



Wrocław University of Technology

th.if.uj.edu.pl/~gulakov/epi.pdf
(Network's) Models of
epidemiology

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USM

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Poland**



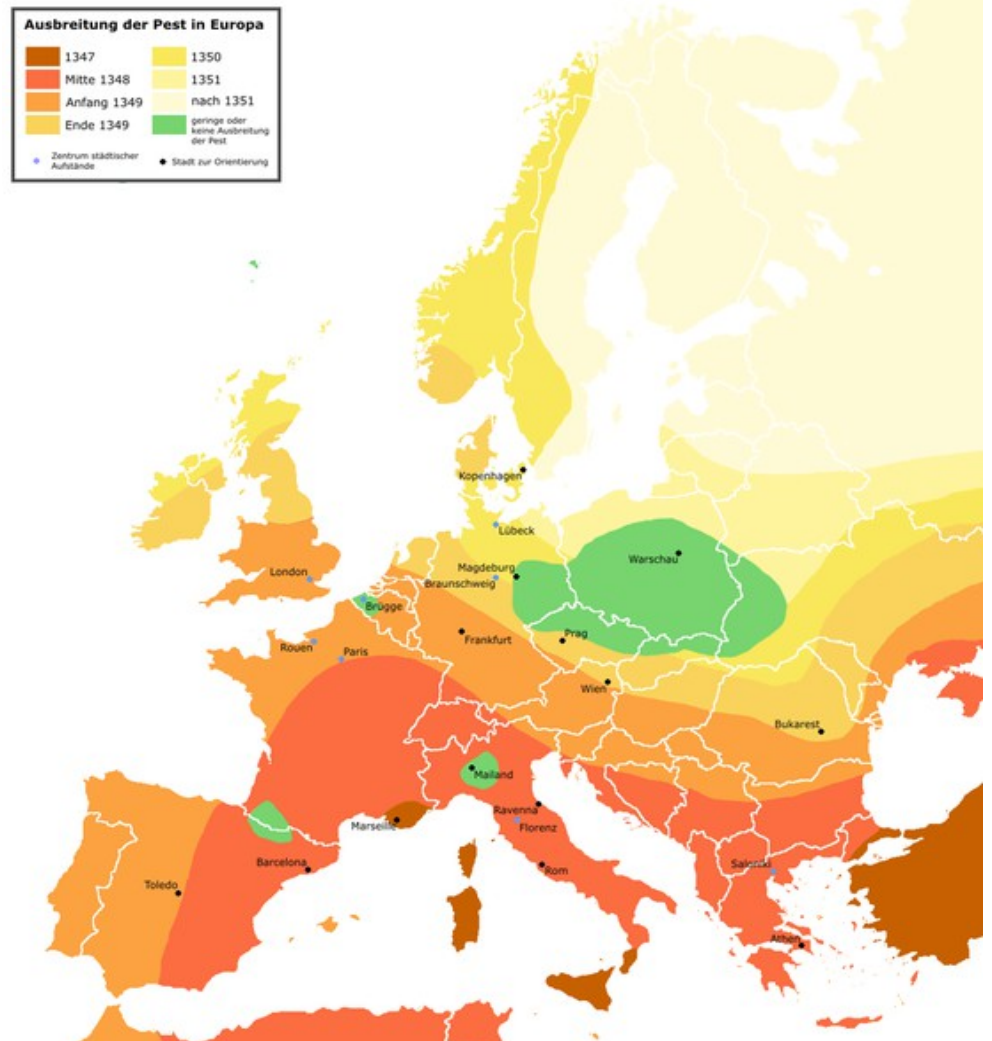
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- 2) Differential equations & Bernoulli model
- 3) Agent based models
- 4) Cellular automata/ Networks
- 5) Economic Consequences to Society of Pandemic H1N1 Influenza
- 6) Sexually Transmitted Infections (HPV)
- 7) MRSA in Hospitals
- 8) STOP – ACTA viral spread



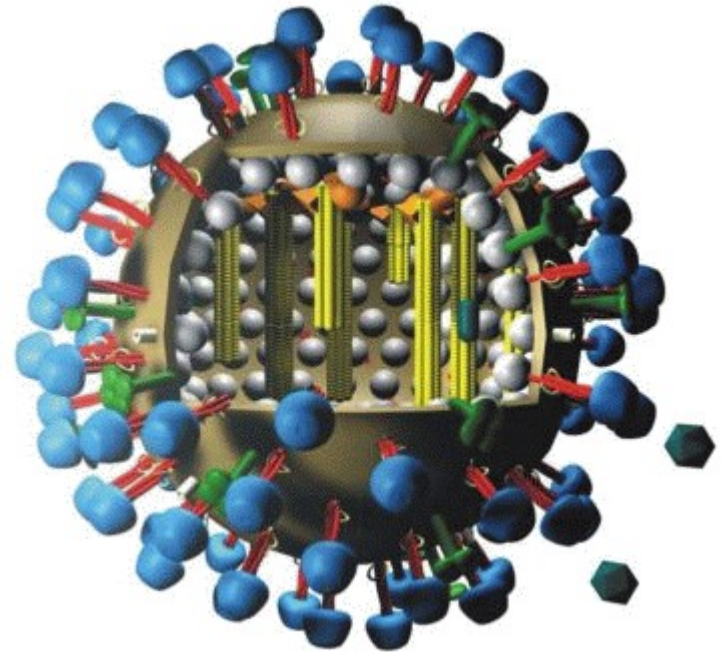
Epidemics

Black Death (PDE)





Epidemics



H5N1 influenza - bird flu 2005
H1N1 influenza - swine flu 2009
(Networks)



Epidemics



Plant's diseases - rhizobia
(CA)



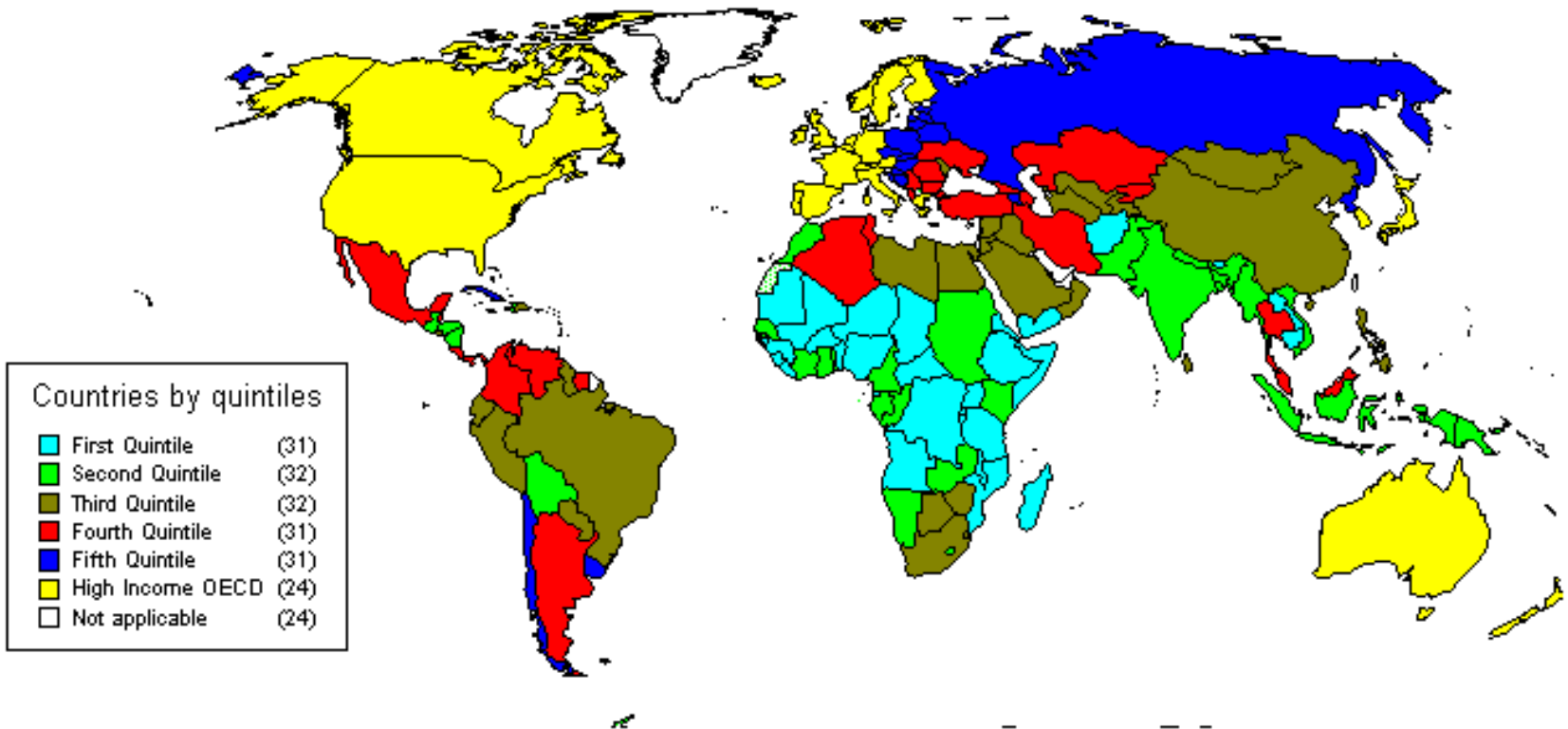
Epidemics



Animal's diseases
Mad Cow - BSE
(CA, Networks)



Epidemics



Differential equations vs Networks

Data!!!



Before differential equations, Bernoulli Model

Wrocław - from the beginning of smallpox epidemiology modeling up to eradication of disease



In Poland smallpox **last time appeared in Wrocław in 1963**, but it was stopped by the actions of the government and epidemiologists. Moreover smallpox was eradicated by WHO in 1979. **Bernoulli (1760) actually used data provided from Wrocław to estimate his model.**



Before differential equations, Bernoulli Model

This Swiss mathematician **was the first to express the proportion of susceptible individuals of an endemic infection** in terms of the force of infection and life expectancy. His work describe smallpox, which cause a lot of epidemics in big European cities at his time. Smallpox devastated earlier the native Amerindian population and was an important factor in the conquest of the Aztecs and the Incas by the Spaniards.



Before differential equations, Bernoulli Model

I simply wish that, in a matter which so closely concerns the well-being of mankind, no decision shall be made without all the knowledge which a little analysis and calculation can provide.

Daniel Bernoulli, presenting his estimates of smallpox
Royal Academy of Sciences-Paris, 30 April 1760



Before differential equations, Bernoulli Model

Bernoulli based at work of famous British **astronomer** – **Edmund Halley** „An Estimate of the Degrees of the Mortality of Mankind, drawn from curious Tables of the Births and Funerals at the City of Breslaw” published in Philosophical Transactions 196 (1692/1693).

In 17th century English Breslaw means Breslau-German name of Wrocław.



Before differential equations, Bernoulli Model

Survivors according to Halley	Not having had smallpox	Having had smallpox	Catching smallpox each year	Dying of smallpox each year	Total smallpox deaths	other diseases each year
1300	1300	0				
1000	896	104	137	17,1	17,1	283
855	685	170	99	12,4	29,5	133
798	571	227	78	9,7	39,2	47
760	485	275	66	8,3	47,5	30
732	416	316	56	7	54,5	21
710	359	351	48	6	60,5	16
692	311	381	42	5,2	65,7	12,8
680	272	408	36	4,5	70,2	7,5
670	237	433	32	4	74,2	6
661	208	453	28	3,5	77,7	5,5
653	182	471	24,4	3	80,7	5
646	160	486	21,4	2,7	83,4	4,3
640	140	500	18,7	2,3	85,7	3,7
634	123	511	16,6	2,1	87,8	3,9
628	108	520	14,4	1,8	89,6	4,2
622	94	528	12,6	1,6	91,2	4,4
616	83	533	11	1,4	92,6	4,6
610	72	538	9,7	1,2	93,8	4,8
604	63	541	8,4	1	94,8	5
598	56	542	7,4	0,9	95,7	5,1
592	48,5	543	6,5	0,8	96,5	5,2

Table 1. Smallpox in Wrocław [D. Bernoulli]



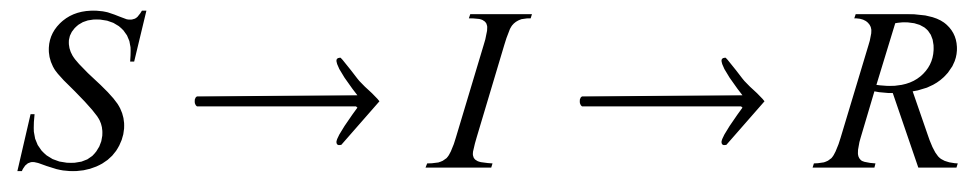
Before differential equations, Bernoulli Model

Bernoulli has constructed table with 'natural state with smallpox', in contradistinction to the third column, which shows the 'state without smallpox' and which gives the number of survivors each year assuming that nobody must die of smallpox. Difference between second and third column gave him **a gain in people's lives**. He introduced 'total quantity of life' of the whole generation.



