MATH.EN.JEANS

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PANDEMICS

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The problem statement

A disease is spreading At every moment for each patient occurs that:

- 1) The patient could infect another entity with a certain probability
- 2) The patient could heal with a certain probability
- 3) The patient could die with a certain probability.

What could happen considering different probabilities? Is it better to vaccinate a part of the population or to isolate the population in small groups?

The static framework

Statistical approach with a Java numerical simulation

Contained infection on a square matrix

Setting of INPUT parameters

- Transmissions routes
- Limit of movement
- Quarantine

These three new parameters were subsequently added and analysed

Extraction of OUTPUT parameters

The simulation

MAIN RULES:

- The disease spreads from a single cell (zero patient)
- The infection could spread the 8 adjacent cells
- A cell can be infected by an adjacent infected cell
- Healed cells are immune from the disease
- Dead cells can not spread the disease
- The development of the system occurs checking the condition of **each cell.**

ENDING CONDITION:

The system is left to evolve until there are no more infected entities in the matrix:
Stable matrix: n. of infected=0.

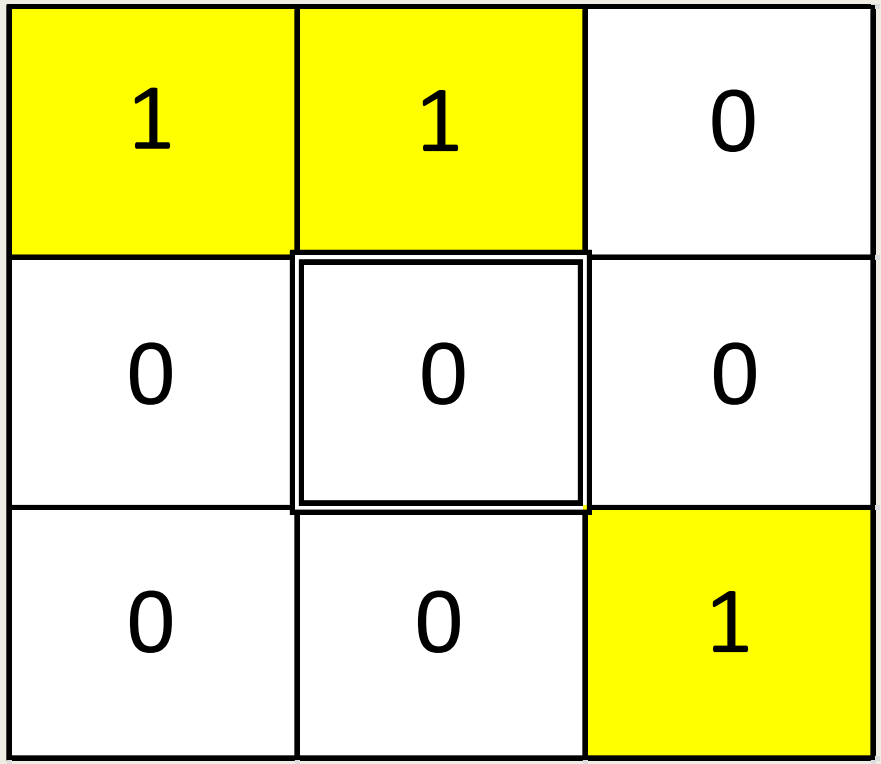
The colors' logic

We have identified four different "conditions" of a single cell:

0	Healthy	White
1	Infected	Yellow
2	Healed	Green
3	Dead	Red

The state of each cell is updated every step according to the values of the parameters added in input

