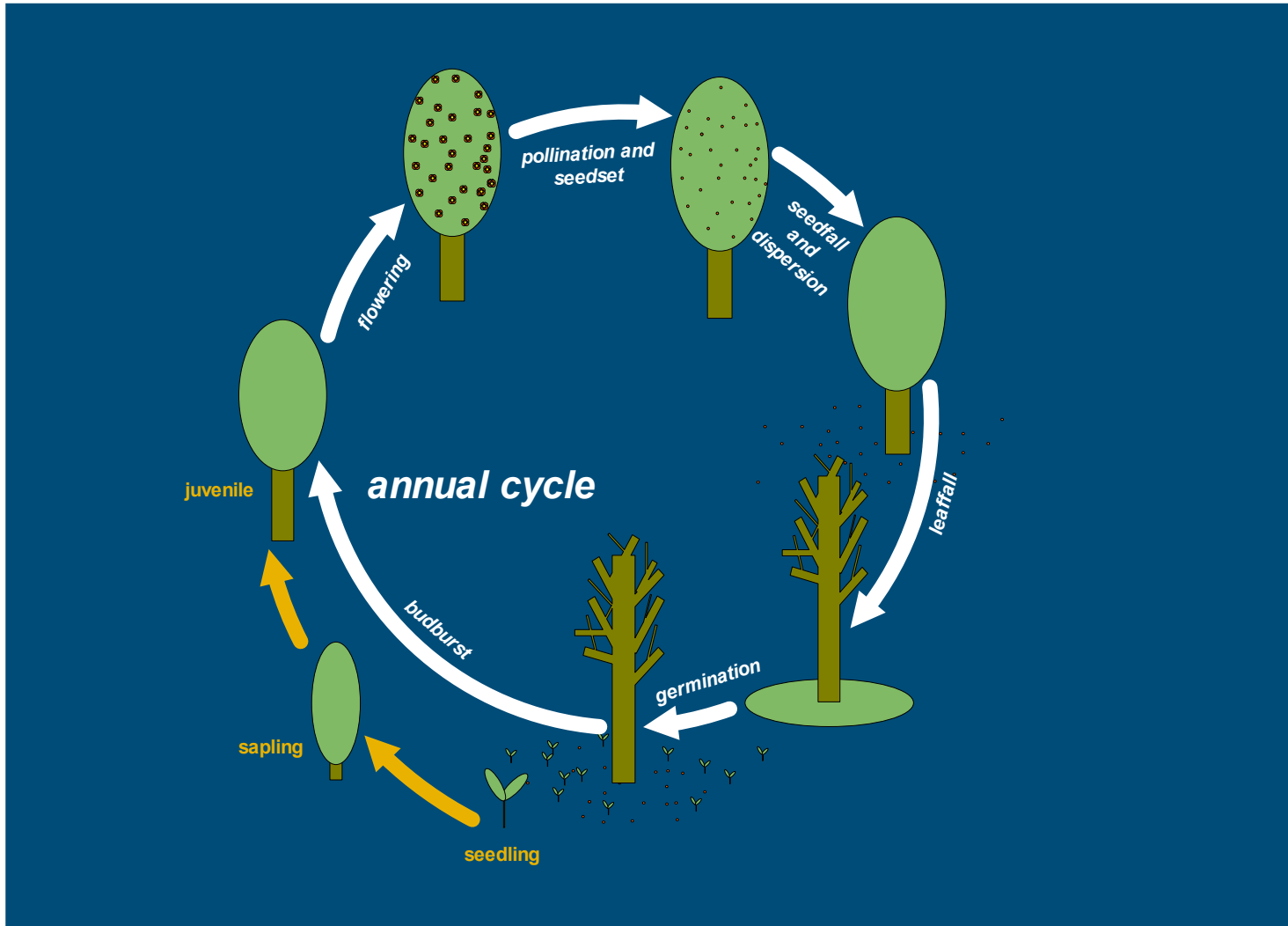
Life and annual cycle



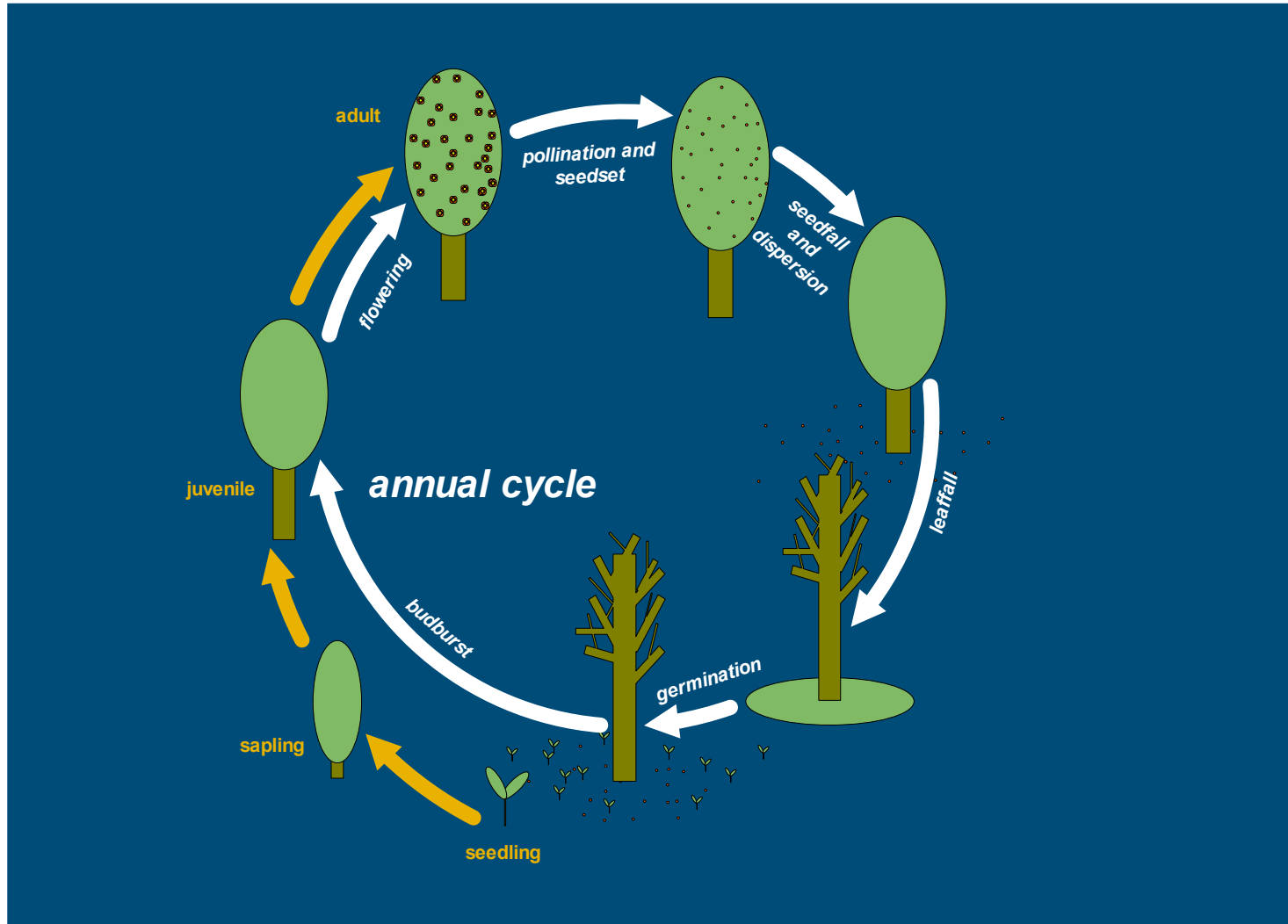
Life and annual cycle



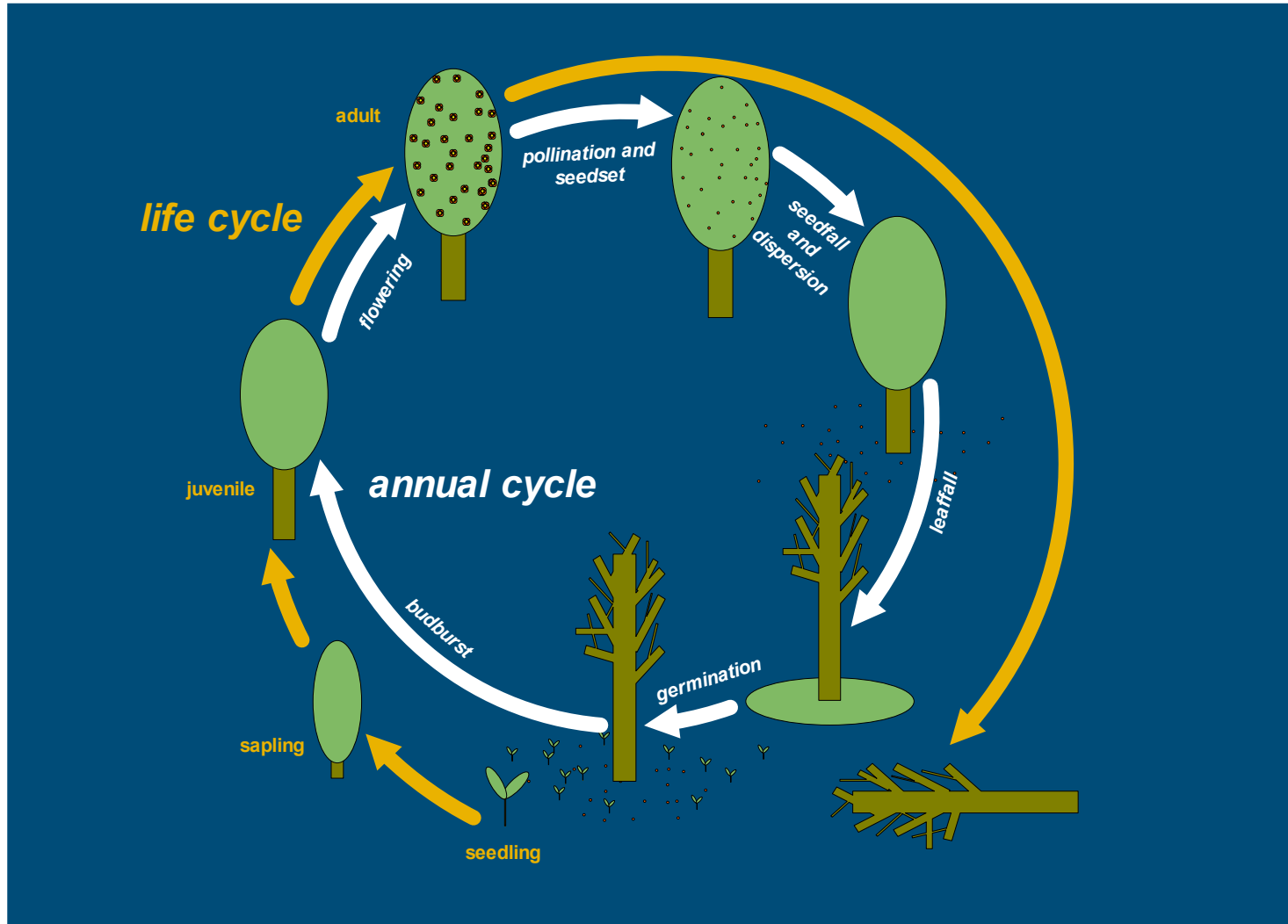
Life and annual cycle



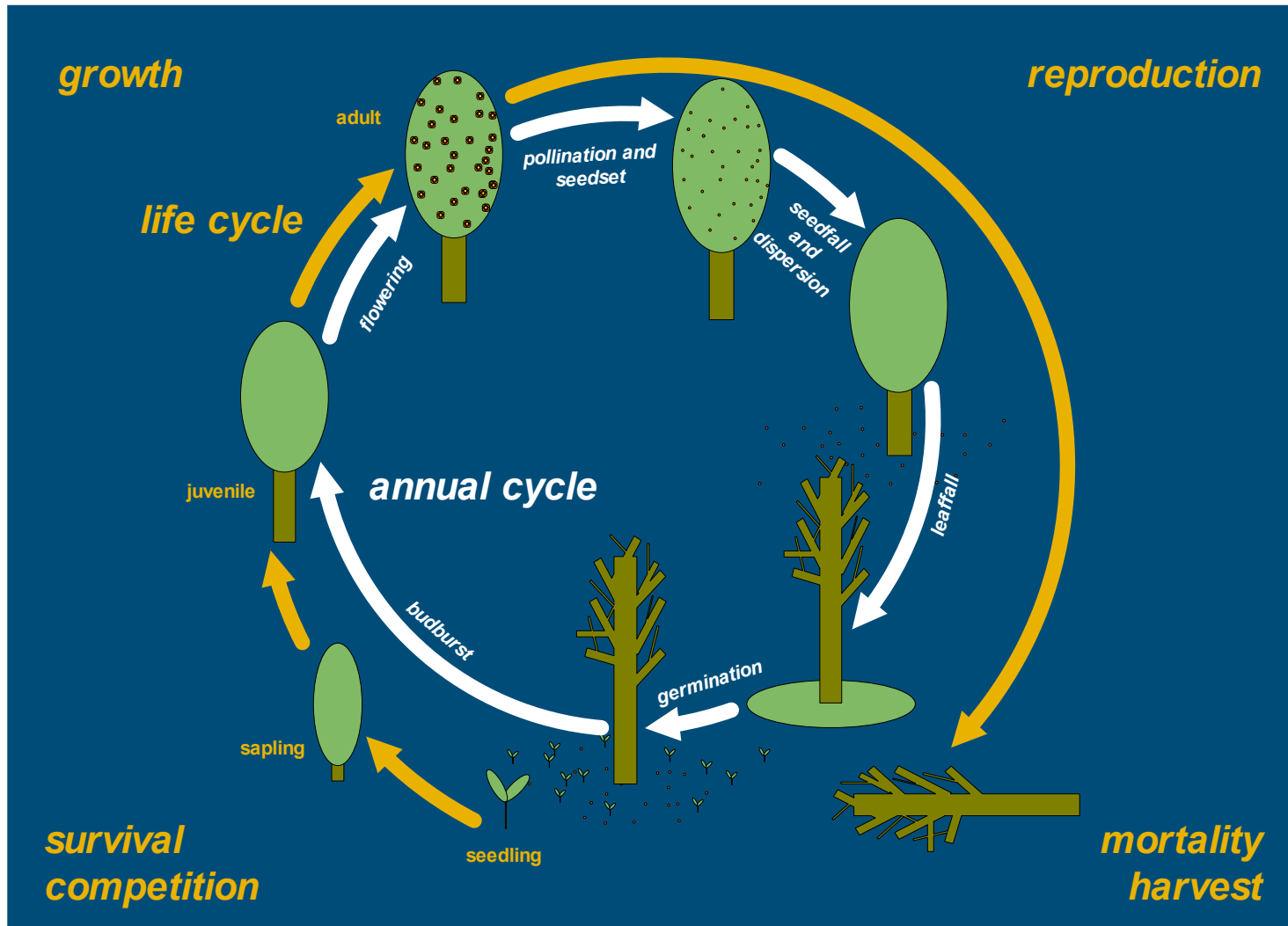
Life and annual cycle



Life and annual cycle



Life and annual cycle



Approach of genetic component of ForGEM

Selection of phenotypic feature relevant in for competition, survival or establishment. E.g.:

- **Timing** (buddburst, flowering, germination,)
- **Tolerance** (frost, wind throw, drought,)
- **Efficiency** (resource utilization => Competition)

Genetic processes: selection & migration

Quantify genetic model for phenotypic trait, default:

- 10 loci; 2 alleles per locus per trait
- no recombination
- additive genetic variance
- no mutation