Differential equations

Suppose that population is divided into three classes: the susceptibles (S) who can catch the disease; the infectives (I), who can transmit disease and have it; and the removed (R) who had the disease and are recovered (with immune) or isolated from society. Schema of transition can be represented:



W. O. Kermack and A. G. McKendrick, 1927



Differential equations

$$\frac{dI}{dt} = rSI - aI ,$$

$$\frac{dS}{dt} = -rSI ,$$

$$\frac{dR}{dt} = aI$$

Where transmission rate is: $r = \beta C / N$

β – infectivity rate, C – contact rate, a – recovery rate



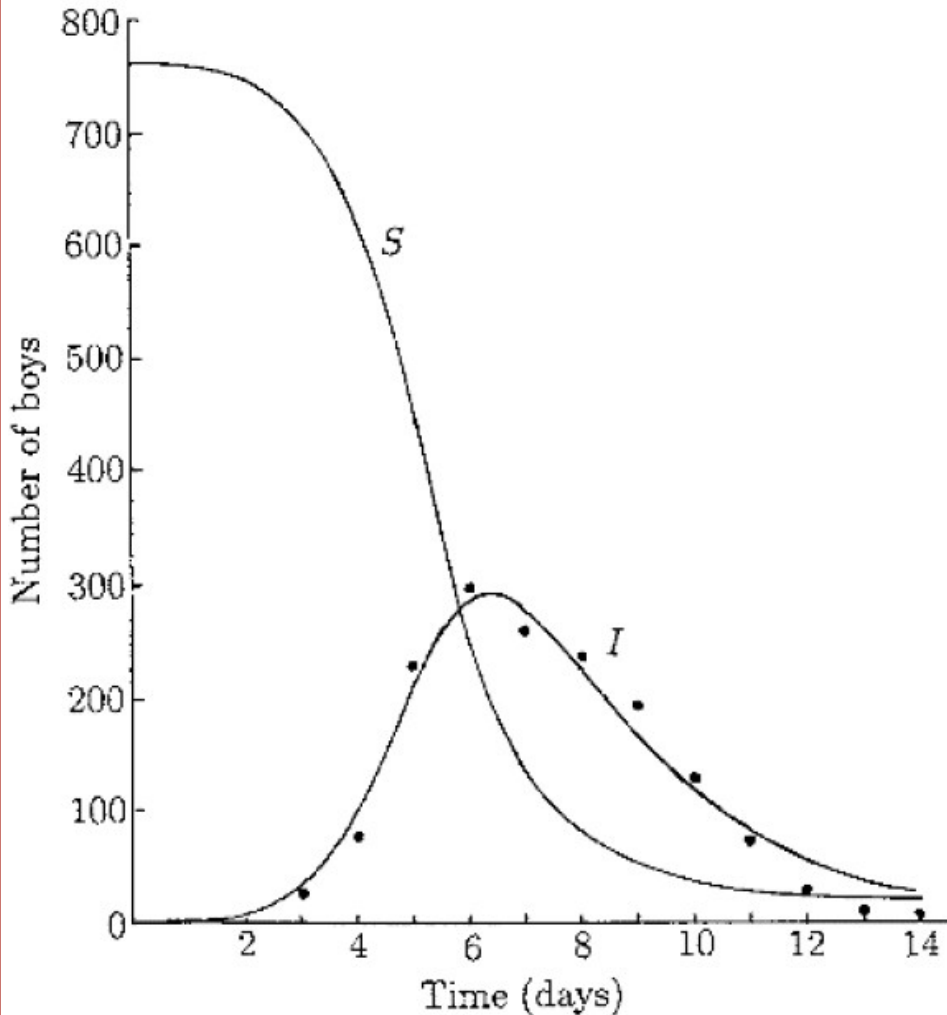
Differential equations

$$R_0 = \frac{r S_0}{a}$$

where R_0 is basic reproduction rate of the infection. This rate is crucial for dealing with and an epidemic which can be under control with vaccination for example. Action is needed if $R_0 > 1$, because epidemic clearly ensues then.



Differential equations



Influenza epidemic data (●) for a boys boarding school as reported in UK in 1978. The continuous curves for I and S were obtained from a best fit of numerical solution of SIR system with parameters: $S_0=762$, $I_0=1$, $S_C=202$, $r=0,0022/\text{day}$.



Agent-based models

Differential equation vs Agent-based models

Network of contacts:

In an SIR-type model, the population is split into three different groups and the majority of the population is placed in the susceptible compartment. All information about society is used in microsimulation, so it can give better prediction, then differential equations



Agent-based models vs DE

Differential equations were first applied to describe and predict those phenomena (in use since the 18th century when even the definition of „differential equation” has not been known). Epidemiological models that treat transmission from the perspective of differential equations do exist in older literature, but recently agent-based models appear even more often. Both approaches use variations of SIR (susceptibles - infectives - removed) concept, so sometimes **the same problem could be solved in both ways**. Not always, because computer simulation has changed the world of mathematical modeling, agent-based models give better predictions and some hints for decision-makers even parallel development of numerical methods for differential equations. On the other hand, **differential equations allow us to understand the core process, which could be missing in the agent-based approach**. As a result, both perspectives are common among epidemiologists and **depend on theoretical or applied aspect** percentage representations differ.

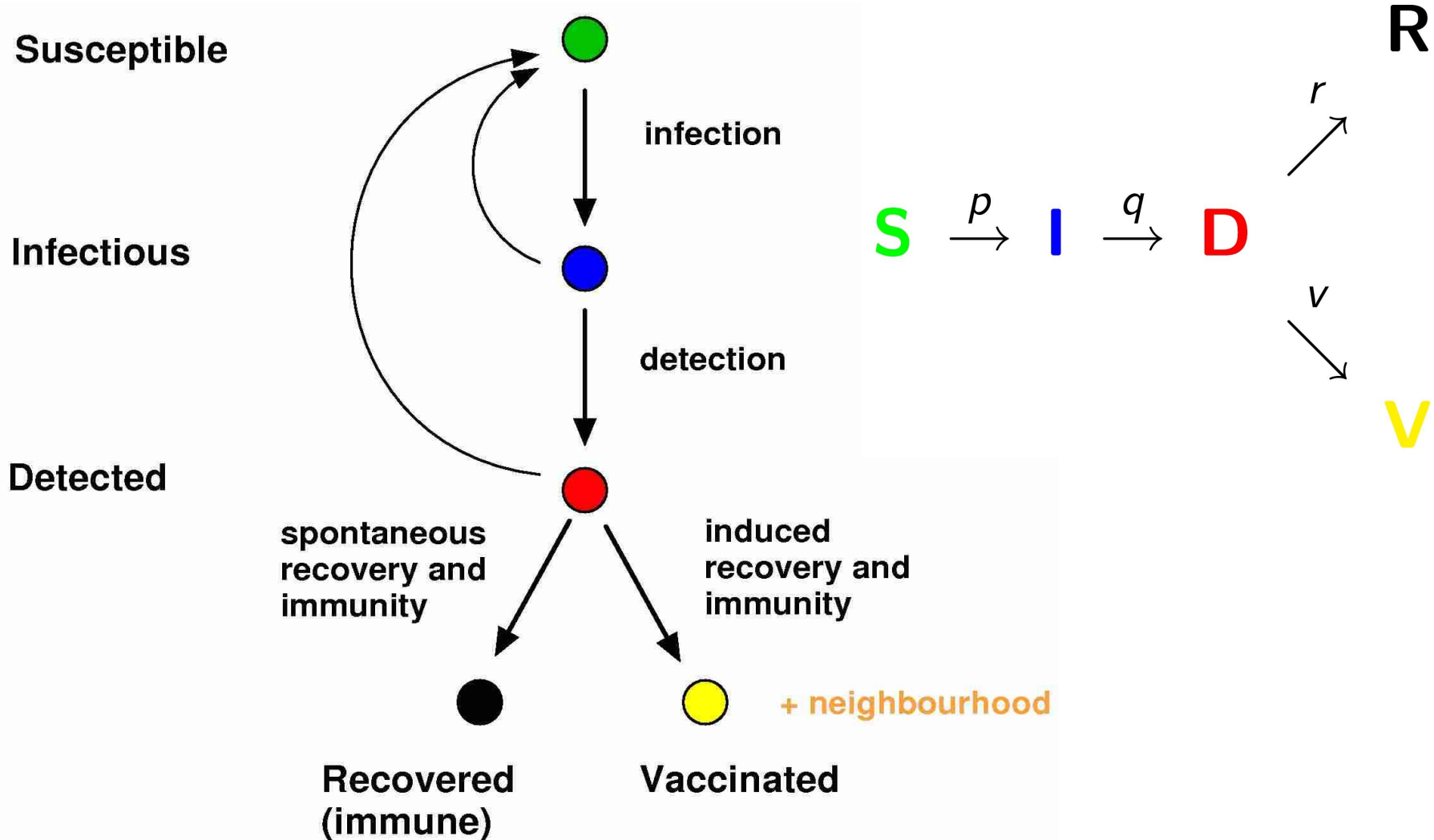


Cellular Automata

Cellular Automata were invented in early 50th. They are based on some designed topology of elements which have some possible number of states and they can evaluate in time. A cellular automaton may be also a collection of "colored" cells on a grid of specified shape that evolves through a number of discrete time steps according to a set of rules based on the states of neighboring cells.

