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Epidemic Modeling with Cellular Automata

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Outline

State of the art

- Modeling of epidemy is both of theoretical interest and practical importance,
- There exists several mathematical models of epidemy
- Cellular Automata can serve as a basig modeling tool for such spatial phenomena,
- There exists several models of epidemy with CA in the literatur, but only classical CA are in use.

Modeling used classical CA

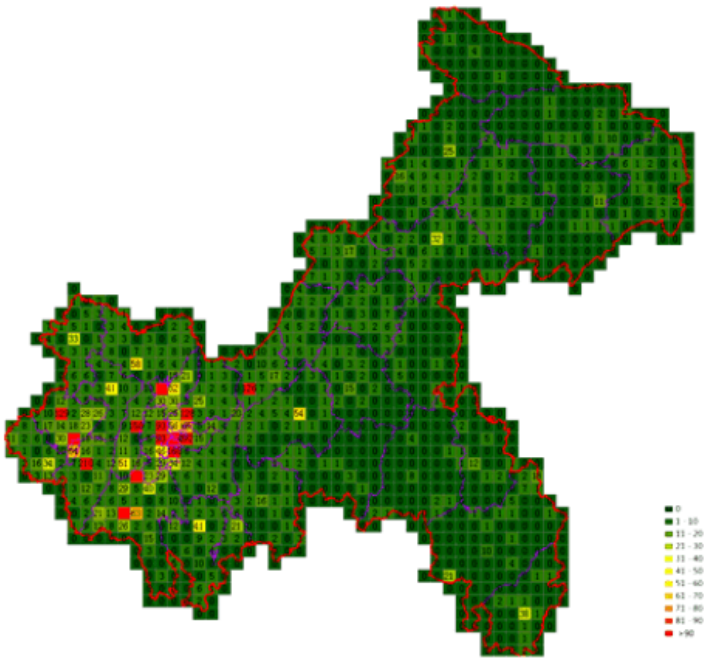

Figure 1. The distribution of HIV/AIDS infectives, 1995-2009.

Figure: HIV modeling used classical CA

Epidemic modeling

- Daniel Bernoulli - first matematical epidemic model - Structure of Bernoulli's model - the population is divided into susceptibles, i.e. those who have not yet been infected, and immunes, i.e. those who have been immunized for the rest of their life after one infection.
- SIS, SIR, SEIR, SIRS
- Threshold analysis - The model is based solely on the user's response to the drug, and it is shown that when a certain combination of susceptible population size, individual susceptibility, and infectiousness does not exceed a critical threshold value, there will be only few users.
- Reed–Frost model - is one of the simplest stochastic epidemic models. It was formulated by Lowell Reed and Wade Frost in 1928 and describes the evolution of an infection in generations.

Epidemic as conflict

parties to the conflict

- virus expansion,
- treatment, vaccine.

Epidemic is a spatial conflict with two actors (virus and human).