- initial allelic frequency based on equilibrium assumption (Nei)
- allelic effects such that mean and variance of trait in observed population are met

Modeling genetics

Creating new individuals from parents:

New (parameter) *value* = genetic model + value drawn from distribution
(based on environmental variance)

Deterministic part:

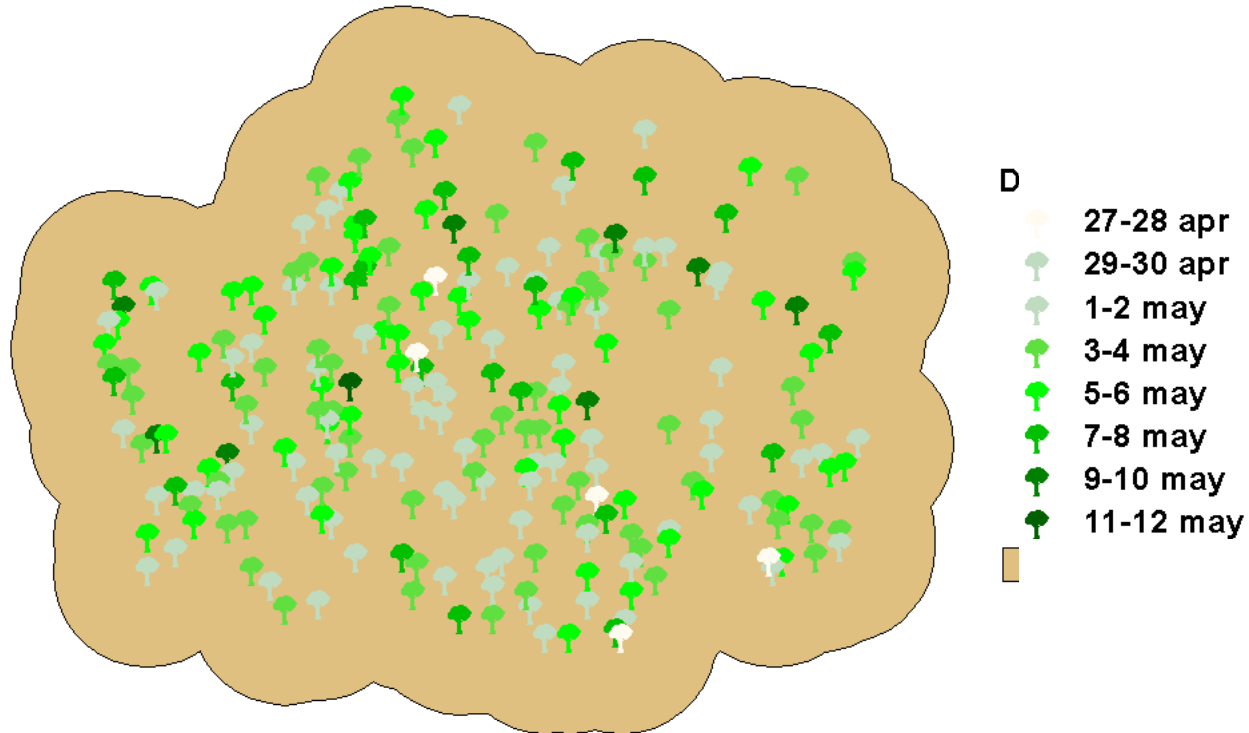
- To keep track of genome define Genome subsystem of tree/seed
- DNA model (e.g. GLM): Allele value on Locus defines a parameter value in equation
- Haploid, diploid, ...
- Multi locus, multi alleles, initial allele distribution

Probabilistic part:

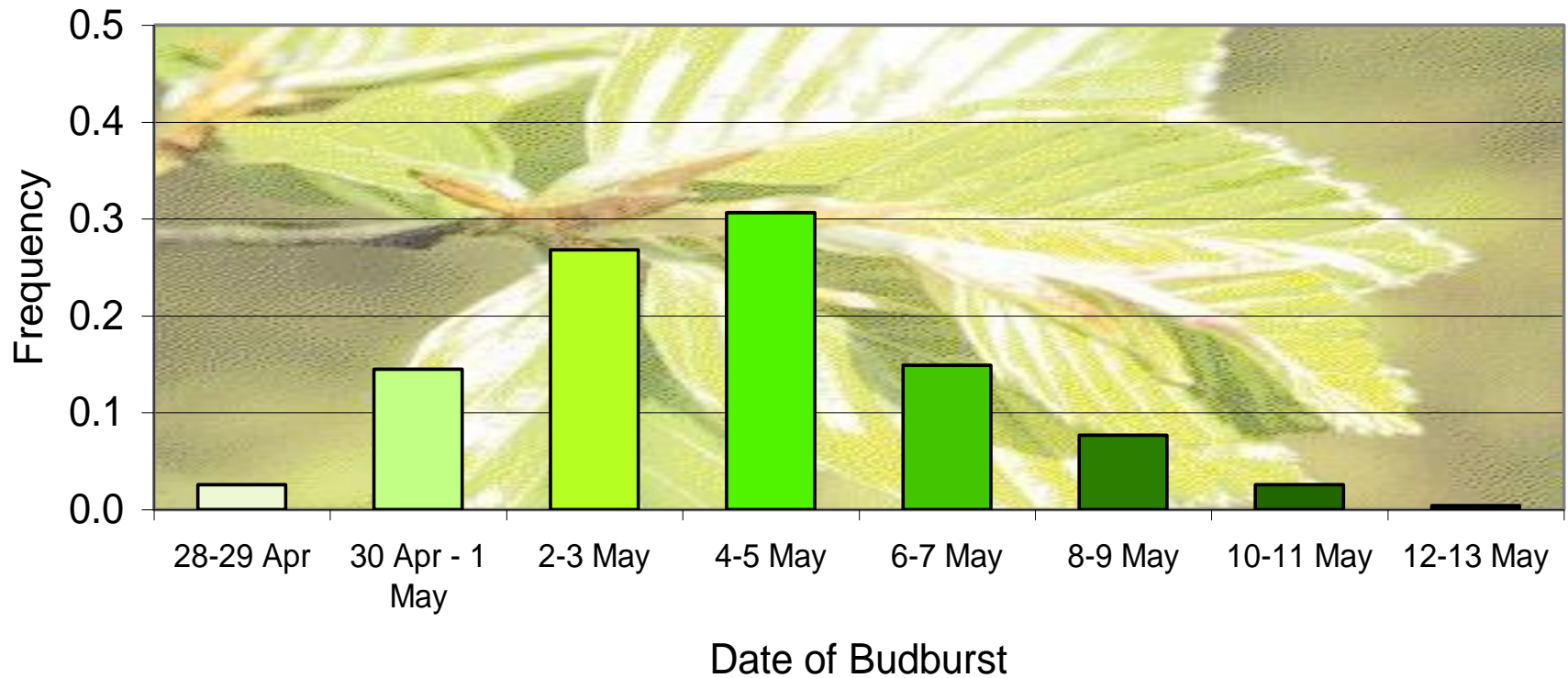
- Create new distribution on basis of the *value* of parents and draw from that distribution
- Need genetic variance and environmental variance