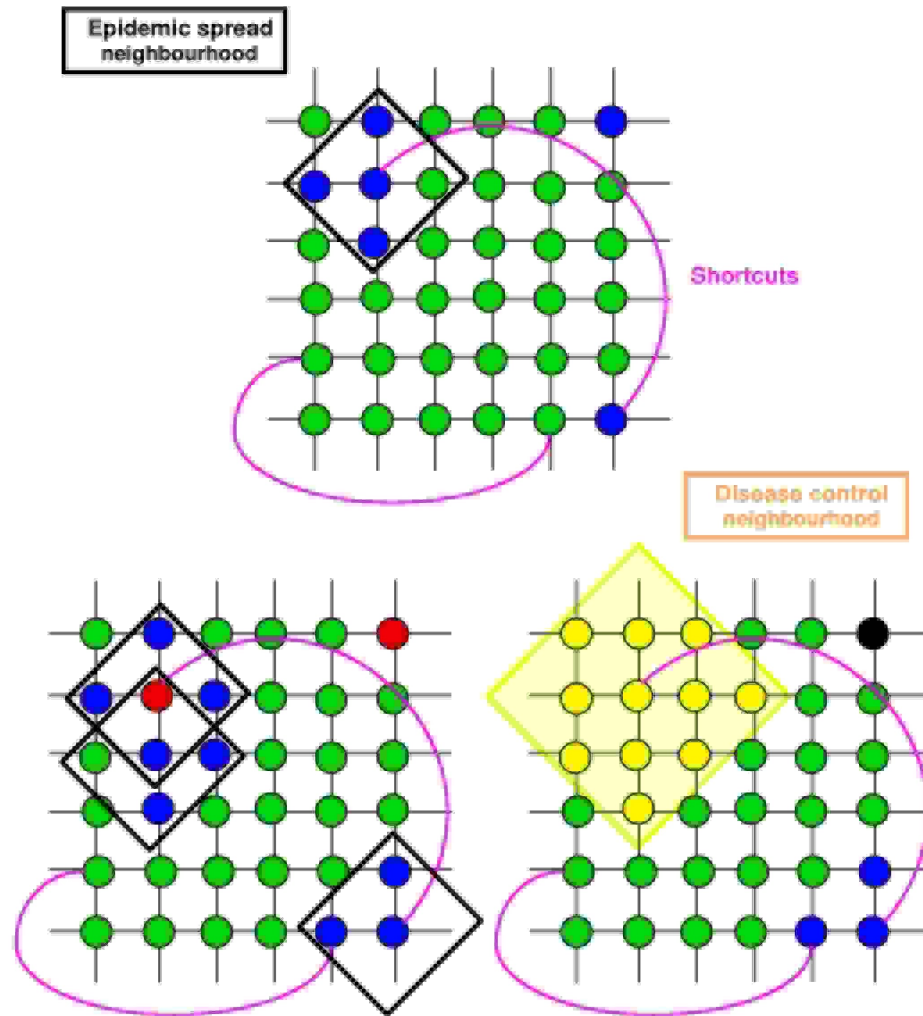


Cellular Automata





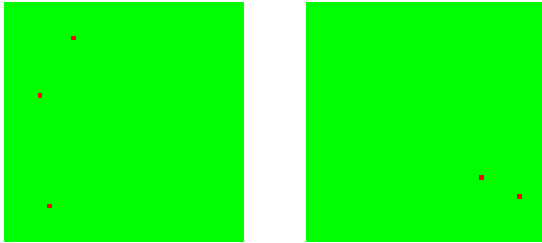
Cellular Automata



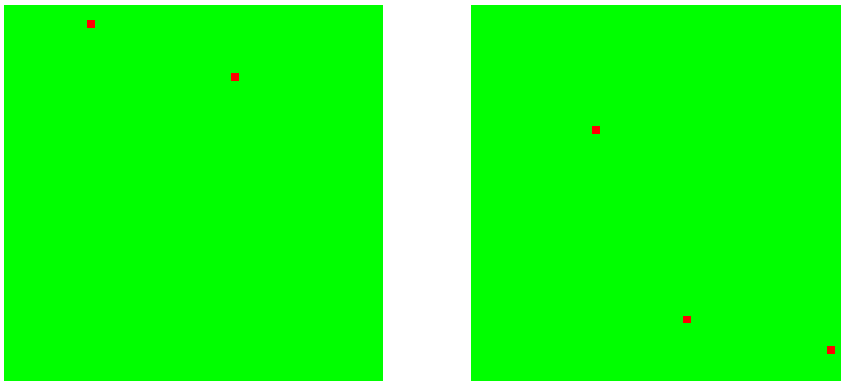


Cellular Automata

No additional links



With additional links





Network Theory - introduction

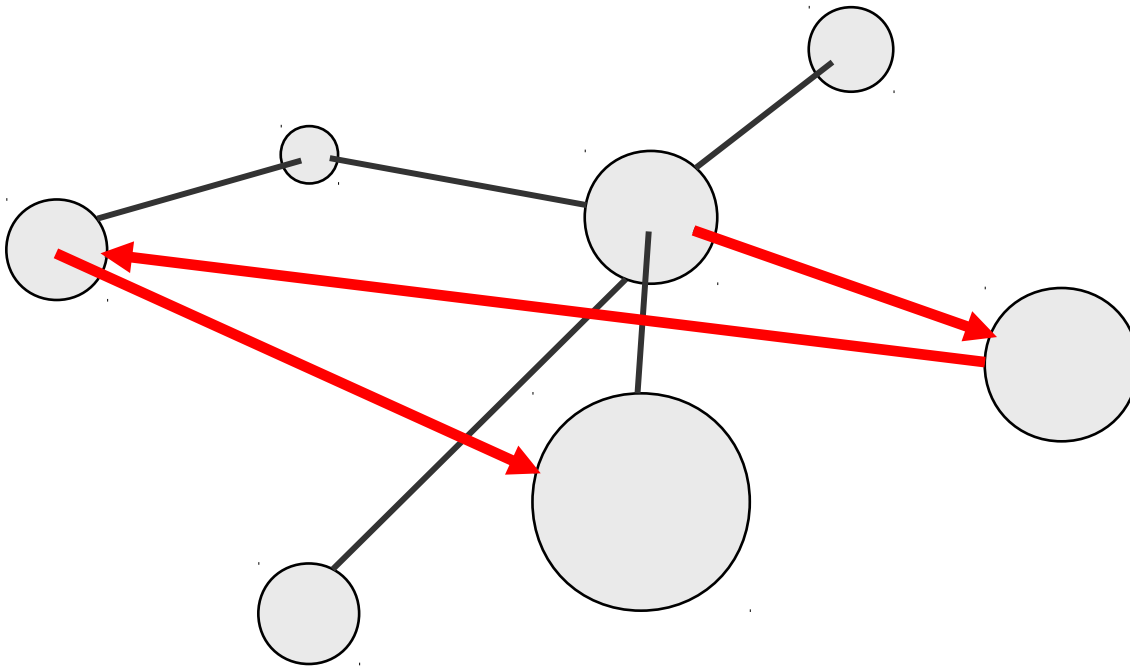
An agent/object's actions are affected
by the actions of others around it.

NETWORK

Actions, choices, etc. are not made in isolation
i.e. they are contingent on others' actions, choices, etc.



Network Theory - terminology



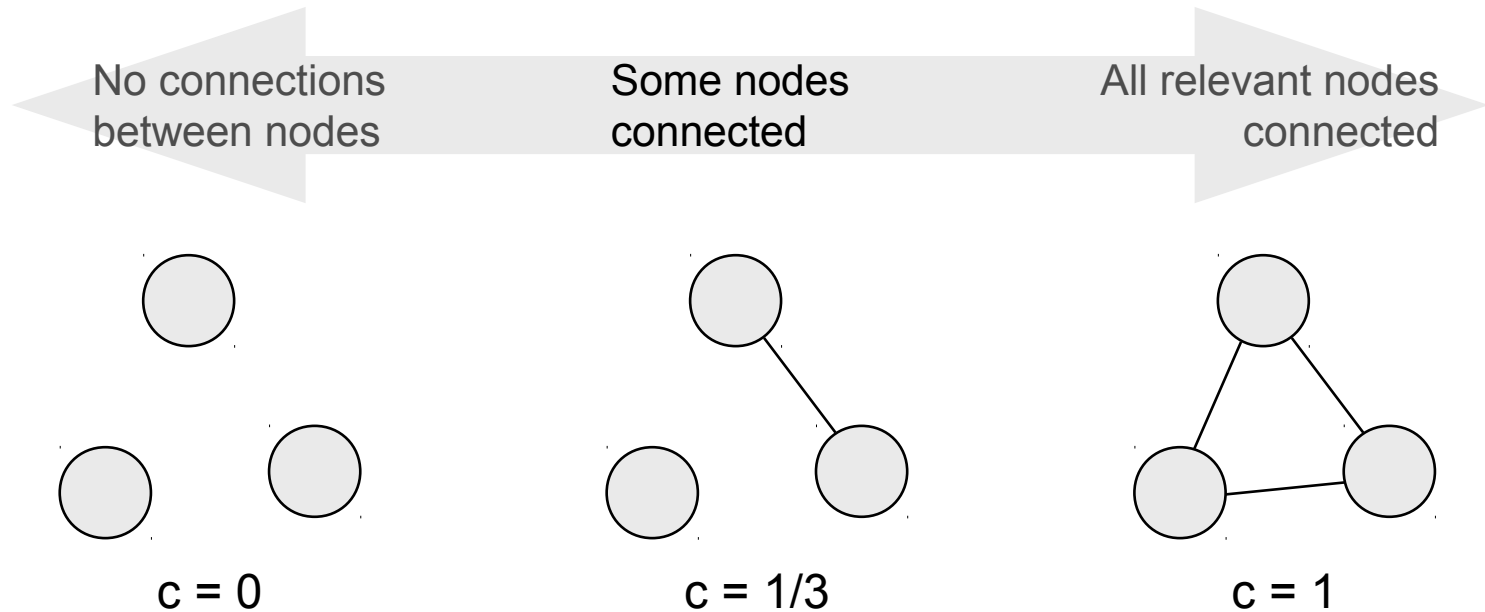
Node = individual components of a network e.g. people, power stations, neurons, etc.

Edge = direct link between components (referred to social networking as a relationship between two people)

Path = route taken across components to connect two nodes



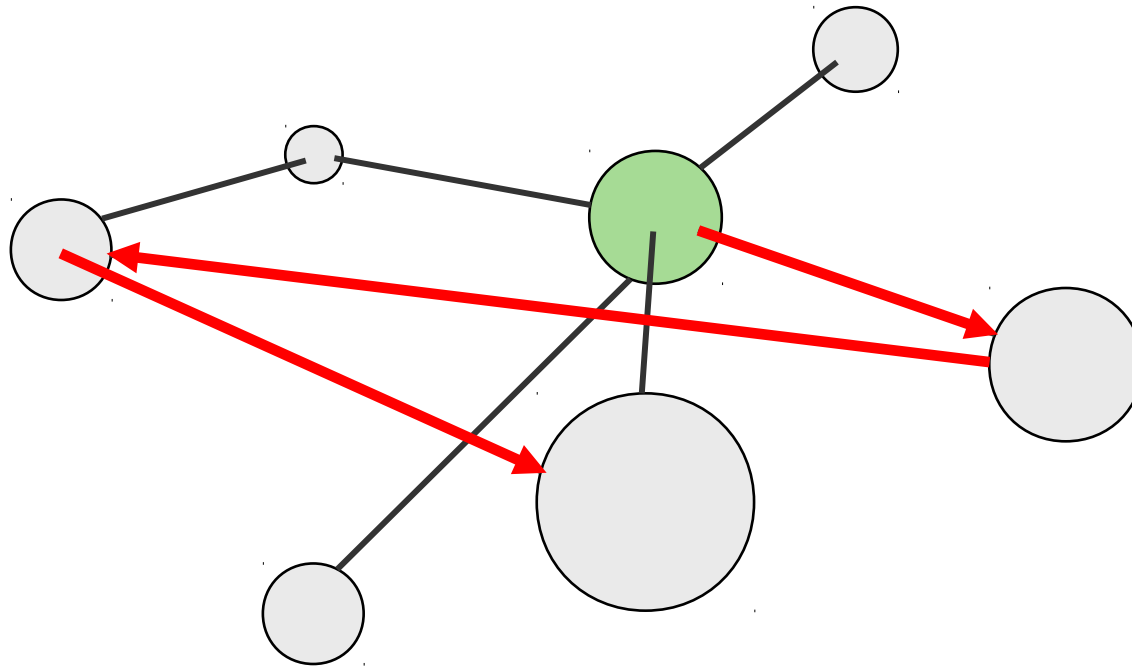
Network Theory - clusters



Clustering coefficient counts number of triangles in networks



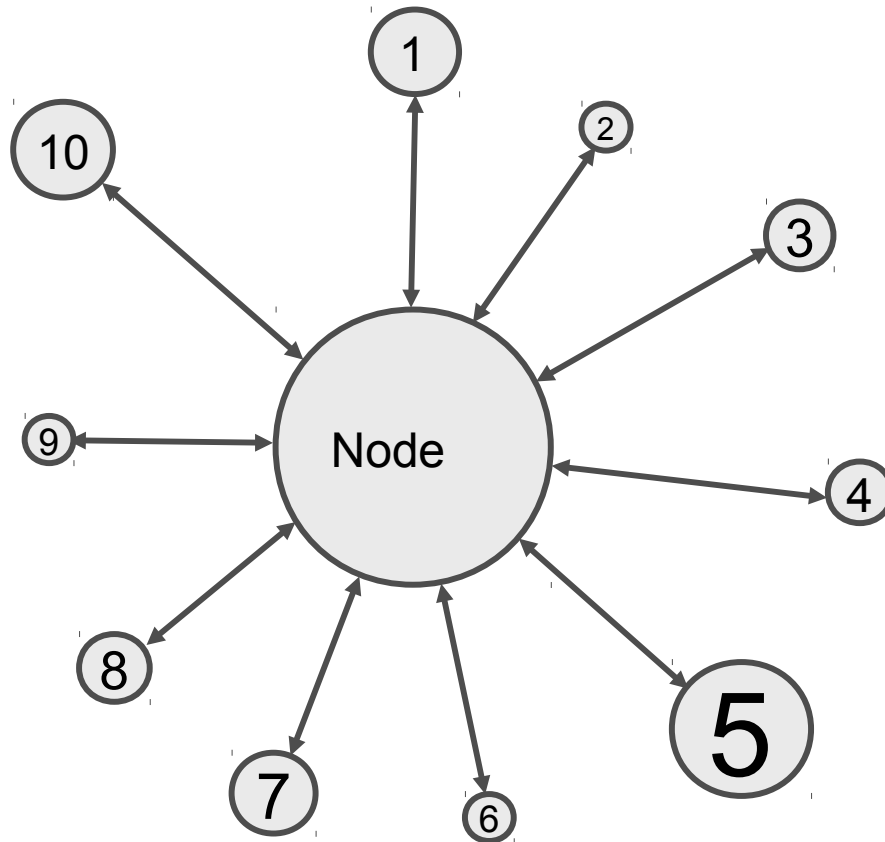
Network Theory - paths



Average path length



Network Theory - node's degree

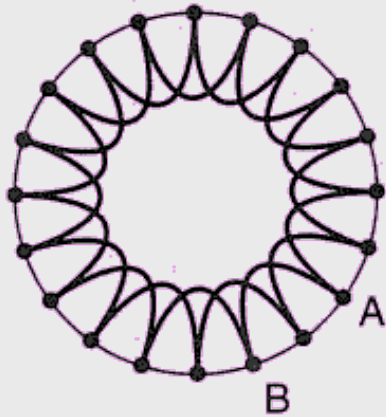


Degree distribution

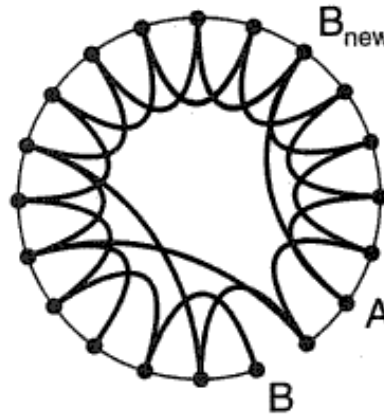


Network Theory - randomness

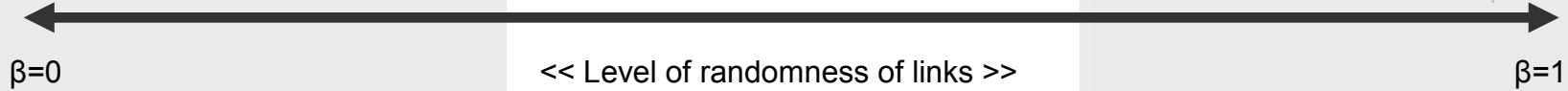
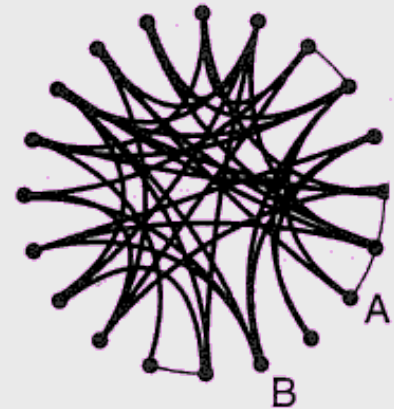
1. Grid/lattice network
(structure, order)



