

Asymmetric cellular automata for the modelling of ecological systems

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1. Modelling with cellular automata in ecology

Cellular automata (Wolfram 1986, Toffoli/Margolus 1987) in combination with individual based or individual oriented approaches (Caswell 1989, DeAngelis/Gross 1992) have successfully been used to build spatially explicit models of population dynamics. Current examples are a fox-rabies-model (Thulke et al. 1999), or a grasshopper model (Schröder 2000). Combination of such models with geographical information systems (GIS) allows to integrate real landscape data quite easily. The software tool RAMAS[©]GIS for example combines a generic metapopulation model (Hanski, 1999) with a raster-based GIS providing habitat data. As a result it can be used for population viability analysis (PVA) based on concrete data (Akçakaya 1998).

Traditionally, cellular automata cover the investigated area with a regular pattern of cells which are identical in shape (usually squares) and size. These cells are related by a simple, regular neighborhood relation. In population ecology, each cell models the local population dynamics by a life-cycle model.

The simple structure of such models is undoubtedly an advantage for formal analysis. But – as also discussed in (Wittmann 2000) – we can consider the uniform structure of cells to be an essential disadvantages of this approach: If e.g. concrete spatial situations (for example barriers like streets or rift valleys between neighbored cells) can be modelled at all, then only in simplified manner. To get more realistic results, one can use a generalized definition of cells and their neighborhood, as e.g. in cellular systems (Wunsch 1977).

A second disadvantage of traditional cellular automata consists in the lack of a global layer to model common, dynamic conditions (e.g. weather) for all cells. Such ‘global variables’ are important to model correlation between local dynamics of the cells.

Therefore, in this paper we introduce a generalized, spatially explicit approach (ACA: asymmetric cellular automata) for modelling of ecological systems which allows the depiction of heterogeneously structured landscapes as

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well as dispersion processes or correlation more easily. Although such demands lead to a more complex modelling approach, our proposal can be described completely and briefly in a formal manner. So, models built by this approach are semantically unambiguous. Moreover, the formal approach of ACA can be used as a specification of a software framework which also allows to integrate vector-based geographical information systems (GIS) into models.

2. ACA: The formal approach

As usual for modelling techniques, one can divide the approach into a specification of static components and dynamic behavior.

2.1 Static components

An Asymmetric Cellular Automaton (ACA)

$$(C, N, T, (names_G, G), (names_S, S), (names_D, D), (names_O, O), \alpha, \mu, o)$$

consists of the following components:

Cells of the automaton Let C be a (finite) set of cells. A cell $c \in C$ is an area which is bounded by edges of a convex polygon. The set C of cells need not to cover a whole area of investigation. Different cells do not intersect except in common edges of the bounding polygons.

Topology of the automaton The topology of an ACA is not restricted to a symmetric grid as it is in traditional cellular automata. A neighborhood relation of the cells is used for describing the topology: The degree of neighborhood of two cells is defined very generally by the function

$$N : C \times C \rightarrow \mathbb{R}^{\geq 0}$$

This allows e.g. to specify $N(c, c')$ as length of the common edges of c and c' or to specify asymmetric neighborhood relations. The neighborhood relation allows to model regular 2D- or 3D-topologies as well as arbitrary interconnections of cells.

Time base A discrete, ordered set T of points in time with a minimal element t_0 founds the dynamic change of the state of cells. Throughout this paper we set $T = \mathbb{N}$.

Global state The global state $(names_G, G_1, \dots, G_g)$ consists of a list of g attribute names $names_G$ and a domain G_i for each attribute. The attribute values may change in time. A time series γ (see below) assigns to each $t \in T$ the global attribute values $\gamma_t \in G = (G_1 \times \dots \times G_g)$.

On one hand the global state contains common external data for all cells of the ACA, on the other hand the global state may aggregate data from the cells. Components of this global state may be e.g. weather conditions or the total

number of individuals in the area under investigation.

As an extension, a global output function defined on G could define an observable effect of the complete automaton.

State of cells The state of each cell is determined by values of its **static** and **dynamic** attributes ($names_S, S_1, \dots, S_s$) and ($names_D, D_1, \dots, D_d$) which both consist of name-lists and associated domains. Attribute names and sets of possible values are the same for all cells.