Import pollen, seeds or even individuals from outside study area

Phenotype (budburst) parent trees

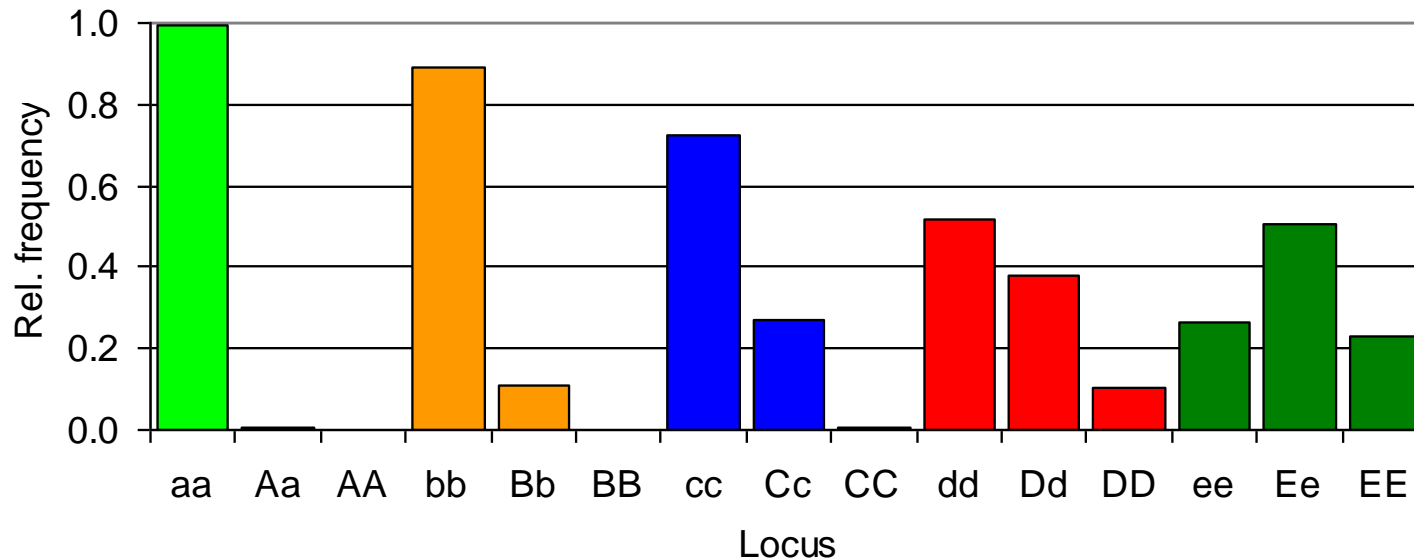


Budburst frequency over 235 adult trees



Example allele frequencies in population

Genotype frequency 235 adults trees



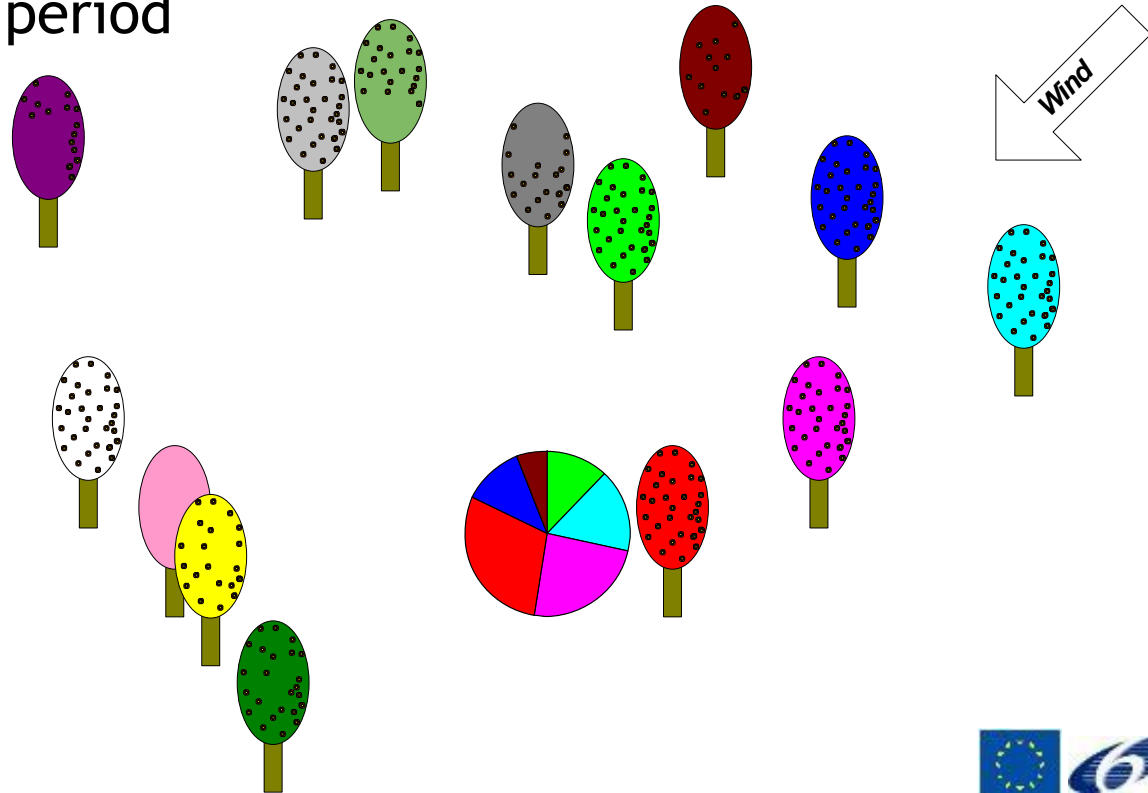
Procedure:

- Assign a allelic value to each allele
- Add all values together
- Add environmental deviate

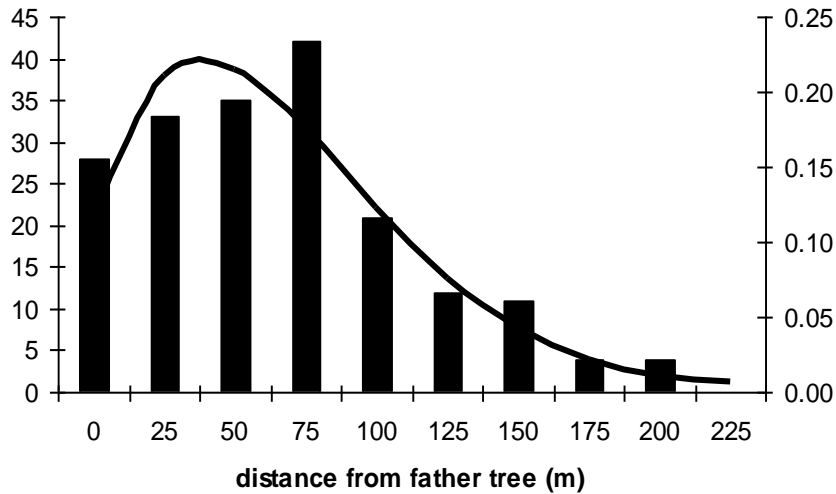
Pollination

Fraction pollen at mother tree:

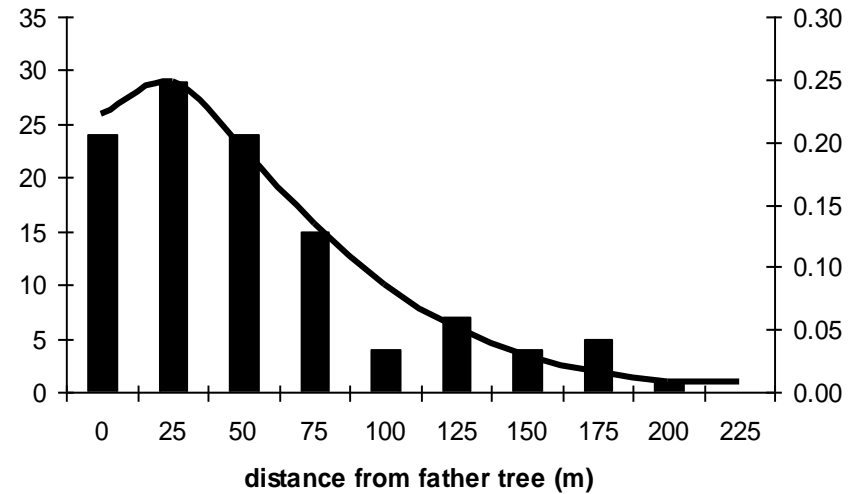
- Wind direction and -speed
- Number of flowers
- Overlapping flowering period
- Self pollination
- Pollen from outside
- Compatibility



St Baume

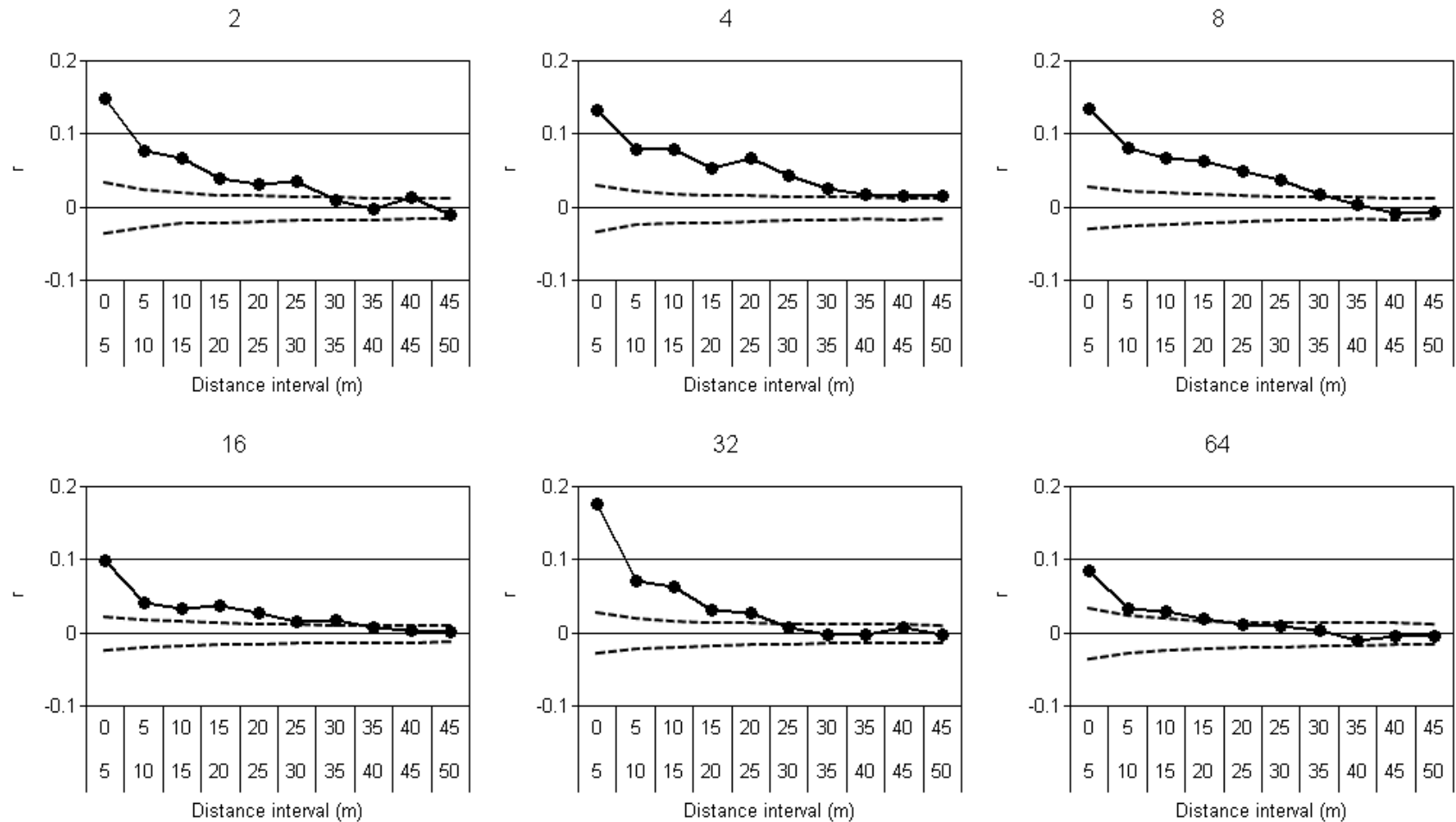


Ventoux



Observed and estimated pollen dispersal curve in France.

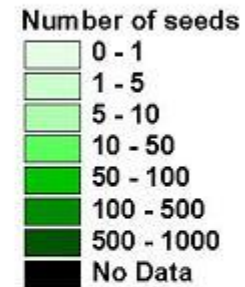
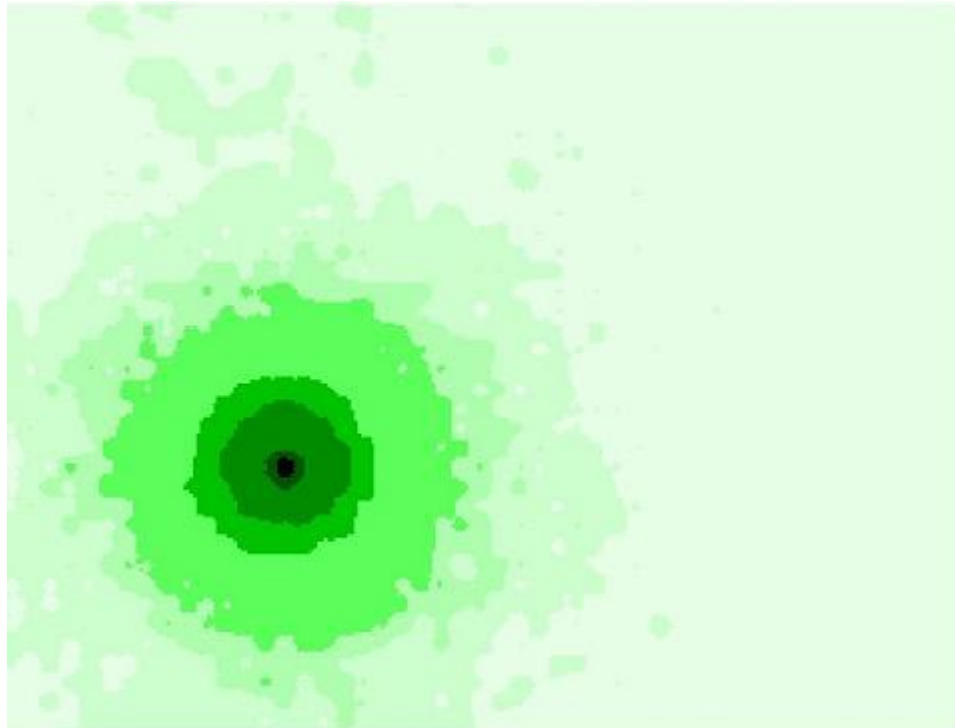
Sensitivity analysis