2. Small-world network
(a mix of order and randomness)



3. Random network
(randomness)

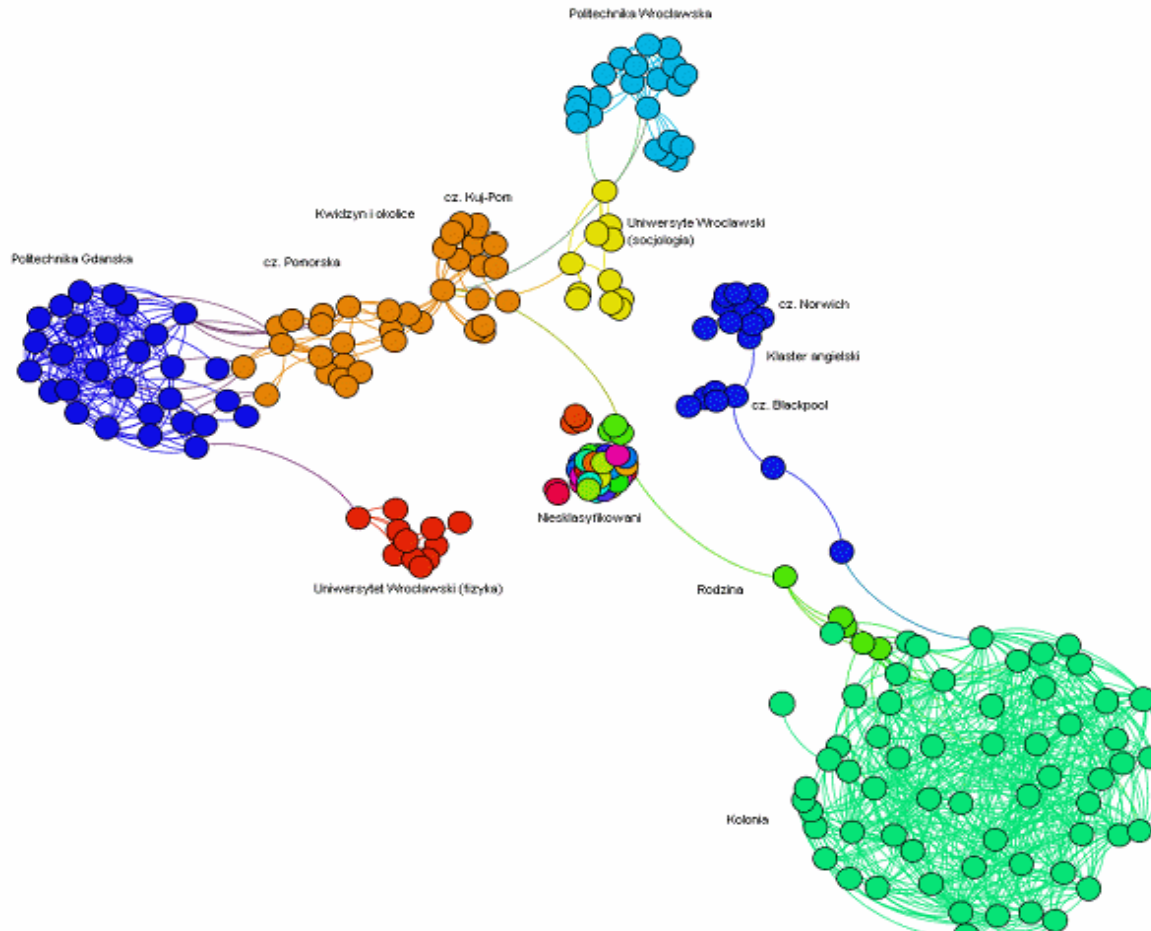


<< Level of randomness of links >>

Randomness



Network Theory - communities



Communities detection

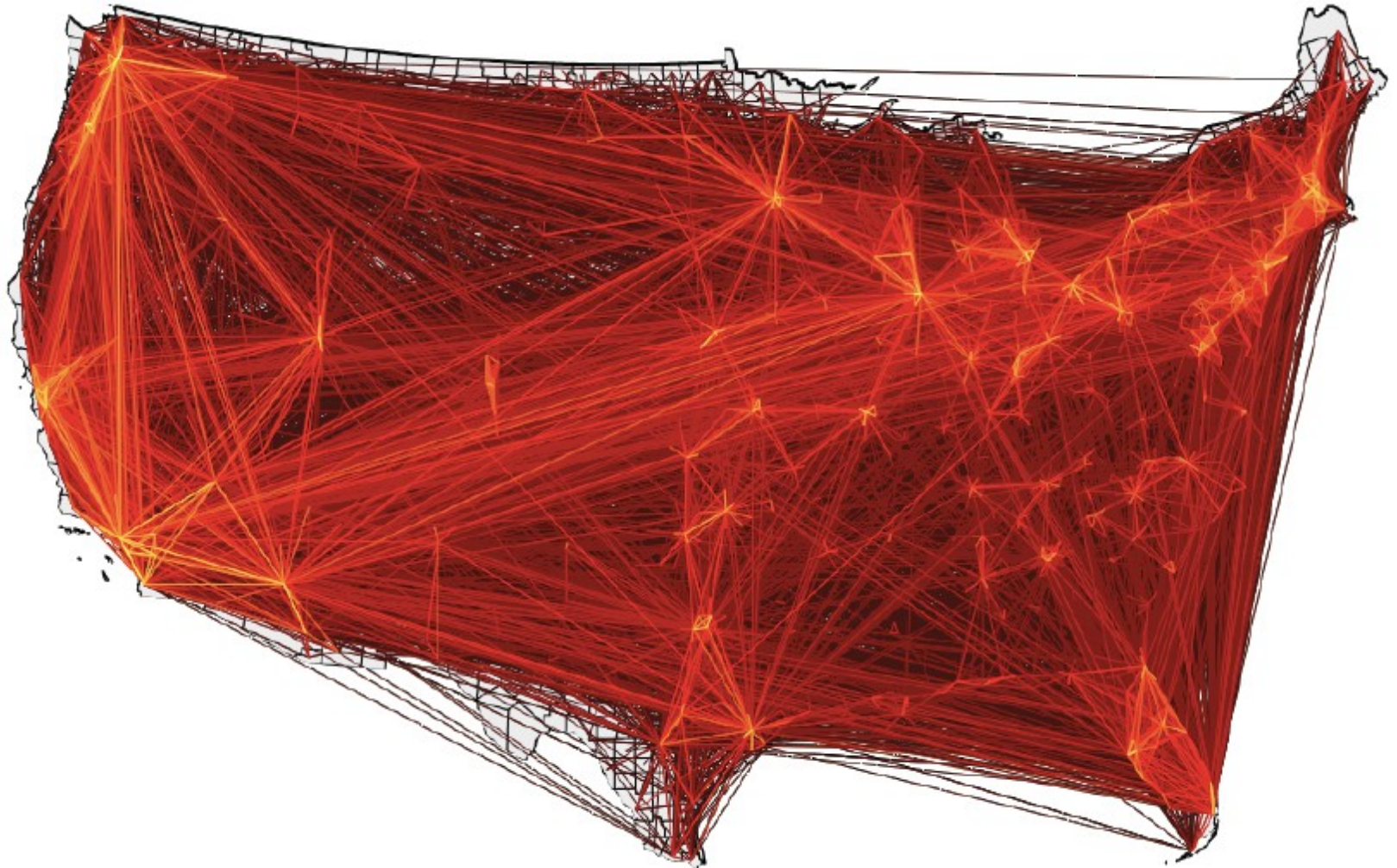


Where's George



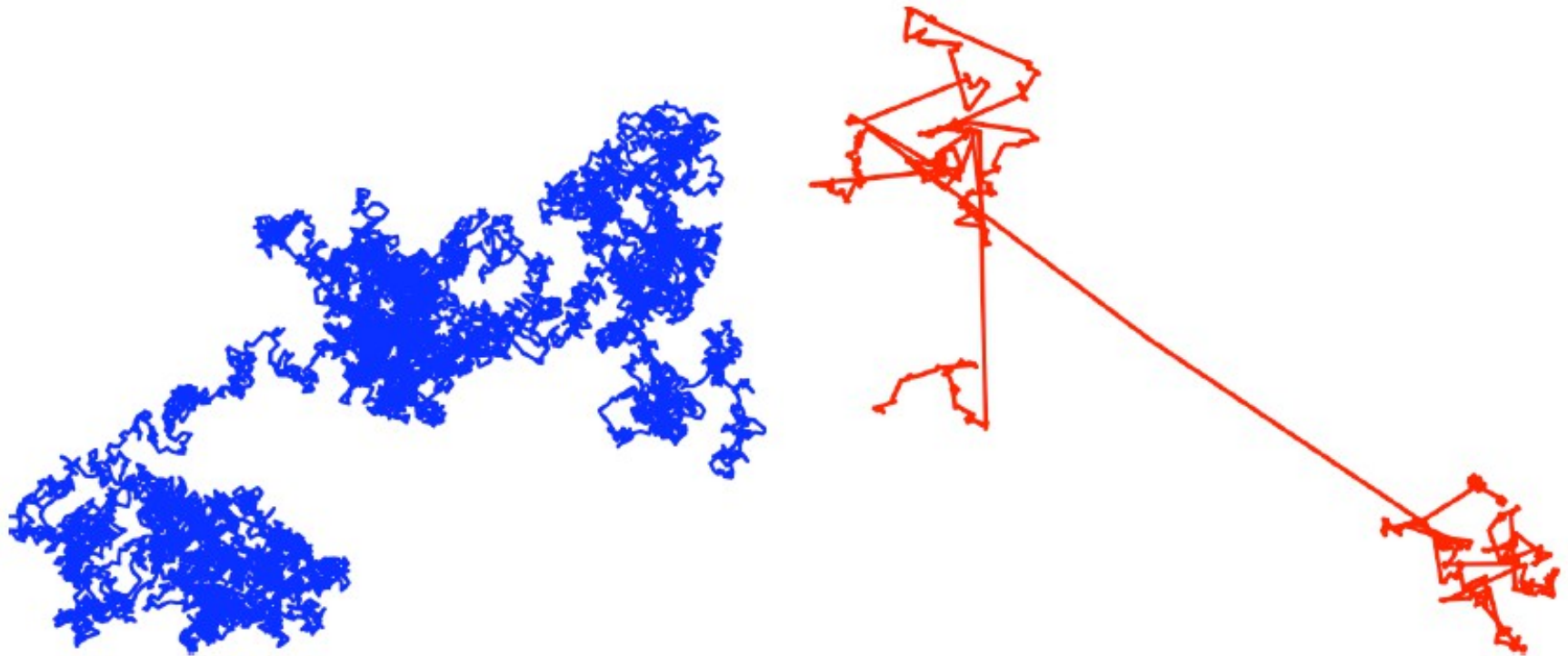


Where's George





Where's George



2 scales of
movements



H1N1 - introduction

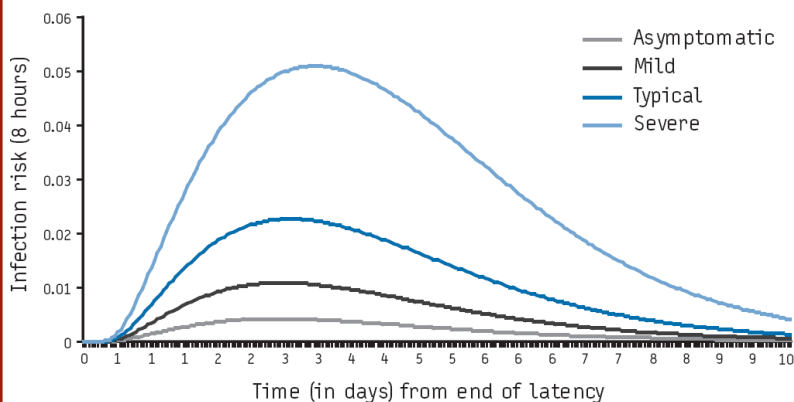




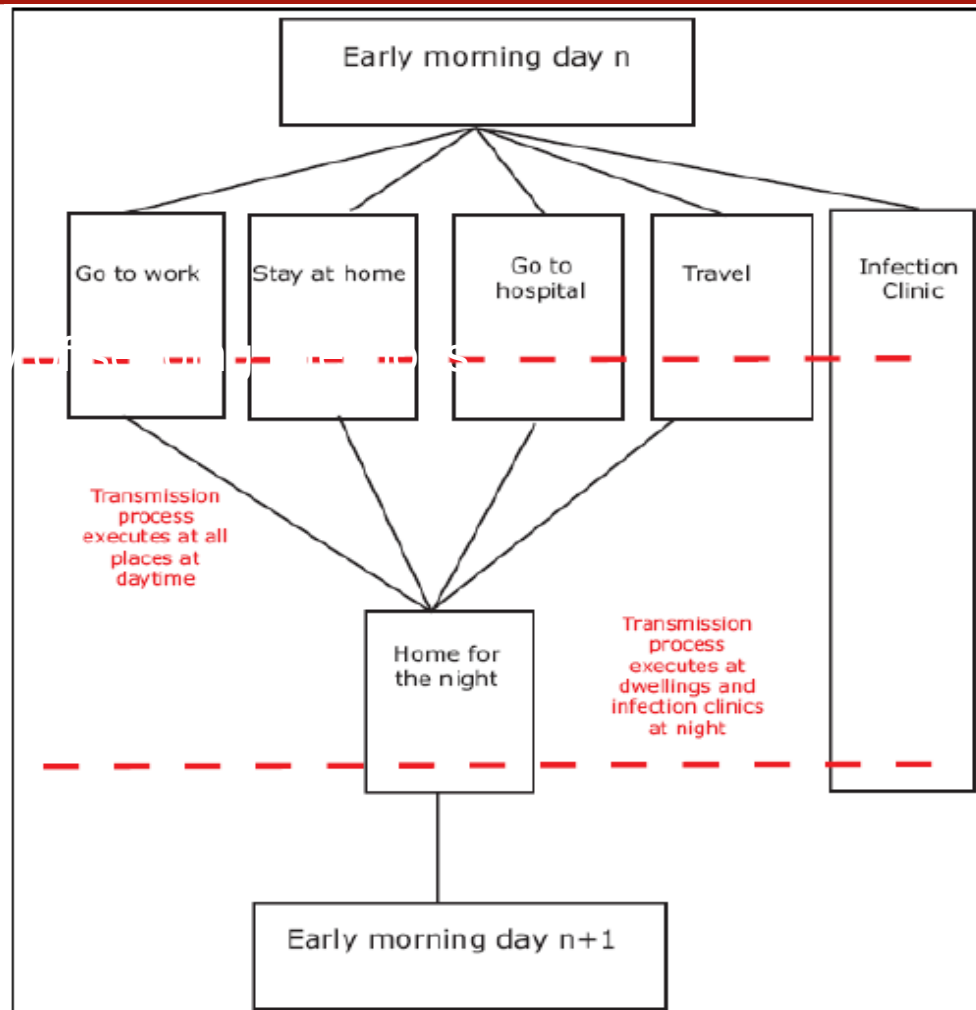
H1N1 - MicroSim

Disease transmission is performed twice daily at 9 am and 5 pm. Programme checks where are all persons during that day hours and night hours.

We have for example profiles of probability of sending infections



Profile of probability (sending H1N1) [adopted F. Carrat]



The daily routines for the simulated persons. [L. Brouwers]



H1N1 - Realization

The outbreak of pandemic influenza in Sweden starts depend of method in June or in September. R_0 -value corresponding approximately to 1.4 in main model, because that was observed in New Zealand during their outbreak. The viral infectivity is markedly initially R_0 value of approximately 2.1 in preliminary method.

$$R_0 = \frac{-\ln\left(\frac{A}{S_0}\right)}{1 - \frac{A}{S_0}}$$

Immunity was calibrated in model to obtain R_0 - 1.4

S_0 : Total number of susceptible individuals before the outbreak

A: Total number of susceptible individuals after the outbreak

This formula is defined as is the average number of individuals a typical person infects under his/her full infectious period, in a fully susceptible population.



H1N1 - Cost & Vaccination

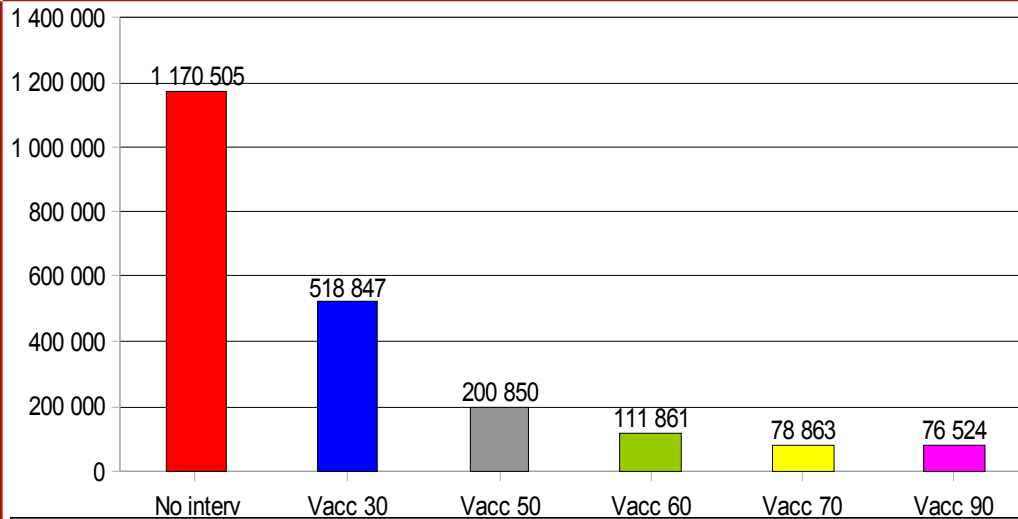
To compare the societal costs of the scenarios, the following costs—obtained from health economists at the Swedish Institute for Infectious Disease Control—were used.

- Cost of one day's absence from work, for a worker: SEK 900.
- Cost of treatment by a doctor in primary care: SEK 2000.
- Cost of one day's inpatient care: SEK 8000.
- Cost of vaccine and administration of vaccination for one person: SEK 300.

