Cellular automaton models for selected invasive pests and pathogens

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The models were developed in EU-funded project called ISEFOR

The project dealt with invasive pests and pathogens

Project partners were from UK, Italy, France, Sweden, Finland, Russia, Poland, Austria and some other countries
Species selection - principles

- Should be invasive
- May cause serious damage
- Environmental requirements should be known
- Occurrence map (raster) of host species should be available
- Different cases should have different spread mechanisms
  - Different CA model variants obtained
  - Each CA can be used for other species having similar spreading mechanisms
Selected species (experts)

- Pinewood nematode (Christelle Robinet)
- Ash dieback (Thomas Kirisits, Jan Stenlid)
- Pitch canker (Paolo Capretti)
- Siberian moth (Dmitri Musolin)
- Dothistroma needle blight (Steve Woodward)
- Emerald ash borer (Marc Kenis)
- Alder Phytophthora (Andrea Vannini, Alberto Santini)
- Rejected
  - Mountain pine beetle (not invasive)
  - North American seed bug (too complicated, studied elsewhere)
Cellular automaton (CA)

- Has been used to simulate
  - Spread of forest fires
  - Expansion of cities
  - Optimize land use
  - Spread of diseases

- Temporal and spatial aspects -> spatio-temporal

- Cell-based
  - States (healthy, infected, spreadable, dead)
  - Rules: how the states of cells change
Model features

- More fine-grained than a typical CA
  - Healthy: no infected trees
  - Infected / spreadable: many sub-states
    - 1 tree infected (or spreadable)
    - 2 trees infected
    - ...
    - 50 000 trees infected
  - Dead: all trees dead
Model features

- **Mechanistic**
  - The same mechanisms simulated that cause the spread
  - No statistical fitting required

- **Spread depends on**
  - Biological parameters
    - Can be measured (at least in theory)
    - Flight distance of spores and insects
    - Predation and parasitization
    - Number of off-spring / female
  - Controllable parameters
    - Can be decided (at least in theory)
    - Entries in harbours and border stations
    - Transportation of cargos
    - Delivery of infected seedlings
Model features

- **Stochastic**
  - Most of the simulated mechanisms are stochastic
  - Destination of transportation
  - Flight of spores and insects
  - Infection
- **Single simulation is just a possibility**
  - One realization of a stochastic process
- **Simulation needs to be repeated many times**
- **Results in a risk map**
  - Probability that the pathogen or pest has reached a certain location by certain year
Species 1

PINE WOOD NEMATODE

MÄNTYANKERÖINEN
Pinewood nematode (PWN)

- Native in North America
- Invasive in Japan, China, ..., Portugal, Spain
- Enters via imported timber and wooden packages
- Causes Pine Wilt Disease
- Kills Eurasian *Pinus* trees rapidly

- PWN is carried by longhorn beetles, *Monochamus*
PWN biology

Healthy

Infected
- Beetles feed and PWN enters the tree (year 1)

Symptomatic, wilt disease
- Beetles lay eggs (year 1)

Asymptomatic (year 1 onwards)

Spreadable
- PWN transferred from tree to beetle (years 2 or 3)

Dead

Saprophytic
- Beetles lay eggs on deadwood (year 1)

Dispersal to another healthy tree

Healthy
Effect of climate and climate change

- Becomes symptomatic if summer is warm enough
1 = transportation of cargo
2 = flight from wood to tree
3 = flight from tree to tree

E = Entry point
P = People
H = Host tree
D = Deadwood object
Saprophytic cycle

- Lays eggs also on harvesting residues, windthrown trees, etc.
- Assumed
  - Suitable material for saprophytic spread available in every cell
  - Begins when the first living tree of the cell is infected
  - Ends when all trees are dead
  - Annual amount of insects emerging from deadwood is constant
Inputs

- CORINE land cover map (250 m)
  - Conifer and mixed conifer
- EFI tree species (1000 m)
  - Coverage of hosts
- Population density map
  - Destination of cargos
- Elevation map
  - Affects the probability of warm July -> Symptomatic spread
- Entry points
  - Location
  - Number of entries per year
Model parameters

- maximum flying distance (default 7000 m)
- mean flying distance (1500 m)
- maximum transportation distance (700 km)
- max no. of infected trees per cell (30)
- no. of tries to find a cell with healthy pines (10)