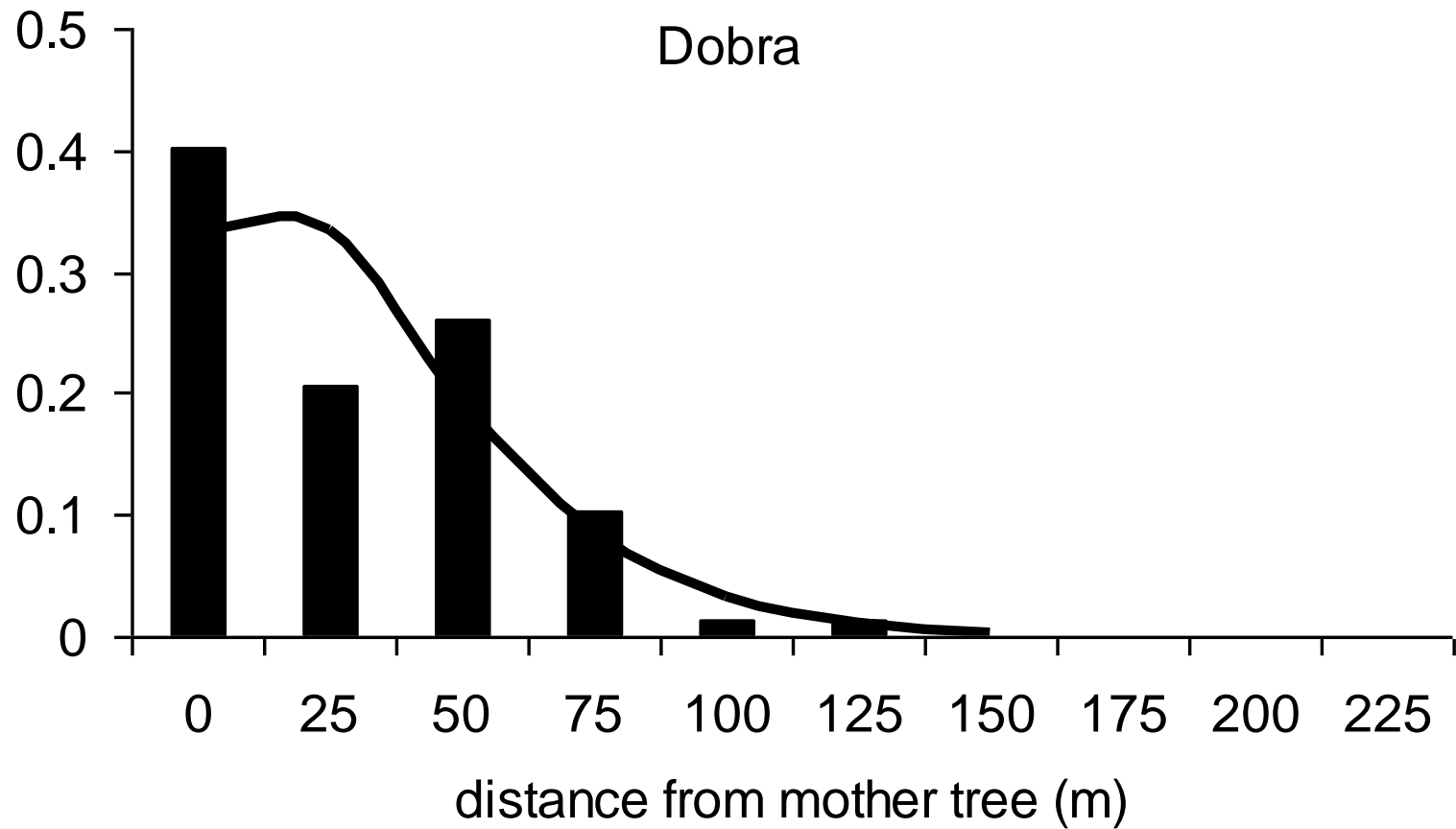


Effect of pollen dispersal distance (expectation of Weibull curve) on spatial genetic structure (t=300yr)

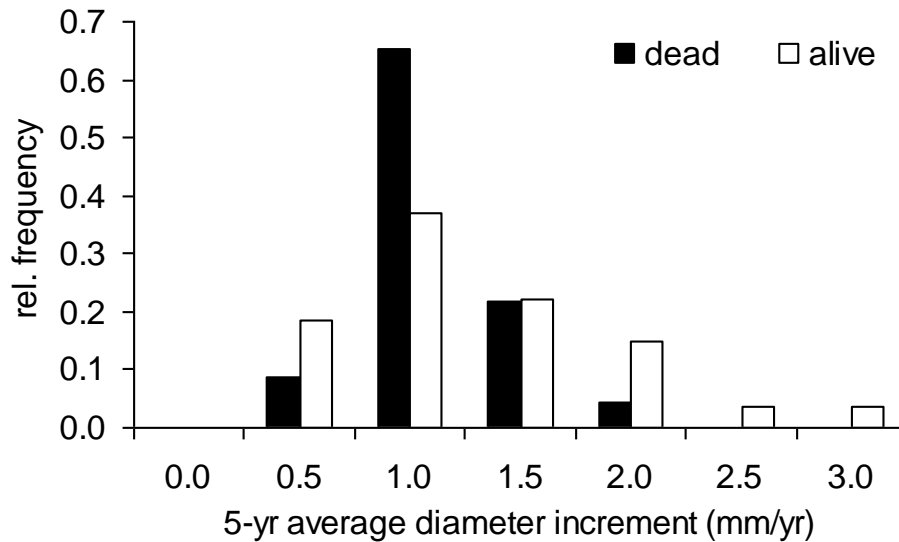
Seed dispersal

Depends on distance function to tree

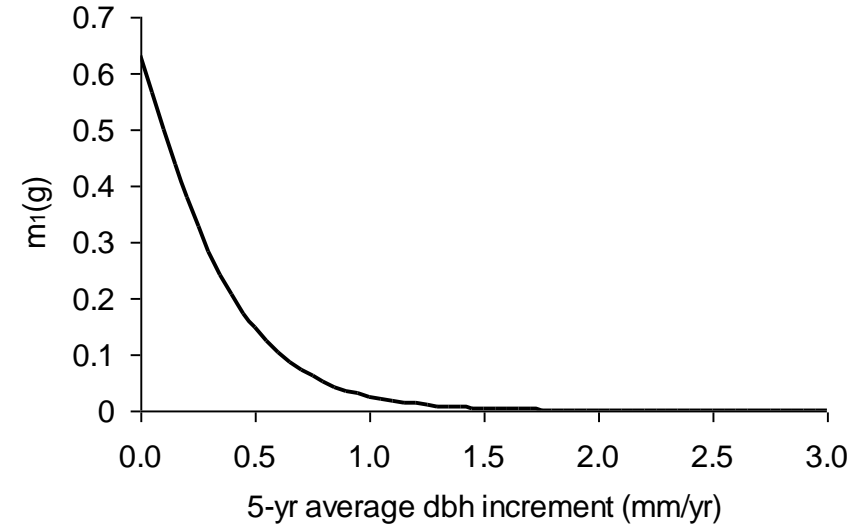




Observed and estimated seed dispersal curve in Austria



Observed distribution of diameter increment of currently living and currently dead trees



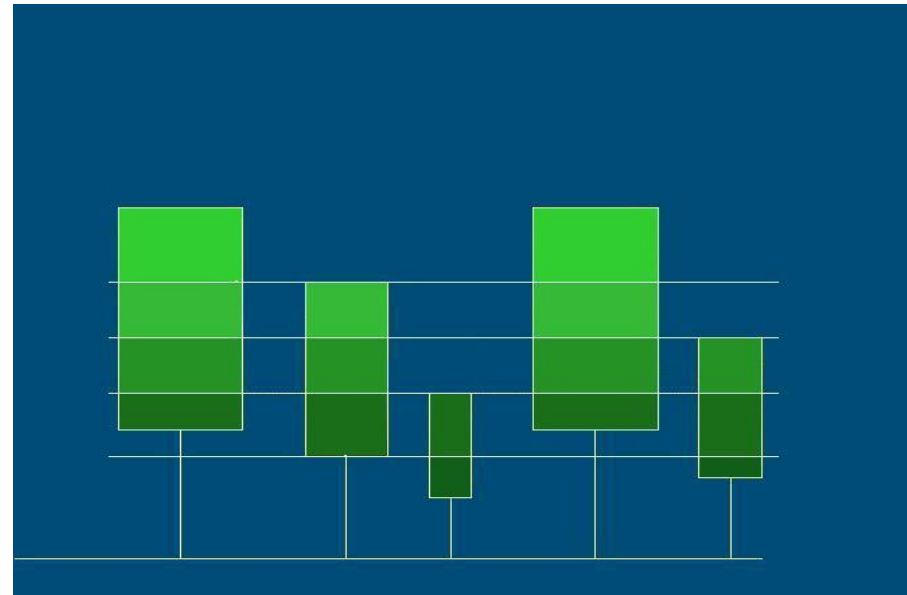
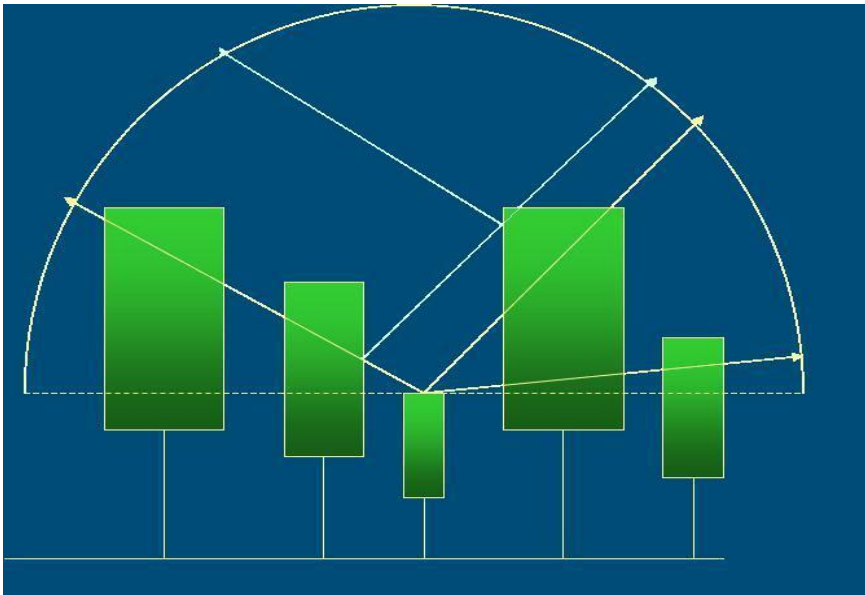
Derived probability of annual mortality depending on growth (Kobe & Pacala)

Light interception

Ray tracing or Gap model

Gap model for seedling and ray tracing for 'adults'