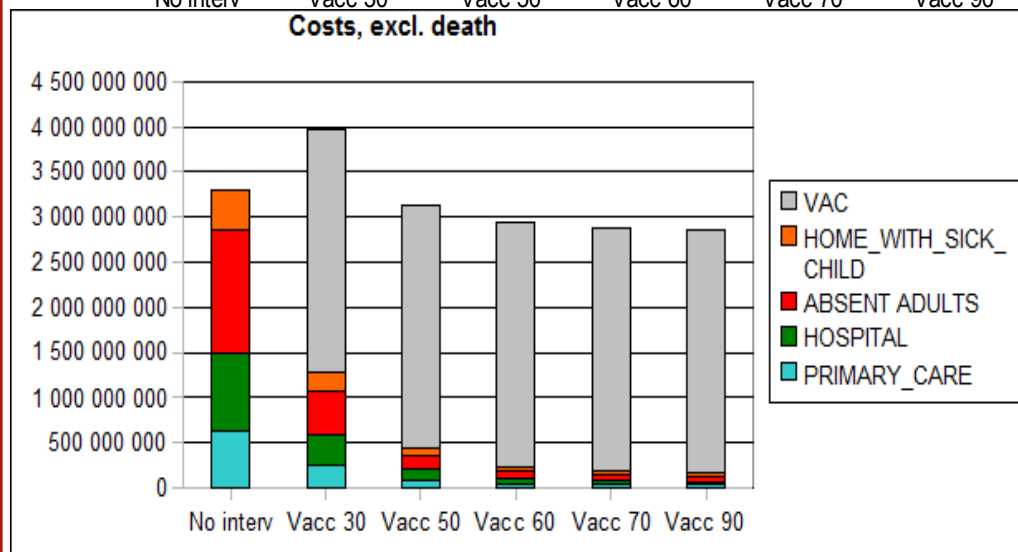
The following scenarios were compared: no response, the vaccination coverage of 30%, 50%, 60%, 70% or 90% in simulation.



H1N1 - Results



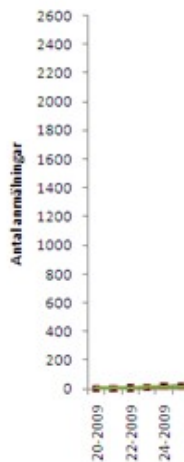
No. of infections (upper graph) and cost of pandemia (lower graph) for different scenarios [by L. Brouwers].





H1N1 - Simulation & Reality

No. of infections per week in simulation (upper graph by L. Brouwers) and cases collected by The Swedish Institute for Infectious Disease Control (lower graph by SMI).



Viral spread with or without emotions in online community





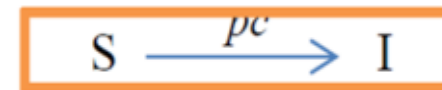
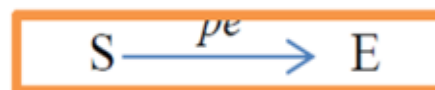
Viral spread with or without emotions in online community

- **modeling the behavior of online community (spread of virals) exposed by external impulses**
- **observation of virtual world**
- **two modes of experiments: with or without award and one natural (spontaneous organization against ACTA)**



Viral spread with or without emotions in online community

Event	proportion of unique invitations	probability of resending invitation per invitation	probability of resending invitation if get invitation
Epidemiological notation	probability of being exposed per contact (pe)	probability of infection per contact (pc)	probability of infection if exposed (p)
Non-incentivized	0.31	0.07	0.24 (std=0.23)
Stop-ACTA	0.87	0.33	0.38 (std=0.28)
Incentivized	0.14	0.07	0.48 (std=0.26)





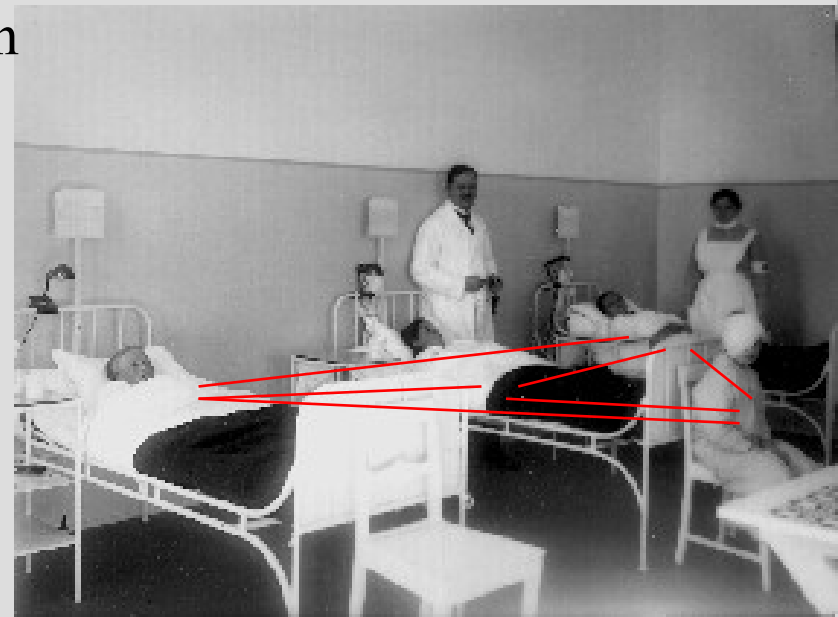
KUZI



MRSA - Background and Social Network

The bacterium Meticillin Resistant Staphylococcus Aureus (**MRSA**) is resistant against more than half of all antibiotics and is known to alone be **the largest care related the infection problem.**

For such a infectious diseases, where a **close contact** is needed for a transmission to occur, the individual's position in **the contact network is important** for the person's risk to get infected. The awareness of the importance of contact network has brought methods from sociological studies of social networks into the area of preventive infectious disease protection work.





