UNIVERSITÀ DEGLI STUDI DI TORINO

Research Education Outreach CCA

An Agent-Based Model to simulate the Covid-19 epidemic diffusion, with the use of Genetic Algorithms to optimize vaccinations

G. Pescarmona[1] P. Terna[2] A. Acquadro[1] P. Pescarmona[3] G. Russo[4] S. Terna[5]

[1] University of Torino, Italy

[2] University of Torino, Italy, retired & Fondazione Collegio Carlo Alberto, Honorary Fellow, Italy

[3] University of Groningen, The Netherlands

[4] Centro Einaudi, Torino, Italy

[5] tomorrowdata.io

CCA – March 29th, 2021

Outline

Objectives of the model

- We propose an agent-based model to simulate the Covid-19 epidemic diffusion, with Susceptible, Infected, symptomatic, asymptomatic, and Recovered people: hence the name S.I.s.a.R. The scheme comes from S.I.R. models, with (i) infected agents categorized as symptomatic and 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.
- The model includes the structural data of Piedmont, but it can be readily calibrated for other areas. The model manages a realistic calendar (e.g., national or local government decisions), via a script interpreter.

Tool and links

- We use NetLogo, at `https://ccl.northwestern.edu/netlogo/`.
- S.I.s.a.R. is at `https://terna.to.it/simul/SIsaR.html` with information on model construction, the draft of a preliminary paper also reporting results, and an online executable version of the simulation program, built using NetLogo.
- A short paper is published at `https://rofasss.org/2020/10/20/sisar/`

G. Pescarmona, P. Terna, A. Acquadro, P. Pescarmona, G. Russo, and S. Terna. How Can ABM Models Become Part of the Policy-Making Process in Times of Emergencies—The SISAR Epidemic Model. *RofASSS*, 2020.

The scale and the items

- 1 : 1000.

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

The interface and the information sheet

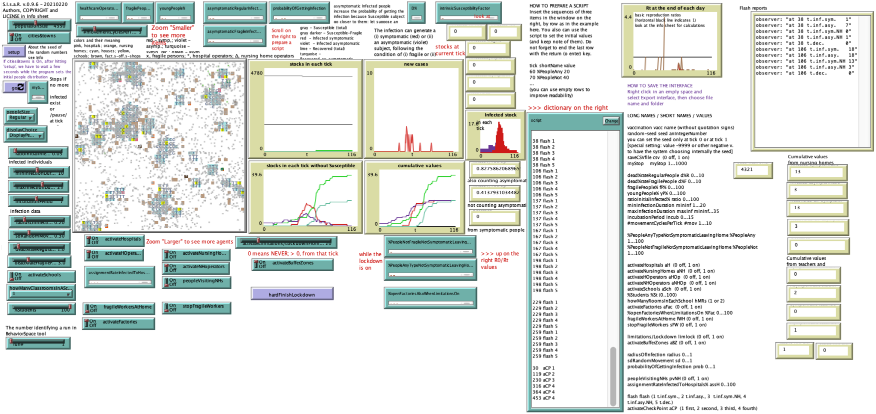

Figure 1: The interface

The interface and the information sheet

WHY THE NAME?

```
S – Susceptible
I – Infected
s – symptomatic
a – asymptomatic
R – Recovered
```

with capital letters referring the *classic* S.I.R. model, also in Wikipedia.

Website

The model has a website.

PRELIMINARY NOTE

This is a simulation with random events, please do not take it as a sure forecasting machine: it is a reasoning machine, a sort of very complex "what if" mental experiment.

The New York Times offers us an analysis on the The Covid-19 Riddle: Why Does the Virus Wallop Some Places and Spare Others? (open link). At the end of the article, we read: *Roll of the Dice - Finally, most experts agree that there may be no single reason for some countries to be hit and others missed. The answer is likely to be some combination of the above factors, as well as one other mentioned by researchers: sheer luck.*

In the same way, in the simulations run with this model we can have very different outcomes as we change the initial seed of the random numbers. Those values are determining mainly the movements at a tiny scale and so the interactions-infections chains.

We can use the model in a comparative way, observing different range of results with different initial conditions (parameters).

Finally, to have a reference at an actual situation, the model is related to the Piedmont scale, with 4,350 agents vs. 4.35 millions of inhabitants. The scale 1 to 1000 is over-represented in the case of schools, with their classrooms with a realistic number of students, apartments with a realistic quantity of inhabitants, and likewise workspaces, hospitals, nursing homes.