Infection spreading

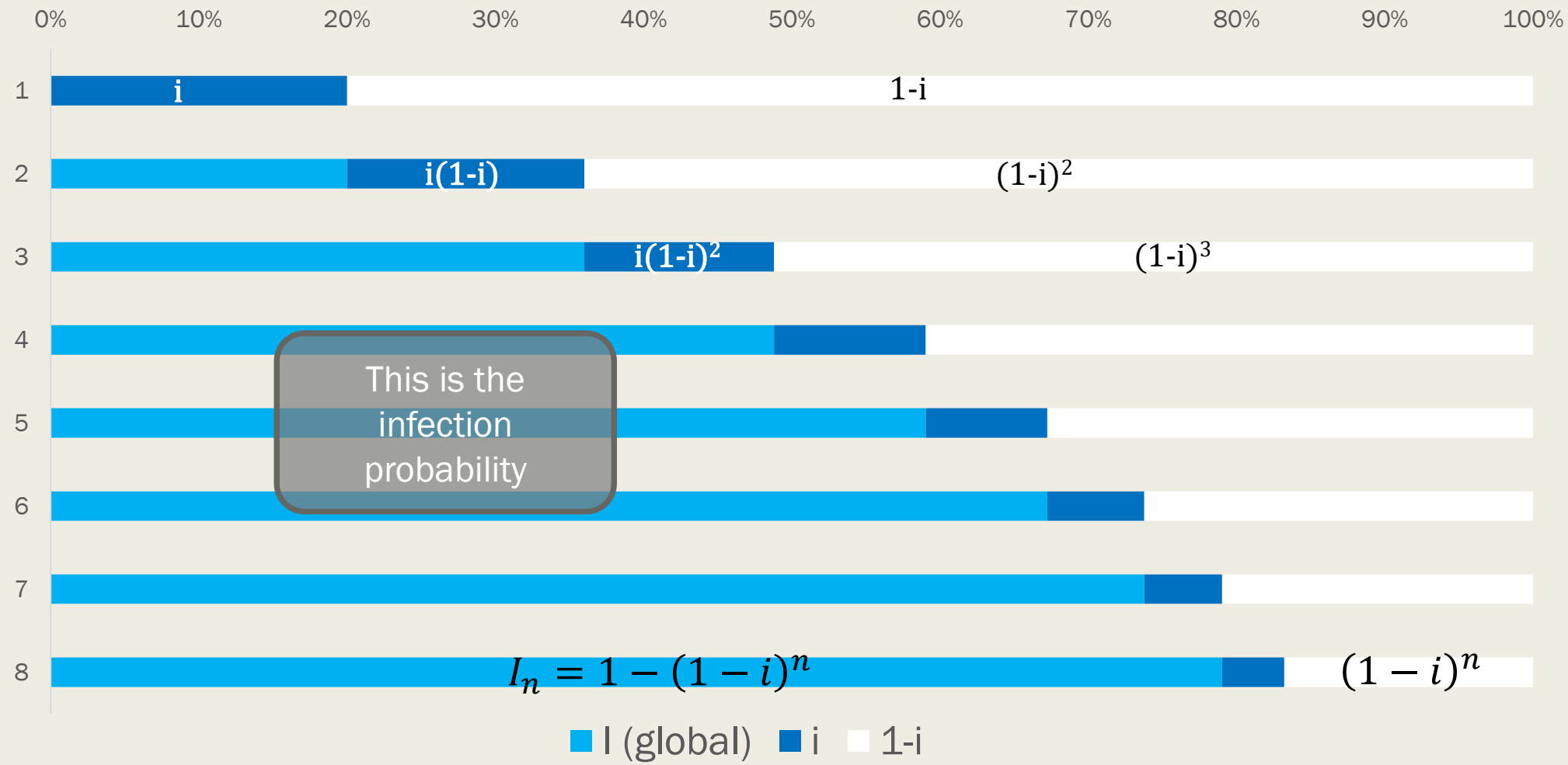


n= 2

Starting on a cell where the state is 0, we count the number ***n*** of the infected cells among the 8 adjacent.

The probability of infection I_n depends on i and n

Evaluating a cumulative infection probability I_n

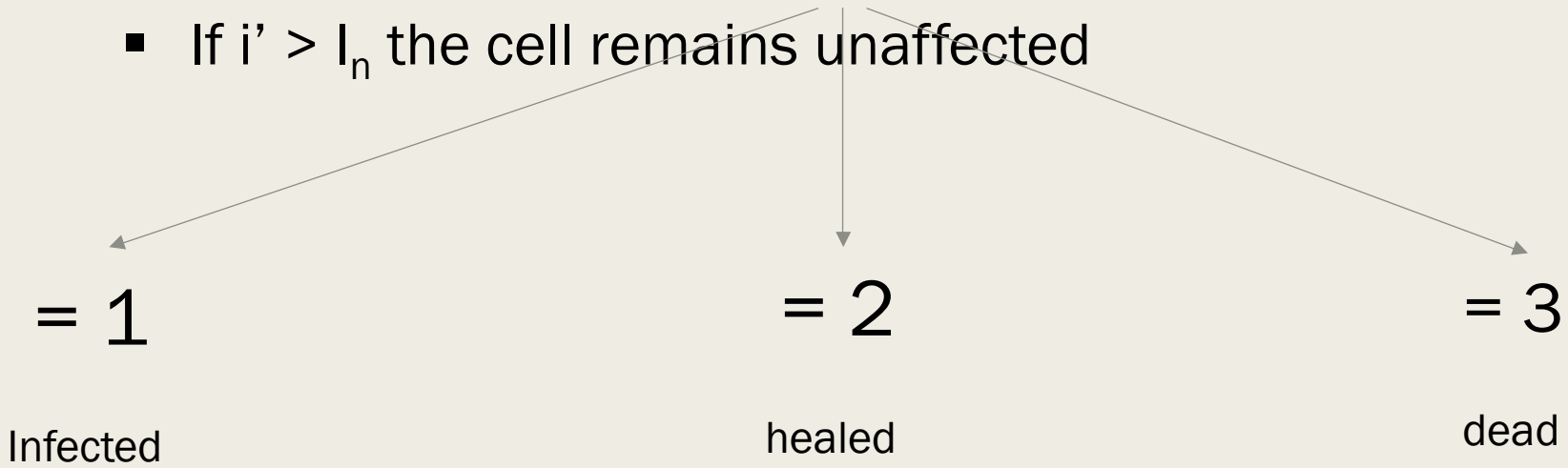


Infection spreading and disease evolution

The infection is evaluated through the generation of a random number **i'**:

For a healing probability (h), created with a random generator the cell state can change in this way

- If $i' \leq I_n$ the cell state changes to 1 = infected
- If $i' > I_n$ the cell remains unaffected



Some real diseases

Data from medical literature were used to make the simulation more realistic

→ **7 diseases** have been chosen to analyse their characteristics:

The course of illness (N): the duration of a disease, that is the number of days after which the patient is definitely healed or dead

Disease	Basic reproductive ratio (R_0)	Mortality Rate (D)	Course of illness (N days)
1) Ebola	2	50%	30
2) SARS	3,5	15%	45
3) Pertussis	14,5	0,35%	80
4) Diphteria	6,5	15%	12
5) Measles	15	0,35%	20
6) Mumps	5,5	0,01%	20
7) Flu	1,65	0,03%	7

The mortality rate (D): the percentage of deaths in a given area, assumed as the cumulative probability to be death after N days from the contagion

The basic reproductive ratio ($R0$): the average number of cases a single patient generates over the course of the infectious period (assumed as the whole duration of the disease)

From diseases to probabilities

From these raw data we tried to derive formulas for the relevant probabilities with the following reasonings.

Probability of infection (i): can be defined as the ratio between the number of new cases generated by the single patient and the maximum number of tries this could have attempted over the course of illness (the duration times the number of adjacent cells).

$$i = R_0/8N$$

Disease	Infectivity (i)	Mortality (d)	Healing probability (h)
1) Ebola	$0{,}8\%$	$2{,}28\%$	2%
2) SARS	$1{,}0\%$	$0{,}36\%$	4%
3) Pertussis	$2{,}3\%$	$0{,}004\%$	7%
4) Diphteria	$6{,}8\%$	$1{,}35\%$	15%
5) Measles	$9{,}4\%$	$0{,}2\%$	25%
6) Mumps	$3{,}4\%$	$0{,}0005\%$	37%
7) Flu	$2{,}9\%$	$0{,}004\%$	69%

Probability of death (d): by reversing the reasoning shown before for the cumulative infectivity I_n by n nearby infectious patients, this probability can be derived as follows.

$$D = 1 - (1 - d)^N \rightarrow d = 1 - \sqrt[N]{1 - D}$$

Probability of healing (h): can be defined in the same way, just assuming the cumulative healing rate to be complementary to the mortality one.

$$H = 1 - D \rightarrow h = 1 - \sqrt[N]{1 - H} = 1 - \sqrt[N]{D}$$

The estimated probabilities

- As shown in table on the side, for each of the 3 parameters i, d and h some values have been calculated with the obtained exponential functions:
  - 7 values for i
  - 8 values for d
  - 7 values for h
- Despite these values are arbitrary they cover with greater density the «*low value*» zones of the parameter space, where most real diseases are expected to be found
- The values have been cross-referenced obtaining:

$7 \times 8 \times 7 = 392$ disease models to simulate

ESTIMATED PROBABILITIES		
Probability of infection (i)	**Probability of death (d)**	**Probability of healing (h)**
0,8%	0,0004%	2%
1,2%	0,002%	4%
1,8%	0,008%	7%
2,7%	0,035%	13%
4,1%	0,15%	22%
6,3%	0,66%	39%
9,4%	2,9%	70%
	12,5%	

The data collection

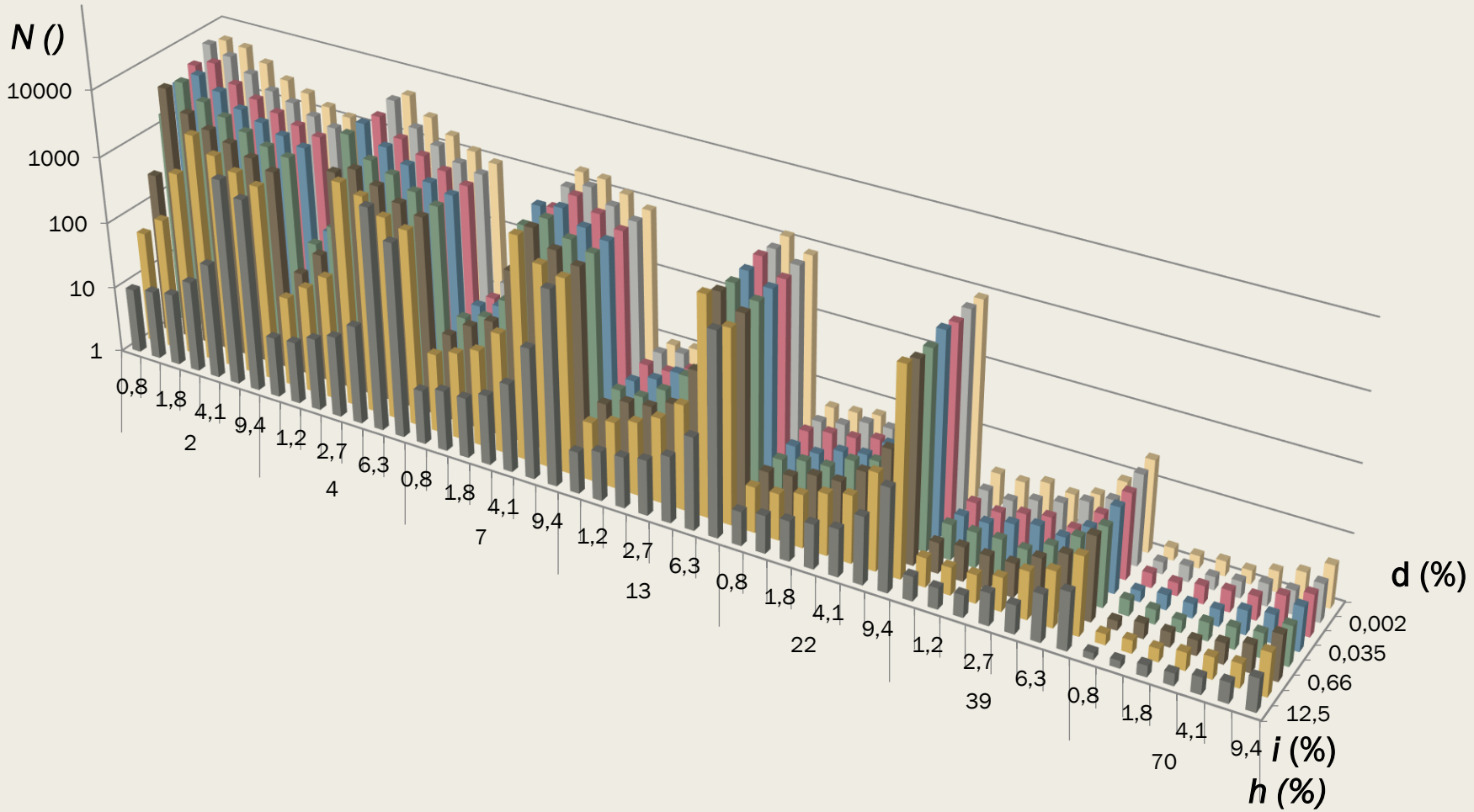
Given the random nature of the phenomenon, in order to get a significative statistics with fairly stable behaviours, the simulation has been ran 100 times over a 501×501 cells matrix, for each disease model. After each run, the following 4 data have been extracted:

The percentage of **not-infected patients** ($\boldsymbol{NI}$)
The percentage of **dead patients** ($\boldsymbol{D}$)
The percentage of **healed patients** ($\boldsymbol{H}$)
The number of **days spent** (cycles ran) before stability ($\boldsymbol{N}$)

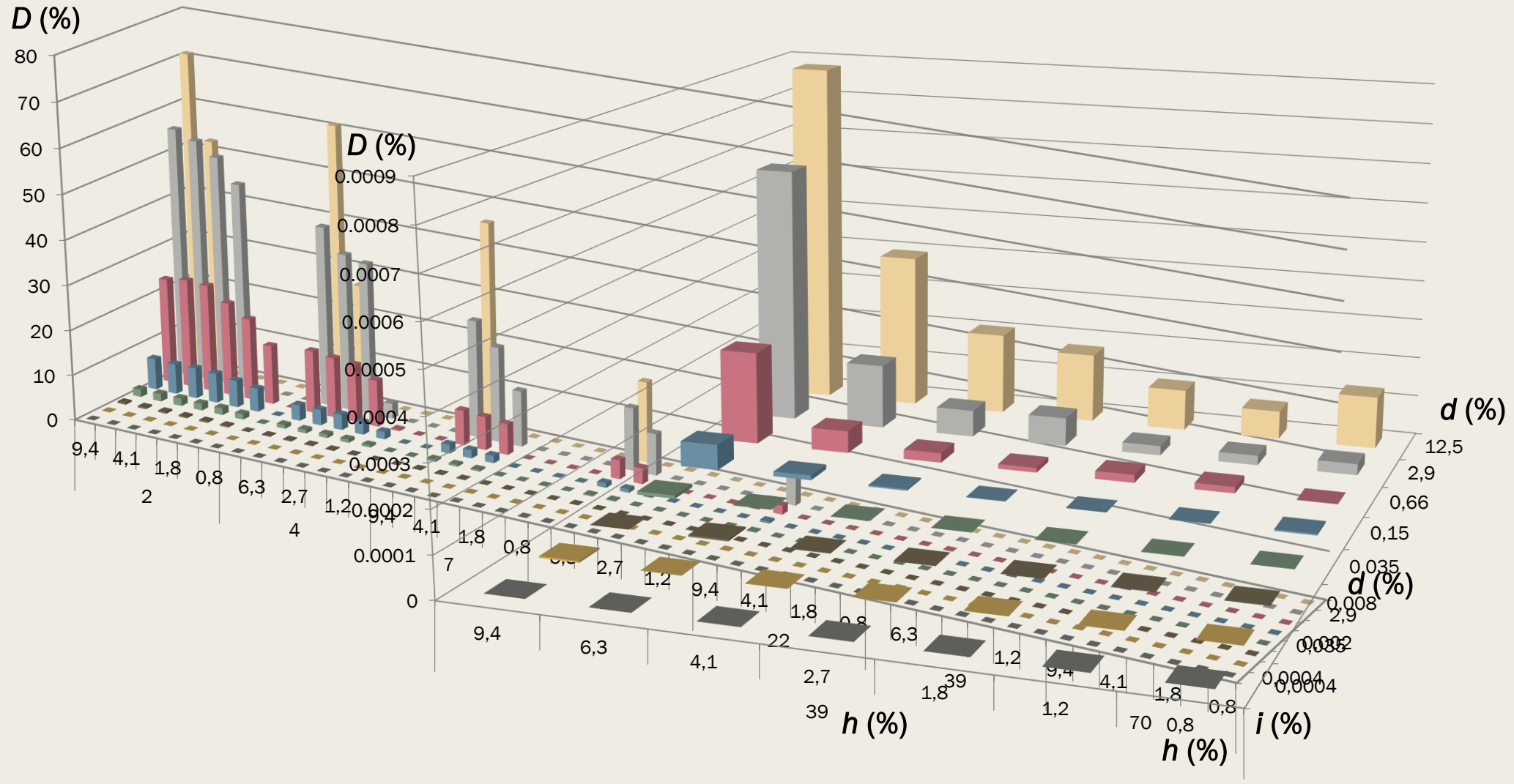
For each simulated model the 100 values obtained for each of the aforesaid parameters have been used to calculate an **average value** and the corresponding ***standard deviation*** σ