- multiplier for the probability of warm summer
- multiplier for the number of transportations per entry point
Host coverage and entry points
Human population density
Probability of spread
Species 2

ASH DIEBACK

SAARNENSURMA
History

- First detected in northeast Poland 1992
- Has invaded almost ash forests of Europe
- Gives a possibility to compare simulated and observed spread

- *Chalara fraxinea*
- Anamorph of non-pathogenic *Hymenoscyphus albidus*
- At present the causal agent of ash dieback is named as *Hymenoscyphus pseudoalbidus*
Records of the spread

Compiled by Thomas Kirisits, based on literature records and personal communications from experts, as part of the EU-funded project ‘FORTHREATS’ and ‘ISEFOR’ (see also Timmermann et al., 2011)

The blue shaded area shows the distribution range of common ash, Fraxinus excelsior (© EUFORGEN)

Explanation of symbols:
Year – year of first record of ash dieback (based on disease symptoms) in the respective countries (or, for Germany, different parts of the country);
? – no information on the presence/status of ash dieback available;
0 – ash dieback not present (personal communications, sometimes also unpublished observations by T. Kirisits or I. M. Thomsen);
0? – ash dieback likely not present, but experts were not totally sure.
Ways of spread of ash dieback

1. Transportation of infected ash seedlings from nurseries (entry mechanism)

2. Sporulation of infected ash trees (main mechanism)

3. Spread of spores in jet streams (long-distance jumps)

4. Infection of new nurseries by airborne spores
Climatic suitability = \( p(\text{Temp}) \times p(\text{Rain}) \)
Rainfall index

Precipitation and temperature rasters for current and future climate

Climatic conditions interpolated for each simulation year and location
A possible path

N = nursery
S = seedling lot
T = tree

1: nursery delivers infected seedlings
2: seedlings infect a tree
3: tree infects another tree
4: tree infects a nursery
Spreading distance & spore density

Probability or relative spore density

Distance from source, km
1. Transportation of seedlings

- Nurseries send infected seedling lots to ash forests
  - Probability of accept random destinations depends on ash percentage of the cell

- Infected seedlings send spore dispatches
  - Spore flight distance drawn from negative exponential distribution

- One tree of the destination cell is infected with probability depending on
  - Climatic suitability: p(Temp) × p(Rain)
  - Density of healthy ash trees
2. Spread by spores from infected cells

- Spore density around an infected cell depends on
  - Proportion of spreadable ash trees in donor cell
    - Relative spore density at donor cell
  - Distance from donor to recipient (negative exponential)
    - Effect of distance on spore density

Each healthy tree at recipient cell is infected with the probability of

\[ \text{DonorSporeDensity} \times f(\text{Distance}) \times p(\text{Temp}) \times p(\text{Rain}) \]
3. Jet steam spread

- Each infected tree sends spore dispatches to jet streams
- Spores are transported over long distances to random directions
- Flight distances are drawn from negative exponential distribution
- One tree of the recipient cell is infected with a probability depending on:
  - Density of healthy ash trees
  - Climatic suitability
4. Infection of new nurseries

- Spores dispersed from trees may also infect a clean nursery
- This nursery becomes a new entry point
- Included in the model since happens in real life

Note: Each spread mechanism may be switched on/off
Model inputs

- EFI map of the percentage of ash (1×1 km)
- Precipitation and rainfall (Worldclim, CIAT)
- Entry points = infected nurseries
  - Coordinates
  - First/last year of transportations of seedlings
  - Max distance of transportations (200 km)
  - Number of infected seedling transportations / year (30)
  - Number of spore dispatches / transportation (100)
Coverage of *Fraxinus excelsior* in Europe
Spread of Ash dieback during 25 years

Green 2012-2017
Spreading trees 2017
Species 3

PITCH CANKER

PIHKAKORO
**Biology**

- *Fusarium circinatum* causes pitch canker in pine and Douglas fir
- Present in USA, Japan, Korea, South Africa
- In Europe: Iberia and Italy
- Spreads in:
  - Infected seedlings (nursery to forest)
  - Spores (seedling to tree, tree to tree)
  - Insect vectors (tree to tree)
  - Other contaminated material (soil, wood)
- Infects wounds, may kill the tree
Entry mechanism