We look also to the time series of the total infected people in Piedmont.

VIEWING THE MODEL

In the desk version, we can use both the *continuous* view, observing all the agents' movements and the "on tick" one, faster but updating the screen only at the end of each tick. To set the view, we use a chooser in the top part of the screen.

In the web version we have uniquely the *on tick* feature.

The desk version also allows 3D view: right click on the map of the world and choose *Switch to 3D View*.

HOW IT WORKS

Scripting capability

The code can manage a script to set the parameter modifications occurring while the simulation is running. Explanations in the right side of the interface.

The simulation starts at tick 1, but we can already set the initial values at tick 0.

A trick: (i) via **setup** set all the default values for the experiments at tick 0 and then (ii) modify those that we want change before hitting **go**.

Special item "flash"

With the "flash" item, followed by 1 or 2 or 3, we obtain a flash output in the window to the far right, with data at the beginning of the tick for: (1) total infected symptomatic people; (2) total infected asymptomatic people; (3) total infected symptomatic people in NH; (4) total infected asymptomatic people in NH;(5) total deceased.

Special item "activate check point"

With the "aCP" (activate checkpoint) item, followed by n with n in [1,6] as closed interval, we collect data at the tick of the aCP command. In BehaviorSpace, we can send (or not) the checkpoint data to the table of the results; we have six possible checkpoints, each reporting stocks of infected symptomatic people, infected asymptomatic people, deceased people. The data are at the beginning of the tick.

Figure 2: The information sheet, about 20 pages

The world

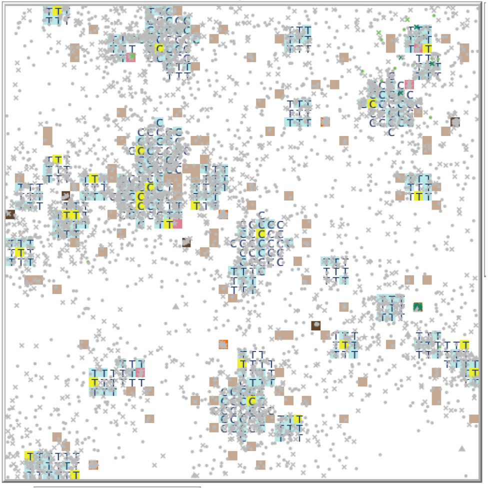

Figure 3: The world

The world 3D

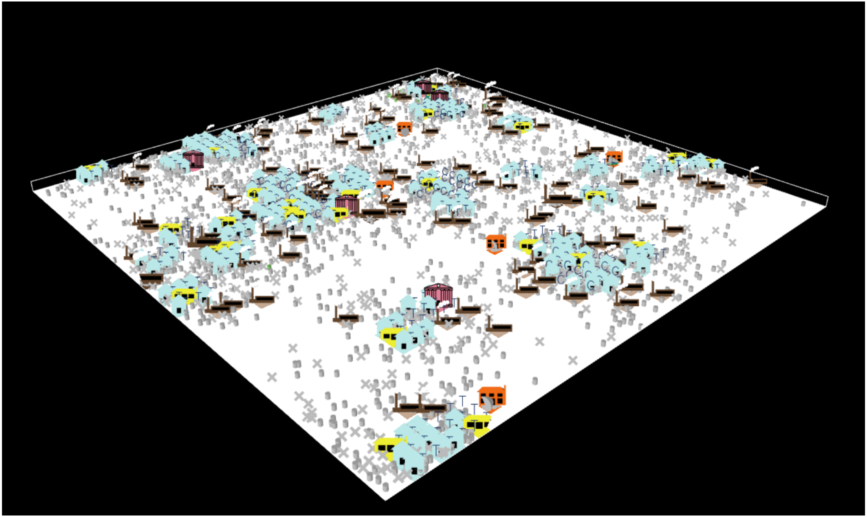

Figure 4: The world 3D

The agents

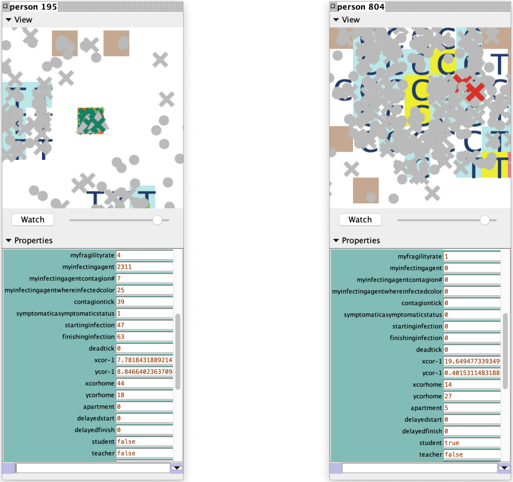

Figure 5: Probes to different agents

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.
  We represent 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)