Purpose: amount of energy intercepted by the plant

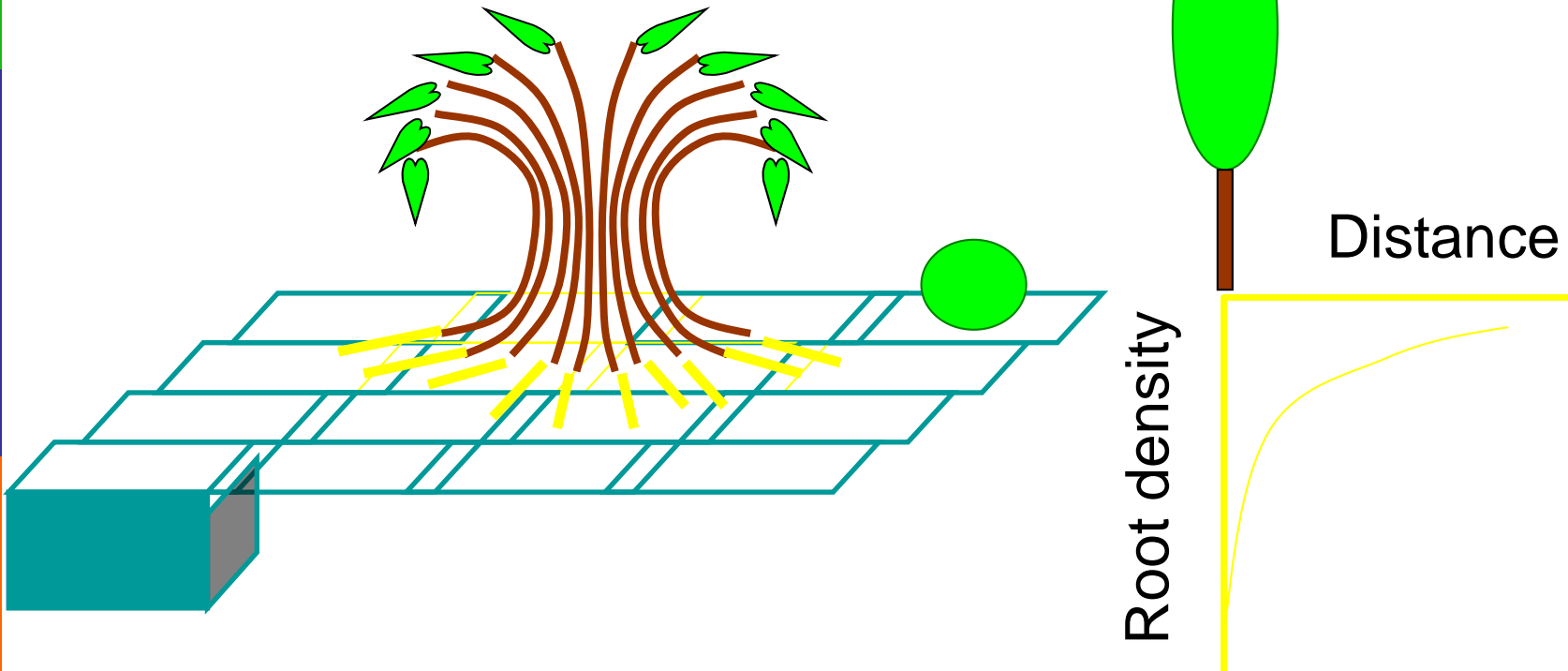


Water use

Gas exchange (e.g. temp, humidity, radiation) => water need

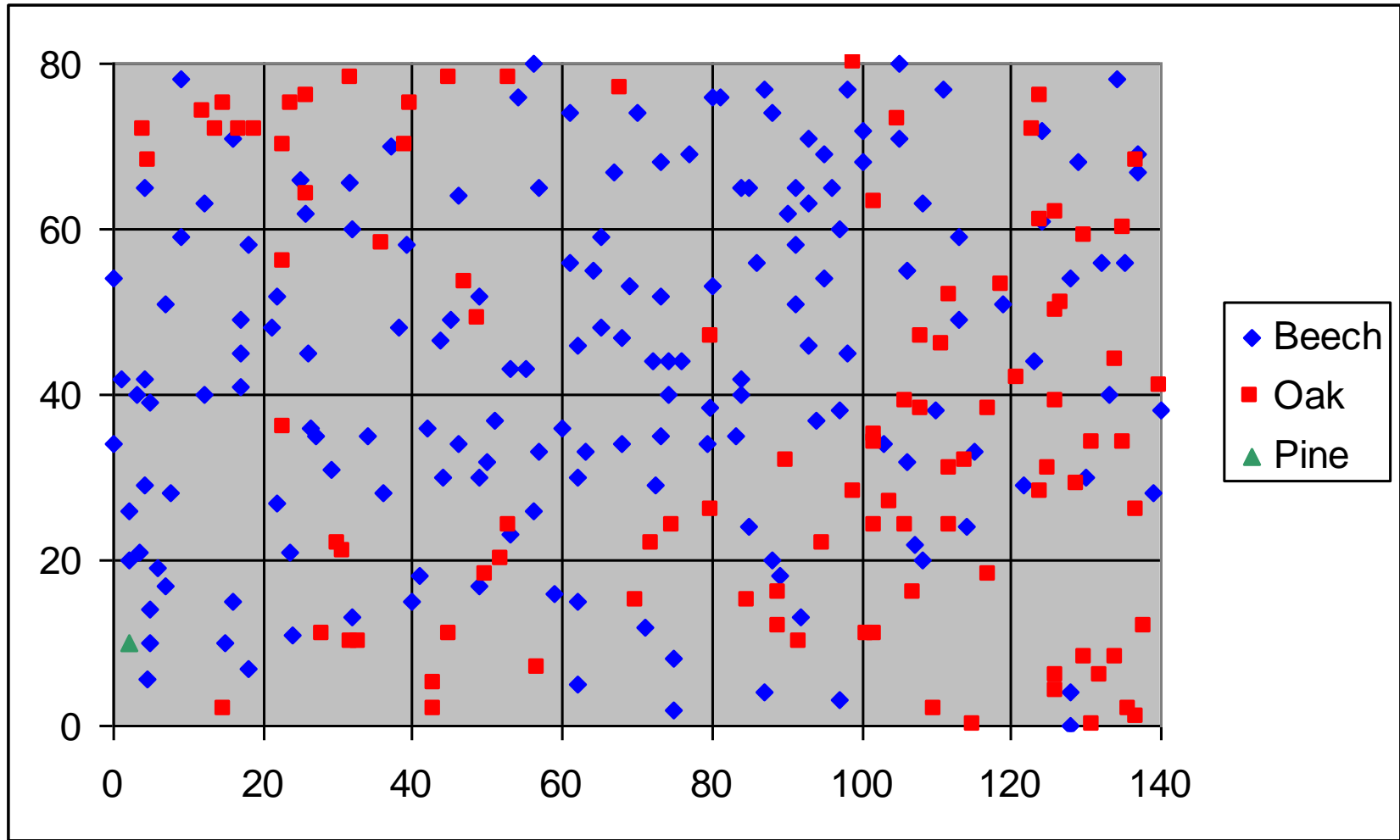
Dependent on root density per pocket

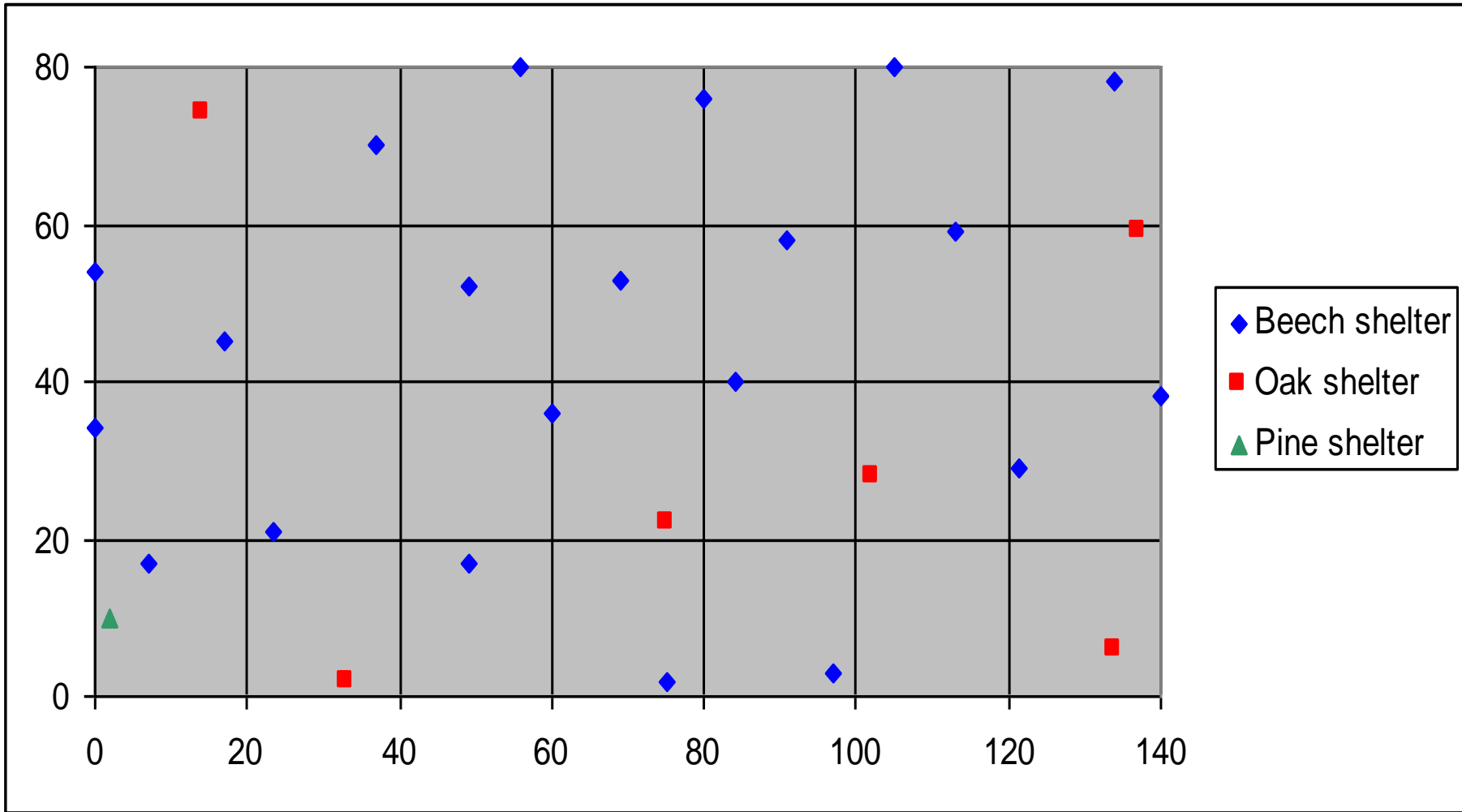
Water exchange between pockets

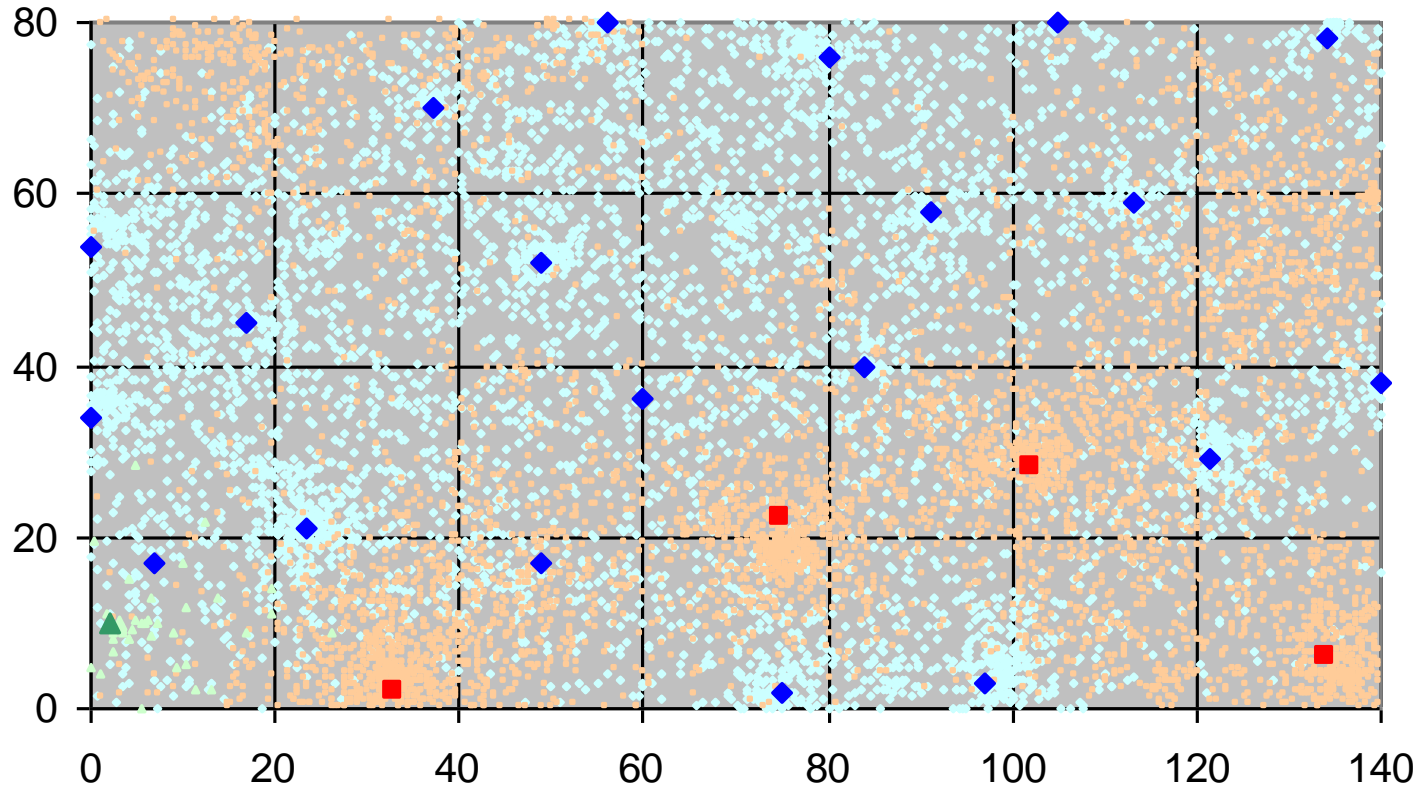


- Sheltercut
- Group selection
- Future tree selection

Sheltercut: initial situation

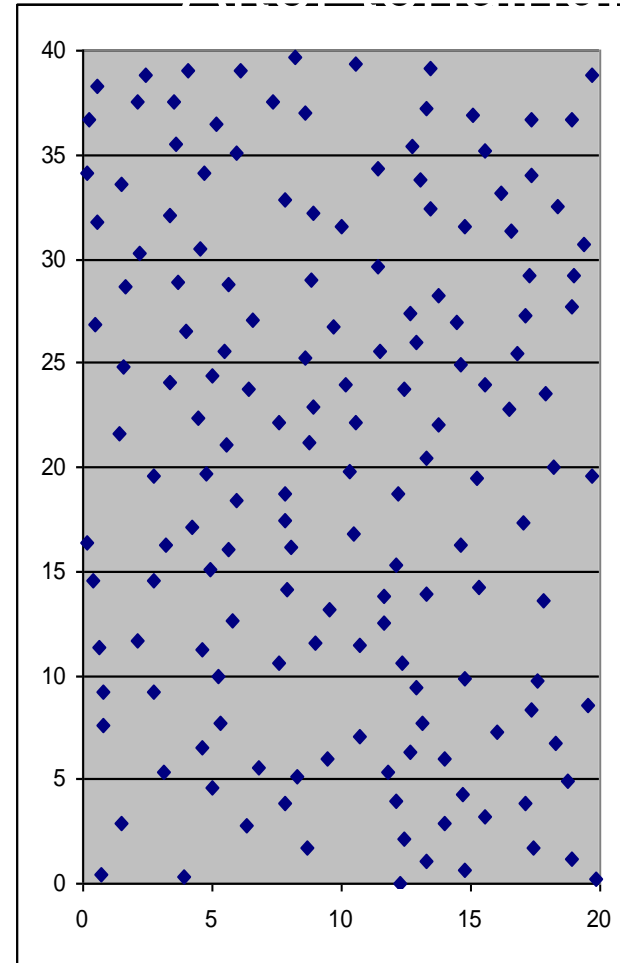
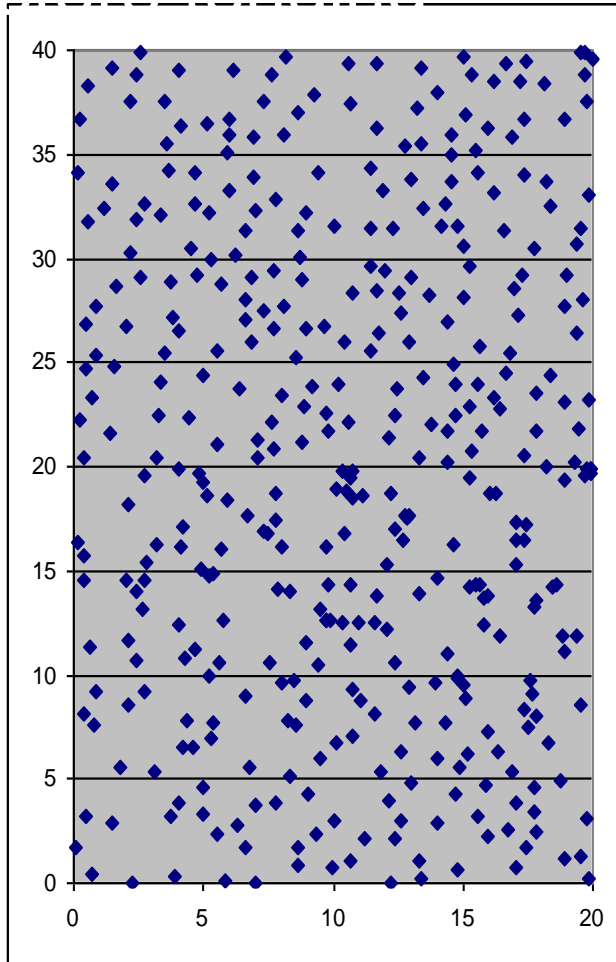




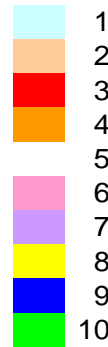


- ◆ Beech regeneration
- ◆ Oak regeneration