A predefined function σ assigns to each cell $c \in C$ the values of its static attributes $\sigma(c) \in S = (S_1 \times \dots \times S_s)$. Values of static attributes may differ between different cells, but a static attribute of a cell is constant relating to time. Static attributes may be e.g. the size of the area, the quality of the modelled habitat, or the type of landscape modelled by the cell. A special static attribute, which a cell c can use by default, is its embedding $N(c) := \sum_{c' \neq c} N(c, c')$ in the topology of the automaton. These attributes could be initialized from a GIS layer.

A time series δ (see below) relates a cell c to its value $\delta_t(c) \in D = (D_1 \times \dots \times D_d)$ at a given point of time $t \in T$. Dynamic attributes may be e.g. the number of individuals in a cell, or the amount of food available. Values of these attributes might be stored in a GIS layer during simulation.

2.2 Dynamic behavior

Dynamics of the ACA is based on three functions:

Global change A function α computes a new global environment for every time step of the simulation of the automaton. This function depends on the old state of the environment, the state of all cells of the automaton and an external stimulation to the automaton: $\alpha : G \times I \times \prod_{c \in C} (S \times D) \rightarrow G$ computes a global state $\gamma_t \in G$ at a given time $t \in T$, where I is a value of an *external influence*. The external influence may be e.g. a time series of weather data, or may include external events as catastrophes.

Self modification $\mu : S \times D \times O \times G \rightarrow D$, which computes the new value of the dynamic attribute from the values of static and dynamic attributes, the influence of all neighbor cells and the global state.

E.g., an ACA can compute the new population size of the cell under certain weather conditions (global state) depending on the old population size, its neighborhood and the habitat quality.

Effect of a cell to its neighbors $o : S \times D \times G \rightarrow O$ determines a set of attribute values named by $names_O$ as an external effect of a cell. O must be a vector space. One can use this *output* of a cell e.g. to determine all emigrants of a cell in a dispersion process. The effect of o on the local state of a cell has to be taken into account when defining the cell's self modification function μ . Starting at a fixed **initial state** (γ_0, δ_0) of the ACA, and given a sequence

I_0, \dots, I_t, \dots of external influences and a definition of static states $\sigma(c)$ for each cell c , a sequence $(\gamma_0, \delta_0), (\gamma_1, \delta_1), \dots, (\gamma_t, \delta_t), \dots$ of states is (inductively) defined by

$$\begin{aligned} \gamma_{t+1} &:= \alpha(\gamma_t, I_t, \mathbf{X}_{c \in C}(\sigma(c) \times \delta_t(c))) \\ \delta_{t+1}(c) &:= \mu(\sigma(c), \delta_t(c), \underbrace{\sum_{c' \in C} (N(c, c') \cdot \underbrace{o(\sigma(c'), \delta_t(c'), \gamma_t)}_{\text{influence of cell } c'})}_{\text{effect of the neighborhood to } c}) \end{aligned}$$

By this, a cell distributes its output to other cells proportionally to their degree of neighborhood.

Generally speaking, semantics of an ACA depends only on the interpretation of the data types in G, S, O, D , the global change function α , the self modification function μ , and of the output function o . If e.g. all data types are (subsets of) domains of numbers, and all functions are arithmetic functions, an ACA has unambiguously defined formal semantics.

3. A spatially realistic metapopulation model

The spatially realistic model in (Hanski, 1999) models habitats of a population as cells, which are scattered in an unsuitable area. The cells are different in size and can be occupied or empty. The dynamics of a cell is determined by its size, the extinction rate of its population (which depends on the habitat's area), and the colonization pressure of the other cells. We will realize this irregular model as an ACA in a first step. In a second step we will add stochastic global influences which will enable an even more realistic model.

Each suitable habitat is a cell of the ACA. The static attributes of a cell c are its area $c.area$, its extinction rate $c.ext = 1/c.area$ and its position $c.pos$ in the 2-dimensional space. The state $c.state \in \{occupied, empty\}$, the colonization rate $c.col$ and the probability of occupancy $c.occ$ are the dynamic attributes of a cell. So, we get $\sigma(c) = (c.area, c.ext, c.pos)$ and $\delta(c) = (c.col, c.occ, c.state)$.