LCCA

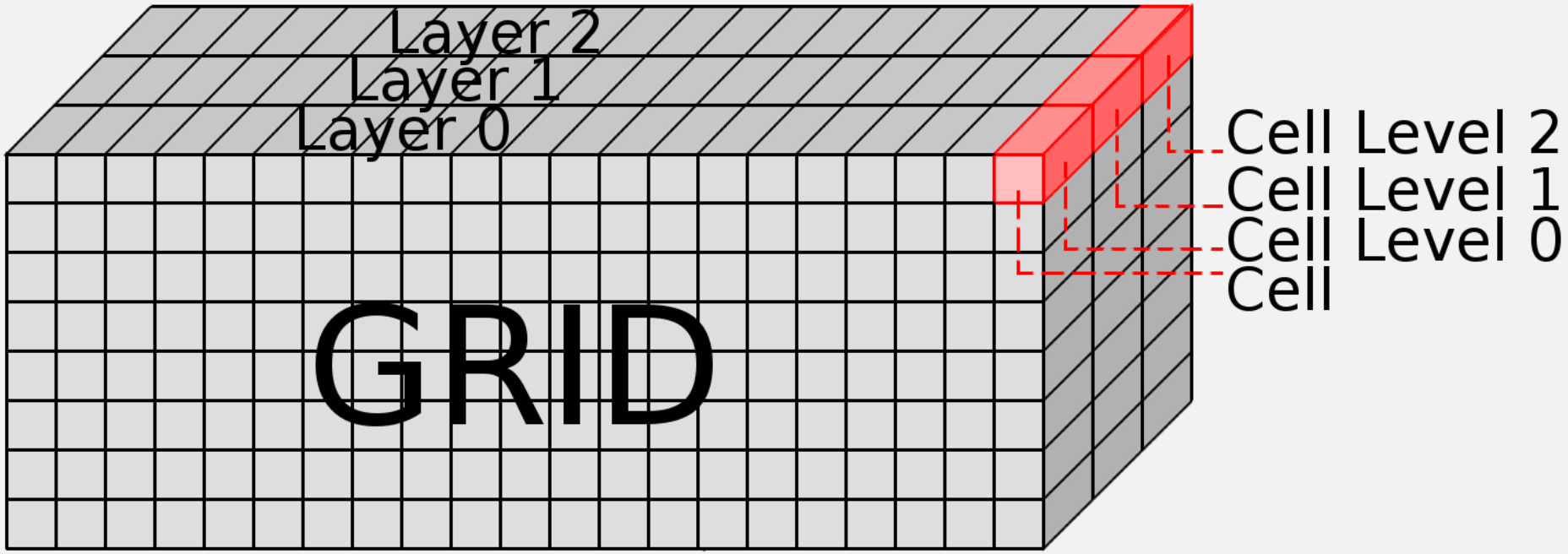

Figure: Graphical presentation for MultiLayered Cell use in LCCA

Movement phase

- Select a random cell (infected peoples) from the countries,
- For each of the individuals in the cell, randomly select a neighbouring cell and move the individual into it (cell not being full),
- Repeat from step one until all the cells in the area have been accounted for,
- In every cells where was infected peoples set virus and time for 24h in Layer 1,
- Every infected man heve set time = 216h in Layer 2,
- Compute contact infections,
- Repeat from step four for the next cell until all cells have been accounted for.

Rule

Virus Layer:

- live time (max 24h)
- A type flu - $Z(C_{1n}) = xy * Zar_A * W$
- B type flu - $Z(C_{1n}) = xy * Zar_B * W$

Medicine Layer:

- Spread of virus (max 216h)
- A type flu - vactine person - $C_{2n} = 0,6 * Z(C_{1n})$
- B type flu - vactine person - $C_{2n} = 0,4 * Z(C_{1n})$
- resistant person - $C_{2n} = 0 * Z(C_{1n})$
- $C_{2n} = Z(C_{1n})$

Modeling results

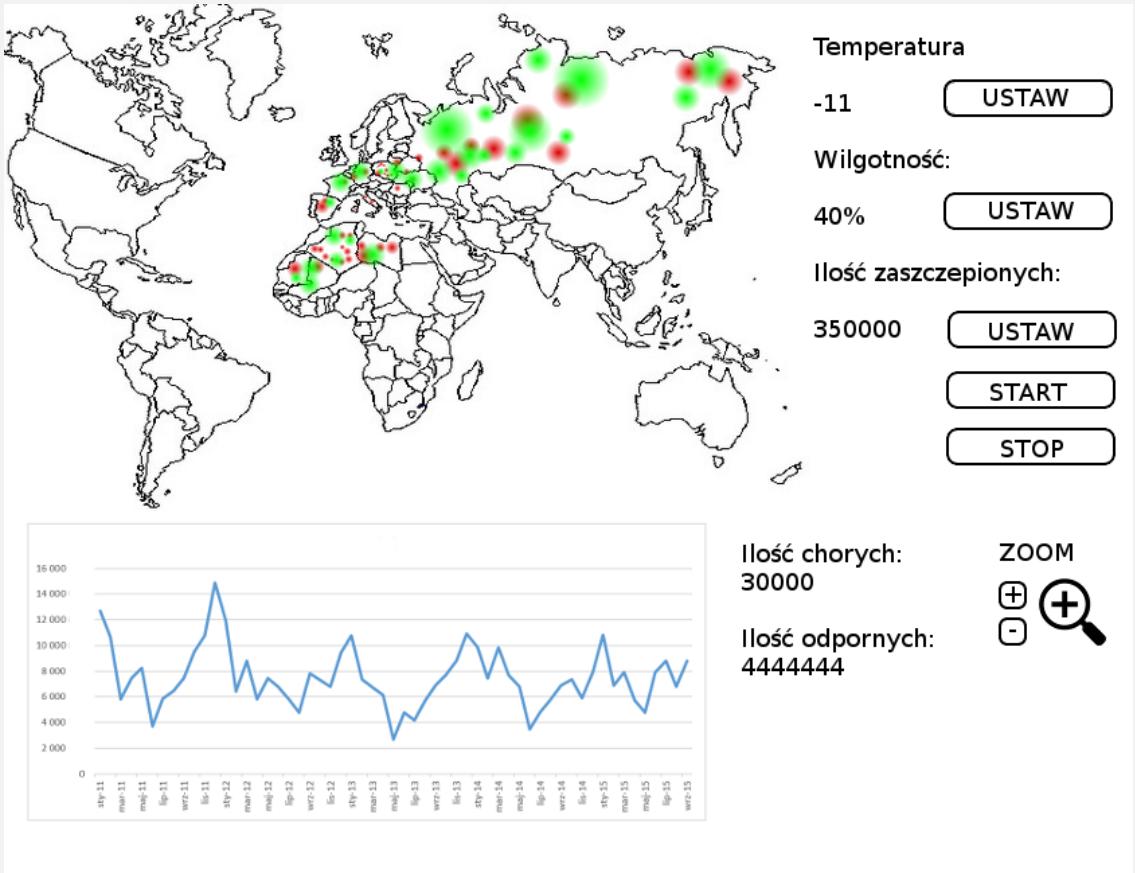

Figure: Modeling results

Problems and future work

Problems under investigation:

- modeling the rules of propagation and interaction (x, y parameters),
- validation of the rules,
- validation of the final results,
- model tuning,

Bibliography

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