

ABMs	The virus model	How the model works	Exploring cases	Factual/counterfactual analyses	Planning vaccination campaigns	A new model	NetLogo
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Agent Based Models

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slides at <https://terna.to.it/abmMC.pdf>



Outline

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Epidemics without and with control

Actual data

Factual/counterfactual analyses

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Introduction

An experiment with GA

A new model

NetLogo

ABMs

The virus model

How the model works

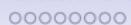
Exploring cases

Factual/counterfactual analyses

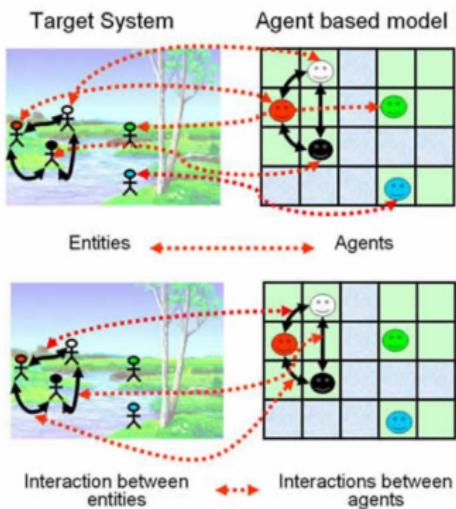
Planning vaccination campaigns

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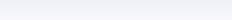


Introduction



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>



Many tools and a scheme



*From Santa Fe Swarm(1995,
<http://www.swarm.org>) to SLAPP, in
 Python and with a better time
 management*



SLAPP

Swarm-Like Agent Protocol in Python

Here you have SLAPP v.0.91 (in the [SLAPP repository](https://github.com/terna/SLAPP3/) you have related material and old versions).

A reference manual is coming (expected with version 1.0, in June 2015).

Five chapters of a forthcoming book will be related to SLAPP.

SLAPP logo: credits to [Steve Rogers](#).

ABMs

The virus model



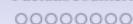
How the model works



Exploring cases



Factual/counterfactual analyses



Planning vaccination campaigns



A new model



NetLogo



A scheme

agents

in a collection

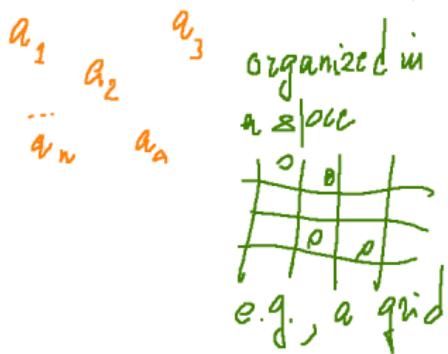
$[a_1, a_2, \dots, a_n]$

a_1
...
 a_n

may be, many
collections

A scheme

agents



A scheme

agents

a_1 a_2 a_3
... a_n a_n

organized in
a space



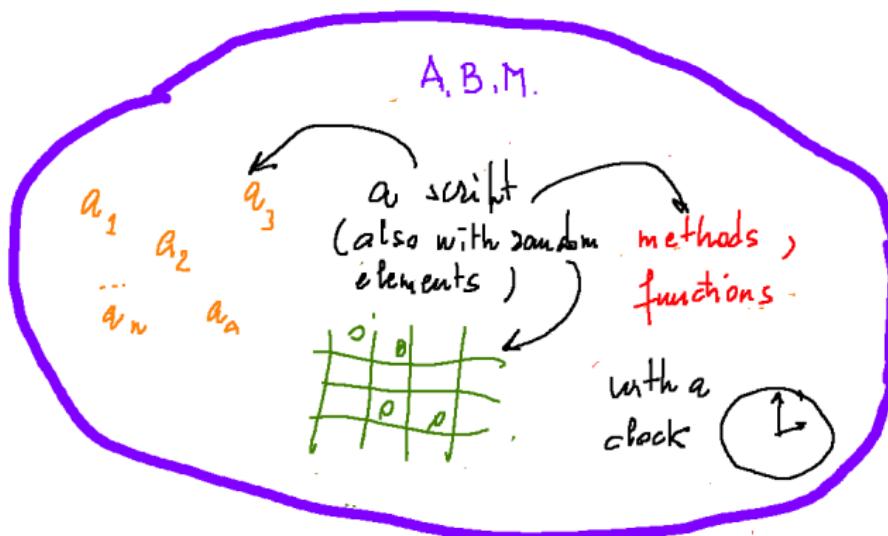
Executing "orders"

as methods,
functions

e.g.,

eat
move
buy
stock
...

A scheme

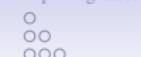




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An ABM on virus diffusion: a paper describing the model

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>.



Introduction

- A micro-based model of interacting agents, following plausible behavioral rules into a world where the Covid-19 epidemic is affecting the actions of everyone.
- The model works with:
 - i infected agents categorized as symptomatic or asymptomatic and
 - ii the places of contagion specified in a detailed way, thanks to agent-based modeling capabilities.
- 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.

