Parliamo di pandemia, con formule e modelli

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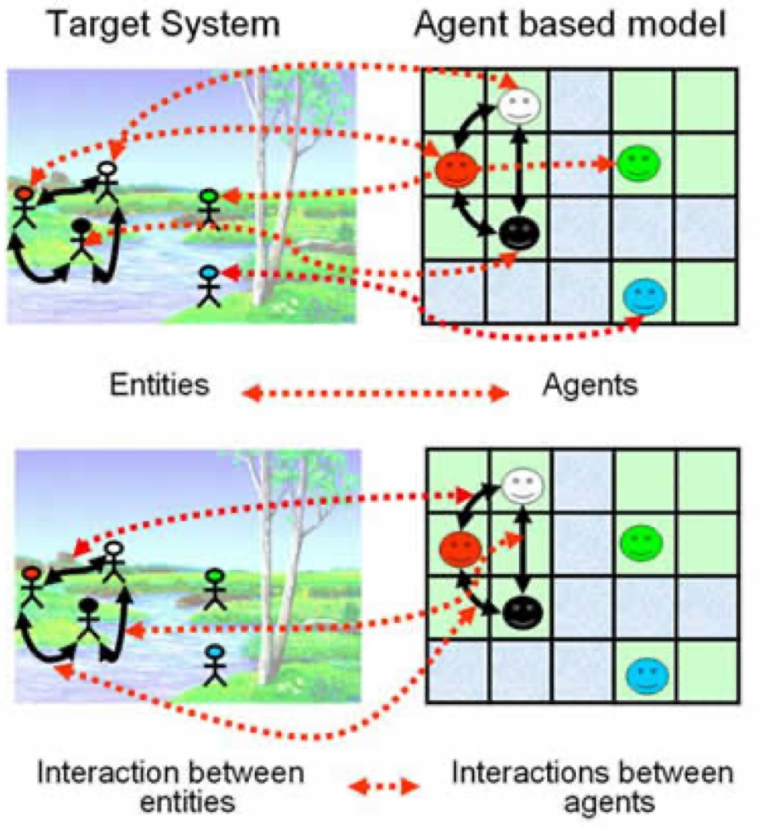
Introduzione



From M. Galán, L.R. Izquierdo, S.S. Izquierdo, J.I. Santos, R. del Olmo, A. López- Paredes, B. Edmonds: Errors and artefacts in agent-based modelling. *Journal of Artificial Societies and Social Simulation*, 12 (1):1, 2009. ISSN 1460-7425.

http://jasss.soc.surrey.ac.uk/12/1/1.html

Un modello ad agenti sulla diffusione del virus: un articolo che lo descrive

G. Pescarmona, P. Terna, A. Acquadro, P. Pescarmona, G. Russo, E. Sulis, and S. Terna. *An Agent- Based Model of COVID-19 Diffusion to Plan and Evaluate Intervention Policies*, 2021. https://arxiv.org/abs/2108.08885.

Descrizione

- Un modello microfondato con agenti che interagiscono, seguendo regole comportamentali plausibili in un mondo dove l'epidemia di Covid-19 sta influenzando le azioni di tutti.
- Il modello opera con:
  - i agenti infetti classificati come sintomatici o asintomatici e
  - ii ta luoghi di contagio specificati in modo dettagliato, grazie alle capacità di modellizzazione basata sugli agenti.
- The infection transmission is related to three factors: the infected person's characteristics and those of the susceptible one, plus those of the space in which a contact occurs.

- The micro-based structure of the model allows factual, counterfactual, and conditional simulations to investigate both the spontaneous or controlled development of the epidemic. Examples of counterfactual situations are those considering:
  - i different timing in the adoption of the non-pharmaceutical containment measures;
  - ii alternative strategies focusing exclusively on the defense of fragile people.
- The model generates complex epidemic dynamics, emerging from the consequences of agents' actions and interactions, with high variability in outcomes, but frequently with a stunning realistic reproduction of the contagion waves that occurred in the reference region.
- We take charge of the variability of the epidemic paths within the simulation, running batches of executions with 10,000 occurrences for each experiment.

- The AI and inverse generative sides of the model come from constructing a meta-agent optimizing the vaccine distribution among people groups—characterized by age, fragility, work conditions—to minimize the number of symptomatic people (deceased persons come from there).
- We can characterize the action of the planner both:
  - i introducing ex-ante rules following "plain" or "wise" strategies that we imagine as observers or
  - ii evolving those strategies via the application of a genetic algorithm.
- The genome is a matrix of vaccination quotas by people groups, with their time range of adoption.

The model

- As the agents can be Susceptible, Infected, symptomatic, asymptomatic, and Recovered, the name of the model is S.I.s.a.R., with the capital letters recalling the S.I.R. scheme.
- We use NetLogo (https://ccl.northwestern.edu/netlogo/).
- S.I.s.a.R. is at https://terna.to.it/simul/SIsaR.html with information on model construction, and an online executable version.
- A paper is published at https://arxiv.org/abs/2108.08885
- The model includes the structural data of Piedmont, an Italian region, but we can easily calibrate it for other areas. The simulation reproduces a realistic calendar (e.g., national or local government decisions) via a dedicated script interpreter.

The scale and the items

- 1 : 1000, for a population of 4,350,000 people.

- Houses.
- Schools.
- Hospitals.
- Nursing homes,
- Factories.