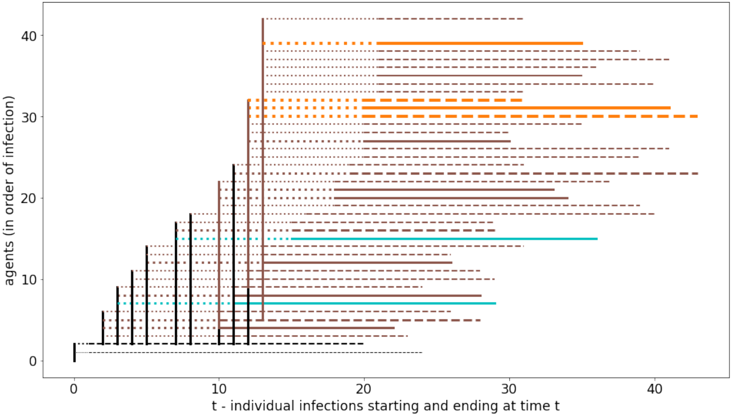

Figure 6: A case with containment measures, first 40 infections: workplaces (brown) and nursing homes (orange) strictly interweaving

Examples (2/2), whole epidemic

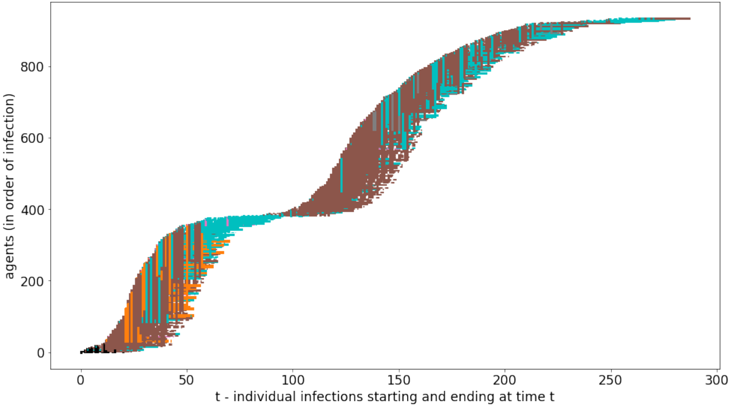

Figure 7: A Case with containment measures, the whole epidemics: workplaces (brown) and nursing homes (orange) and then houses (cyan), with a bridge connecting two waves

A contagion sequence suggesting policies: in Fig. 8 we can look both at the places where contagions occur and at the dynamics emerging with different levels of intervention.

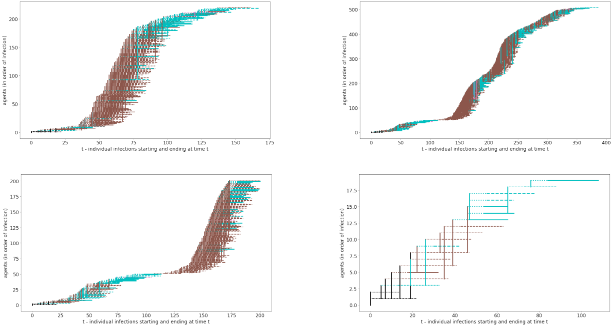

Figure 8: (*top left*) an epidemic with regular containment measures, showing a highly significant effect of workplaces (brown); (*top right*) the effects of stopping fragile workers at day 20, with a positive result, but home contagions (cyan) keep alive the pandemic, exploding again in workplaces (brown); (*bottom left*) the same analyzing the first 200 infections with evidence of the event around day 110 with the new phase due to a unique asymptomatic worker, and (*bottom right*) stopping fragile workers and any case of fragility at day 15, also isolating nursing homes