ABMs

The virus model

How the model works

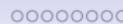
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- The micro-based structure of the model allows factual, counterfactual, and conditional simulations to investigate both the spontaneous or controlled development of the epidemic. Examples of counterfactual situations are those considering:
 - i different 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.

ABMs

The virus model

How the model works

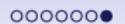
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The world 3D

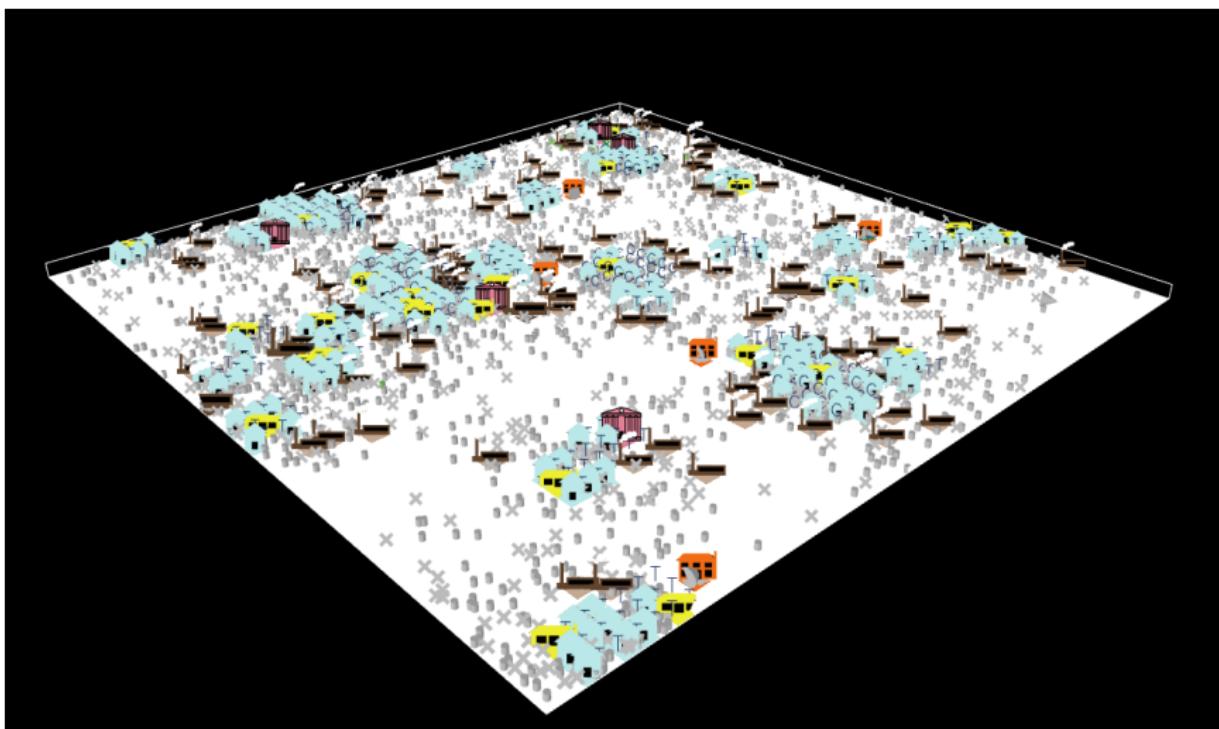


Figure 1: The world 3D

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A circular scheme

S.I.s.a.R outline

People that cannot move stay at home
 Other steps, if any ($K > 1$)
 Going out of the home to walk, shop, etc.
 Diffusing infection, among any people moving
 in any place,
 but school (only students and teachers enter there);
 here interpersonal distance is relevant,
 with `radiusOfInfection`

Agents' interaction [D]

Emerging immunity in vaccinated people (if any)
 Managing infections: emerging after incubation or recovering
 Diffusing infection in factories and school, among stable people there
 (interpersonal distance are not relevant here, as people are in an enclosed space
 Diffusing infection, among any people moving in any place, but school
 (only students and teachers enter there); here interpersonal distance is relevant, with `radiusOfInfection`

Daily actions and activities

12 AM

Daily actions and activities

day continuation
other steps
(if any)

early morning
& first day step

after first step

Sending people at home: the day starts at midnight, sending people
 at home (or holding them in hospitals or in nursing homes).

Diffusing contagion at home, in hospitals, nursing homes
 contagion => `probabilityOfGettingInfection * intrinsicSusceptibility`

interpersonal distance are not relevant here,
 as people are in an enclosed space

Agents' interaction [A]

$K = \#movementCyclesPerTick$ determines
 the number of actions/movements in a day

K steps, with some action uniquely
 in step 1 (go to work or school)

Going to: work, school, generically out of the
 home to visit persons (n . homes), shop, etc.