The world 3D

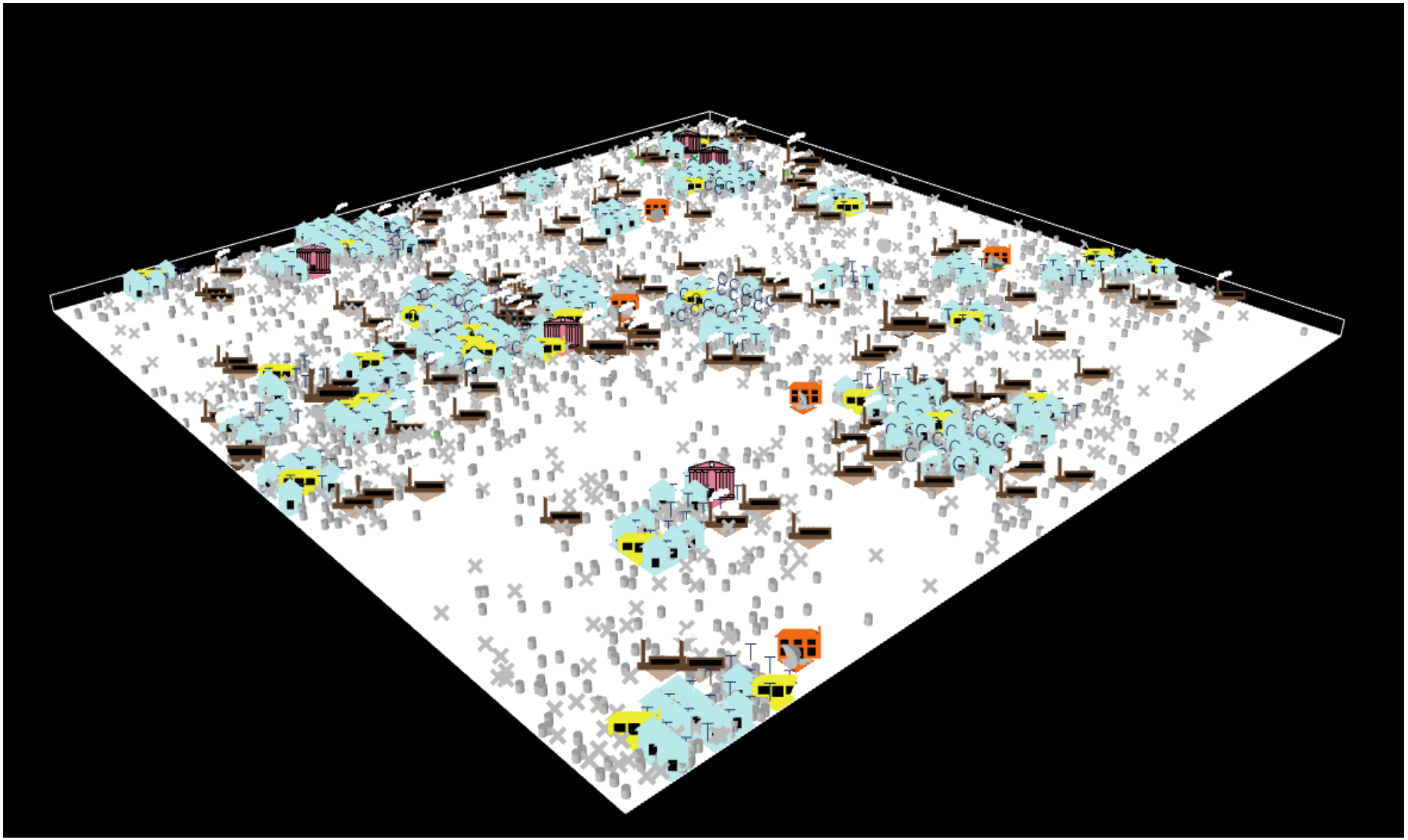


Figure 1: The world 3D

A circular scheme

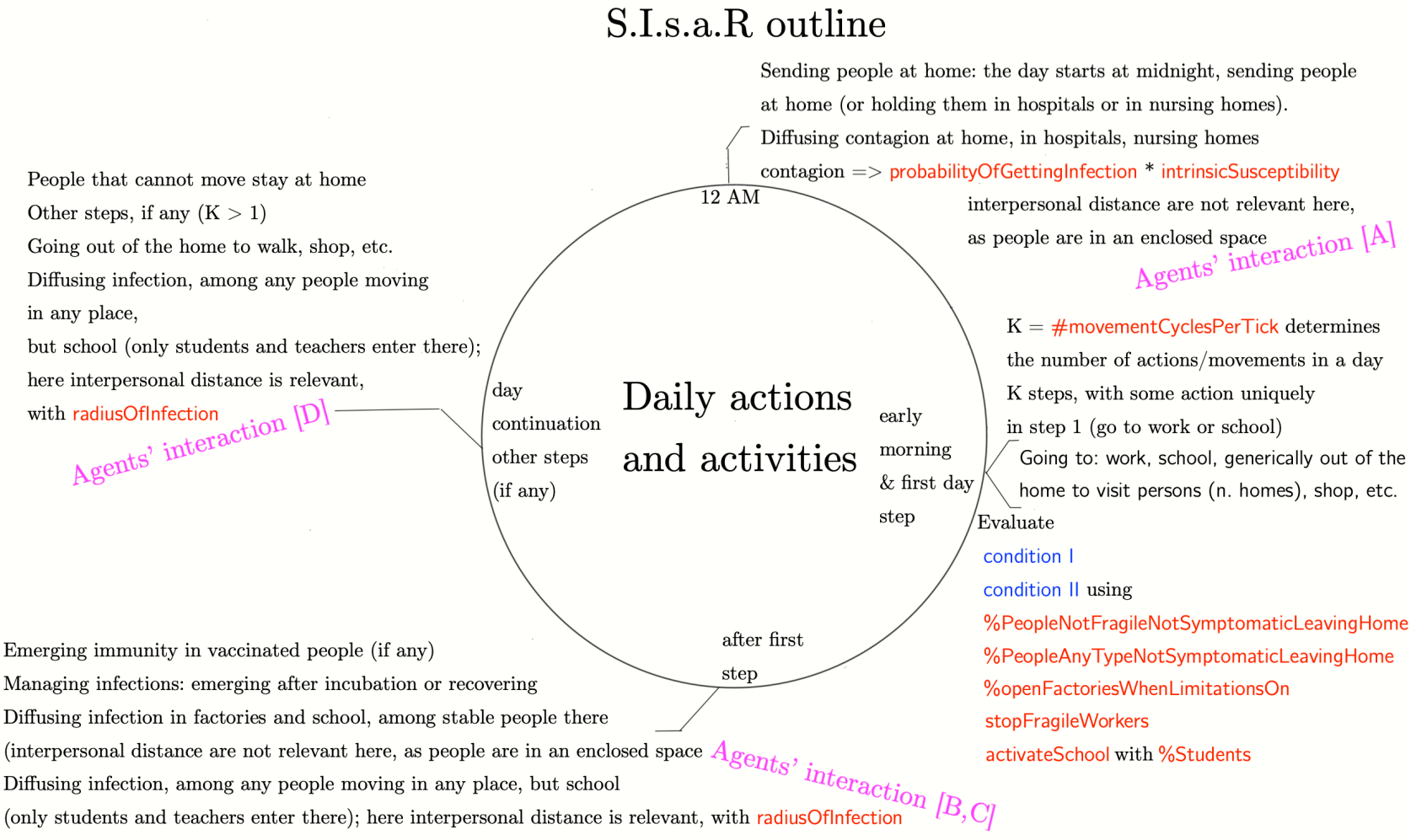


Figure 2: The scheme: def. and values of the parameters at https://terna.to.it/simul/howSIsaRworks.pdf

Contagion representation

- The model allows analyzing the sequences of contagions in simulated epidemics, reporting the places where the contagion occur.
- We represent:
  - i each infected agent as a horizontal segment (from the starting date to the final date of the infection) with vertical connections to other agents if they receive the disease from the specifically represented agent;
  - ii the new infected agents via further segments at an upper level.
- With colors, line thickness, and styles, we display multiple information.
- This enables understanding at a glance how an epidemic episode is developing. In this way, it is easier to reason about countermeasures and, thus, to develop intervention policies.

Examples (1/2)

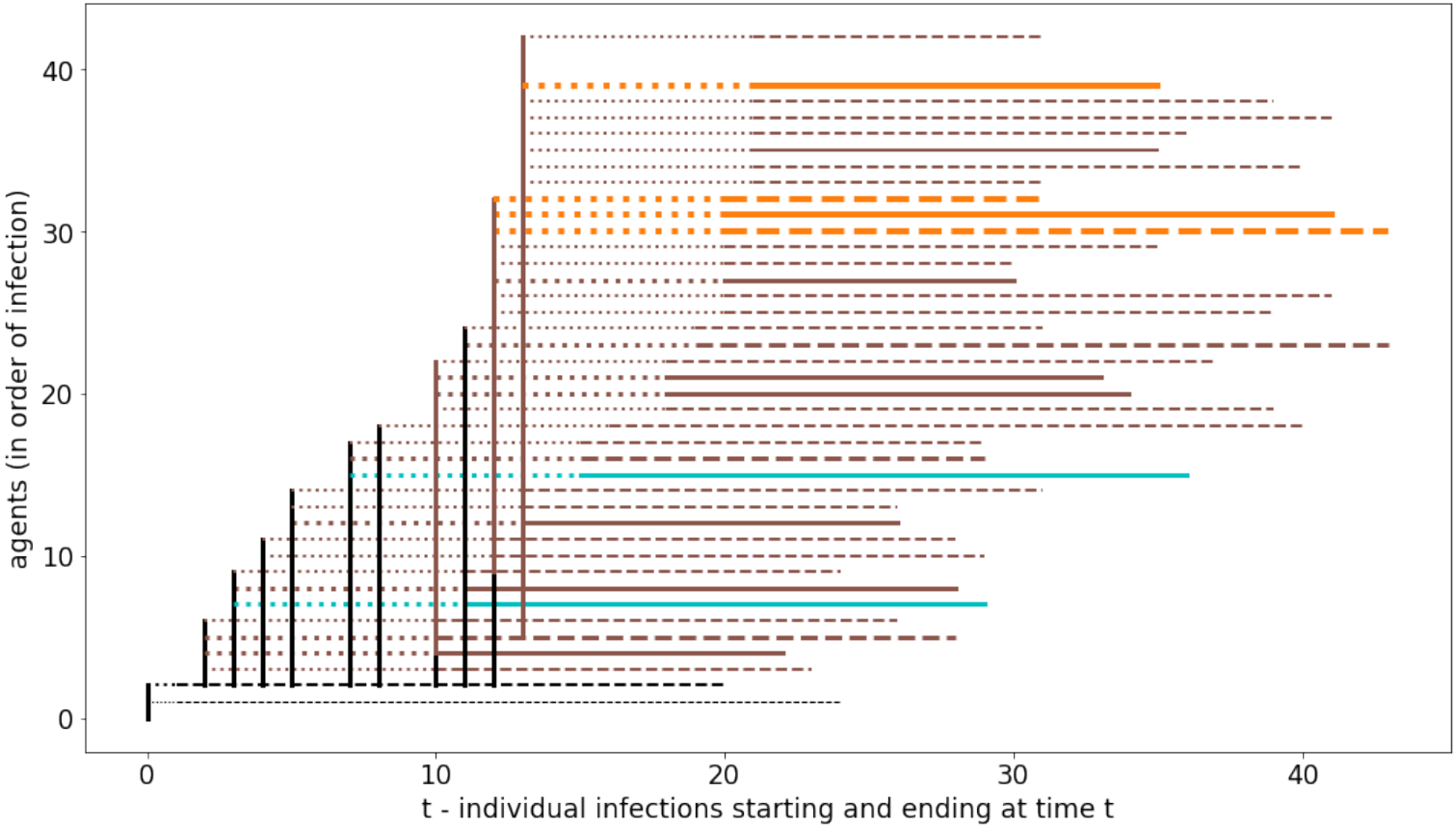


Figure 3: A case with containment measures, first 40 infections: workplaces (brown) and nursing homes (orange) strictly interweaving