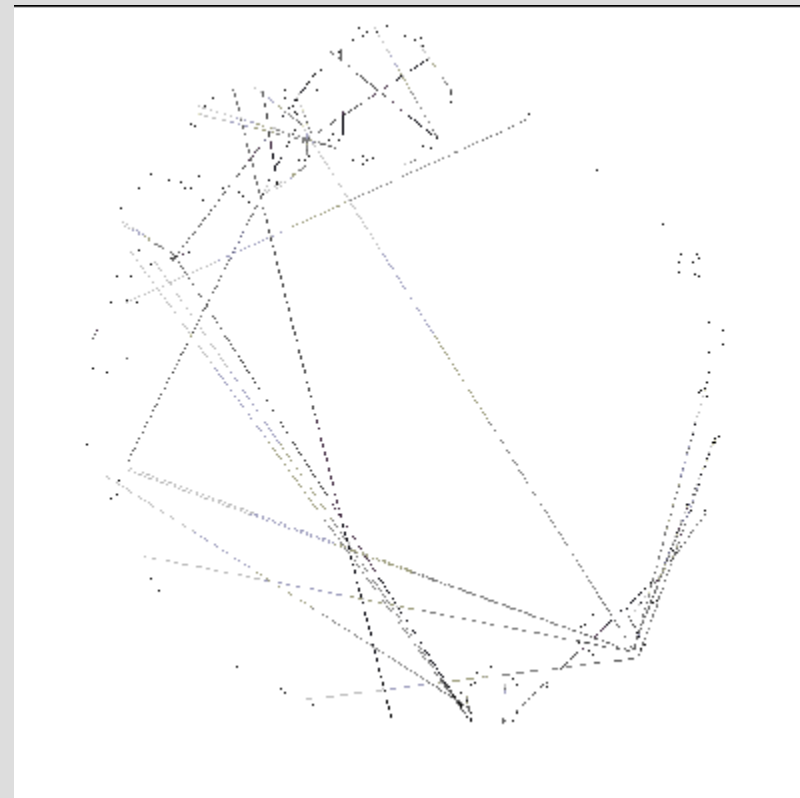
KU SI



The MRSA outbreak in Stockholm 1999-2005

- 1337 Cases
- Population 2 314 517 Patients
- 210 different types of MRSA
- UK-E15 is the most frequent one
- The outbreak is now under control

Dataset contains information about all in- and outpatient visits within Stockholm County during the period outbreak and a registry over diagnosed MRSA cases.





MRSA – Method of realization

We study matrix of disease transition in hospitals population. This matrix P is our first goal. **In rows are Infected and in Columns people, who could sent infection.** Elements of matrix are probabilities, what Infection was sent by indicated person. Diagonal elements are probabilities of being infected by someone out of hospital, but they are in first approximation zeros. **Unfortunately $\frac{1}{4}$ of all infected are patients, who had no contact with no other infected person.**



Probabilities calculation is based on time of contact (time of sharing the same ward)



Metropolis Monte Carlo algorithm

We have matrixes P_t , Q_t and P'_t for each year but there are not normalized.

Formula for individual change state in one time step can be written as:

$$p_i(t) = 1 - \exp\left(-\sum_j \sqrt{P_t(i, j)} \cdot s - \sum_j \sqrt{Q_t(i, j)} \cdot k - \sum_{j'} \sqrt{P'_t(i, j')} \cdot m\right)$$

Using characteristics of exponent we can rewrite formula above in multiplicative form, because our goal is to know who could infected patient i .

$$p_i(t) = 1 - \Pi_j (P_{i<-j}(t)) \cdot \Pi_j (Q_{i<-j}(t)) \cdot P'_{i<-indirect}(t)$$

Where:

$P_{i<-j}(t)$ represents that j send infection to i in year t on ward connections
($Q_{i<-j}(t)$ equivalent on clinic connections)

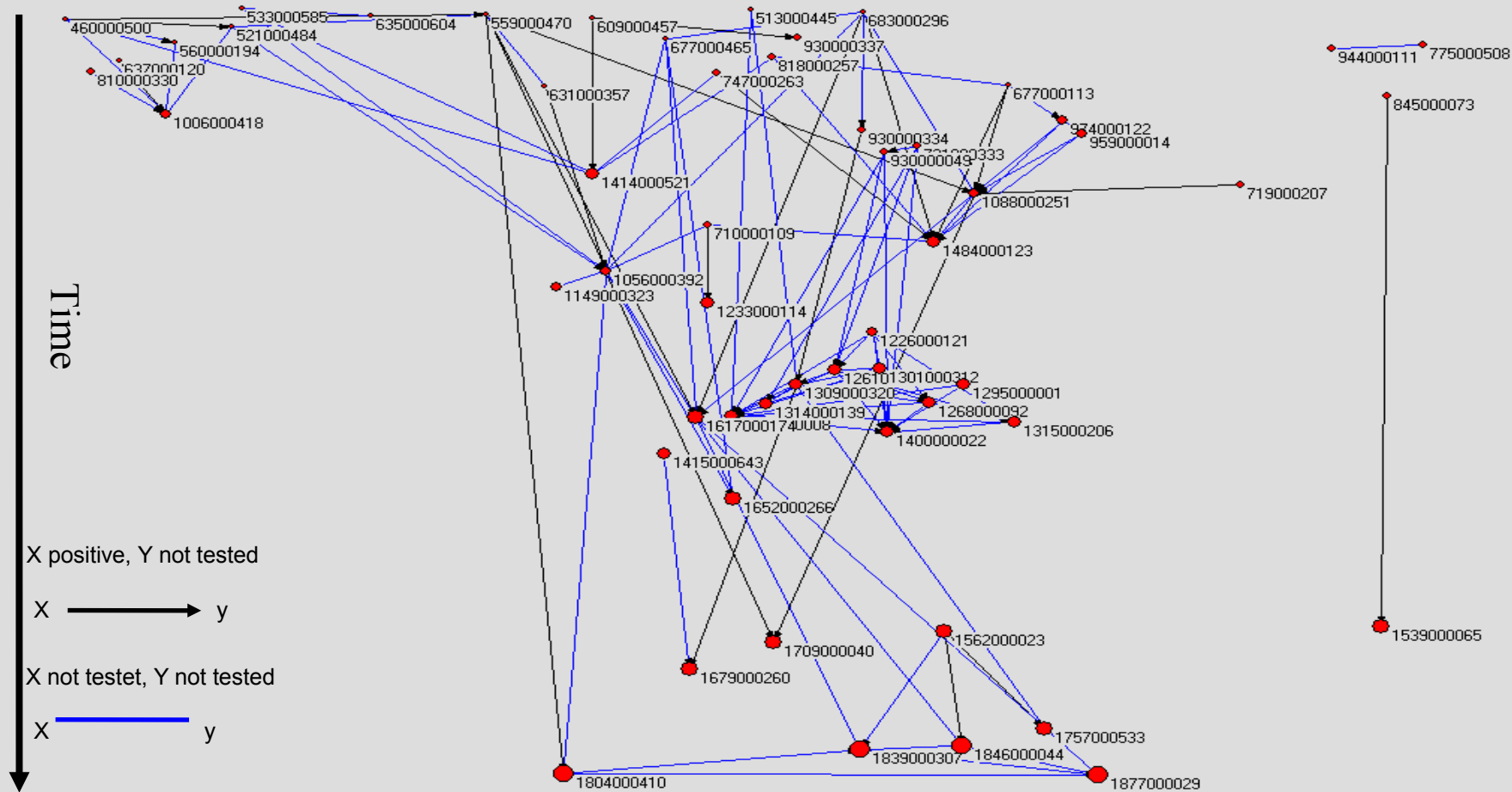
$P'_{i<-indirect}(t)$ is the representation of being infected indirectly in year t .

We need 3 parameters:



Summary

One step to get most likely paths of transmission





Sexually transmitted infections (STI)

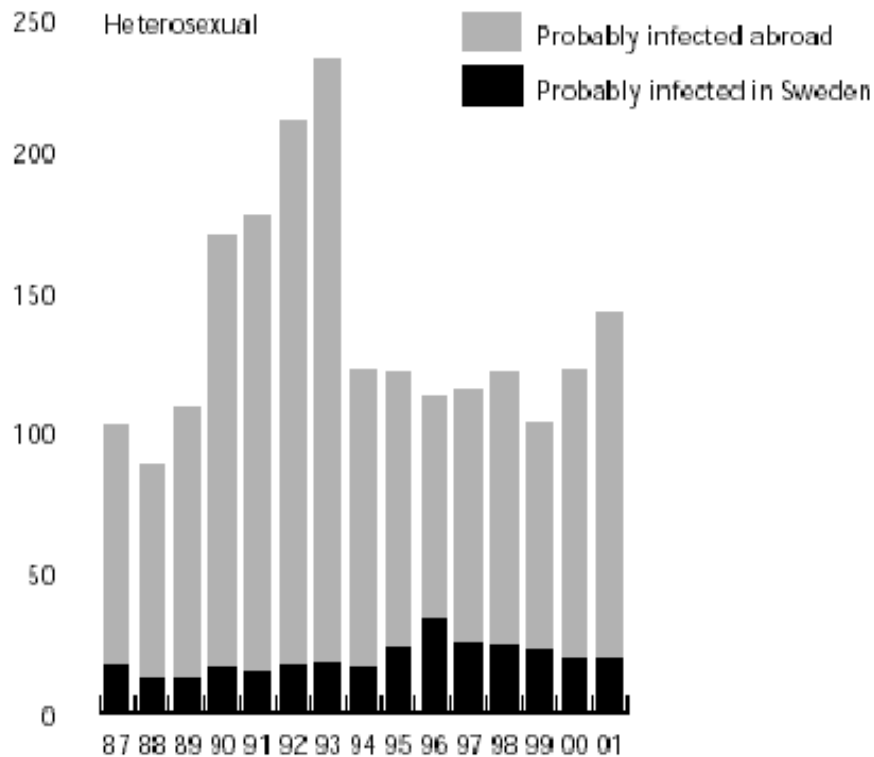




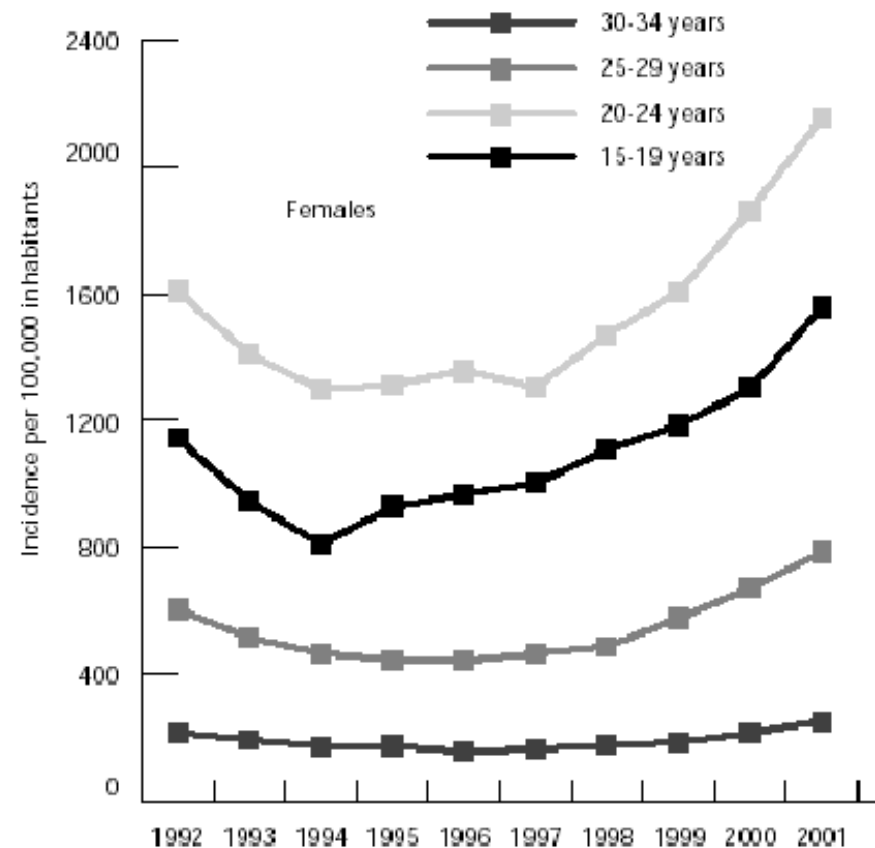
STI - problem

Probability of transmission per contact (β)

HIV 0,08-1,7%

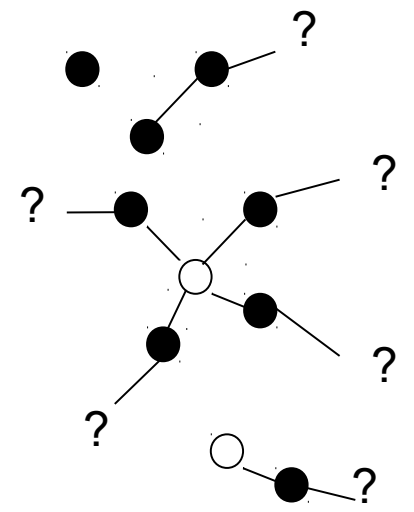
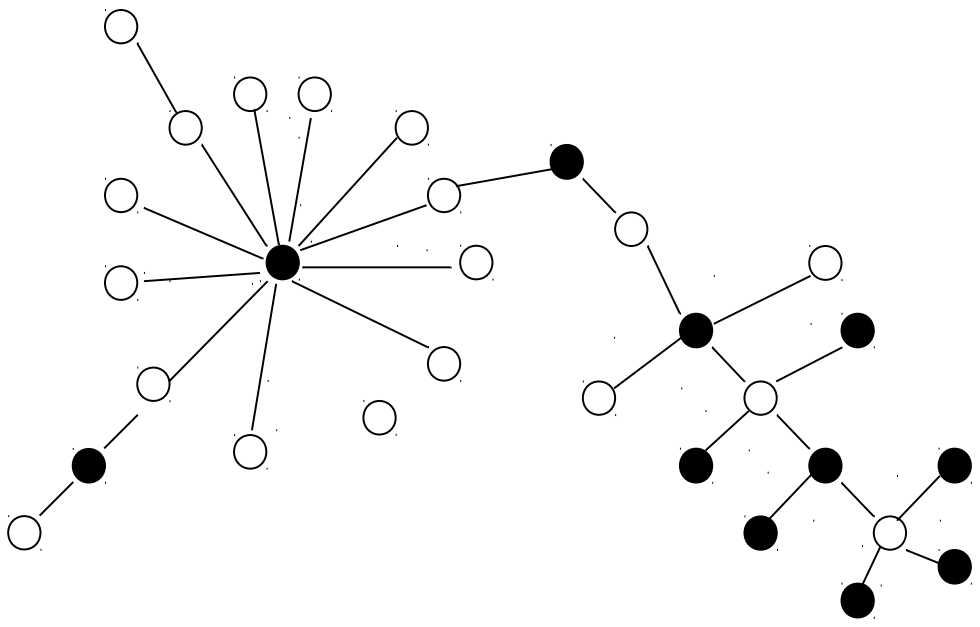