Nursery sends infected seedling lots (thick arrows)

Infected seedlings send spores to trees (thin arrows)
Two tree-to-tree spread mechanisms

1: By spores
Simulated by spore density fields

2: By insect vectors
Simulated by sending infected insects to random directions
Infection probability

- Infection at recipient cell depends on
  - Host density
  - Ecoclimatic index
  - Relative spore density (when spore density field is used)

- Relative spore density
  - At donor:
    - \( \frac{N(\text{Spreadable})}{N(\text{Maximum})} \)
  - At recipient:
    - \( \text{DonorDensity} \times \text{DistanceEffect} \)
Eccolimatic index

- Calculated for two time points with CLIMEX
  - Current and 2100 (Scenario A1B)
Ecoclimatic index

- Climate change included in simulations
  - Ecoclimatic index interpolated for each simulation year

In 2100
## Climatic change in A1B scenario by year 2100 in Europe

<table>
<thead>
<tr>
<th>A1B scenario</th>
<th>North of latitude 50</th>
<th>South of latitude 50</th>
</tr>
</thead>
<tbody>
<tr>
<td>Winter temperature change, °C</td>
<td>+4.5</td>
<td>+3.0</td>
</tr>
<tr>
<td>Summer temperature change, °C</td>
<td>+3.0</td>
<td>+4.0</td>
</tr>
<tr>
<td>Winter rainfall change, %</td>
<td>+15</td>
<td>0</td>
</tr>
<tr>
<td>Summer rainfall change, %</td>
<td>+10</td>
<td>-20</td>
</tr>
</tbody>
</table>
Host density & Entry points

Three southernmost entry points exist currently

Four other points assumed in a 100-year simulation
Probability of spread in 20 years, 3 entry points
Probability of spread in 100 years, 7 entry points
Biology

- *Dendrolimus sibiricus*, coming from the east
- Defoliates conifers: *Larix, Abies, Picea, Pseudotsuga*
- Two-needle pines less vulnerable
- Adult moth lays eggs on needles
- Larvae overwinter in litter
- Start eating needles next spring
- The tree becomes susceptible to bark beetles etc.
- Siberian moth has many enemies; viruses, predators, etc.
- Outbreak is usually over in 2–3 years
Model

- **Entries**
  - In imported cargos via eastern border stations
  - Cargos transported to places where people are living
  - Adult moths emerge from contaminated materials
  - Fly to forests of host trees, can fly long distances (max 50 km)
  - Mated adult females lay eggs on needles

- **Tree-to-tree spread**
  - New adults fly to new trees
  - Many eggs, many off-spring
  - Viruses, parasites and predators stop population growth
Spread mechanism

1: Cargos transported to inhabited places. Moths emerge from contaminated cargos and fly to host trees.

2: Some female moths mate, find a host tree, avoid enemies and produce offspring (shaded H).

3: Off-spring continue the outbreak.

E = Entry point
P = People
H = Host tree
Simulation of entries

- Destinations of cargos depend on human population density
- Destinations of moths emerging from cargos depend on
  - Availability of healthy host trees
  - Ecoclimatic index of the cell in that year
- Mating probability depends on population density
Simulation of cell-to-cell spread

- Off-spring density at donor cell depends on
  - Number of spreading trees within the cell
  - Predation & parasitization = f(number of spreading trees)

**Recipient density** depends on **donor density** and **distance**
- Off-spring density field generated around each infected cell

- The number of new infestations within a recipient cell depends on
  - Off-spring density at recipient cell
  - Density of healthy host trees
  - Ecoclimatic index
Mating and enemies

- Non-predated
- Mating
- Relative success

Probability vs. Proportion of spreadable trees in the cell
Inputs

Host species & entry points
Inputs

Human population density
Inputs

Ecoclimatic index
<table>
<thead>
<tr>
<th>Outputs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Probability of spread</td>
</tr>
</tbody>
</table>
Outputs

Infection year

Number of spreading trees
Species 5

**DOTHISTROMA NEEDLE BLIGHT**

**PUNAVYÖKARISTE**
Biology

- *Dothistroma septosporum* needle blight (DNB)
- Red band needle blight
- Worldwide
- Corsican pine, lodgepole pine, radiata pine, ponderosa pine, Austrian pine and maritime pine
- Causes defoliation of older needle age classes
- Trees may die
- First detected in Europe in 1911
- Climate change increases northward spread?
Spread mechanism