Examples (2/2), whole epidemic

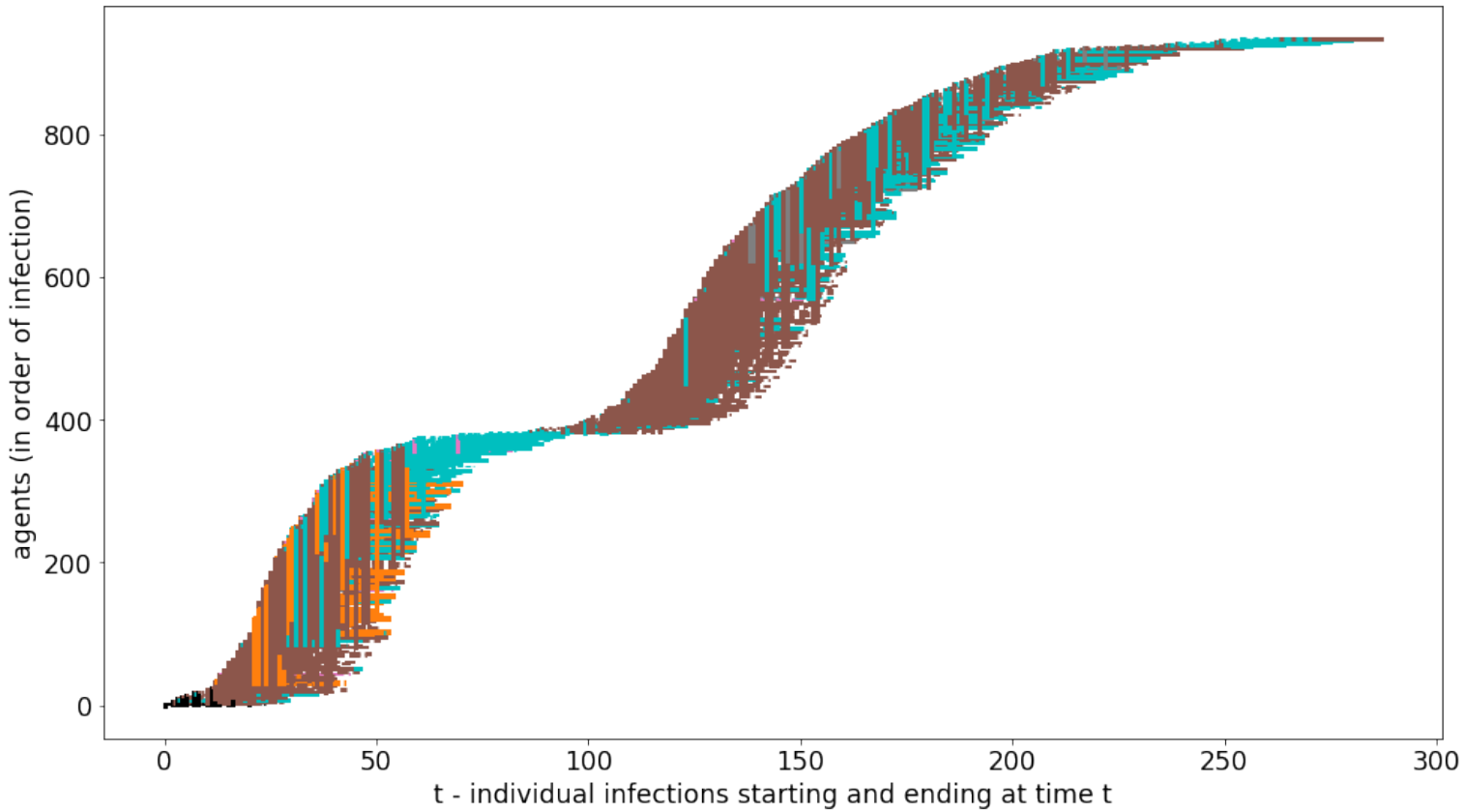


Figure 4: A Case with containment measures, the whole epidemics: workplaces (brown) and nursing homes (orange) and then houses (cyan), with a bridge connecting two waves

Simulation batches

- We explore systematically the introduction of factual, counterfactual, and prospective interventions to control the spread of the contagions.
- Each simulation run—whose length corresponds to the disappearance of symptomatic or asymptomatic contagion cases—is a datum in a wide scenario of variability in time and effects.
- We need to represent compactly the results emerging from batches of simulation repetitions, to compare the consequences of the basic assumptions adopted for each specific batch.
- Besides summarizing the results with the usual statistical indicators, we adopt the technique of the heat-maps.
- Each heat-map reports the duration of each simulated epidemic in the x axis and the number of the symptomatic, asymptomatic, and deceased agents in the y axis. The z axis is represented by the colors, as in the logarithmic scale on the right of each picture.
- In our batches we have 10,000 runs.

10,000 epidemics without control in Piedmont

	symptomatic	totalInfected&Deceased	duration
count	10000.00	10000.00	10000.00
mean	969.46	2500.45	303.10
std	308.80	802.88	93.50

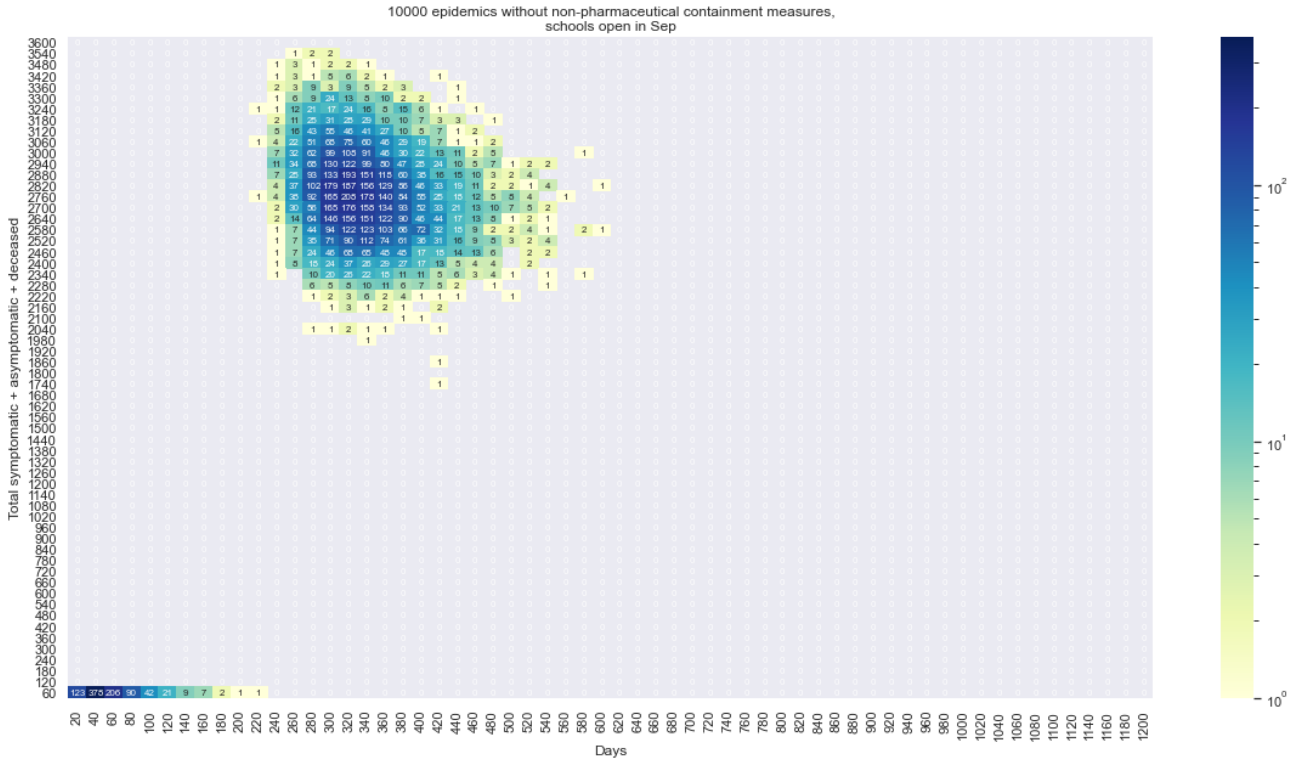


Figure 5: Without non-pharmaceutical containment measures

10,000 epidemic with basic control in Piedmont

	symptomatic	totalInfected&Deceased	duration
count	10000.00	10000.00	10000.00
mean	344.22	851.64	277.93
std	368.49	916.41	213.48