Chlamydia 2-60%





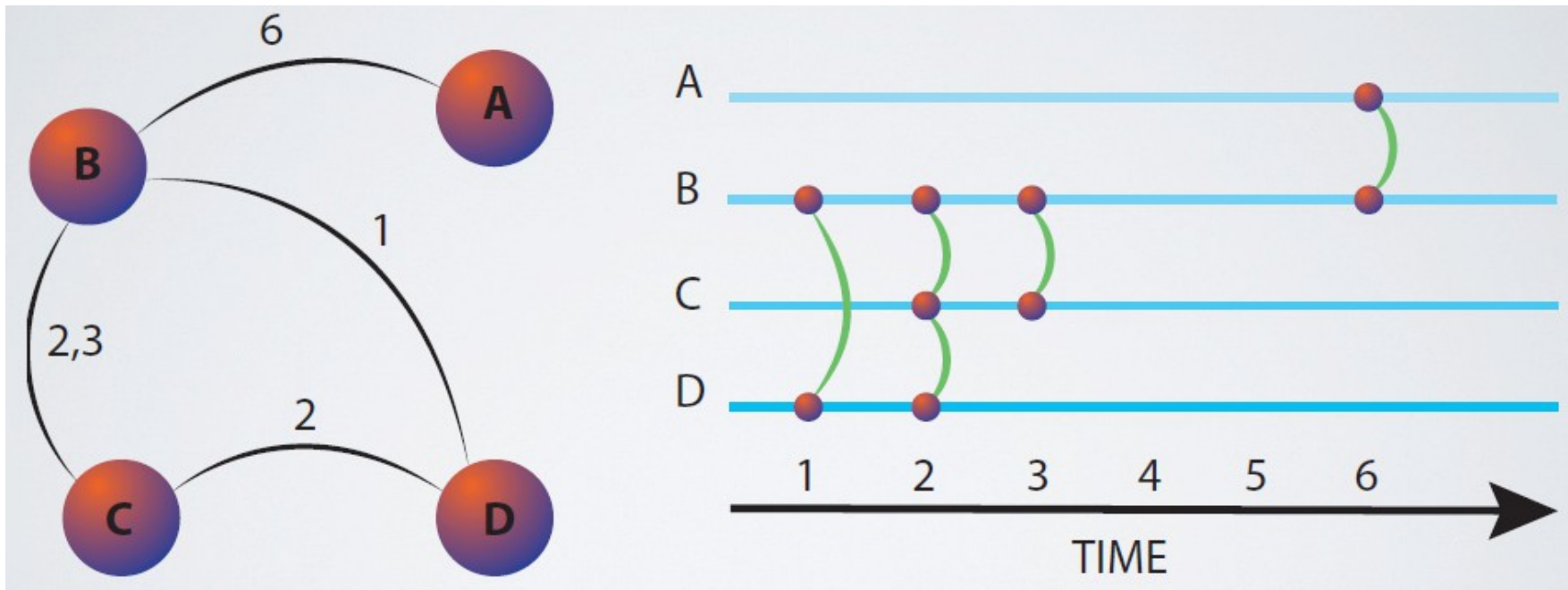
STI - networks



○
●
Men
Female

STI - model

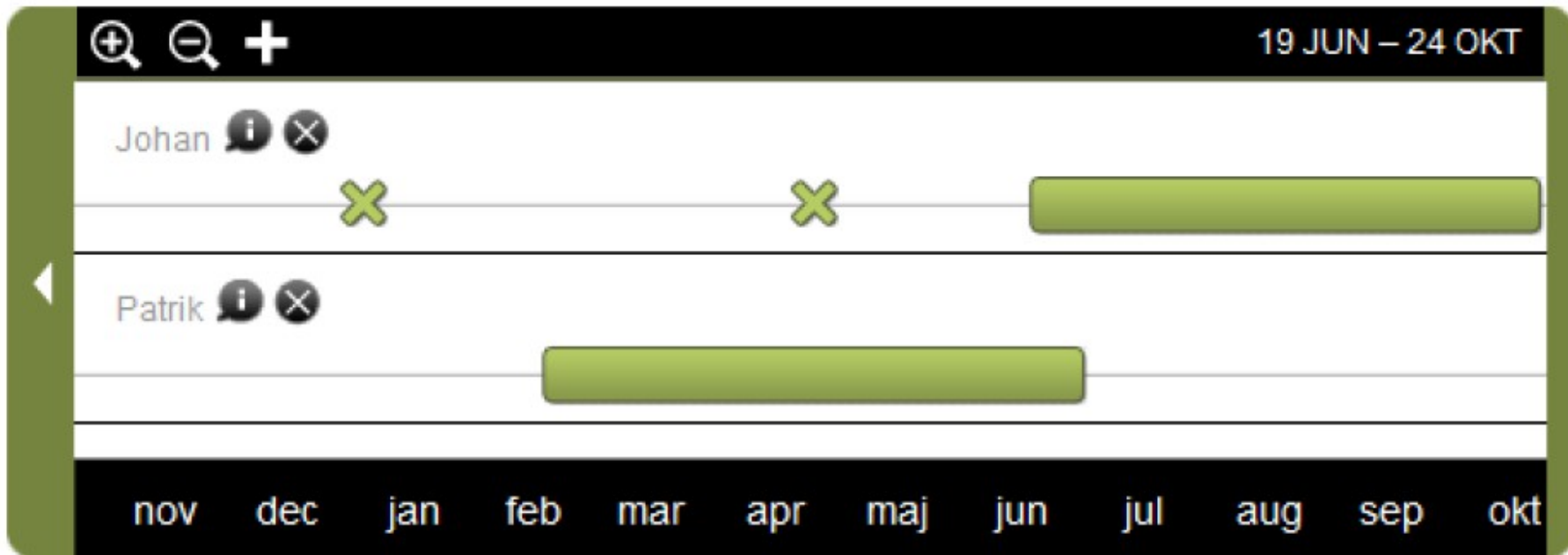
Time and intensity of contacts does matter





STI - future...

Research in plans





UNIwersytet Jagielloński
w Krakowie



Stockholm
University

Studying possible outcomes in a model of sexually transmitted virus (HPV) causing cervical cancer Poland



UNIwersYTET JAGIELLOŃSKI
W KRAKOWIE

Epidemiology of HPV



Stockholm
University

- **Human papillomavirus, or HPV, is a sexually transmittable virus infection, which is not only the main, but also necessary risk factor for developing cervical cancer - second most common type of cancer in women.**
- **The infection is transmittable via sexual contact.**
- **The time between getting infected by HPV and developing a cancer can be twenty years or more, therefore a dynamic model of human behavior would be very useful, so that simulations can be made and different scenarios compared.**

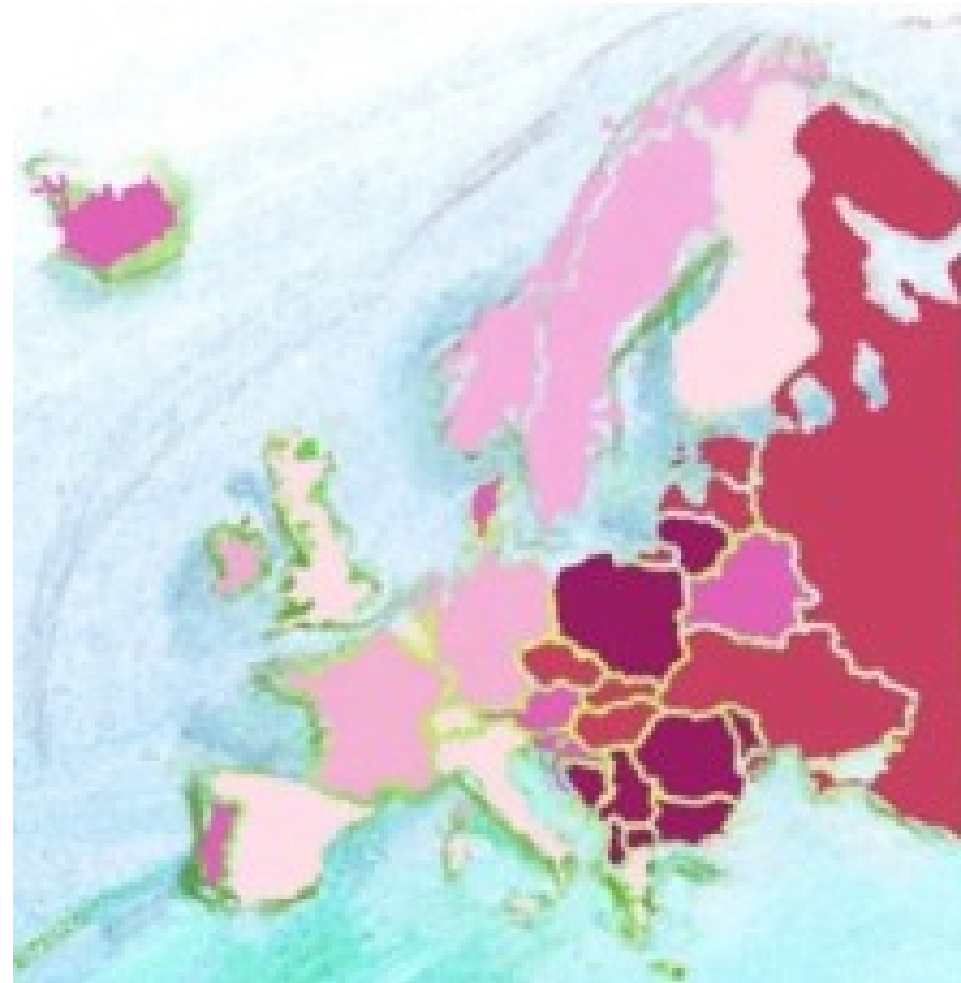


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Future?



Stockholm
University



Mortality of cervical cancer



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W KRAKOWIE

Epidemiology of HPV

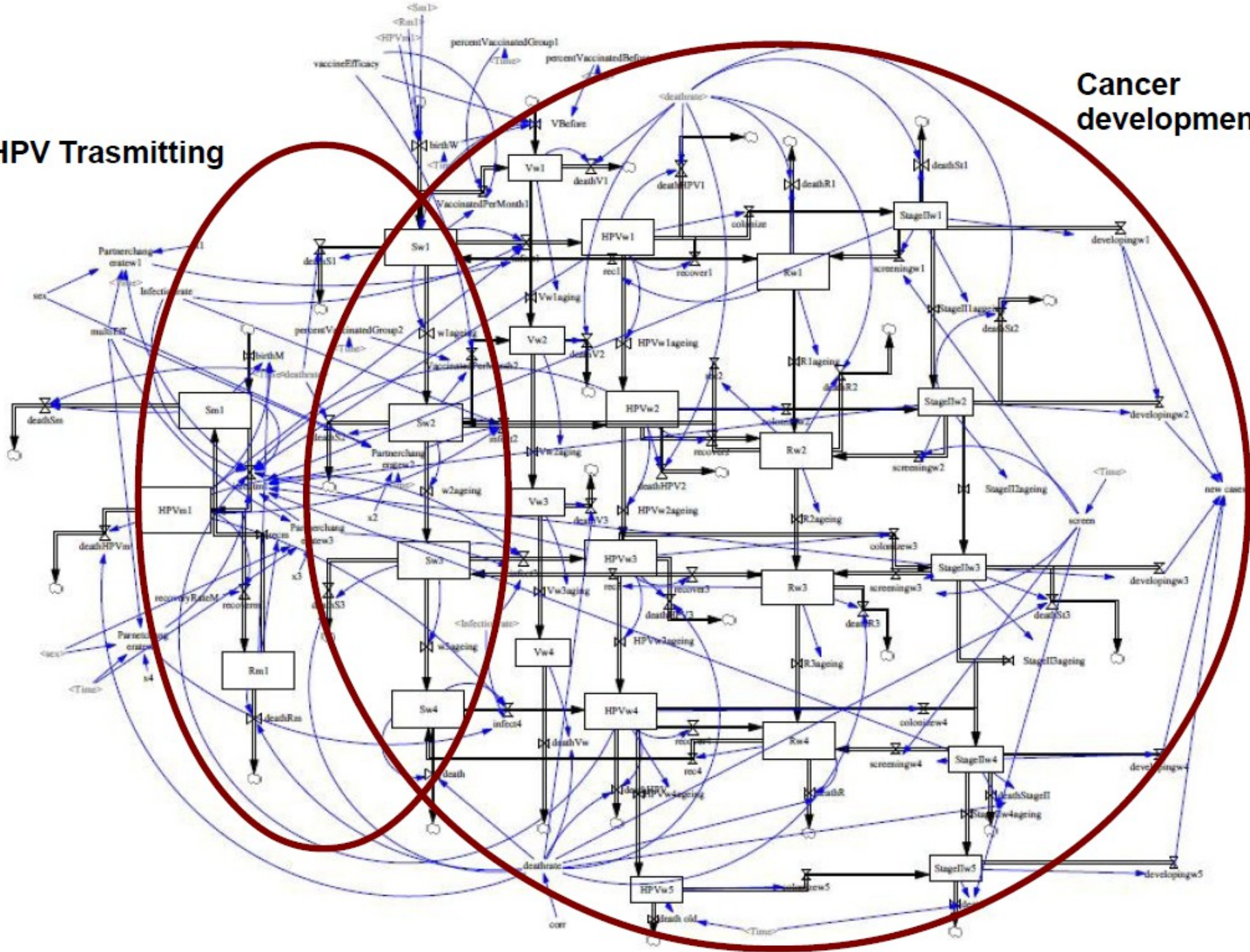


Stockholm
University

- **Among the oncogenic HPVs, the most severe one is type 16, present in about half of all cervical cancer cases.**
- **Recent studies have shown that the main safety precaution with respect to cervical cancer is going to be a combination of vaccination and screening - since only type specific vaccines are available and there are as many as 15 high risk HPVs.**