Given the great number of parameters involved, in order to compare the data output with the input probabilities, the resulting data have been analysed using ***pivot tables***.

The course of the pandemic



The mortality rate



Some simple results

Firstly…

- If i is high enough to infect approximately all the population, the relation between *H* and *D* stands as:

$$\frac{H}{D} \not\simeq \frac{h}{d}$$

Decreasing i this stable behaviour is quickly lost with variable results

A check with some real diseases

Measles

- Known data:
  - *Basic Reproductive Ratio* $R_0 = 15$
  - *Mortality Rate* $D = 0{,}035\%$
  - *Duration* $N = 20\ days$
- Estimeted parameters:

$$i = 9{,}4\%,\ d = 0{,}02\%,\ h = 25\%$$

- The most similar simulated model:

$$i = 9{,}4\%, d = 0{,}035\%,\ h = 22\%$$

$\rightarrow$ Estimated mortality rate $D = 0{,}157\%$

Ebola

- Known data:
  - *Basic Reproductive Ratio* $R_0 = 2$
  - *Mortality Rate* $D = 50\%$
  - *Duration* $N = 30\ days$
- Estimeted parameters:

$$i = 0{,}8\%,\ d = 2{,}28\%,\ h = 2\%$$

- The most similar simulated model:

$$i = 0{,}8\%, d = 2{,}9\%,\ h = 2\%$$

$\rightarrow$ Estimated mortality rate $D = 67{,}5\%$

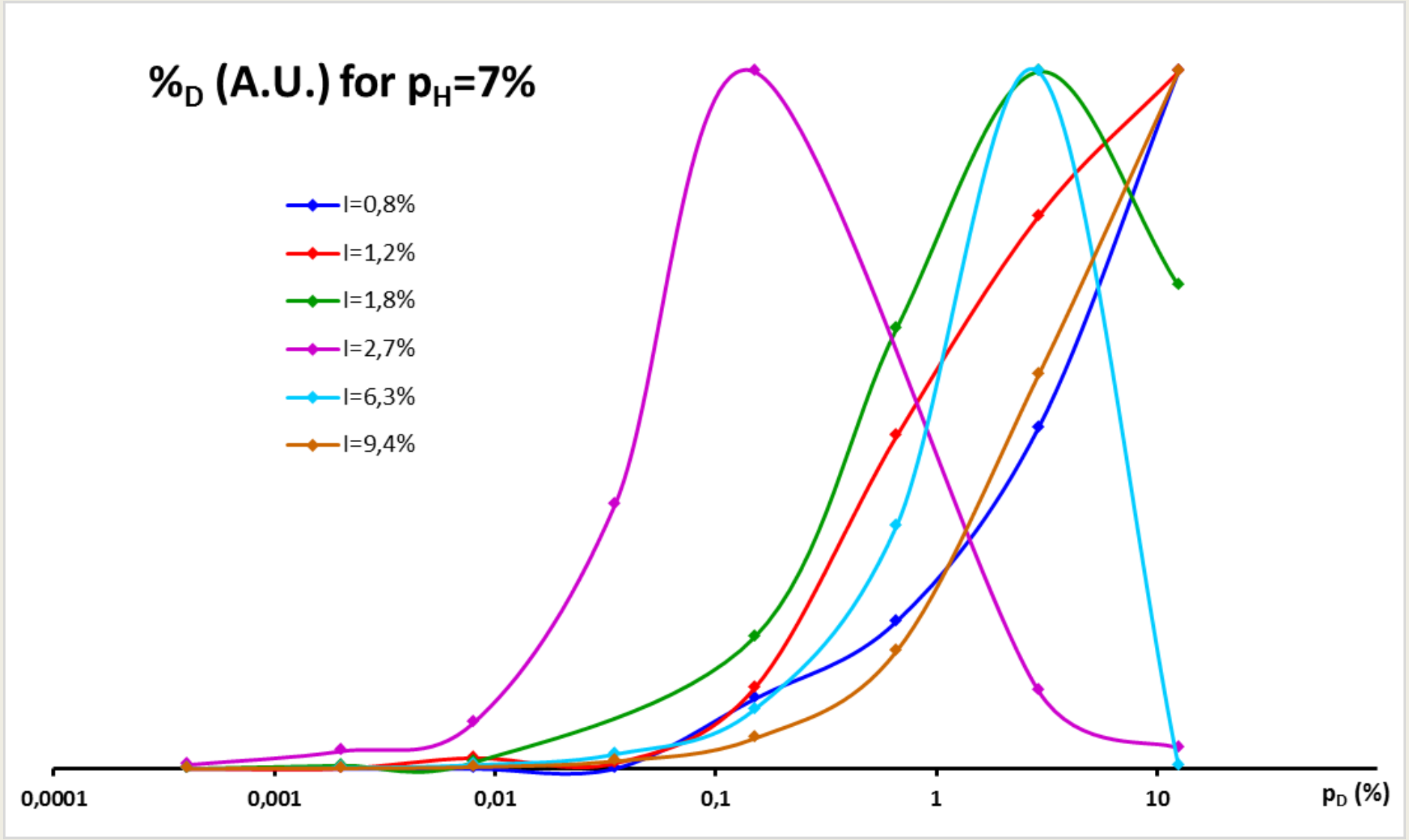
Some simple results

The mortality rate graphs have been analysed fixing 2 of the 3 input probabilities each time, and studying the obtained data as a function of the third one.
Two different kind of results have been obtained.

- For fixed i and d, the mortality rate D decreases monotonically with increasing h

- For fixed i and h, the mortality rate D often shows absolute maxima for $d \neq d_{MAX}$ (this behaviour results reasonable if one thinks that a too much murderous disease can experience difficulties to infect enough people to spread…)

D vs d for fixed h and various i



Some interesting fits I

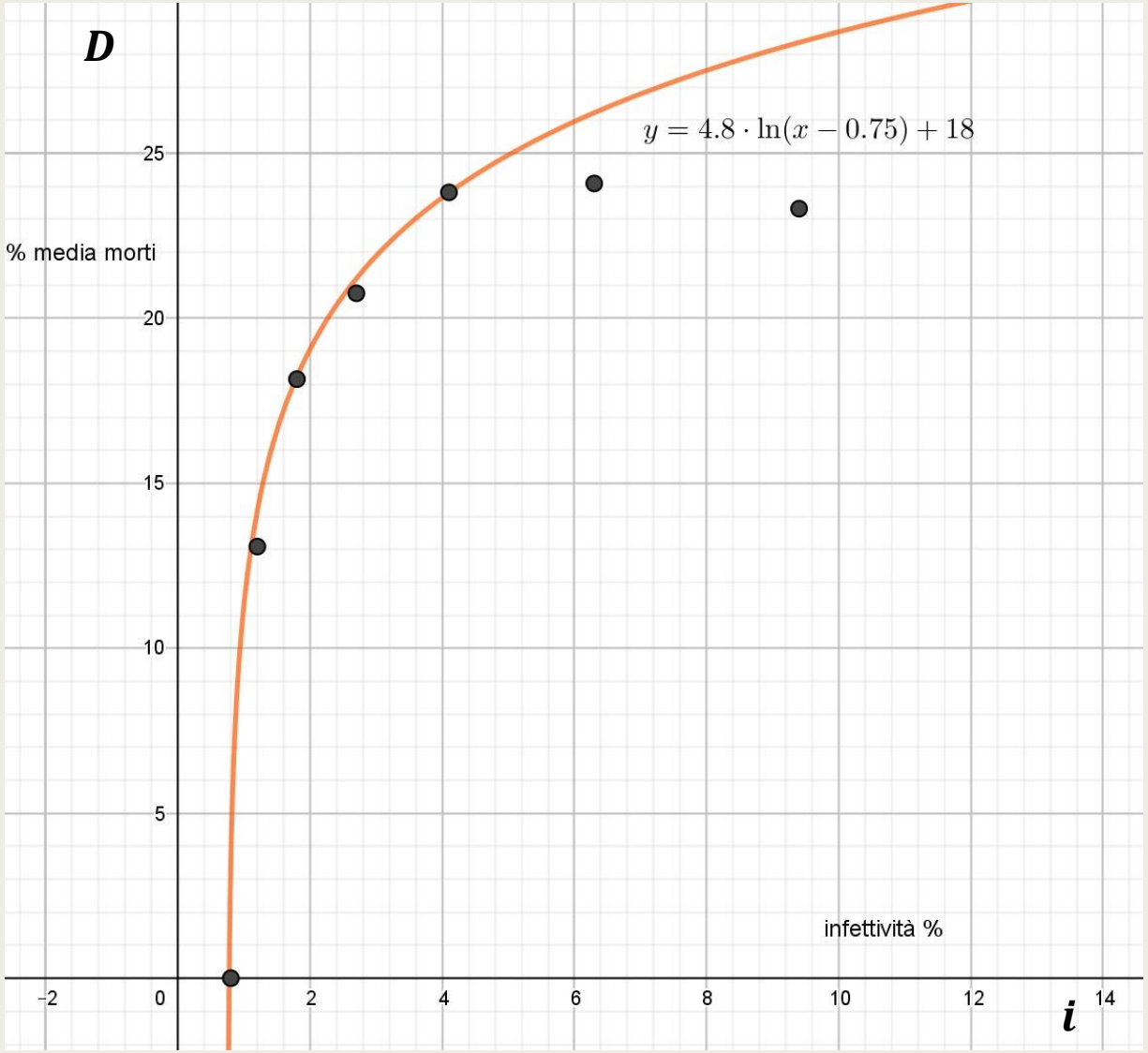
D vs i for fixed h and d

This is logarithmic model for the increasing part of the graph

$$y = a \cdot \ln(x + b) + c$$

y: D(%) x: i(%)