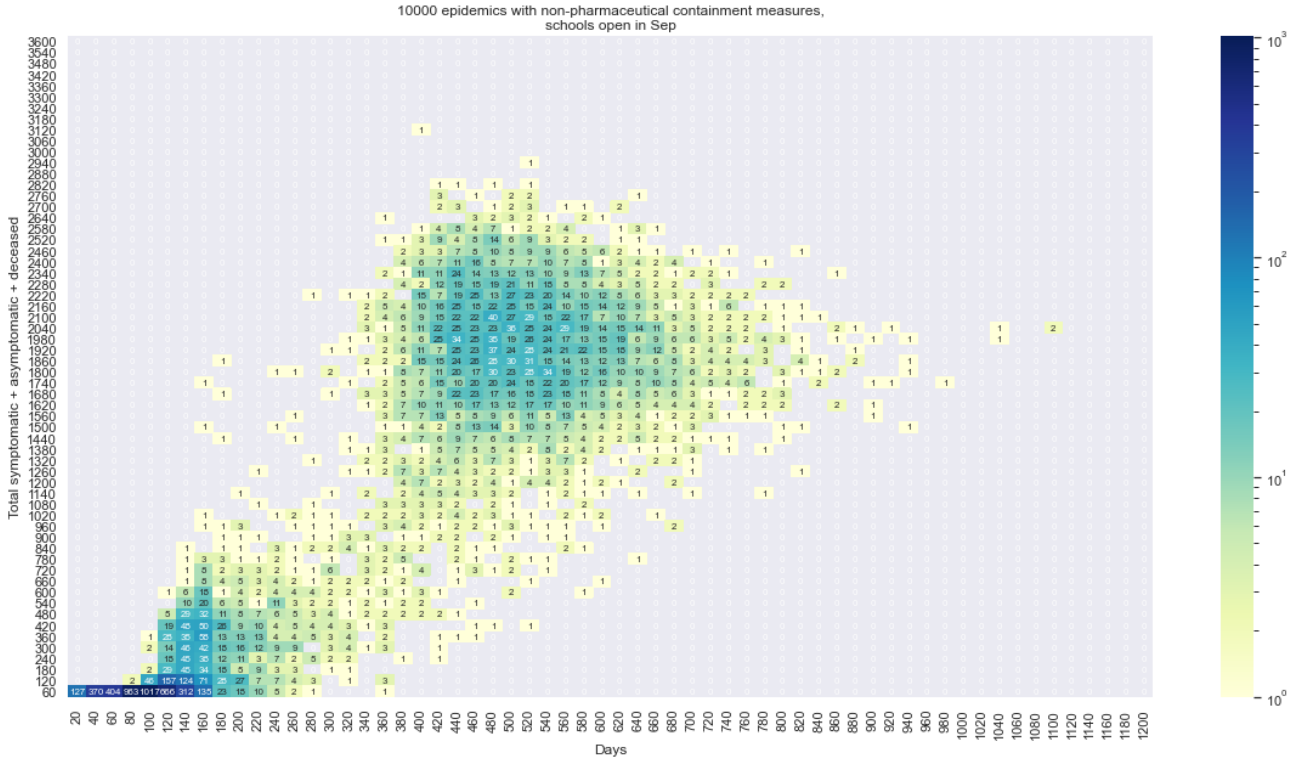


Figure 6: First wave with non-pharmaceutical containment measures

Key points in Summer and Fall 2020

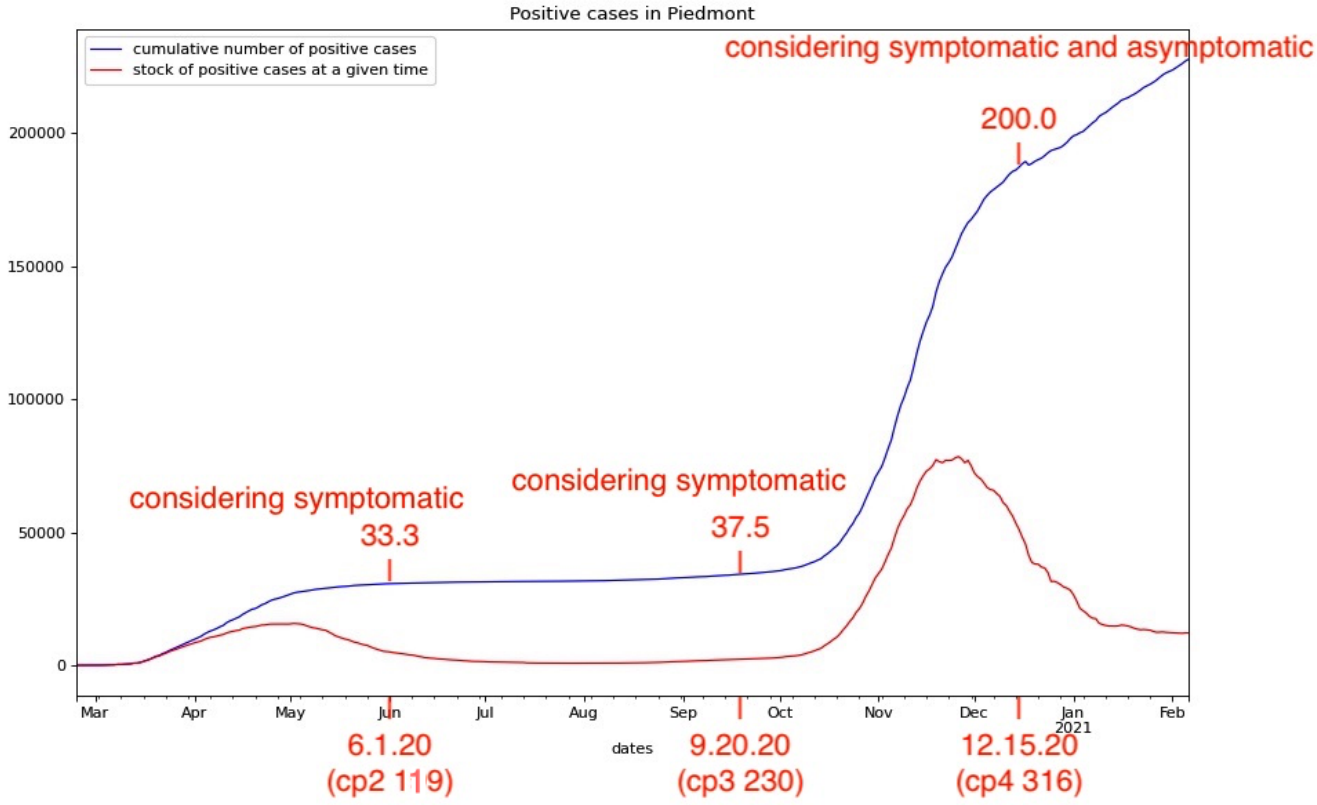
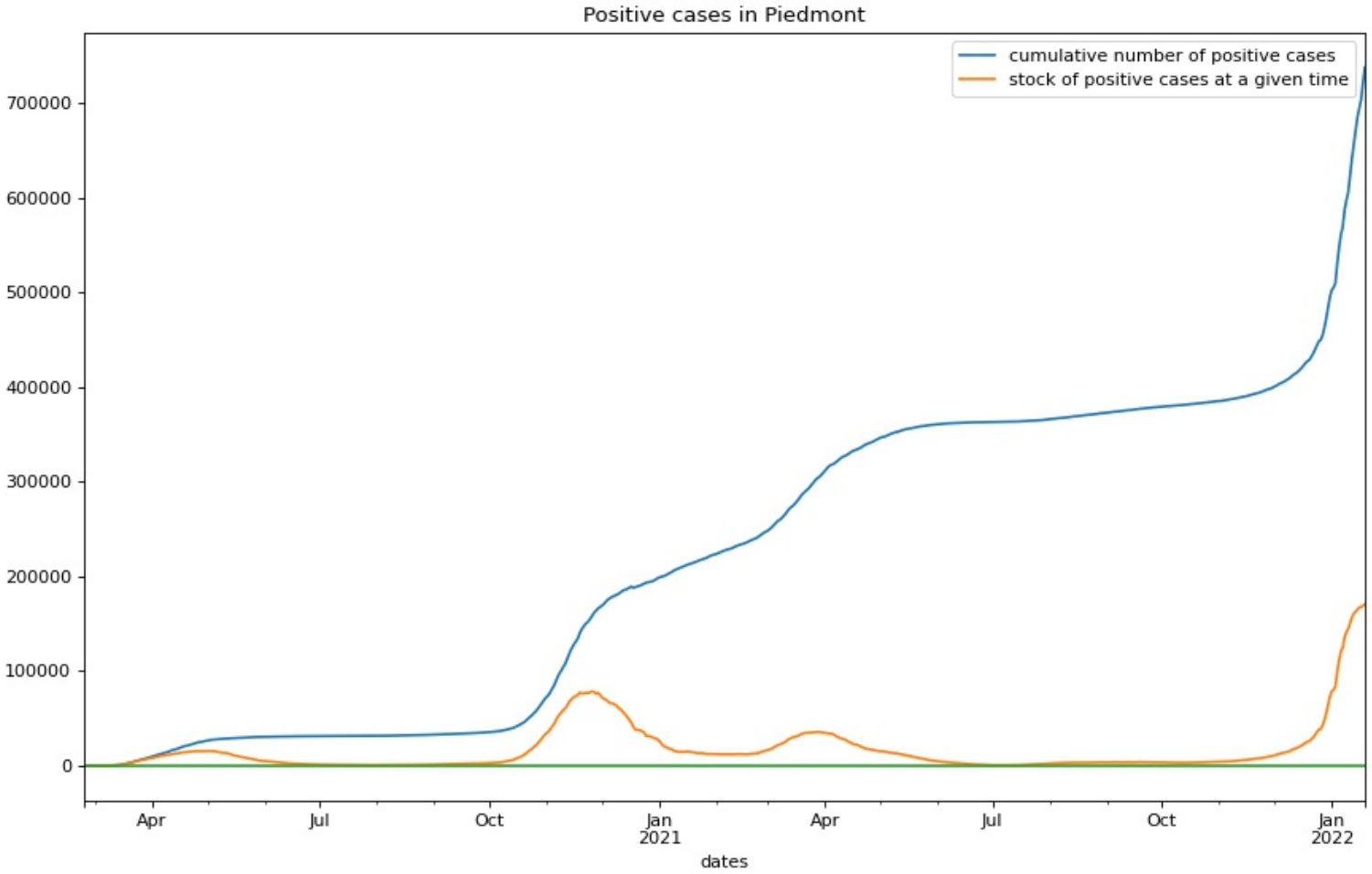


Figure 7: key points in epidemic dynamic in Summe and Fall 2020

Non homogeneous data

- Following the Civil Protection Department web site http://www.protezionecivile.it/web/guest/department, we find the repository https://github.com/pcm-dpc/COVID-19.
- In the first wave we had uniquely data about symptomatic infected people, but from October 2020 data are mixed.
- In the above *git* repository, in October and November 2020 we had "Positive cases emerged from clinical activity", unfortunately then reported as "No longer populated" (from the end of November 2020, my observation) and "Positive cases emerging from surveys and tests, planned at national or regional level", again "No longer populated" (from the end of November, my observation).
- Using those two series, it was possible to estimate a subdivision between symptomatic and asymptomatic cases, which is no longer possible.

Updated series, with a third wave (data at January 19th, 2022)



Spontaneous second wave, without specific measures

170 epidemics stable in Summer 2020 out of 10,000, rule: at Jun 1, 20 select if sym. (10, 70], actual v. 33.3 & at Sep 20, 20 select if sym. (20, 90], actual value 37.5; **140** at Dec 15, 20, rule: sym.+asym.>Sep 20, 20, actual value: 200.0.