Evaluate

`condition I`

`condition II` using

`%PeopleNotFragileNotSymptomaticLeavingHome`

`%PeopleAnyTypeNotSymptomaticLeavingHome`

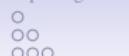
`%openFactoriesWhenLimitationsOn`

`stopFragileWorkers`

`activateSchool` with `%Students`

Agents' interaction [B,C]

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:
 - 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;
 - 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.

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Examples (1/2)

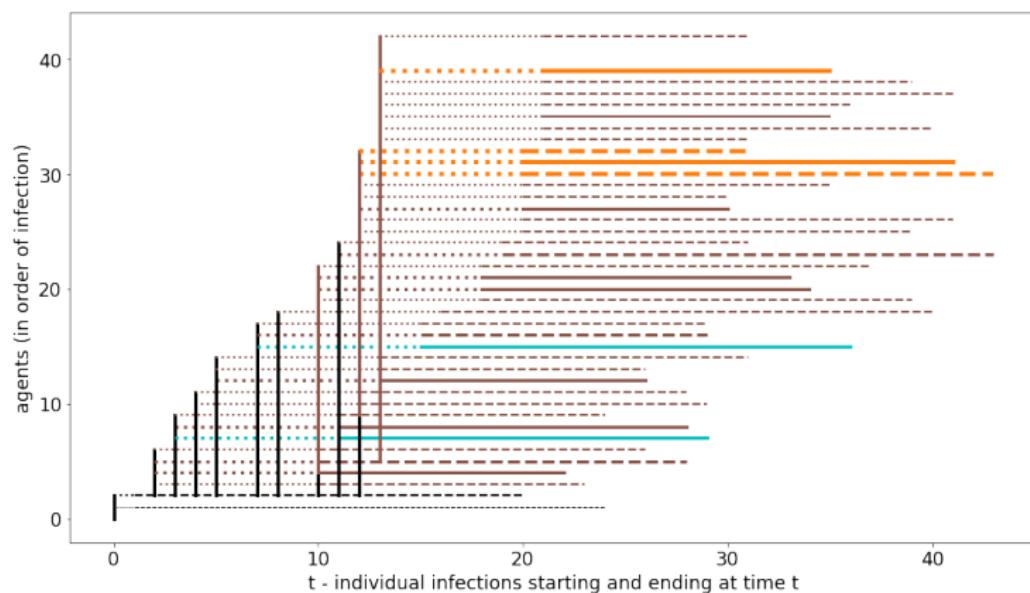


Figure 3: A case with containment measures, first 40 infections: workplaces (brown) and nursing homes (orange) strictly interweaving

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Examples (2/2), whole epidemic

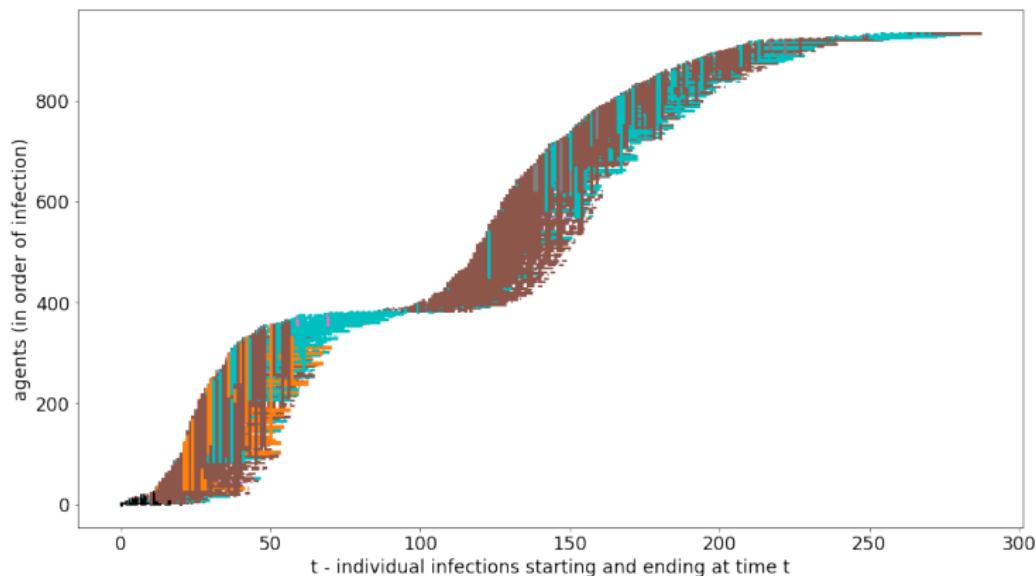


Figure 4: A Case with containment measures, the whole epidemics: workplaces (brown) and nursing homes (orange), and then houses (cyan), with a bridge connecting two waves

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.