- **Entry**
  - Spreads to new regions in infected seedlings
  - Then spreads from seedlings to trees

- **Tree-to-tree spread by airborne**
  - Asexual spores
    - Conidia
    - Main mechanism
    - Short dissemination distance
  - Sexual spores
    - Ascospores
    - Few
    - Longer flight distance
Simulation of entries

- Infected nurseries deliver infected seedlings
- Transported to forests of host species
- Send conidia to surrounding forests
- Number of conidia "dispatches" per seedling lot is a model parameter
- A dispatch infects a tree within the recipient cell with probability

\[ P_{\text{Infection}} = \left[ \frac{N_{\text{healthy}}}{N_{\text{max}}} \right] \times EI \]

*EI* is ecoclimatic index (climatic suitability of the cell)
Simulation of tree-to-tree spread

Conidia: Relative spore density field generated around each infected cell

Ascospores: Individual spore dispatches generated
Simulation of tree-to-tree spread

- **Conidia**
  - Donor density depends on the number of spreading trees
  - Recipient density depends on donor density and distance
  - Number of new infections within recipient cell depends on:
    - Spore density at recipient cell
    - EI of recipient cell
    - Number of healthy host trees

- **Ascospores**
  - A dispatch infects a tree with probability depending on
    - EI of the recipient cell
    - Density of healthy host trees within the cell
Input

Eco climatic index
Current
2100
Scenario A1B
Input

Host occurrence

Entry points
Output

Probability of spread by 2030 (starting in 1970)

Red = high

Green = low
Output

Infection year

Red = before 2007
Green = after 2007
Output

Number of infected trees in 2030

Red > 100/ha

Green < 1/ha
Effect of improved control

Delivery of infected seedlings ends in 2014

Effect on the probability of spread by 2030

Yellow = no effect

Blue = Risk is decreased by 30 percentage units or more
Specie 6

Emerald Ash Borer

Saarnenjalosoukko
<table>
<thead>
<tr>
<th>Biology</th>
</tr>
</thead>
<tbody>
<tr>
<td>- <em>Agrilus planipennis</em>, invasive wood-boring beetle</td>
</tr>
<tr>
<td>- Detected in North America in 2002</td>
</tr>
<tr>
<td>- Has killed tens of millions of trees</td>
</tr>
<tr>
<td>- Spreading westwards in Russia, now in Moscow</td>
</tr>
<tr>
<td>- Spread rate 30–40 km per year</td>
</tr>
<tr>
<td>- Adults lay eggs in bark</td>
</tr>
<tr>
<td>- Larvae eat cambium and sapwood</td>
</tr>
<tr>
<td>- The tree dies in 1–4 years</td>
</tr>
<tr>
<td>- Overwinters in pupal cells</td>
</tr>
<tr>
<td>- New adults emerge next spring</td>
</tr>
</tbody>
</table>
Entry mechanism

- Enters Europe in transported wood (e.g. packages)
- Cargos transported to dwelling places of people
- Adult borers fly from cargos to ash trees
- Mean flight distance 280 m, maximum 1500 m
- Lays 70–90 eggs in May–June
- Probability to lay eggs depends on
  - Host tree density of the destination cell
  - Ecoclimatic index of the destination cell
  - Probability of mating = $f(\text{population density}) = f(\text{density of spreading trees})$
Cell-to-cell spread

Spread by off-spring is simulated by using off-spring density field

Spread in firewood is simulated by generating random firewood destinations
Cell-to-cell spread

- New adults fly to other trees next spring
- Some enemies (woodpeckers, wasps, fungi) may slow down population growth rate
- Number of off-spring within a cell depends on
  - Density of spreading trees
  - Probability to avoid predation and parasitization = $f(\text{density of spreading trees})$
- Number of infections at recipient cell depends on
  - Recipient off-spring density = $f(\text{donor density, distance})$
  - $EI$
  - Density of healthy ash trees
  - Probability of mating = $f(\text{population density})$
Spread in firewood

- Transported firewood is an important additional spread mechanism
- Firewood is prepared from dying (infected) trees!
- The number of firewood parcels prepared per hectare and year is given as model parameter
- Maximum transportation distance another parameter
- Parcels transported to random destinations
- May infect an ash tree, depending on
  - Density of healthy ash trees
  - EI of the destination cell
  - Probability to find a mate
Probability to mate and avoid enemies