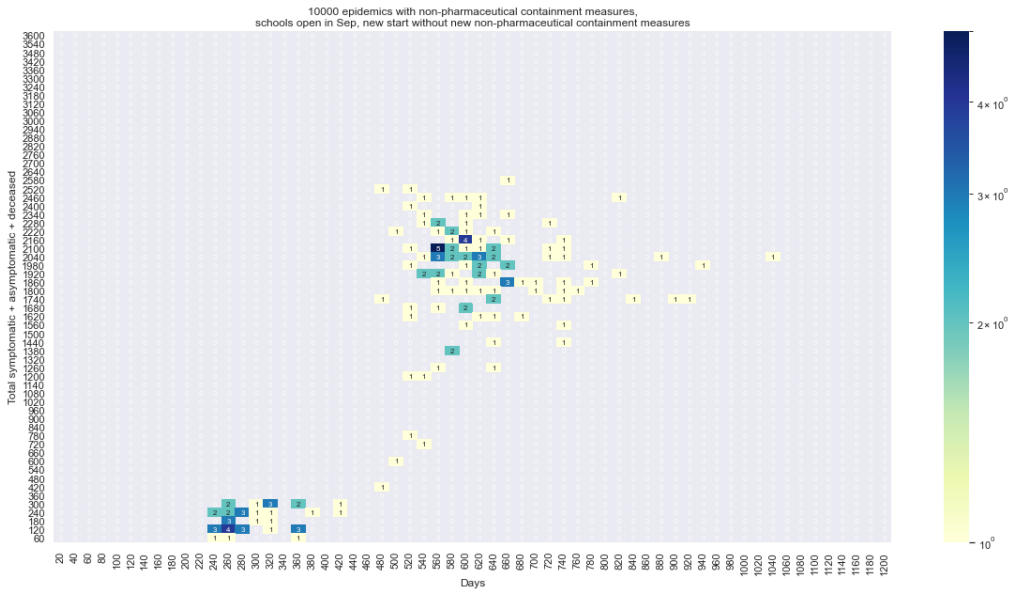


Figure 9: First wave with non-pharmaceutical containment measures, spontaneous second wave, without specific measures

(1000)	Jun 1, 20		Sep 9, 20		Dec 15, 20		Feb 1, 21		May 1, 21		Dec 15, 20 to end		
cum. v.	sym.	all	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	days
count	170.0	170.0	170.0	170.0	140.0	140.0	131.0	131.0	128.0	128.0	140.0	140.0	140.0
mean	37.9	100.2	60.4	159.3	**248.4**	**648.7**	**432.2**	**1109.5**	**656.3**	**1655.5**	701.1	1757.9	594.2
std	16.4	61.0	19.6	71.7	167.4	424.3	220.4	538.4	215.4	513.3	246.4	599.7	118.9

Second w., new infections from outside, without specific measures

1407 epidemics stable in Summer 2020 out of 10,000, rule: at Jun 1, 20 select if sym. (10, 70], actual v. 33.3 & at Sep 20, 20 select if sym. (20, 90], actual value 37.5; **1044** at Dec 15, 20, rule: sym.+asym.>Sep 20, 20, actual value: 200.0.

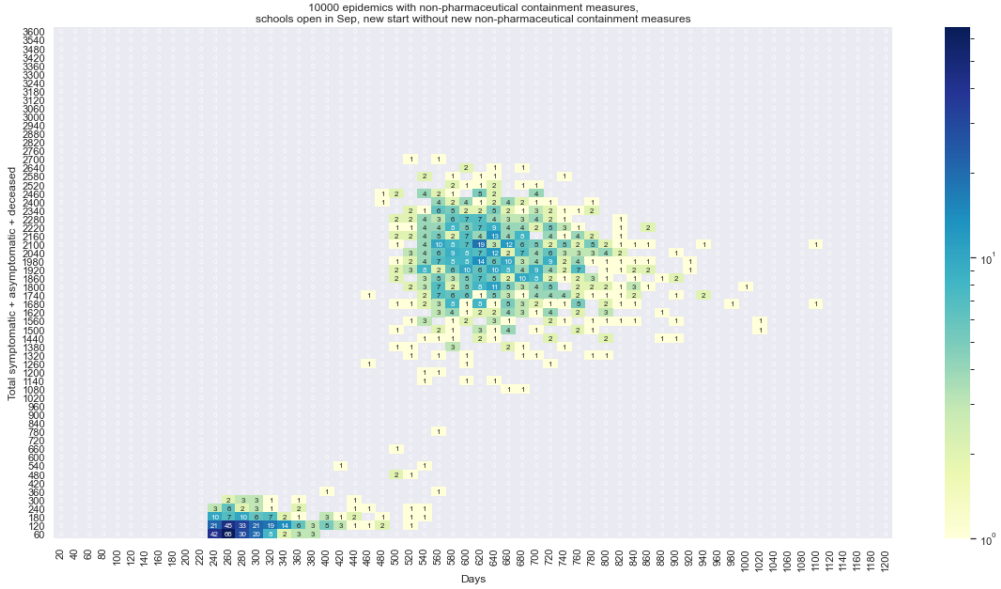


Figure 10: First wave with non-pharmaceutical containment measures, forcing the second wave, without specific measures

(1000)	Jun 1, 20		Sep 9, 20		Dec 15, 20		Feb 1, 21		May 1, 21		Dec 15, 20 to end		
cum. v.	sym.	all	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	days
count	1407.0	1407.0	1407.0	1407.0	1044.0	1044.0	1005.0	1005.0	980.0	980.0	1044.0	1044.0	1044.0
mean	35.6	72.7	40.0	84.1	**180.4**	**462.1**	**354.1**	**900.4**	**623.8**	**1563.3**	726.6	1810.9	620.9
std	14.1	42.6	16.7	52.8	134.6	354.6	213.8	535.4	217.9	527.0	221.9	544.0	110.8

Second w., new infections from outside, with new specific measures

1407 epidemics stable in Summer 2020 out of 10,000, rule: at Jun 1, 20 select if sym. (10, 70], actual v. 33.3 & at Sep 20, 20 select if sym. (20, 90], actual value 37.5; **874** at Dec 15, 20, rule: sym.+asym.>Sep 20, 20, actual value: 200.0.

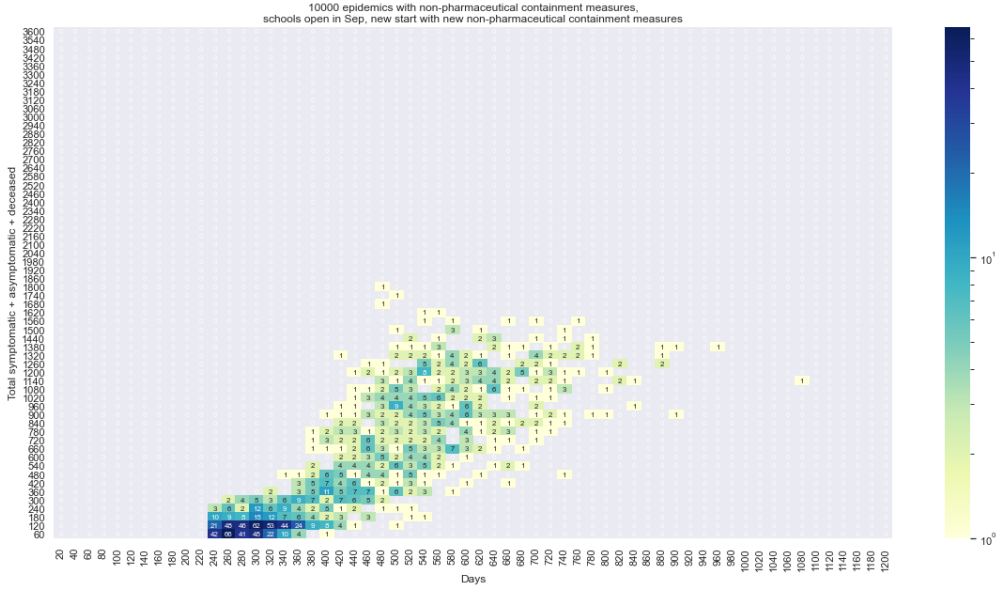


Figure 11: First wave with non-ph. containment measures, forcing the second wave, **with new specific non-ph. containment measures**

(1000)	Jun 1, 20		Sep 9, 20		Dec 15, 20		Feb 1, 21		May 1, 21		Dec 15, 20 to end		
cum. v.	sym.	all	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	sympt.	totalInf.	days
count	1407.0	1407.0	1407.0	1407.0	874.0	874.0	719.0	719.0	523.0	523.0	874.0	874.0	874.0
mean	35.6	72.7	40.0	84.1	**130.0**	**340**.6	**194.4**	**512.8**	**295.7**	**791.2**	252.7	666.4	494.1
std	14.1	42.6	16.7	52.8	83.9	232.6	104.1	276.9	119.1	300.6	156.8	416.4	122.7

Time factor

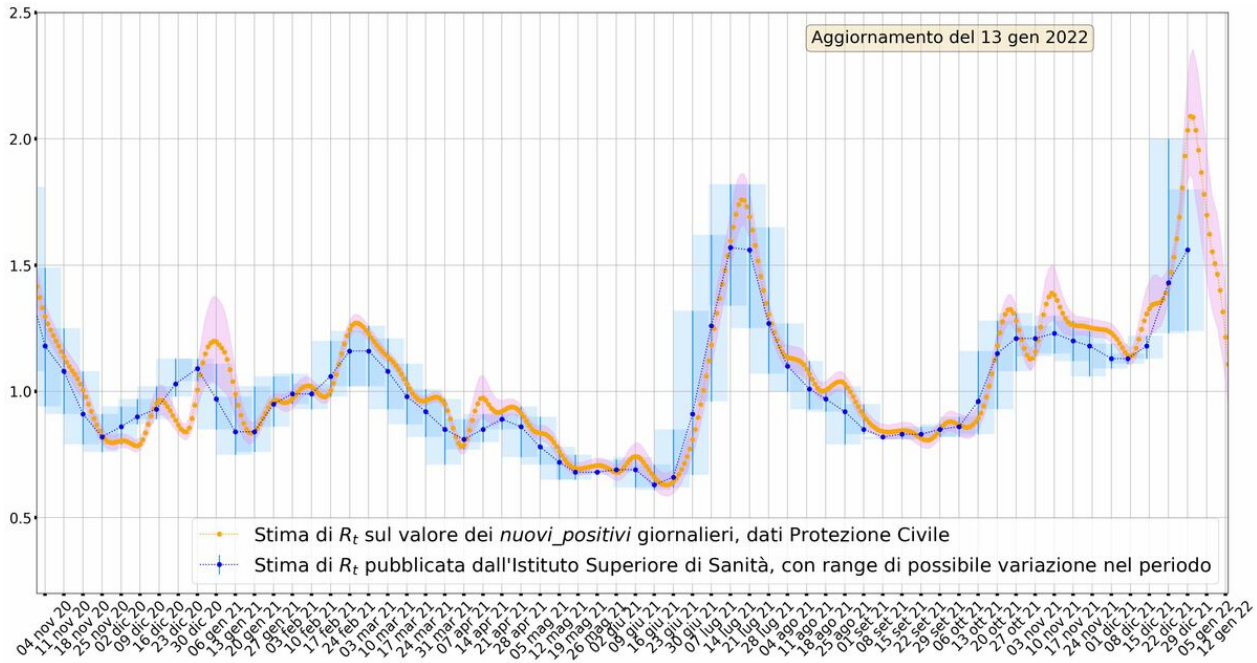


Figure 12: In blue the R_t values as reported by the Istituto Superiore di Sanità and in red the calculation published regularly at https://mondoeconomico.eu by Stefano Terna[1].

