

Lecture overview • Cellular automaton • *The game of life* • Bioinformatics examples • Summary of the course

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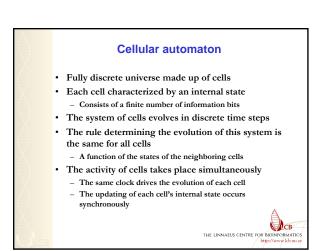
Cellular automaton Idealization of a physical system – Space and time are discrete – Physical quantities (states of the automaton) take only a finite set of values Invented by von Neumann (late 1940s) Extract the abstract mechanisms leading to selfreproduction of biological organisms

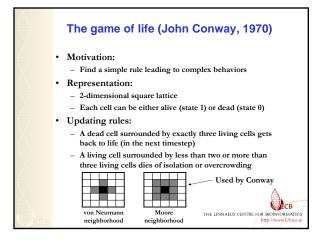
 a system having the capability to produce another organism of equivalent complexity with only its own resources

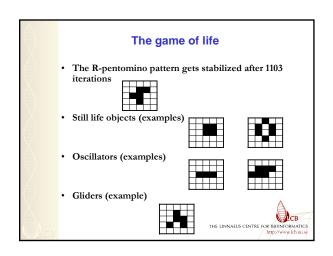
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Can mimic or simulate physical system







The game of life

- The game of life is one of the simplest examples of what is sometimes called emergent complexity or selforganizing systems
- It is the study of how elaborate patterns and behaviors can emerge from very simple rules
- E.g. explains how the stripes on a zebra can arise from a tissue of living cells growing together In Nature we do not know all the rules. The game of
- life lets us observe a system where we do

What can be learnt? E.g.

- Behavior of cells or animals can be better understood using simple rules
- Behavior that seems intelligent, such as we see in ant colonies, might just be simple rules that we don't understand yet
- More: http://www.math.com/students/wonders/life/life.html

Cellular automata - theoretical capabilities

• The game of Life is a CA capable of universal computations

- A computer can be built inside the Life "universe"
- Streams of gliders can be used to send information just as electrical signals are used to send information in a physical computer
- These streams of gliders can react in a way to perform all of the logical functions on which a modern computer is based
- Several interesting special-purpose computers have been constructed

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- Possible to mimic any computation process
- CAs have the capacity to be non-restrictive computational technique THE LINNAEUS CENTRE FOR BIOINFORMATIC

Cellular automata

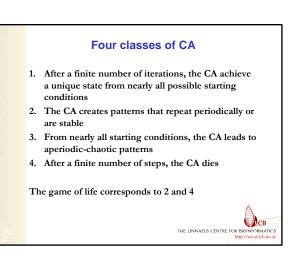
- Provide simple models of complex systems
- A collective behavior can emerge out of the sum of many, simply interacting, components
- A global behavior may obey new laws that are not obviously extrapolated from the individual properties The whole is more than the sum of all parts
- CAs can do more than just behaving similarly to natural
- dynamical processes
- Can represent actual models of a given physical system leading to macroscopic predictions
- The macroscopic behavior of many systems is quite disconnected from its microscopic reality
- E.g. flows of fluid and gas are very similar at a macroscopic scale, in spite of their microscopic nature
- Many physical processes are well suited to the cellular

automata approach

Pattern formation, growth phenomena, etc.

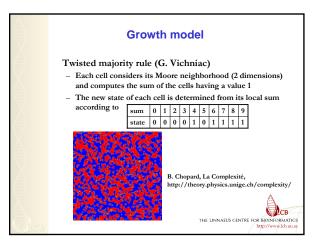


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State transition rules

- The behavior of an CA is a function of the initial conformation and the transition rules
- Although the rules are simple, simulation is the only way to determine the CA's behavior
- Second-order rules
- Use the historic state behavior of cells (current and neighbors) to compute a new state for the current cells Short-term memory in the decision making
- Probabilistic rules
 - State changes are executed according to a probability
 - Could choose from a number of state changes based on their probability
 - CA behaves in a stochastic rather than deterministic Асв THE LINNAEUS CENTRE FOR BIOINFORMATIC manner



Competition models and cell differentiation

- Competitive dynamics
 - Cells compete for some resources at the expense of their nearest neighbors
 - A winner is a cell of state 1 and a looser of state 0
 - No two winner cells can be neighbors
 - Any looser cell must have at least one winner neighbor
- Direct application in biology

Development of drosophila

- 25% of the cells forming the embryo are evolving to the state of neuroblast (that develop into neurons)
- How can we explain this differentiation and the observed fraction?
 - · At the beginning, all cells are assumed equivalent

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Competition models and cell differentiation Competition takes place between adjacent biological cells Each cell produces some substance S The production rate is inhibited by the amount already present in the neighboring cells Differentiation occurs when a cell reaches a level of S above a given threshold Hexagonal lattice (5 neighbors + current) Approximation of the cell arrangement in drosophila embryos S can be either 0 (inhibited) or 1 (active)

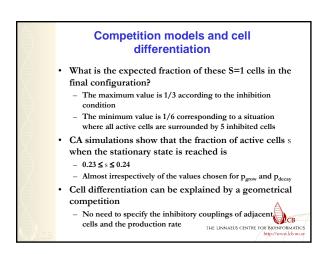
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Competition models and cell differentiation

- Rules
 - A S=0 cell will grow (i.e., turn to S=1) with probability p_{grow} provided that all its neighbors are 0
 - A cell in state S=1 will decay (i.e., turn to S=0) with
 - probability p_{decay} if it is surrounded by at least one active cell
- Evolution stops when no S=1 cell feels any inhibition and when all S=0 cells are inhibited by their neighborhood
 - Cells with S=1 are those which will differentiate
- What is the expected fraction of these S=1 cells in the final configuration?