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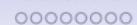
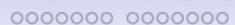
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10,000 epidemics without control in Piedmont

	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

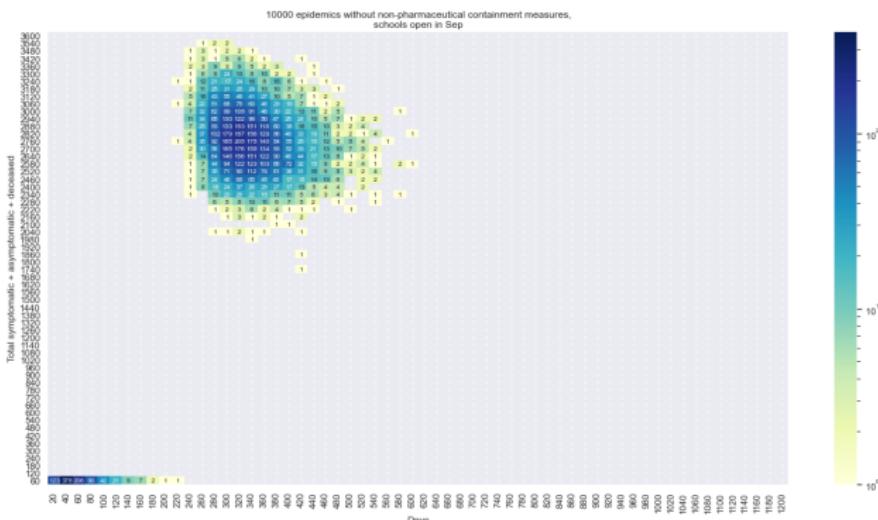


Figure 5: Without non-pharmaceutical containment measures

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How the model works

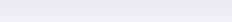
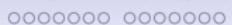
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10,000 epidemic with basic control in Piedmont

	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

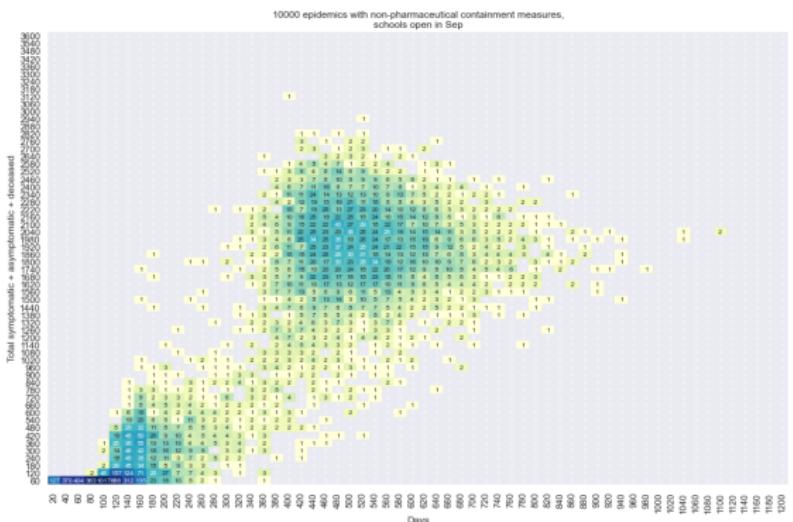


Figure 6: First wave with non-pharmaceutical containment measures

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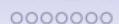
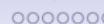
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Key points in Summer and Fall 2020

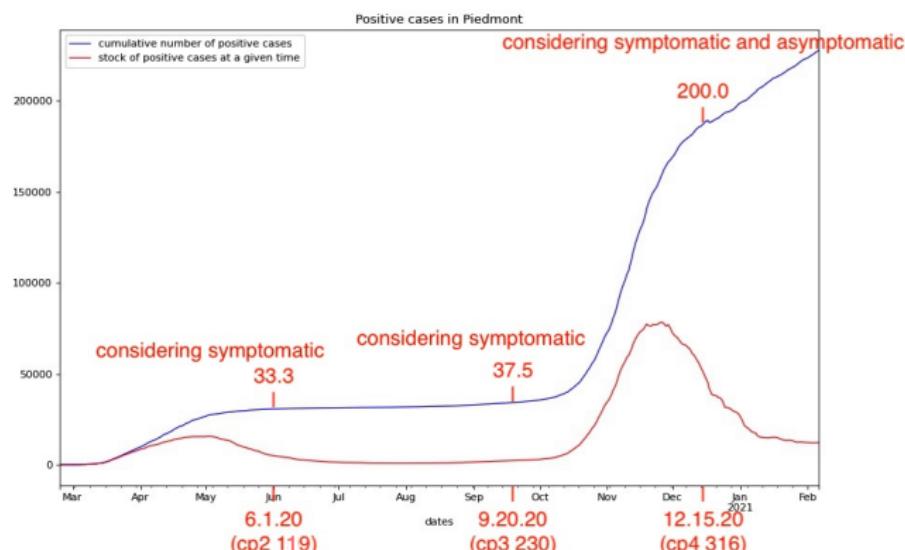


Figure 7: key points in epidemic dynamic in Summe and Fall 2020

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.