[1] Methodology: Section 5.4 at https://arxiv.org/abs/2108.08885

Second w., new infect. from outside, with new specific meas. -20 days[2]

1407 epidemics stable in Summer 2020 out of 10,000, rule: at Jun 1, 20 select if sym. (10, 70], actual v. 33.3 & at Sep 20, 20 select if sym. (20, 90], actual value 37.5; **769** at Dec 15, 20, rule: sym.+asym.>Sep 20, 20, actual value: 200.0.

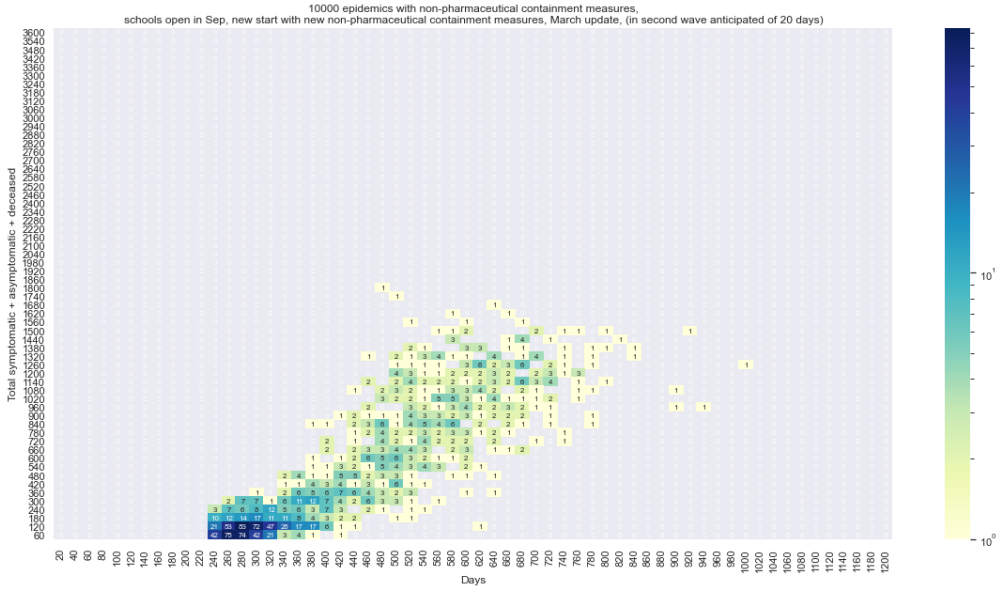


Figure 13: First wave with non-ph. cont. meas., forcing the second wave, **with new specific non-ph. cont. meas., 20 day anticipation**

(1000) cum. v.	Jun 1, 20 sym.	all	Sep 9, 20 sympt.	totalInf.	Dec 15, 20 sympt.	totalInf.	Feb 1, 21 sympt.	totalInf.	May 1, 21 sympt.	totalInf.	Dec 15, 20 to end sympt.	totalInf.	days
count	1407.0	1407.0	1407.0	1407.0	769.0	769.0	637.0	637.0	471.0	471.0	769.0	769.0	769.0
mean	35.6	72.7	40.0	84.1	**112.2**	**294.2**	**172.0**	**467.9**	**276.5**	**748.6**	248.9	663.4	499.3
std	14.1	42.6	16.7	52.8	66.8	188.4	91.5	251.3	112.9	286.9	158.0	417.5	124.1

Fragile persons

- A possible strategy is to stop all fragile people for a given period when R_t starts increasing (also with fragile workers in sick leave, if unable to work remotely).
- We have also relevant social benefits, e.g., schooling, and economic benefits, as activities do not stop

Sec. w., new infect. from outs., stop fragile people. 60 days from Oct. 5th, 2020[3]

1407 epidemics stable in Summer 2020 out of 10,000, rule: at Jun 1, 20 select if sym. (10, 70], actual v. 33.3 & at Sep 20, 20 select if sym. (20, 90], actual value 37.5; **886** at Dec 15, 20, rule: sym.+asym.>Sep 20, 20, actual value: 200.0.

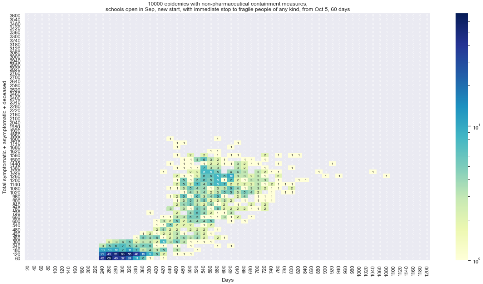


Figure 14: First wave with non-ph. cont. meas., forcing the sec. w.; **in sec. w., uniquely stop fragile people, including fragile workers**

(1000)	Jun 1, 20 sym.	all	Sep 9, 20 sympt.	totalInf.	Dec 15, 20 sympt.	totalInf.	Feb 1, 21 sympt.	totalInf.	May 1, 21 sympt.	totalInf.	Dec 15, 20 to end sympt.	totalInf.	days
count	1407.0	1407.0	1407.0	1407.0	886.0	886.0	761.0	761.0	637.0	637.0	886.0	886.0	886.0
mean	35.6	72.7	40.0	84.1	128.1	326.3	**211.0**	**555.1**	**323.3**	**862.1**	301.1	792.3	515.5
std	14.1	42.6	16.7	52.8	89.6	234.2	118.1	306.7	126.4	315.9	170.7	450.2	116.9

To recap (2020 second wave)

Scenarios		Dec 15, 20 sympt.	Dec 15, 20 totalInf	Dec 15, 20 to end sympt.	end totalInf	days
no containments in forced second wave	count	1044.0	1044.0	1044.0	1044.0	1044.0
	mean	**180.4**	**462.1**	726.6	1810.9	620.9
	std	134.6	354.6	221.9	544.0	110.8
basic containements in forced second wave	count	874.0	874.0	874.0	874.0	874.0
	mean	**130.0**	**340**.6	252.7	666.4	494.1
	std	83.9	232.6	156.8	416.4	122.7
-20 days containments in forced second wave	count	769.0	769.0	769.0	769.0	769.0
	mean	**112.2**	**294.2**	248.9	663.4	499.3
	std	66.8	188.4	158.0	417.5	124.1
frag. p. & workers						

Genetic Algorithms (GAs) and how to use them our case

- An introduction to genetic algorithms (GAs) is at https://en.wikipedia.org/wiki/Genetic_algorithm, with the related Holland's schema theorem at https://en.wikipedia.org/wiki/Holland's_schema_theorem.
- Exploring vaccination sequences, using *genetic algorithms*: a detailed note is at https://terna.to.it/simul/GAresultPresentation.pdf and the analysis is in Section 7 of the paper at https://arxiv.org/abs/2108.08885.
- In our case we have to decide how to assign vaccinations over time to seven groups of persons.
- We evolve populations of models whose parameters correspond to their genome. We create newer and newer populations, randomly extracting models using a roulette having the dimension of the pockets proportional to the fitness. After extraction, we cross the genomes with random copy errors, and so on. Fitness is the total number of symptomatic people (death

How to organize the parameters to produce a genome (the numbers are just examples)

From day	Q. of vaccines (000)	*g1*	*g2*	*g3*	*g4*	*g5*	*g6*	*g7*
373	5	0.1	0.1	0.1	0.1	0.1	0.1	0.1
433	10	0.1	0.1	0.1	0.1	0.1	0.1	0.1
493	10	0.1	0.1	0.1	0.1	0.1	0.1	0.1
553	10	0.1	0.1	0.1	0.1	0.1	0.1	0.1
613	20	0.1	0.1	0.1	0.1	0.1	0.1	0.1
738	end							

Figure 15: From the day of the first column, the quantity of vaccination of each group follows the quotas of the related columns

(000)	*g1*	*g2*	*g3*	*g4*	*g5*	*g6*	*g7*
Susc. at t = 0	133	84	240	1560	1179	254	900
Susc. when vacc. starts	124	81	162	1234	1032	245	891

Figure 16: Susceptible persons at the beginning of the simulation and when the vaccination campaign starts, day 373, Feb. 12th, 2021

2021: planning a vaccination campaign using GAs, with non-pharmaceutical containment measures in action, but without the inclusion of the new external input, i.e., the Omicron variant

- We compare the effect of choosing the vaccination quotas via GAs with two predetermined strategies, considering three hypotheses (vaccinated people: still spread the contagion; do not spread the contagion; do it in the 50% of the case); we show here only the first case results.
- Key dates:
  - in the internal calendar of the model, day 373 is Feb. 12th, 2021, which is effectively the starting point of the vaccinations in the region;
  - the day of the effectiveness of the initial vaccinations, 40 days later, is day 413 (Mar. 22nd, 2021).

Vaccination groups

We take into consideration seven groups in order of decreasing fragility but also considering the exposure to contagion:

- *g1* extra fragile people with three components;
  - due to intrinsic characteristics: people in nursing homes;
  - due to risk exposure:
    - nursing homes operators;
    - healthcare operators;
- *g2* teachers;
- *g3* workers with medical fragility;
- *g4* regular workers;
- *g5* fragile people without special characteristics;
- *g6* regular people, not young, not worker, and not teacher;
- *g7* young people excluding special activity cases (a limited number in *g1*).