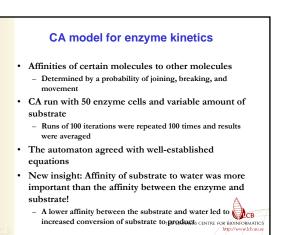




CA model for enzyme kinetics (Kier et al., 1996)

- Model the reaction between an enzyme and substrate in water
- 110*110 grid of cells (12100 cells)
- Can take values of E (enzyme), S (substrate), P (product), and W (water)
- 69 % covered with water, 31% space
- Added ingredients replace water
- Each cell has a probability associated with its movement and its interaction with other molecules
 - Enzymes can interact with S, P, and W, but not ${\bf E}$
 - Extended von Neumann neighborhood (2 steps in each direction)





Simulation of an apoptosis reaction network (Siehs et al. 2002)

- Simulation of the molecular reaction pathways of apoptosis (cell death)
 - Potentially greater understanding of the mechanisms of cancerous cells
 - Cancer is often characterized by the inhibition of the apoptosis process
- 2-dimensional grid
- Complex data structure at each cell
- Registers storing variables relating the current state of the molecules within the cell and its surrounds
- Each of the cells could be in a large number of states due to combination of parameters in registers

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Simulation of an apoptosis reaction network

Registers:

- 1. Type of molecular object(s) occupying the site
- 2. Reaction rate constants for the occupying objects
- 3. Molecular neighborhood (Moore). Types of molecules
- 4. Distribution of local momentum (hard sphere collision model)
- Potential energy status of the molecules at the site (function of the attraction/repulsion of molecules on the site and in the neighborhood)
- 6. Molecular reaction lists (what occurs if two molecules occupy the same site?)
- 7. Reaction product lists (products of the reactions in 6)
- Moved direction (location of each of the molecules at time t+1 given information in 4 and 5)
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Simulation of an apoptosis reaction network

- Each time the CA was updated the following steps were performed
 - 1. Evaluation of molecular collisions and redistribution of
 - kinetic energies
 - Propagation of type information from cells to register
 Computation of the local potential energy situation
 - Computation of the local potential ef
 Evaluation of chemical reactions
 - Evaluation of chemical reaction
 - 5. Computation of the grid positions of the molecules in the next timestep
- 6. Full update of the grid based on 1-5



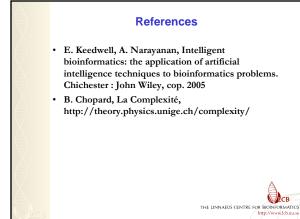
Simulation of an apoptosis reaction network

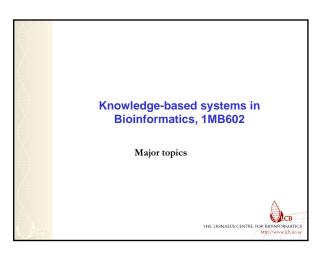
Results:

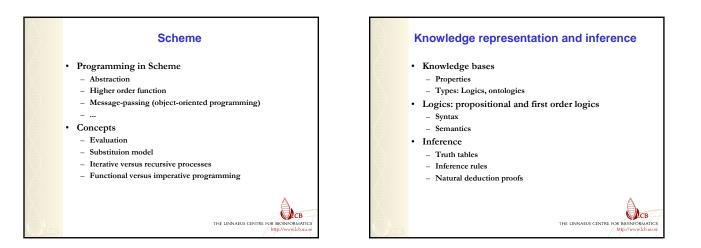
- Authors found a set of experiments where changes in concentration of certain proteins could affect the apoptosis
- An equilibrium existed between several proteins
- Confirmed what was known experimentally
- Replicated expected results for different sets of stimuli
- Able to simulate the process of apoptosis under a number of artificial conditions with a small computational requirement

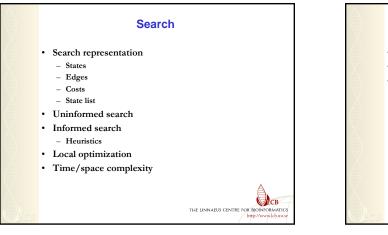
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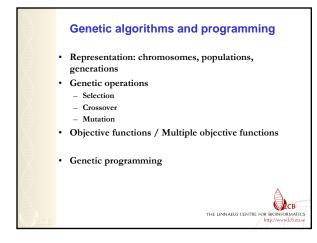


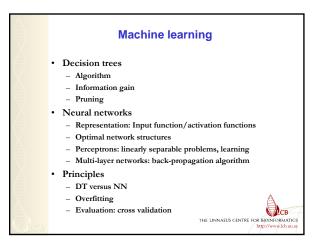






Probabilistic approaches Bayes' rule Machine learning/supervised learning Bayesian (belief) networks Representation Representation





Cellular automatas

- Representation: cells, rules, discrete time
- The game of Life
- Purpose/power
- Possible applications