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

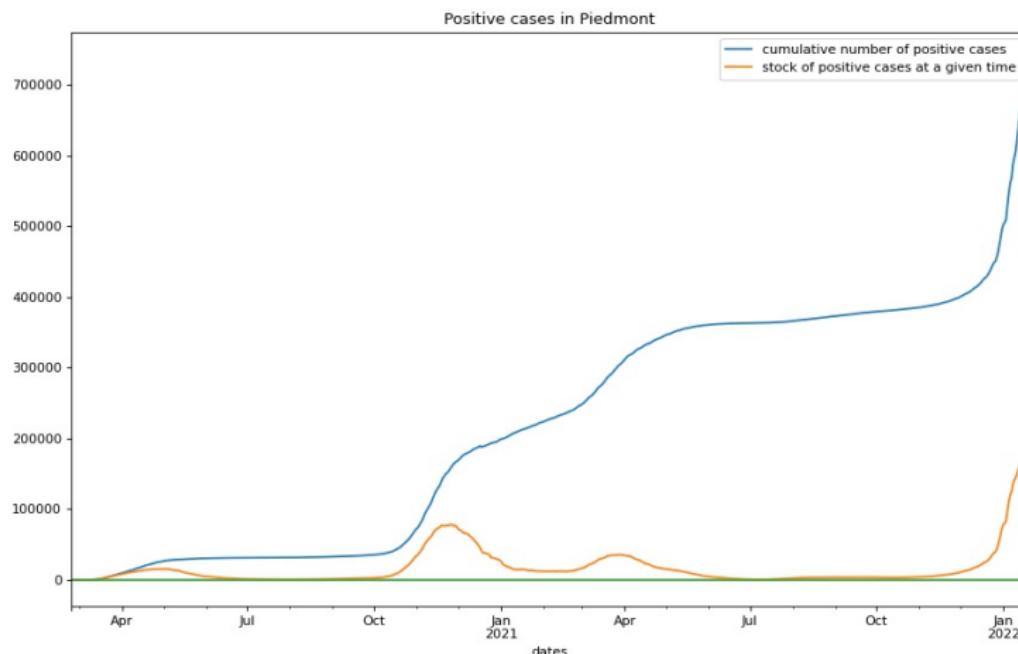


Figure 8: Data for Piedmont

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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.

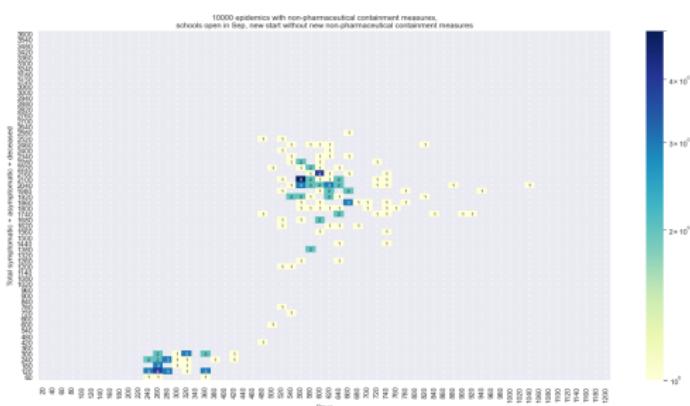


Figure 9: First wave with non-pharmaceutical containment measures, spontaneous second wave, without specific measures

(1000) cum. v.	Jun 1, 20 sym.	Jun 1, 20 all	Sep 9, 20 sympt.	Sep 9, 20 totalInf.	Dec 15, 20 sympt.	Dec 15, 20 totalInf.	Feb 1, 21 sympt.	Feb 1, 21 totalInf.	May 1, 21 sympt.	May 1, 21 totalInf.	Dec 15, 20 sympt.	Dec 15, 20 totalInf.	to end 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

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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) cum. v.	Jun 1, 20		Sep 9, 20		Dec 15, 20		Feb 1, 21		May 1, 21		Dec 15, 20 to end		
	sym.	all	symp.	totalInf.	symp.	totalInf.	symp.	totalInf.	symp.	totalInf.	symp.	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



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+asymp>Sep 20, 20, actual value: 200.0.

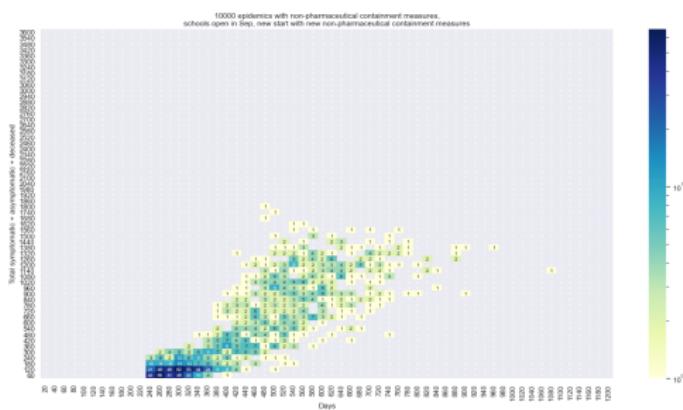


Figure 11: First wave with non-ph. containment measures, forcing the second wave, **with new specific non-ph. containment measures**