A specific realistic case

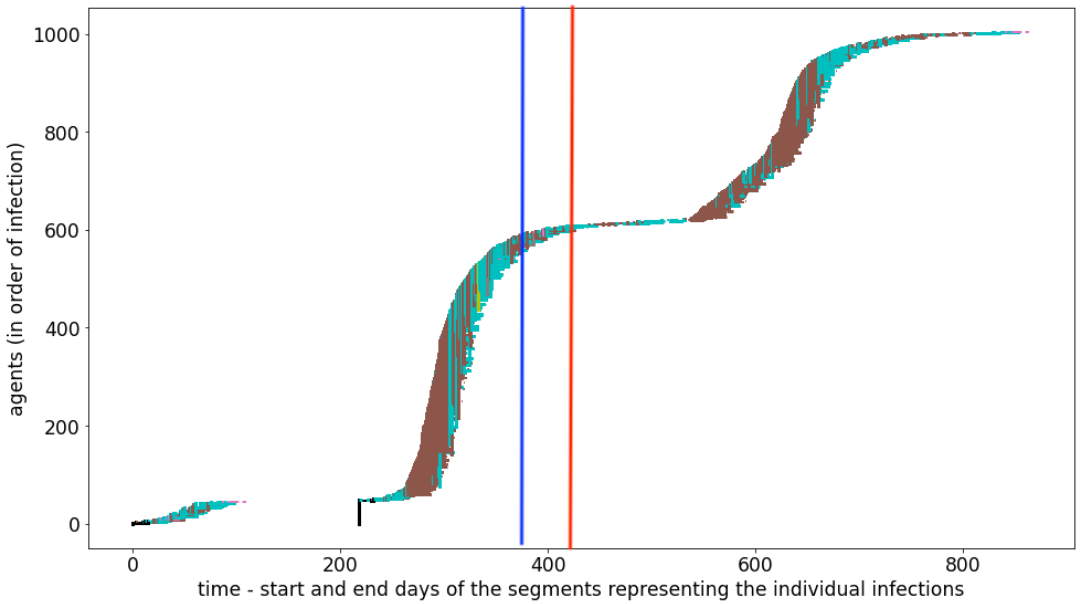


Figure 17: Crucial dates: blue line for the starting point of the vaccination campaign and red line for the start of the effectiveness of the initial vaccinations

Time dynamics without vaccinations

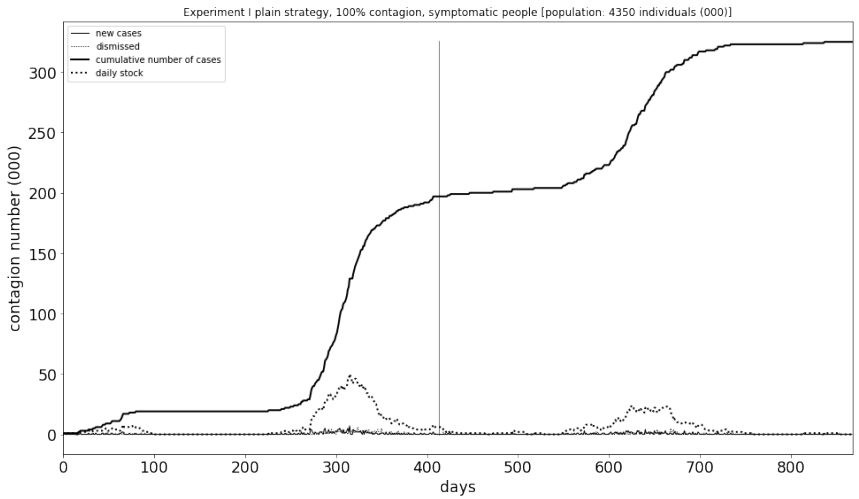


Figure 18: Experiment I, ‘base symptomatic series; the vertical line is at day 413 is not relevant here

Time dynamics with *plain* vac. strategy, vac. people still spreading the infection

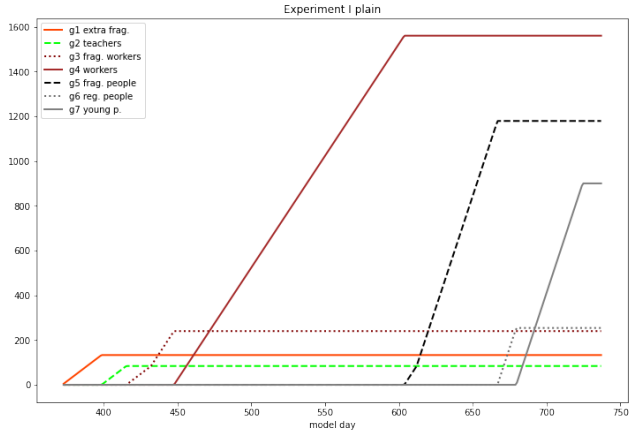


Figure 19: "Plain" vaccination sequence; on the *y* axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)

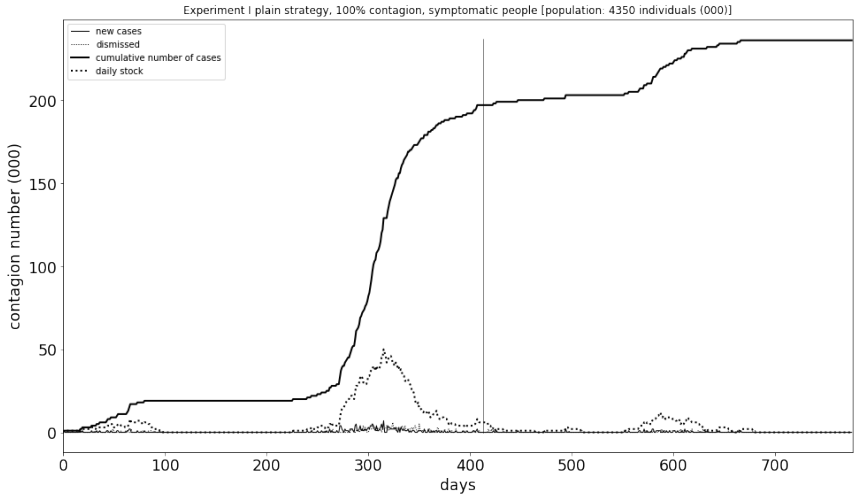


Figure 20: "Plain" vaccination symptomatic series; the vertical line is at day 413, when the effectiveness of first vaccination starts

Time dynamics with *wise* vac. strategy, vac. people still spreading the infection

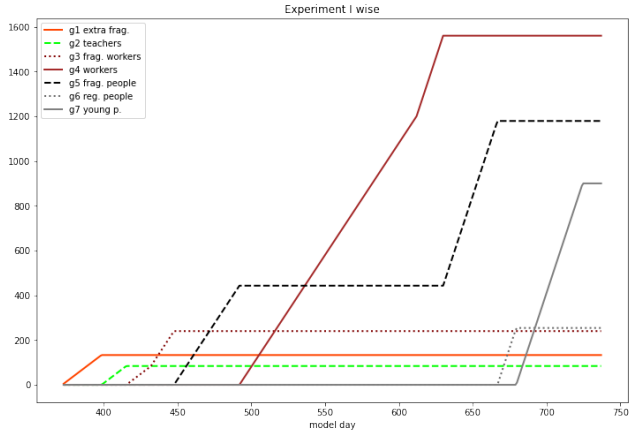


Figure 21: "Wise" vaccination sequence; on the *y* axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)

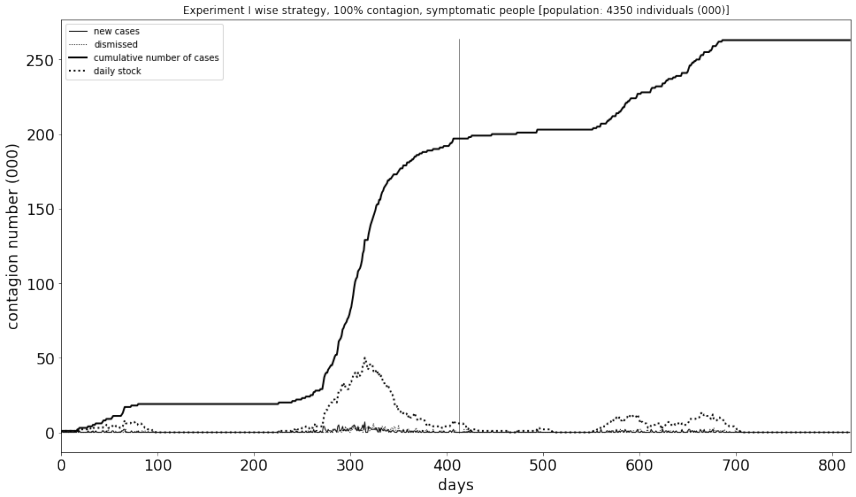


Figure 22: "Wise" vaccination symptomatic series; the vertical line is at day 413, when the effectiveness of first vaccination starts

Time dynamics with best GAs strategy, vac, people still spreading the infection

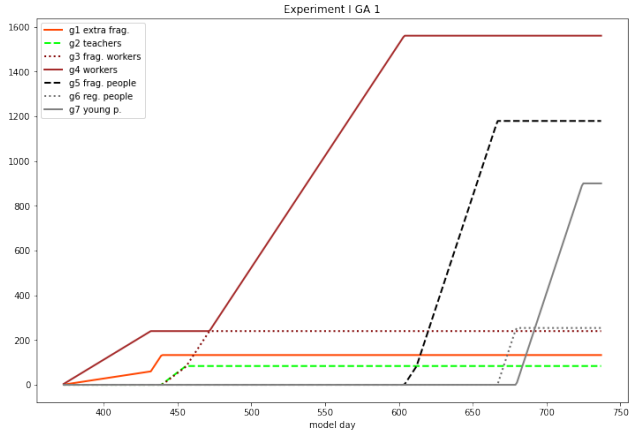


Figure 23: GA 1 vaccination sequence; on the *y* axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)