The model has been attempted with set d and h



Some interesting fits II

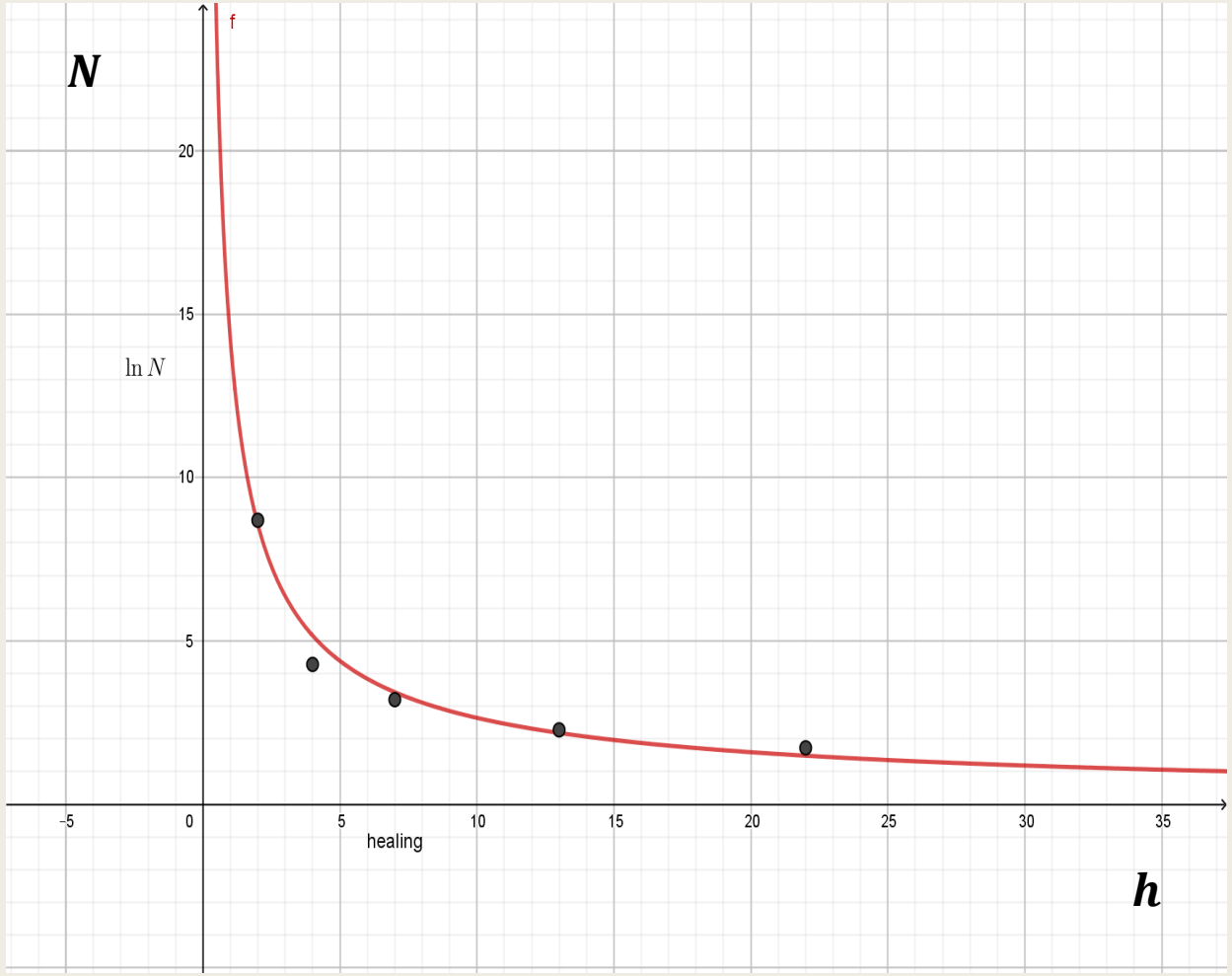
N vs h for fixed i and d

This is the power law model:

$$\ln N = a \cdot h^b$$

where $\mathrm{b} < 0$ and $a > 0$.

The model has been attempted with set i and d



Vaccination

For simulating the effect of a vaccination we can choose a ***%V*** (vaccination percentage) which describe the density of vaccinated people inside the matrix allocated with a random distribution

0	Healthy	White
1	Infected	Yellow
2	Healed	Green
3	Dead	Red
4	Immunized	Blue

We simulated a «measles-like» disease (i=10%, d=0,1% e h=25%) with increasing percentages of immunized people (0 to 99%) each run 100 times

Herd Immunity Threshold (HIT)