(1000) cum. v.	Jun 1, 20		Sep 9, 20		Dec 15, 20		Feb 1, 21		May 1, 21		Dec 15, 20 to end		
	sym.	all	symp.	totalInf.	symp.	totalInf.	symp.	totalInf.	symp.	totalInf.	symp.	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

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Time factor

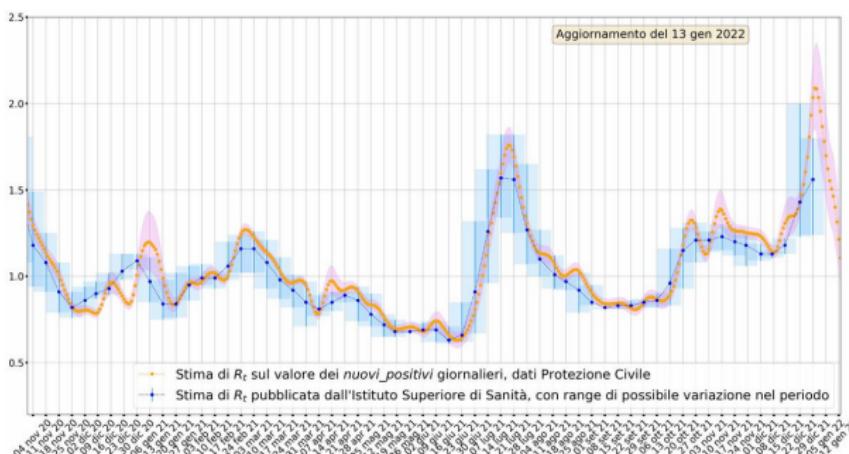


Figure 12: In blue the R_t values as reported by the Istituto Superiore di Sanità and in red the calculation published regularly at <https://mondoeconomico.eu> by Stefano Terna¹.

¹Methodology: Section 5.4 at <https://arxiv.org/abs/2108.08885>

Second w., new infect. from outside, with new specific meas. -20 days²

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.

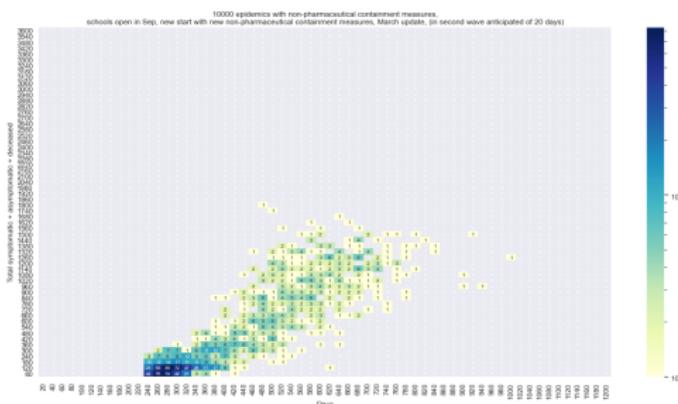


Figure 13: First wave with non-ph. cont. meas., forcing the second wave, **with new specific non-ph. cont. meas., 20 day anticipation**

(1000) cum. v.	Jun 1, 20		Sep 9, 20		Dec 15, 20		Feb 1, 21		May 1, 21		Dec 15, 20 to end		
	sym.	all	symp.	totalInf.	symp.	totalInf.	symp.	totalInf.	symp.	totalInf.	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

²N.B.: (i) anticipation limit Oct 5th, 2020; (ii) also the ending date of each measure is anticipated of 20 days.

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,
2020³

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.

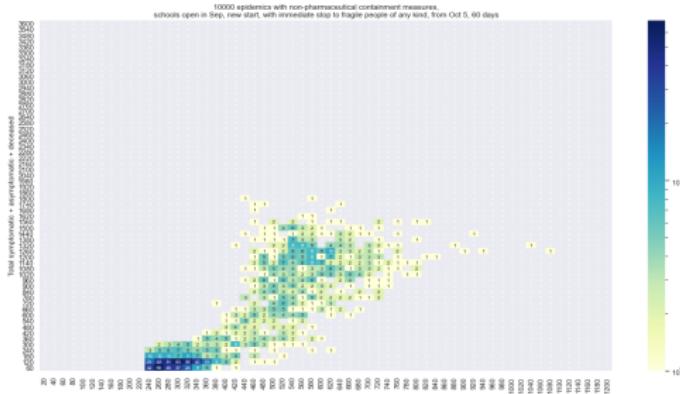


Figure 14: First wave with non-ph. cont. meas., forcing the sec. w.; **in sec. w., uniquely stop fragile people, including fragile workers**

(1000)	Jun 1, 20		Sep 9, 20		Dec 15, 20		Feb 1, 21		May 1, 21		Dec 15, 20 to end		
	sym.	all	symp.	totalInf.	symp.	totalInf.	symp.	totalInf.	symp.	totalInf.	symp.	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

³Schools are always working 100% in this case.