- ◆ Pine regeneration
- ◆ Beech shelter
- Oak shelter
- ▲ Pine shelter

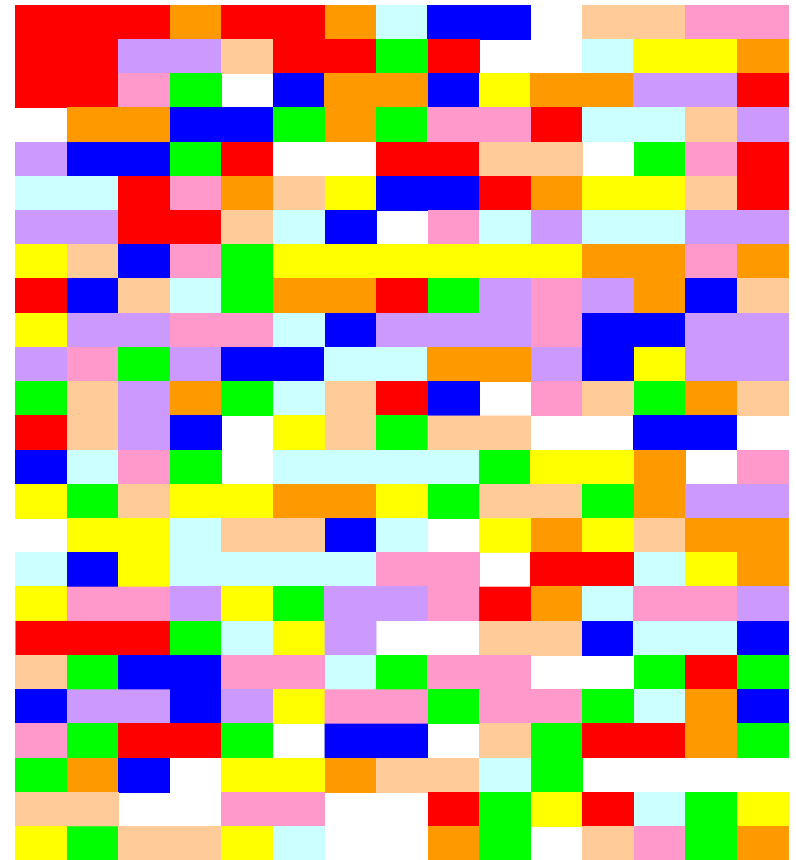
Sheltercut: tending



Small and large gaps

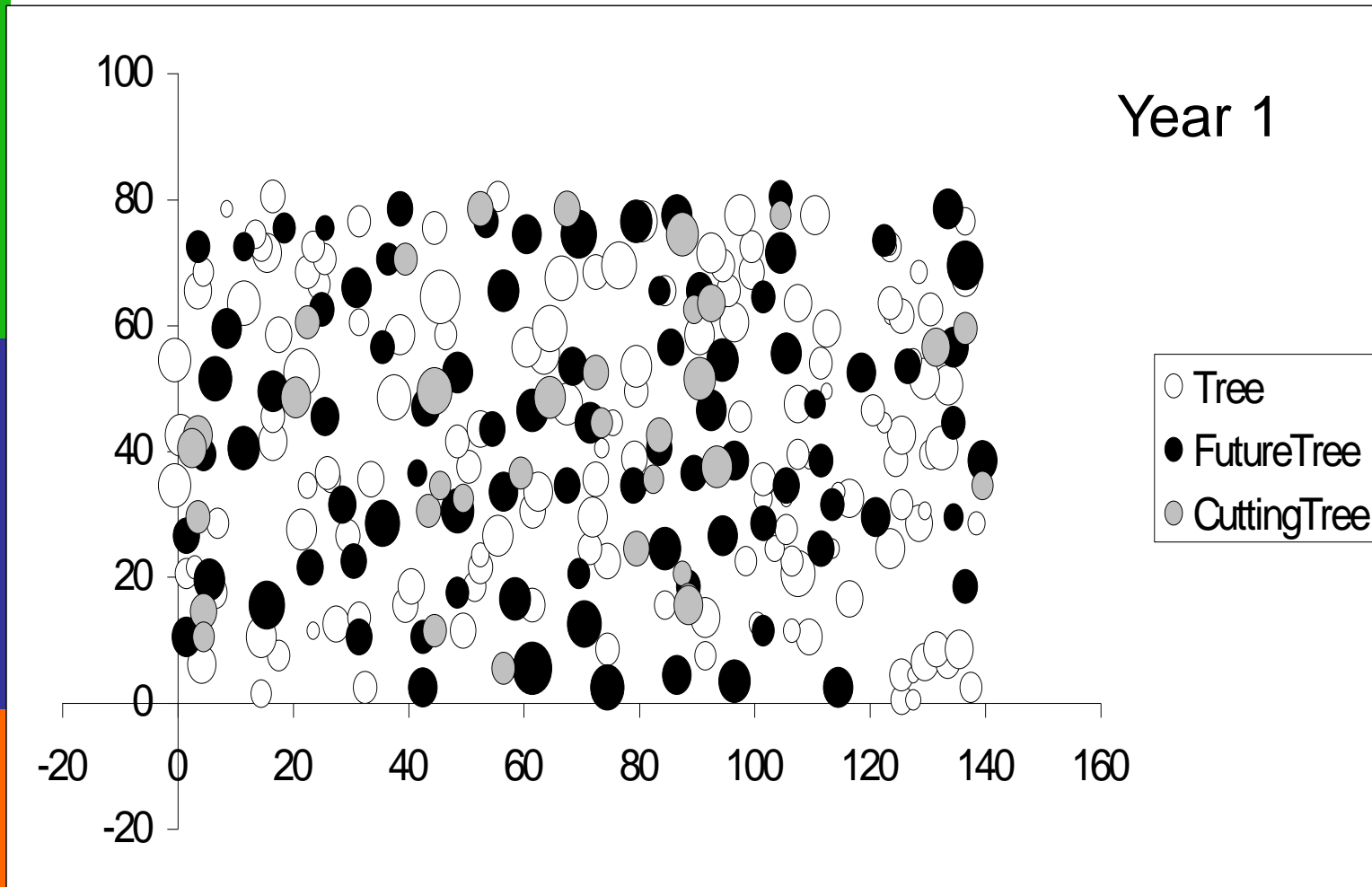


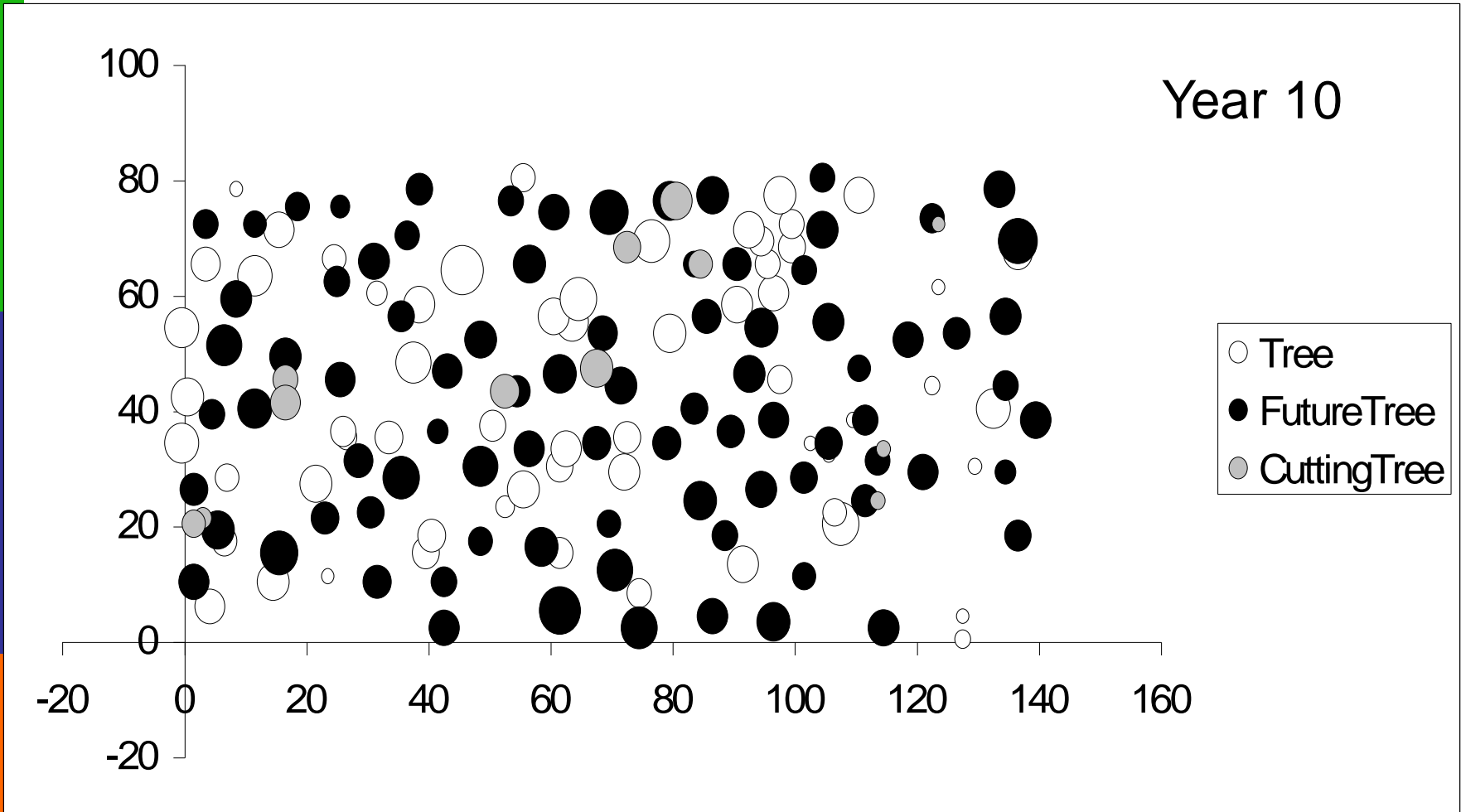
Mainly small



Gridsize: 20x20m

Future tree selection





Structure of the presentation

Modelling principles

The model ForGEM

- genetic components
- eco(physio)logical components
- forest management

Examples: impact of forest management on:

- basal area
- tree density
- phenotypic value of genetic traits
- response of phenotypic trait values
- genetic diversity
- spatial genetic structure