- HIT = percentage of population that must be immunized in order to stop the spreading of the disease:

$$HIT = 1 - \frac{1}{R_0}$$

- This value must be compared with the one obtained from the simulation

Estimation of HIT for a measles-like disease

Theoretical estimation

We extract N from the following system (with a numeric resolution)

$$\begin{cases} d = 1 - \sqrt[N]{(1-D)} \\ h = 1 - \sqrt[N]{D} \end{cases}$$

Then we find R_0

$$i = \frac{R_0}{8N} \Rightarrow R_0 = 8Ni$$

And so

$$HIT = 1 - \frac{1}{R_0} = 0.92 = 92\%$$

Data estimation

With the 0%v file's data we calculate

$$D = \frac{\%\ dead}{1 - \%\ not\ infected}$$

Thus

$$N = \frac{\ln D}{\ln(1-h)}$$

And as shown before we find R_0 and so

$$HIT = 1 - \frac{1}{R_0} = 0.9566 = 95.66\%$$

Movement

In order to simulate a more realistic behaviour, the algorithm has been modified to include the movement of people and different kinds of transmission modes

-1	Empty Cell	Black
0	Healthy	White
1	Infected	Yellow
2	Healed	Green
3	Dead	Red
4	Immunized	Blue

At the beginning of every step, before considering the evolution of the disease, the movement of people to empty cells of the matrix is computed with a random generator

Movement and ways of trasmission

WAYS OF MOVEMENT

- Static
- Walking (max 100 per axis)
- Bike (max 200 per axis)
- Car (max 400 per axis)

WAYS OF TRANSMISSION

- Direct infection (r = 1 cell)
- Droplet (r=5 cells)
- Air (r=10 cells)
- Vector (animals) (r = 20 cells)

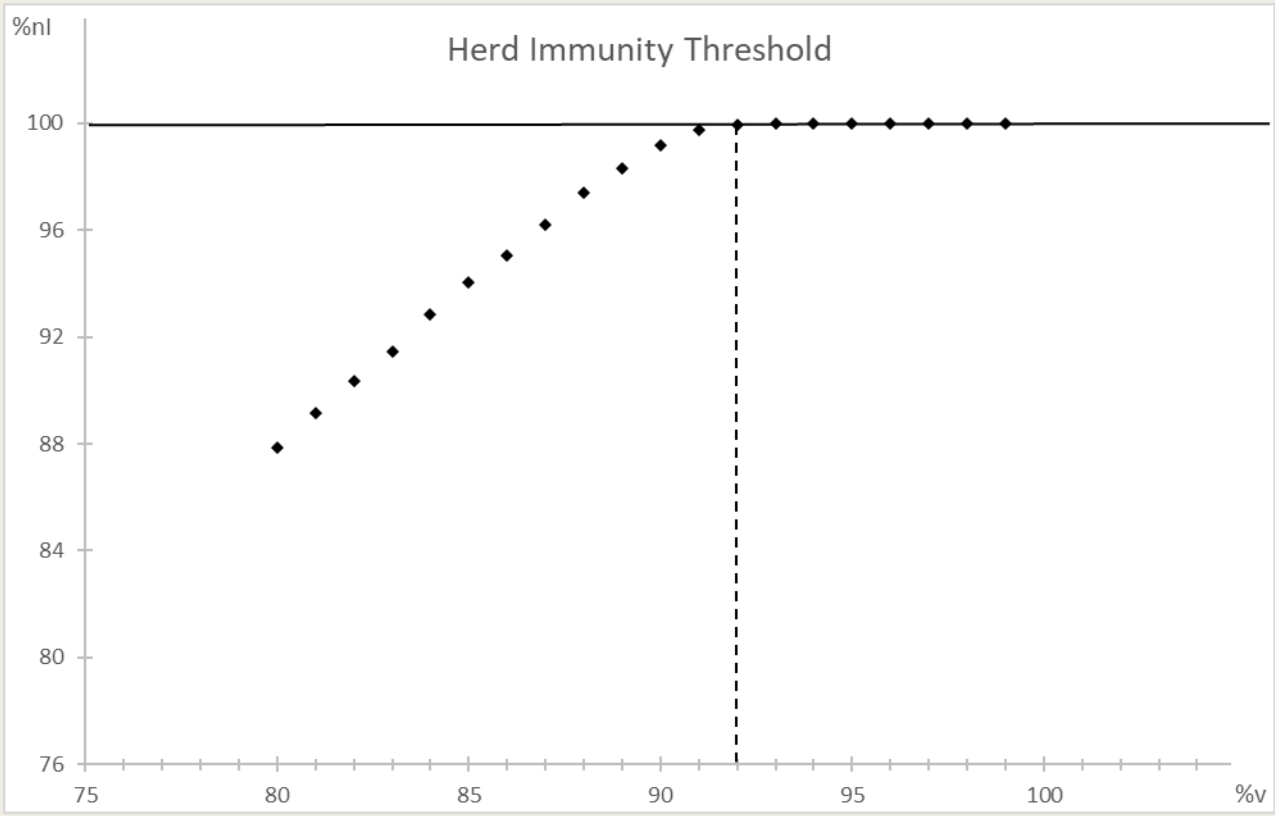
HIT in a more realistic model

«Measles-like» disease
(i=10%, d=0,1% e h=25%) with:

- vaccination (80-99%),
- movement (Car, 400 cells)
- infection radius (Animals, 20 cells)

HIT= 92%

It is found that HIT in the static model is quite similar to the one evaluated in this model



Thanks for your attention

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