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To recap (2020 second wave)

Scenarios			Dec 15, 20 sympt.	Dec 15, 20 totalInf.	to end sympt.	to 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 containments 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. & work- ers control in forced second wave	count	886.0	886.0	886.0	886.0	886.0	
	mean	128.1	326.3	301.1	792.3	515.5	
	std	89.6	234.2	170.7	450.2	116.9	

Table 1: Report of the key results, with count, mean, and std

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%27s_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 people come from there) with the minimum value as the goal.



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

From day	Q. of vaccines (000)	<i>g1</i>	<i>g2</i>	<i>g3</i>	<i>g4</i>	<i>g5</i>	<i>g6</i>	<i>g7</i>
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)	<i>g1</i>	<i>g2</i>	<i>g3</i>	<i>g4</i>	<i>g5</i>	<i>g6</i>	<i>g7</i>
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*).

ABMs

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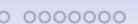
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A specific realistic case

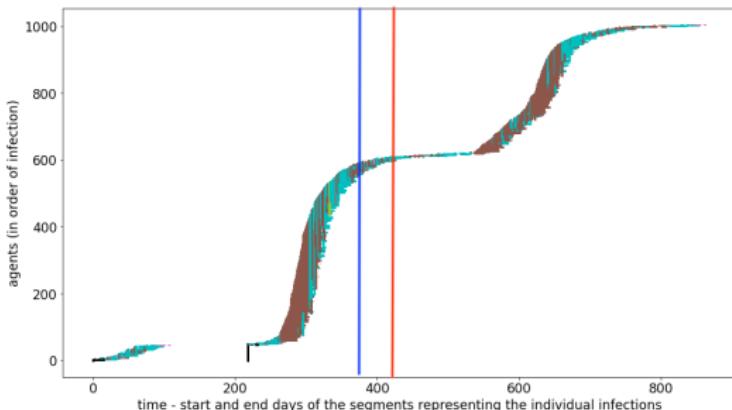


Figure 17: Crucial dates: blue line for the starting point of the vaccination campaign and red line for the start of the effectiveness of the initial vaccinations



Time dynamics without vaccinations

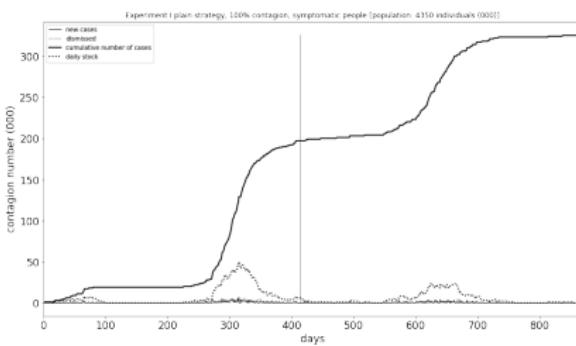


Figure 18: Experiment I, 'base symptomatic series; the vertical line is at day 413 is not relevant here'

ABMs

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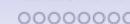
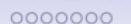
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Time dynamics with *plain* vac. strategy, vac. people still spreading the infection

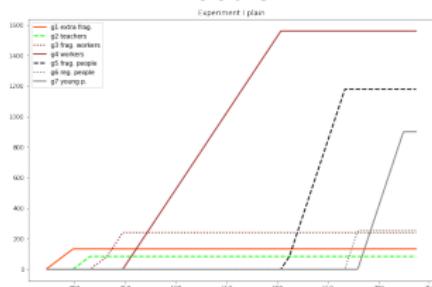


Figure 19: “Plain” vaccination sequence; on the y axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)

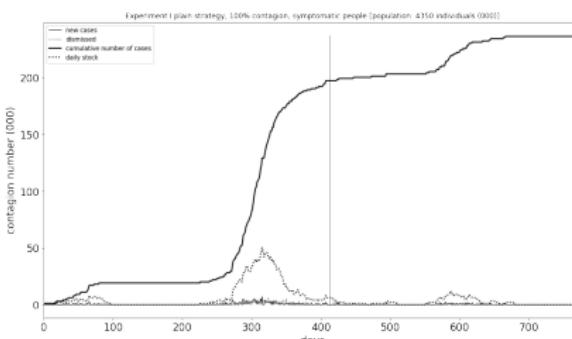


Figure 20: “Plain” vaccination symptomatic series; the vertical line is at day 413, when the effectiveness of first vaccination starts



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

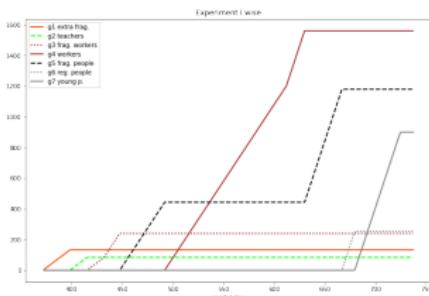


Figure 21: “Wise” vaccination sequence; on the y axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)