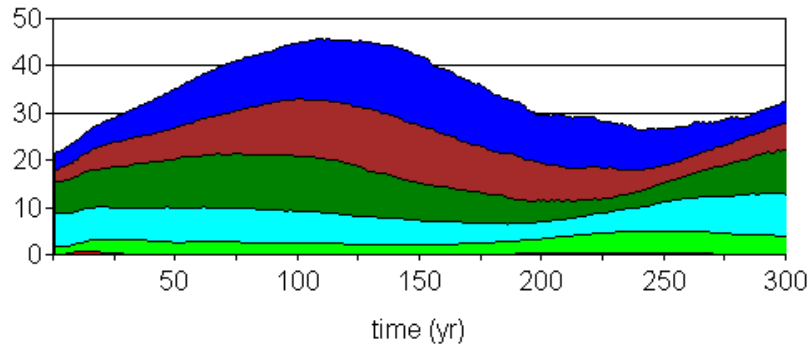
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Modelling the annual cycle

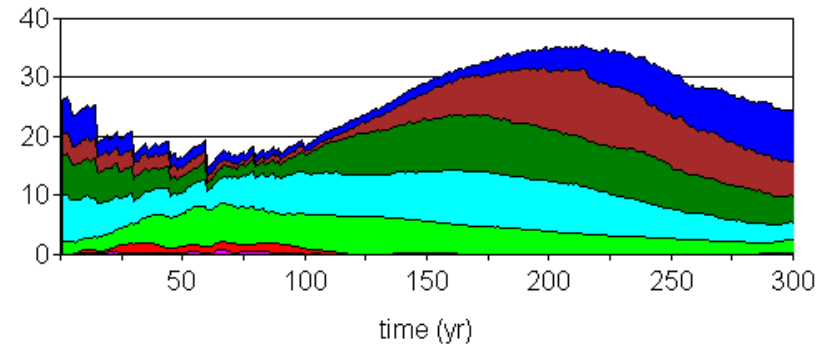
Examples: impact of climate change

Basal area per Dbh-class (m² ha⁻¹)

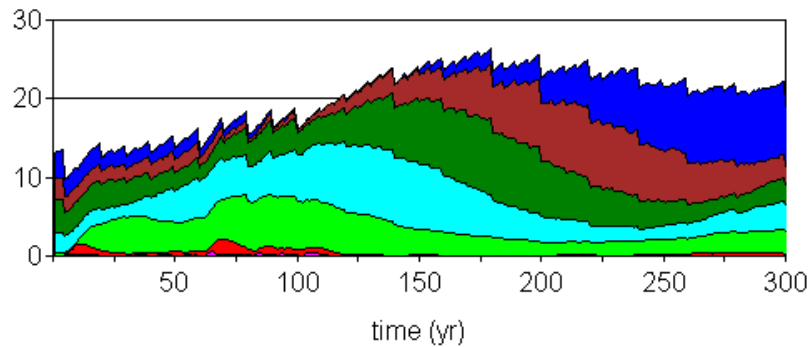
Fagus sylvatica - 1. No Management



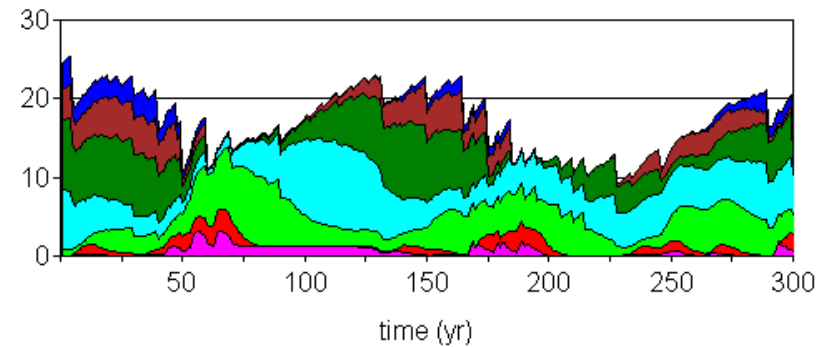
Fagus sylvatica - 2. Nature oriented



Fagus sylvatica - 3. Group selection



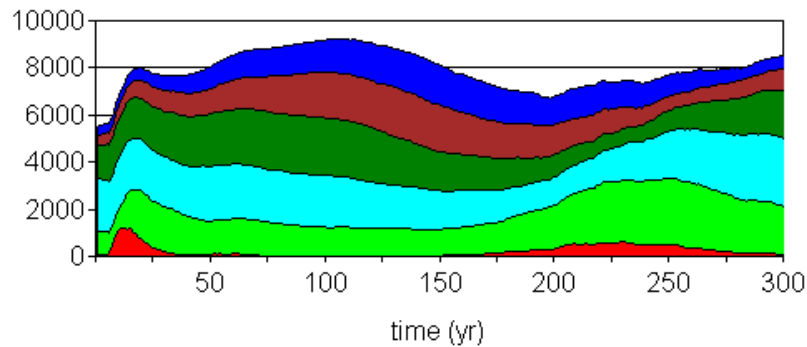
Fagus sylvatica - 4. Sheltercut



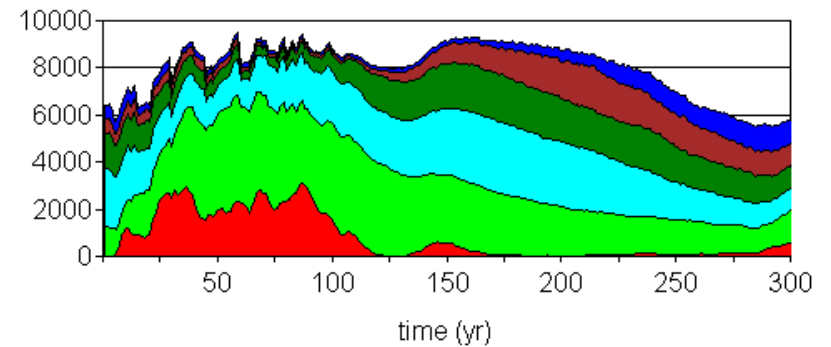
■ Average of Dbh90-500
 ■ Average of Dbh70-90
 ■ Average of Dbh50-70
 ■ Average of Dbh30-50
■ Average of Dbh10-30
 ■ Average of Dbh5-10
 ■ Average of Dbh0-5

Number of trees per Dbh-class (# ha-1)

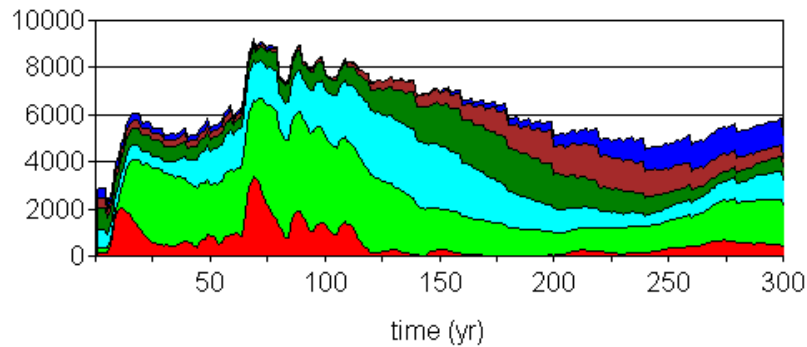
Fagus sylvatica - 1. No Management



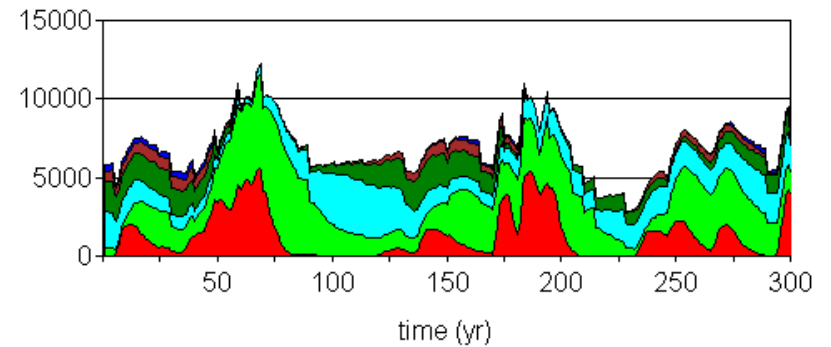
Fagus sylvatica - 2. Nature oriented



Fagus sylvatica - 3. Group selection



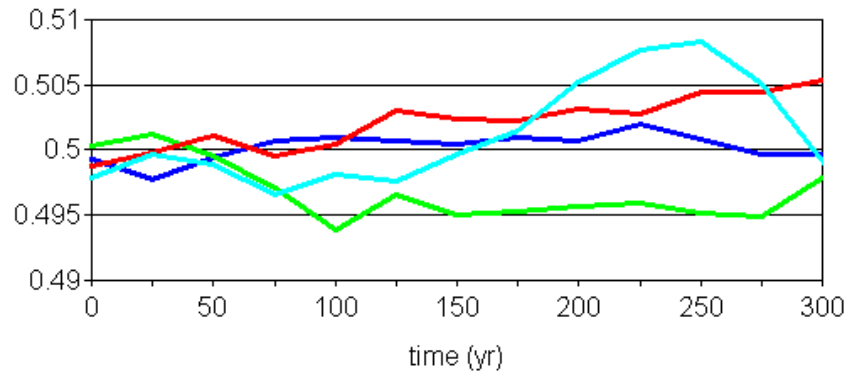
Fagus sylvatica - 4. Sheltercut



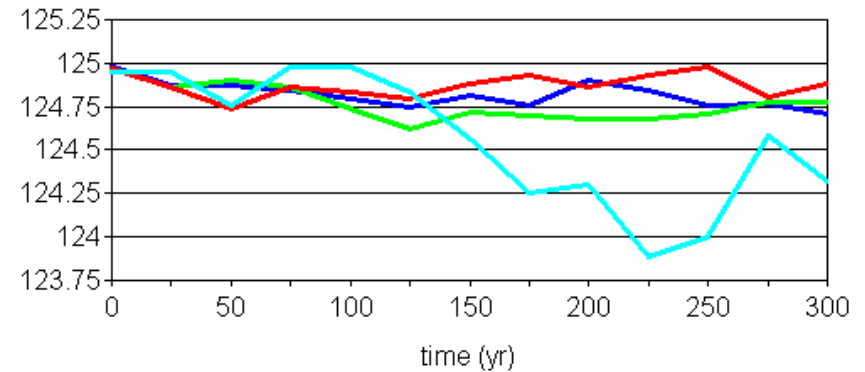
■ Average of Dbh90-500
 ■ Average of Dbh70-90
 ■ Average of Dbh50-70
■ Average of Dbh30-50
 ■ Average of Dbh10-30
 ■ Average of Dbh5-10

Phenotypic value of genetic traits

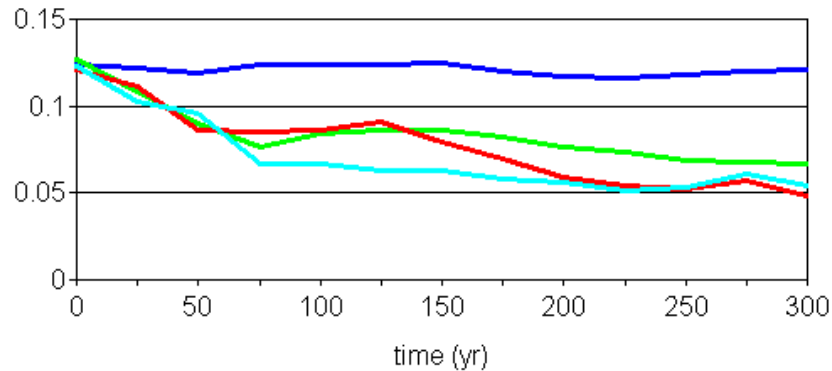
1. Neutral trait



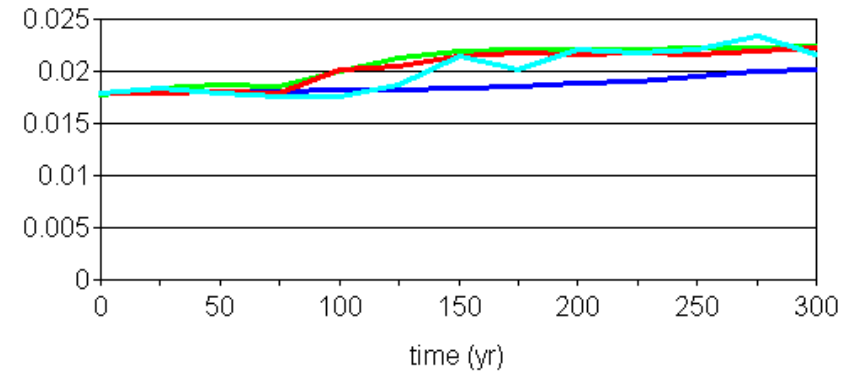
2. Budburst day



3. Spiral grain



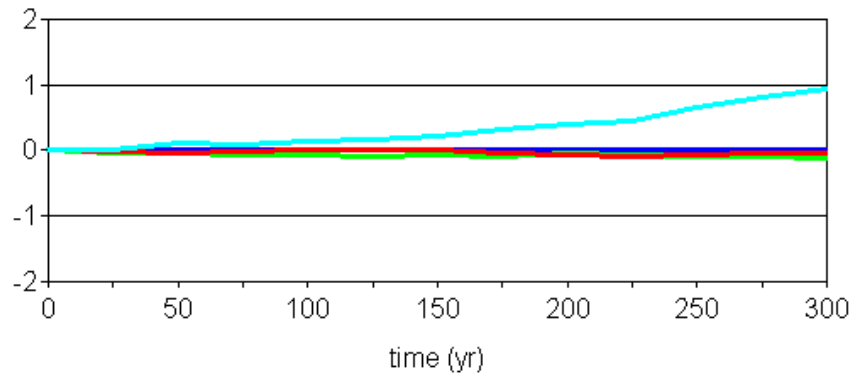
4. C7Hgh



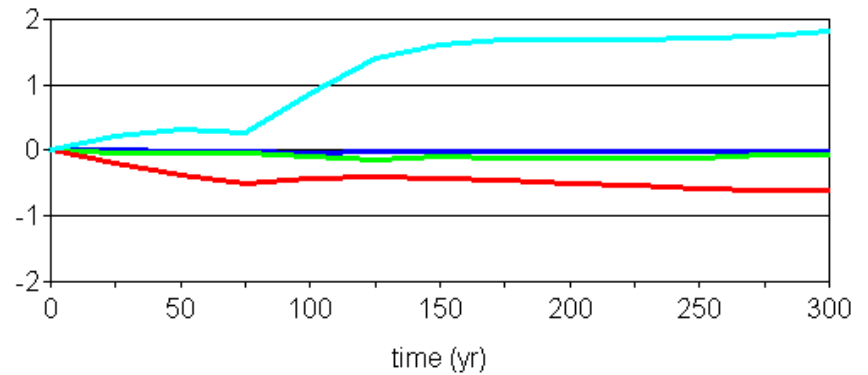
— 1. No Management — 2. Nature oriented — 3. Group selection — 4. Sheltercut