HPV Transmitting

Cancer development





UNIWERSYTET JAGIELLOŃSKI
W KRAKOWIE

Model and simulations



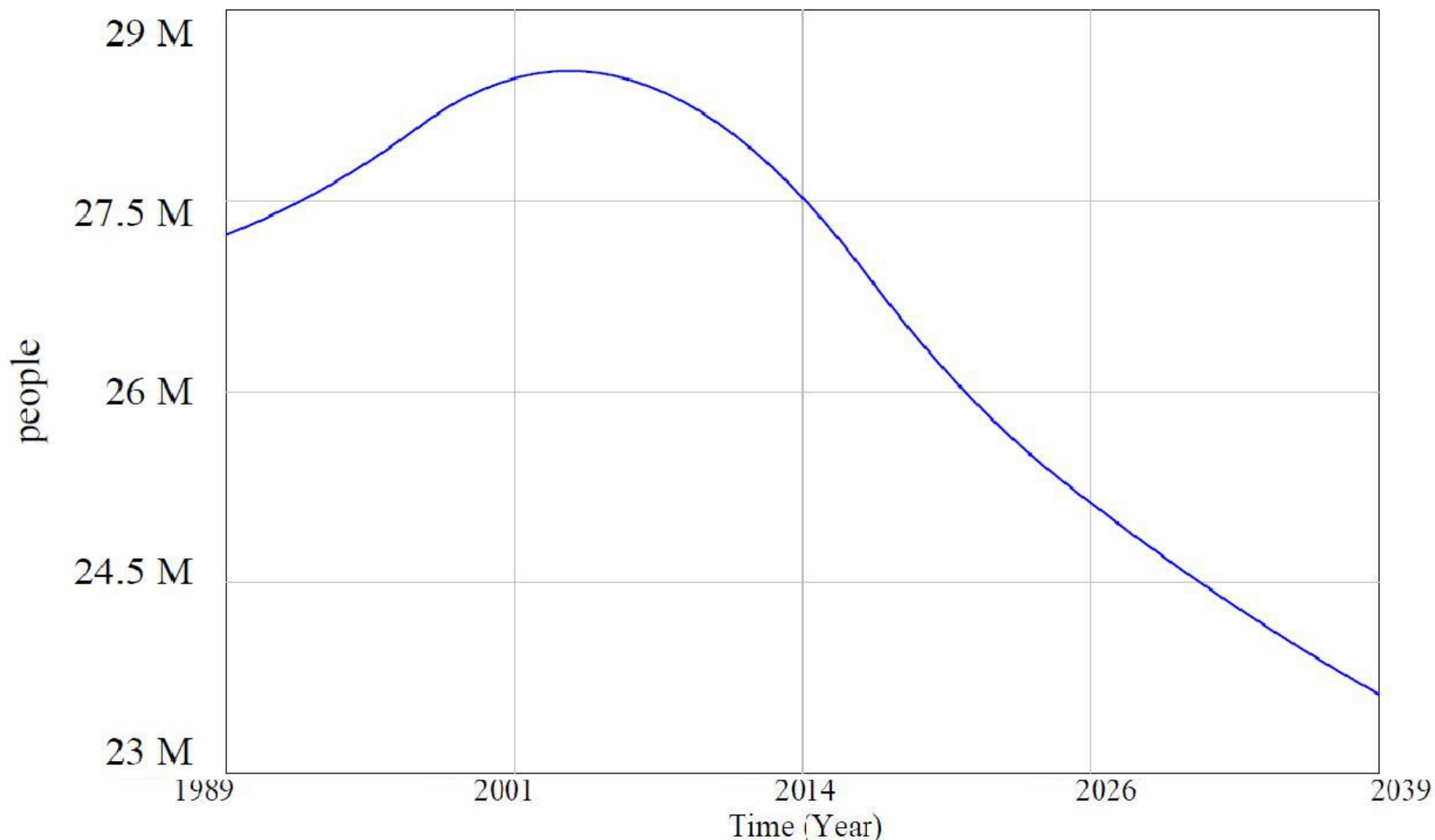
Stockholm
University

- 1) 15-19 (initiation of sexual live)**
- 2) 20-24 (most active sexual group)**
- 3) 25-34 (stabilization of sexual live)**
- 4) 35-64 (sexual stagnation and stronger susceptibility to cancer)**
- 5) <65 (no sexuality and cancer development)**



Model and simulations

Sexually active population

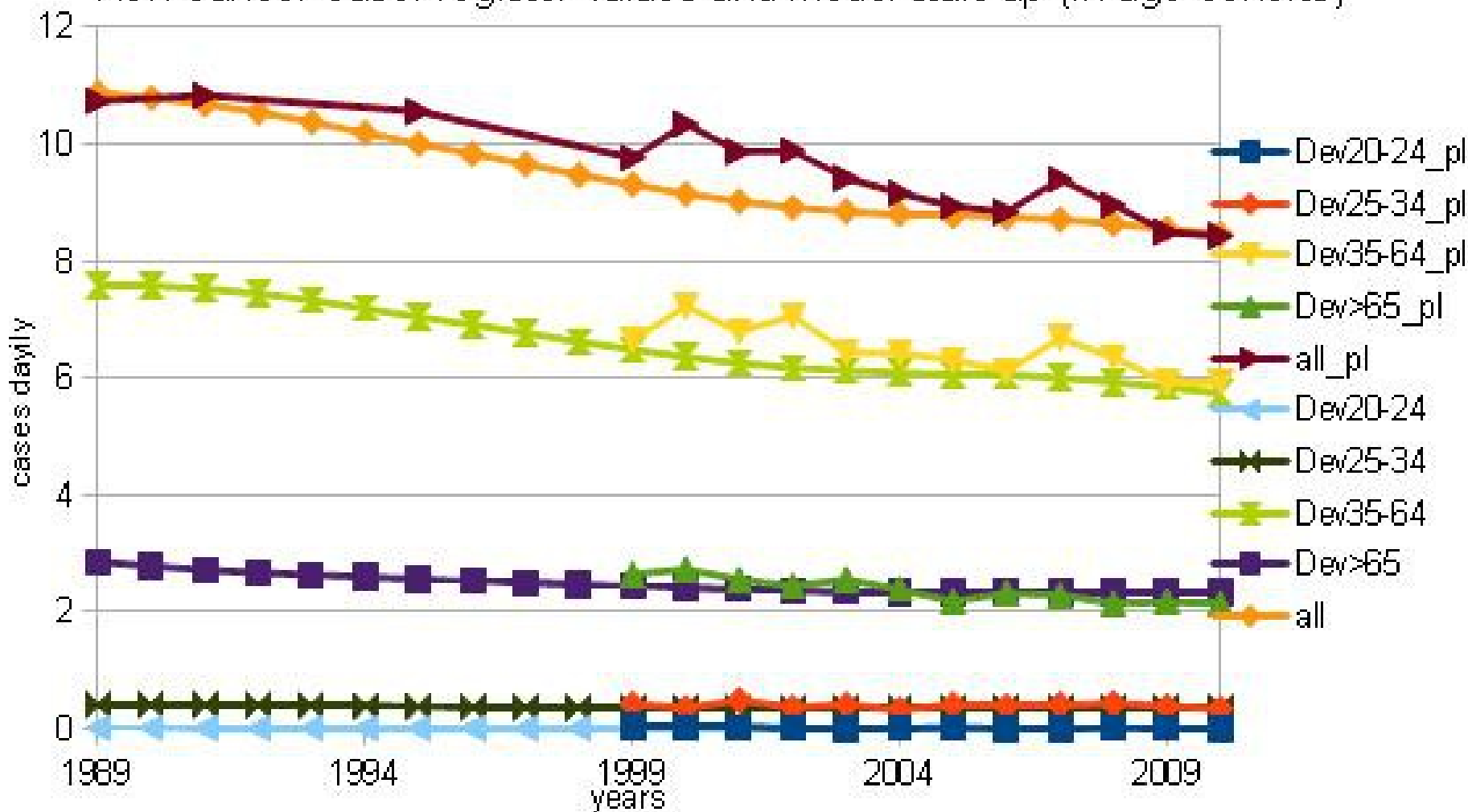




Model and simulations



New cancer case: register values and model start-up (in age cohorts)

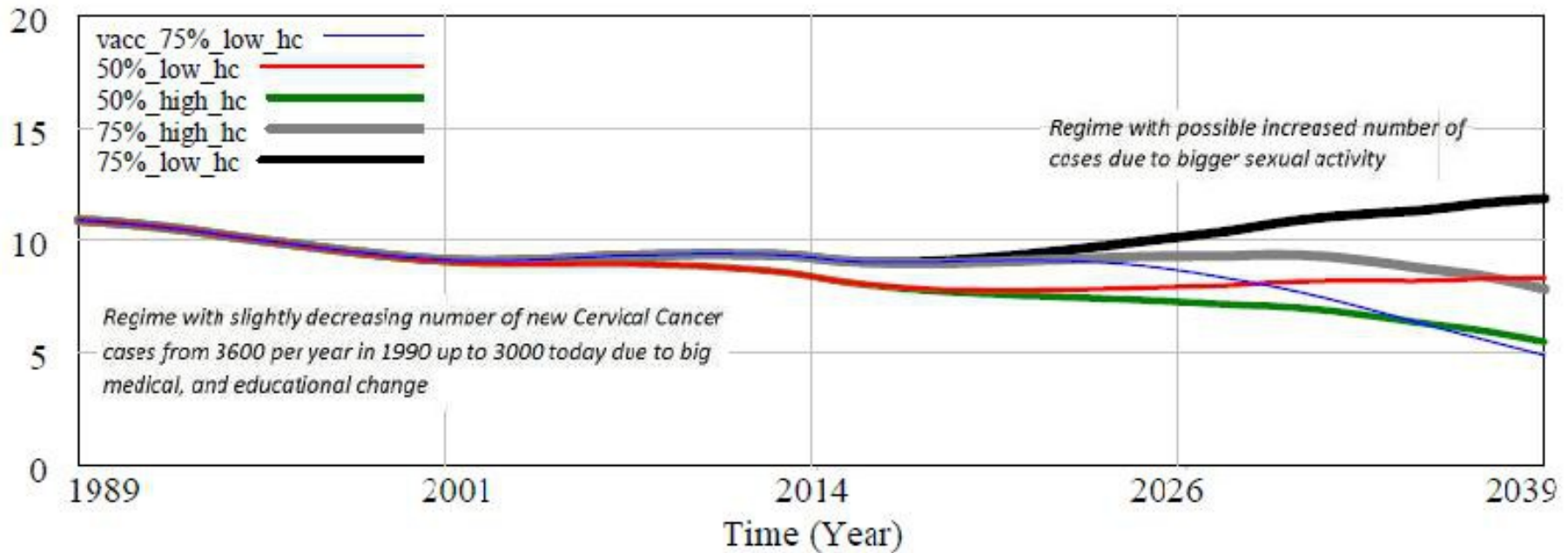




Possible future scenarios



new cases





The End

See you at computer lab to do some
own simulations and data analysis

11.12, 12:45, 236

- th.if.uj.edu.pl/~gulakov/epi.pdf
 - Room 442,
- andrzej.jarynowski@sociology.su.se