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

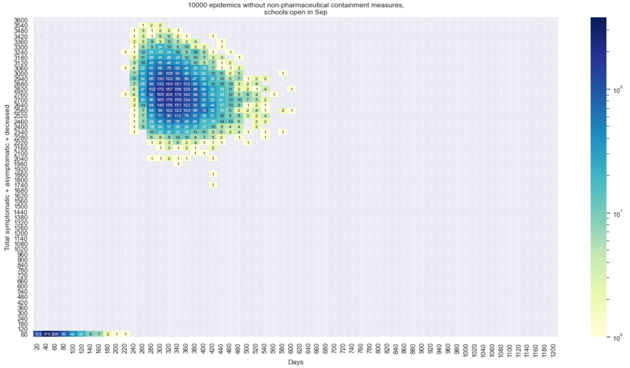

Figure 9: Without non-pharmaceutical containment measures

10,000 epidemic with basic control in Piedmont, first wave

	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

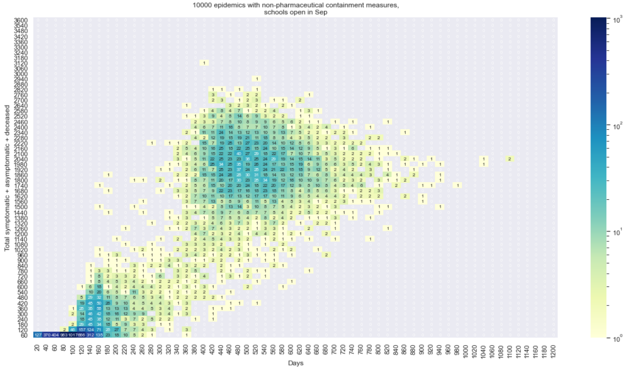

Figure 10: First wave with non-pharmaceutical containment measures

Key points

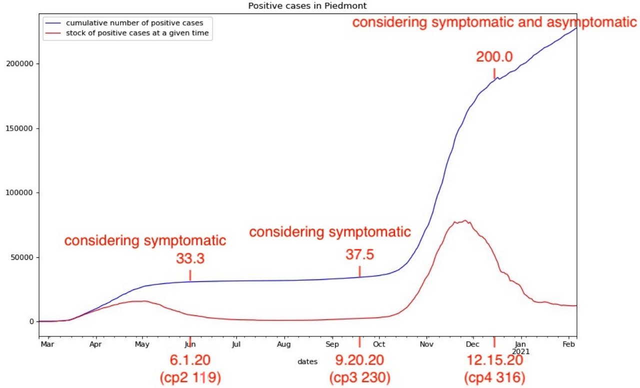

Figure 11: keyPoints

Non omogeneous 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 2021 data are mixed.
- In the above *git* repository, in October and November we had “Positive cases emerged from clinical activity”, unfortunately now reported as “No longer populated” (from the end of November, 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 (close to the end of March)

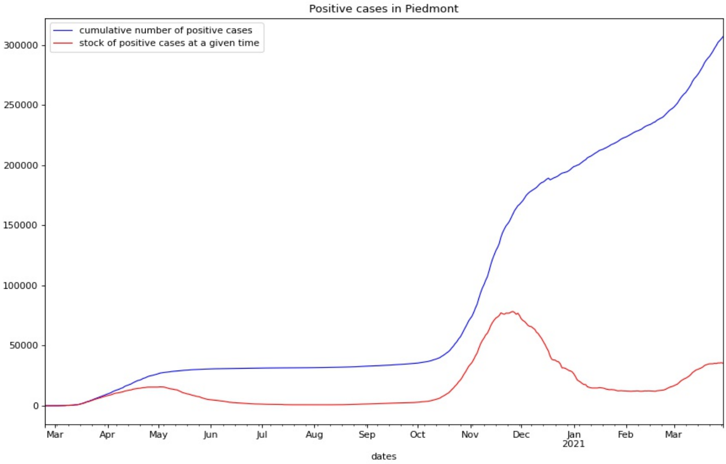

Figure 12: Data for Piedmont

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.

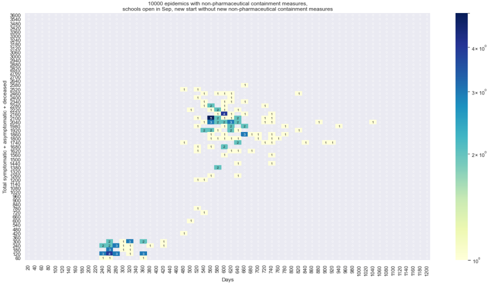

Figure 13: First wave with non-pharmaceutical containment measures, spontaneous second wave, without specific measures

(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	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.