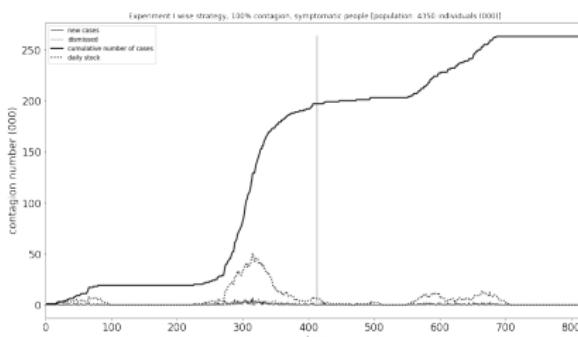


Figure 22: “Wise” vaccination symptomatic series; the vertical line is at day 413, when the effectiveness of first vaccination starts



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

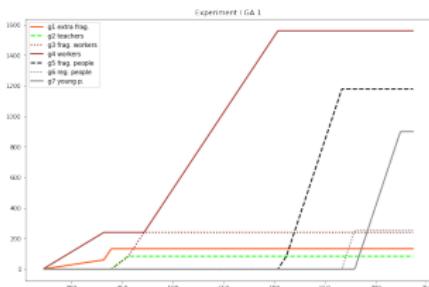


Figure 23: GA 1 vaccination sequence; on the y axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)

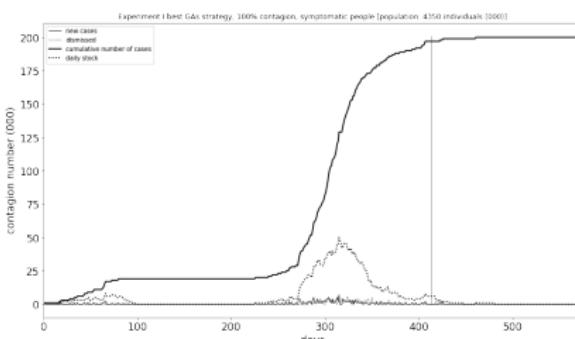


Figure 24: GAs vaccination symptomatic series; the vertical line is at day 413, when the effectiveness of first vaccination starts

Synopsis

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

Case	At day 413	Final no vaccin. (1000)	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)

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A new model: the map

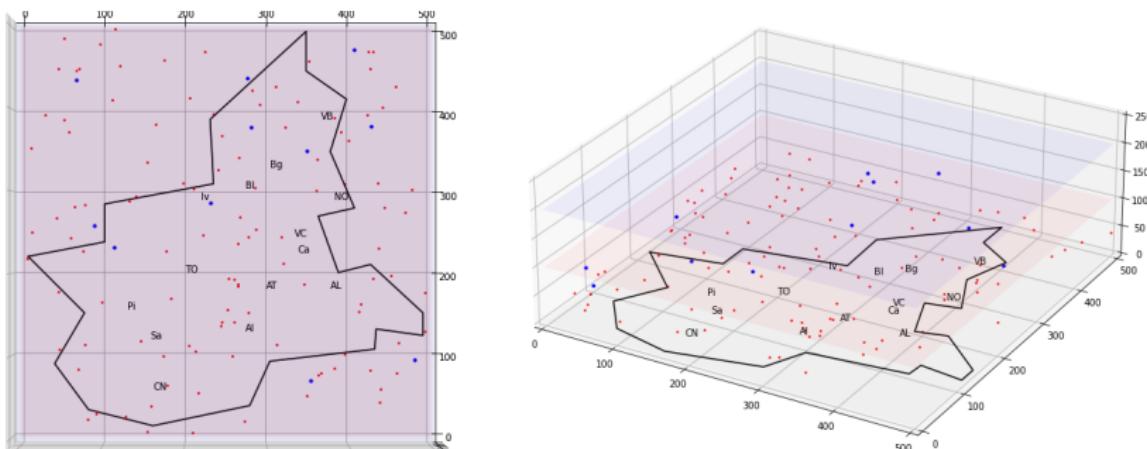


Figure 25: 3D Piedmont

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 ...)

⁴G. 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/>

SLAPP

Swarm-Like Agent Protocol in Python

[View the Project on GitHub](#)
terna/SLAPP



SLAPP

What version of Python do you use?

SLAPP3 uses Python 3

SLAPP2 uses Python 2

Swarm-Like Agent Protocol in Python

At **SLAPP 3**, you have SLAPP running in Python 3 (in the [SLAPP repository](#) you have a lot related material and a large set of old versions; the 2.0.x version is the last one related to Python 2).

We have here also a **Reference Handbook** (it is still a draft and has to be improved).

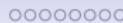
Five chapters of the book of Boero, R., Morini, M., Sonnessa, M., and Terna, P., [Agent-based Models of the Economy - From Theories to Applications](#), are related to SLAPP.

This project is maintained by [terna](#)

Hosted on GitHub Pages — Theme by [orderedlist](#)

The new book of Mazzoli, M., Morini, M., and Terna, P., [Rethinking Macroeconomics with Endogenous Market Structure](#), is deeply based on 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>

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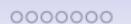
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Many thanks.

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

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