The graph illustrates the relationship between the proportion of spreadable trees in the cell and the probability of non-predation, mating, and relative success.
Input: Host density and entry points
Input: Human population density
Ecoclimatic index

Currently

In 2100 (Scenario A1B)
Probability of spread

In 10 years

and

In 30 years
Other output

Infection year
Red = early
Green = late

Number of infected trees
Red = many
Green = few
Probability of spread if enters only via eastern border stations
Species 7

ALDER PHYTOPHTHORA

LEPÄN MUNASIENI
Biology

- *Phytophthora alni*
- First detected in England in 1993
- Seedlings are infected in nurseries from irrigation water or contaminated soil
- Spreads to alder forests in delivered seedlings
- Found on river sides (> 8 m-wide rivers)
- Spores transported in water
- May spread into alder trees in floods
- Most trees die within few years
Spread mechanism

- Infected nurseries used as entry points
- Infected seedling lots delivered to alder forests
- Infestation depends on
  - Density of alders
  - Distance from river
- Infected trees disseminate spores to the river
- Spores are transported in water
- May infest new trees at destination, depending on
  - Density of alders
  - Distance from river
  - Difference in elevation (no spread upriver)
Input: Coverage of Alnus spp.
Input: Distance to river
Input: Elevation
Output: Probability of spread
A detail from a single simulation

Red: early
Green: late
Blue: river
Dark: Plenty of alder
Simulation software

- **NEMATODI**
- **ASHDIEBACK**
- **PINE RED BAND (SIMULATES ALSO PITCH CANKER)**
- **SMOTH (SIMULATED ALSO EMERALD ASH BORER)**
- **ALNUS**
Simulation software

- Not very user-friendly
  - Only few people use them
- Input rasters are in text files
- Parameters are also in a text file
  - Can be edited with Notepad or WordPad
- Output rasters are saved on text files
- Can be imported to AcrInfo to have nice output
  - Informative colour scheme
  - Raster algebra: effect of control -> difference raster
- Rasters can also be displayed by the simulators
Important to know in ArcInfo

- Spatial reference (coordinate system)
  ETRS_1989_LAEA

- Importing CA rasters to ArcInfo
  ASCII to Raster (Conversion tools)

- Manipulating host cover raster (effect of cuttings)
  - Import to ArcInfo (ASCII to raster)
  - Modify
  - Save as text file (Raster to ASCII)
Example parameter file

1300        ! Maximum flying distance of spores (m)
280         ! Mean flying distance of spores (m)
500000      ! Max transportation distance of seedlings from nursery (m)
100         ! Number of spore dispatches / infected seedling
300         ! Max number of full-sized trees per ha
1           ! Number of insects / infected tree
10          ! Number of tries an insect has to hind host tree
4500        ! Maximum flight length of insect (m)
1000        ! Mean flight length of insect (m)
5           ! Number of years an infected tree is spreading
1           ! Resampling interval (if 2, cell size is doubled)
User interface
Starting a simulation

Siberian moth / Emerald ash borer simulator

Input files:
- Pine raster: Fraxinus.txt
- Entry locations: AshBorerEntryPoints.txt
- Current EI raster: EI_Now_EAB.txt, 2013
- Future EI raster: EI_2100_EAB.txt, 2100
- Human population density: EuropeanPopulation.txt
- Parameter file: AshBorerPara.txt

Output files:
- Summary of results: EAB_Summary.txt
- Infection year raster: EAB_InfectionYear.txt
- Number of dead trees raster: EAB_InfectedTrees.txt
- Number of spreading trees: EAB_DeadTrees.txt
- Probability of spread raster: EAB_InfectionProb.txt

Number of years in a simulation: 20
Number of simulations: 1

[OK] [Cancel]
Selecting output

Simulation completed

Select map output
- Host species: Input
- Current environmental index: Input
- Future environmental index: Input
- Human population: Input
- Infection probability: Based on all simulations
- Infection year: In last simulation
- Proportion of infected trees: In last simulation
- Proportion of spreading trees: In last simulation
- No more map output

You may cut and copy maps from the screen.
Sample output
Healthy forest from Finland