As the degree of neighborhood of two cells c and c' is related to their distance in space, we set $N(c, c') = e^{-ad_{c,c'}}$, where a sets the migration rate of the species and $d_{c,c'} = |c.pos - c'.pos|$ is the Euclidean distance between c and c' . Hanski's model does not include any global influence to the model's dynamics, so we define the global state to be \emptyset and set the global dynamics $\alpha \equiv \emptyset$.

The output $o \in O = \mathbb{R}^{\geq 0}$ of a cell c at time step t is given by

$$o(\sigma(c), \delta_t(c), \gamma_t) = c.area \cdot c.occ \in O$$

The self modification of cell c is determined by the changes of the colonization pressure $c.col$

$$c.col(t+1) = m \sum_{c' \neq c} N(c, c') \cdot o(\sigma(c'), \delta_t(c'), \gamma_t),$$

its probability $c.occ$ of occupancy

$$c.occ(t+1) = (1 - c.occ(t)) \cdot c.col(t+1) + (1 - c.ext) \cdot c.occ(t)$$

and its state

$$c.state(t+1) = \begin{cases} \text{occupied, if } R < c.occ(t+1) \\ \text{empty, if } R \geq c.occ(t+1) \end{cases}$$

where m is the migration range of the modelled species and $R \in [0, 1]$ is an uniform distributed random number.

Combining these computations to the self modification function μ , we see that in this example the new state $\delta_{t+1}(c)$ of a cell C is determined only by the native attributes of c and the effect of the neighborhood:

$$\delta_{t+1}(c) = \mu(\sigma(c), \delta_t(c), \underbrace{\sum_{c' \neq c} N(c', c) \cdot o(\sigma(c), \delta_t(c), \gamma_t), \gamma_t)}_{=c.col(t+1)/m})$$

Now, as a demonstration, we add a global influence to the model from (Hanski, 1999). Let us assume that the migration range m depends on the global weather conditions w . We assume that $w \in \{good, medium, bad\}$ changes on behalf of external stochastic influences $i_t \in I$ which can be read from a database or generated randomly. The dynamics of the global state $\gamma_t = (w)$ at time step t might be given by

$$\gamma_{t+1} = \alpha(\gamma_t, i_t, s_t) = \begin{cases} (good) & , \text{if } i_t \leq 0.3 \\ (medium) & , \text{if } 0.3 < i_t \leq 0.7 \\ (bad) & , \text{if } i_t > 0.7 \end{cases} ,$$

where $s_t = ((\sigma(c), \delta_t(c)))_{c \in C}$ is the state of all cells. As in this example the cells do not effect the global environment, we can neglect s_t .

The computation of the colonization rate $c.col$ is modified by replacing the constant migration rate m with a rate $m(w)$, which varies according to the external influence $\gamma_t = (w)$.

$$m(w) = \begin{cases} 1.2 \cdot m, \text{if } w = good \\ m, \text{if } w = medium \\ 0.7 \cdot m, \text{if } w = bad \end{cases}$$

Instead of this quite simple choice of a global influence to all cells also more complex relations, as e.g. a global regulation of the population density, can be modelled by an ACA. Often such more complex models can not be analyzed mathematically, as Hanski's model, but only by simulation of their dynamics.

This example shows how an ACA structures the complex interaction between local dynamics, global influences, and the effect of the neighborhood to a cell, and enables the modelling of such systems in an unambiguous manner.

4. Outlook

ACA have been shown by an example to be a modelling technique detailed enough to build 'realistic', spatially explicit models of population dynamics where local dynamics can be correlated by a global influence. On the other hand ACA are simple enough to be handled in a formal manner. So they can be used for a formally founded modelling framework. The approach of ACA's introduced here shortly can be generalized in many ways:

- Automata could be structured hierarchically in different levels to allow modelling of different scales of a system.
- Asynchronous state changes as introduced in (Gronewold/Sonnenschein 1998) could be discussed as an alternative to the strictly synchronous behavior of ACA.
- The number of cells and the topology of an automaton could be defined dynamically.

This will be covered by forthcoming papers.

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