Normalised response of phenotypic traits to management

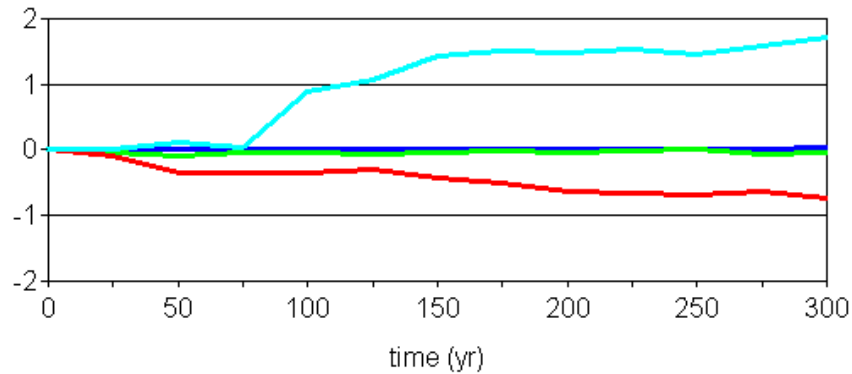
1. No Management



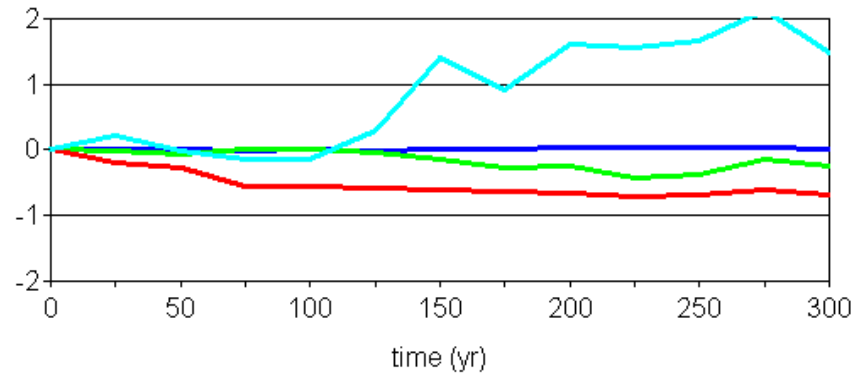
2. Nature oriented



3. Group selection



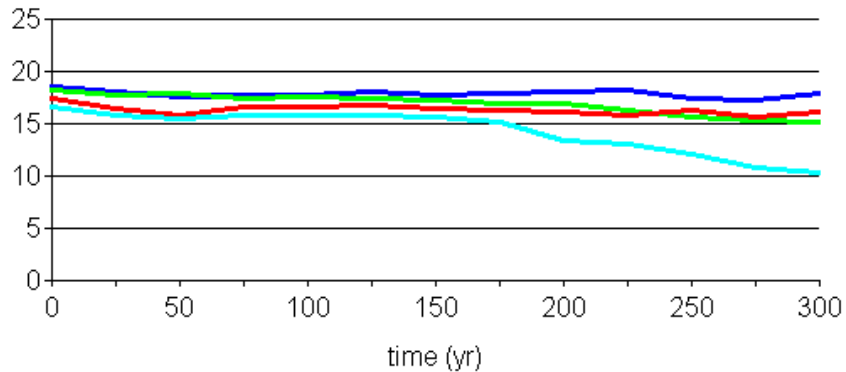
4. Sheltercut



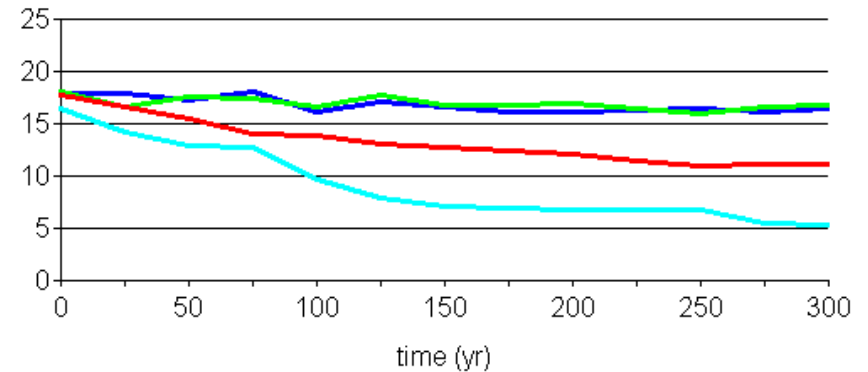
— 1. Neutral trait — 2. Budburst day — 3. Spiral grain — 4. C7Hgh

Genetic diversity

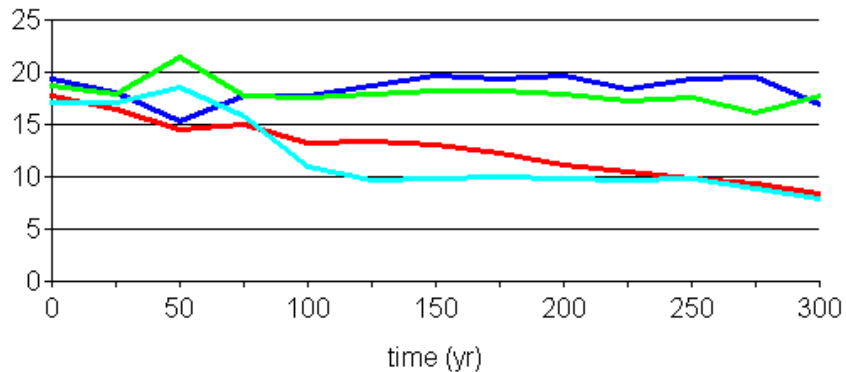
1. No Management



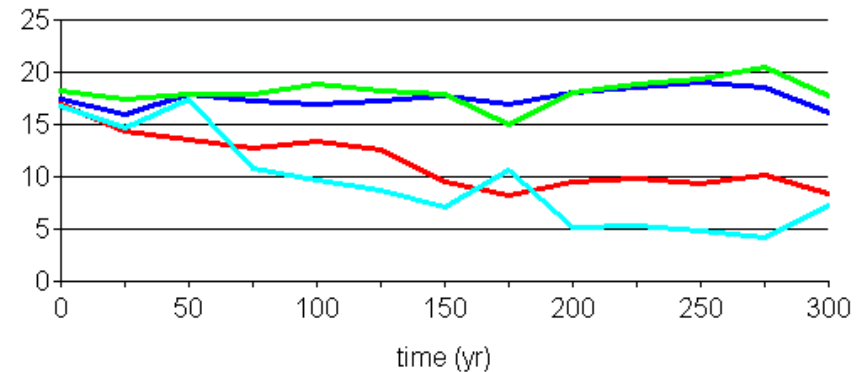
2. Nature oriented



3. Group selection

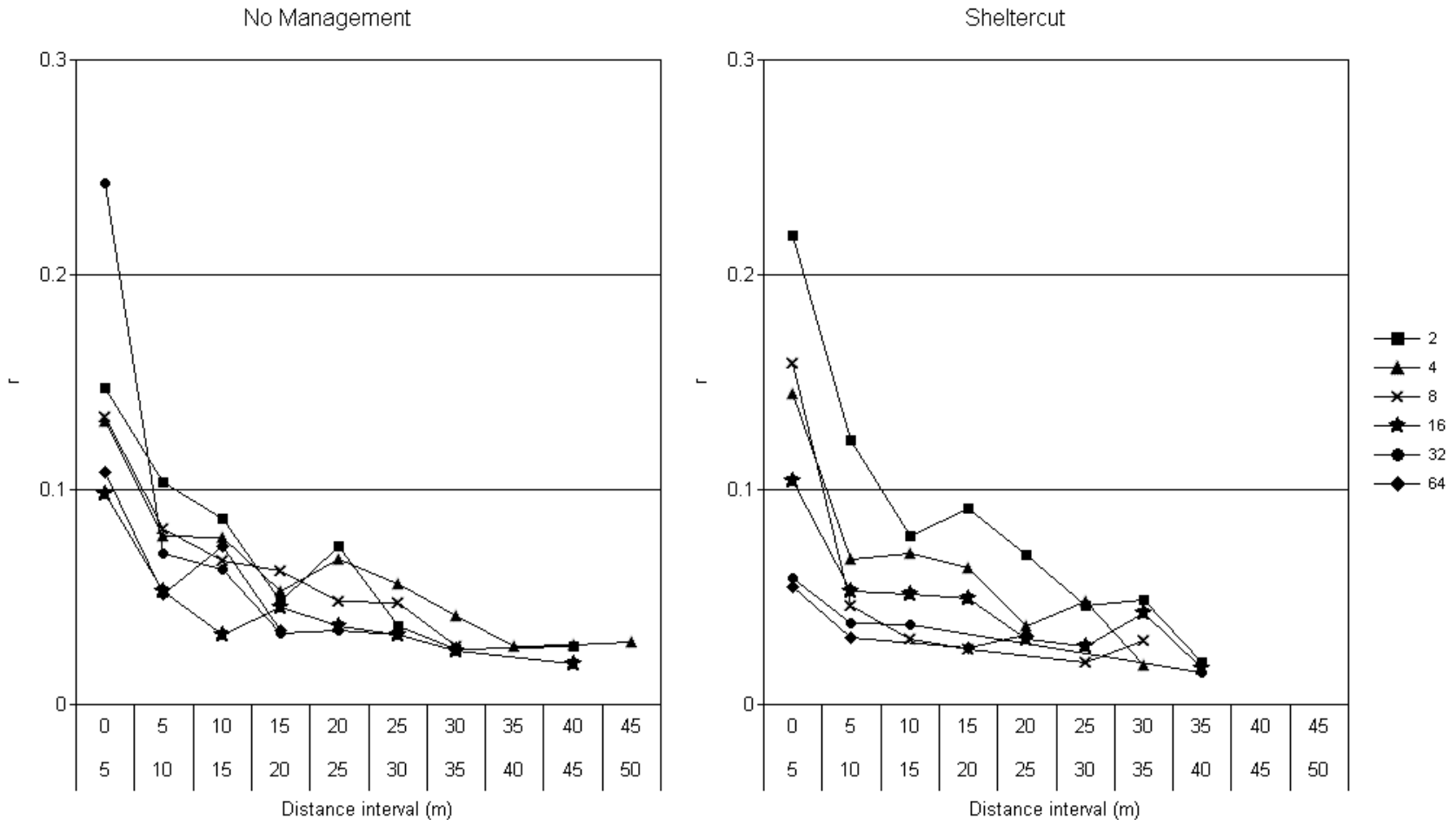


4. Sheltercut



— 1. Neutral trait — 2. Budburst day — 3. Spiral grain — 4. C7Hgh

Interaction of management and pollen dispersal distance on spatial genetic structure



Significant autocorrelations at varying expectations of Weibull distance curve for pollen dispersal (t=300yr)

Some conclusions:

Adaptive ability of a population to environmental changes depends on:

- Available genetic variation for adaptive traits
- Rate of change in genetic composition

Role of management in adaptive response of trees:

- Strongly influences regeneration interval of beech
- => allows population to adapt quicker to environmental changes
- => however, reduces the genetic diversity

time to break...

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