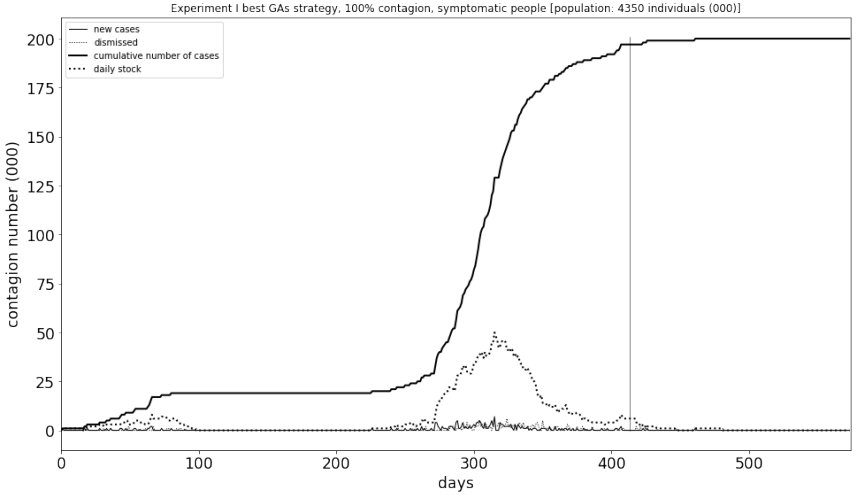


Figure 24: GAs vaccination symptomatic series; the vertical line is at day 413, when the effectiveness of first vaccination starts

Synopsis

Hypothesis: vaccinated people, if infected, are diffusing the contagion.

Case (1000)	At day 413	Final no vaccin.	Final plain vaccin.	Final wise vaccin.	Final GAs vaccin.
I	197	325	236	263	**200**
	-	128	39	66	**3**

Table 2: Results of the vaccination campaigns: only symptomatic people (second row: minus day 413)

A new model: the map

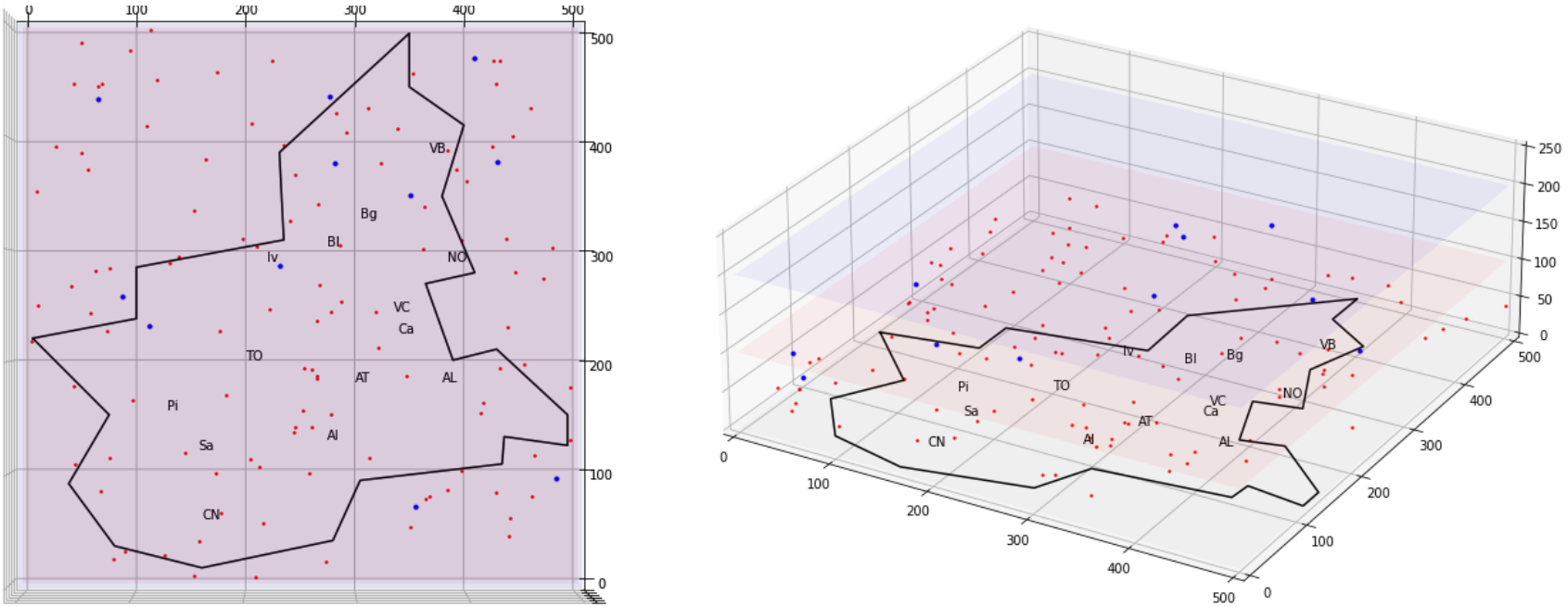


Figure 25: 3D Piedmont

A new model: the scale and the items

- 1 : 100.
- *Infection engine*, https://terna.to.it/simul/InfectionEngine.pdf.
- Houses.
- Schools.
- Hospitals.
- Nursing homes,
- Factories.
- Transportations.
- Aggregation places: happy hours, night life, sport stadiums, discotheques, . . .
- New variants (Delta, Omicron, . . .)
- Networks (family networks, professional networks, high-contact individuals,[4] . . .)

[4] G. Manzo and A. van de Rijt. Halting sars-cov-2 by targeting high-contact individuals. Journal of Artificial Societies and Social Simulation, 23(4):10, 2020. ISSN 1460-7425. doi: 10.18564/jasss.4435. URL http://jasss.soc.surrey.ac.uk/23/4/10.html.

The tool: S.L.A.P.P.

Scientific advertising: https://terna.github.io/SLAPP/

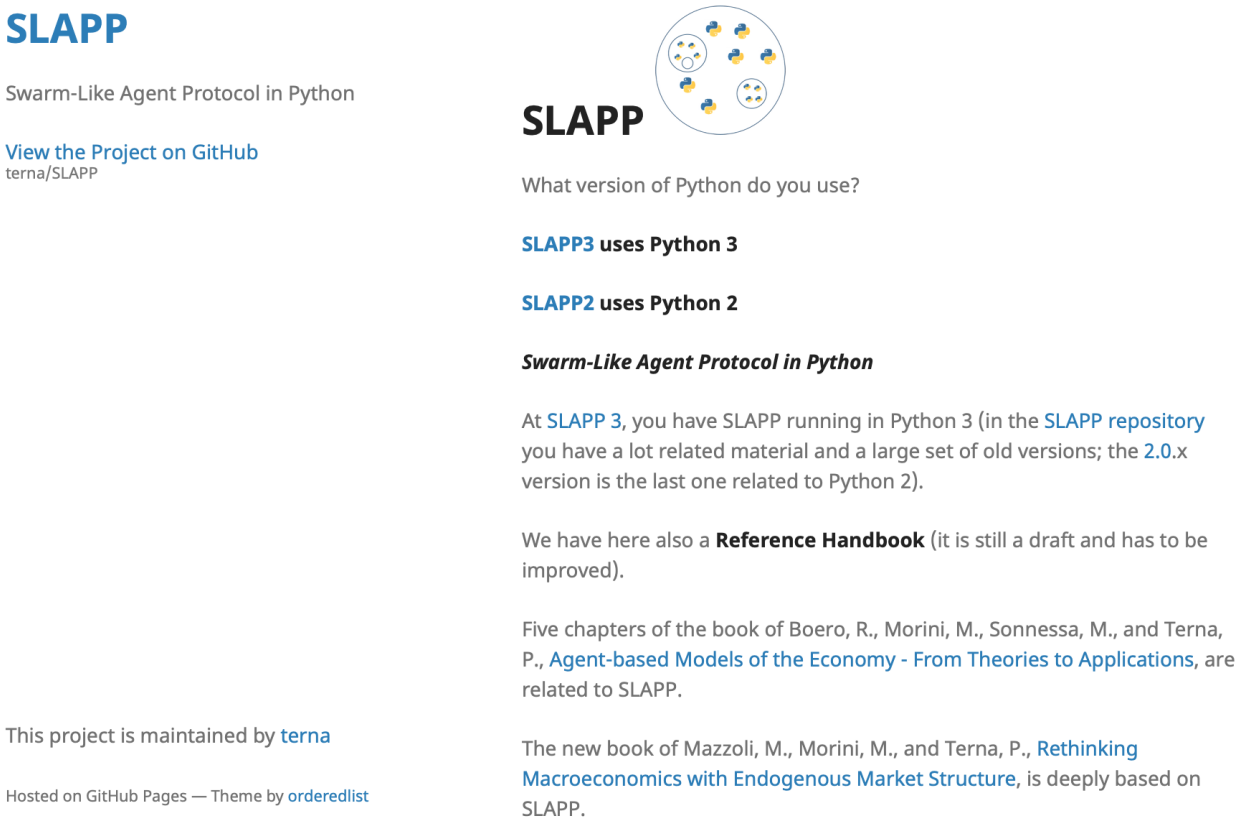


Figure 26: Swarm-Like Agent Protocol in Python

A few steps with NetLogo

NetLogo https://ccl.northwestern.edu/netlogo/
Quoting: “NetLogo is a multi-agent programmable modeling environment. It is used by *many hundreds of thousands* of students, teachers, and researchers worldwide.”

- Start playing . . .
- https://terna.to.it/ChangeColorLightParallelism.html
- https://terna.to.it/ChangeColorStrongParallelism.html
- https://terna.to.it/BenevolentAgents.html

Many thanks.

https://terna.to.it, pietro.terna@unito.it

Slides at https://terna.to.it/abmMC.pdf