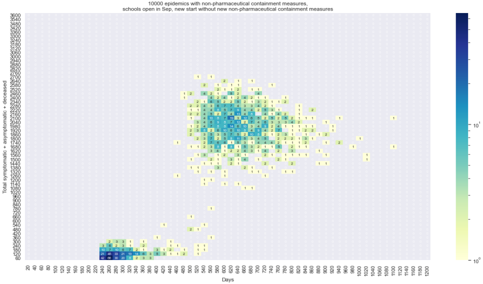

Figure 14: First wave with non-pharmaceutical containment measures, forcing the second wave, without specific measures

(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	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.

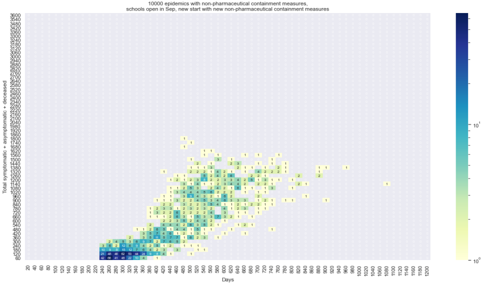

Figure 15: First wave with non-ph.containment measures, forcing the second wave, **with new specific non-ph. containment measures**

(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	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

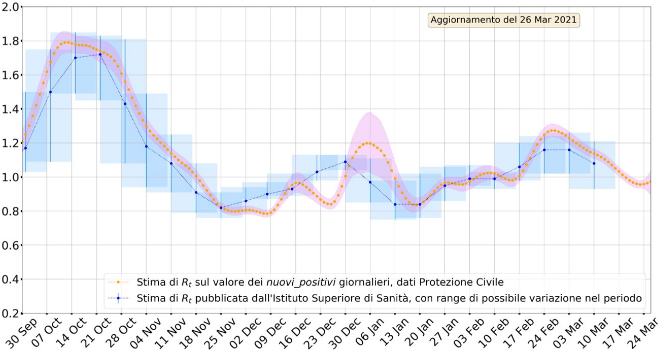

Figure 16: In blue the R_t values as reported by the Istituto Superiore di Sanità and in red the calculation published regularly at `https://mondoeconomico.eu` by Stefano Terna[1].

[1] Methodology: `https://github.com/tomorrowdata/COVID-19/blob/main/notebooks/Rt_on_italian_national_data.ipynb`

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.

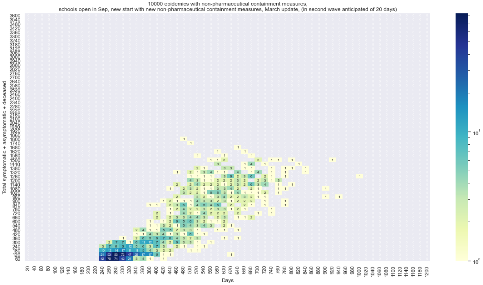

Figure 17: First wave with non-ph.cont. meas., forcing the second wave, **with new specific non-ph. cont. meas., 20 day anticipation**

(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	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

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

Fragile persons and future considerations

- A quite impressive analysis in Nature, Feb. 16, 2021, *The coronavirus is here to stay—here's what that means*

  `https://www.nature.com/articles/d41586-021-00396-2`

  A Nature survey shows many scientists expect the virus that causes COVID-19 to become endemic, but it could pose less danger over time.

- If Nature is right, a possible long-term 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).

  With social benefits, e.g., schooling, and economic benefits, if activities do not stop

- Besides, mainly for the fragile people, adopt prevention and vaccinations.

- A note: the same strategy would also have been surprisingly efficient now, for the second wave.

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

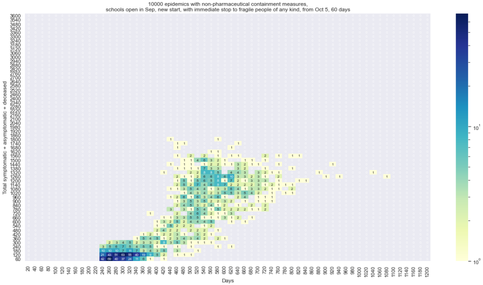

Figure 18: First wave with non-ph, cont, meas., forcing the sec. w.; **in sec. w., uniquely stop fragile people, including fragile workers**

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

[3] Schools are always working 100% in this case.

To recap (second wave)

Scenarios		Dec 15, 20 sympt.	Dec 15, 20 totalInf.	Dec 15, 20 to end sympt.	Dec 15, 20 to end totalInf.	Dec 15, 20 to end days
no containments in spontaneous second wave	count	140.0	140.0	140.0	140.0	140.0
	mean	**248.4**	**648.7**	701.1	1757.9	594.2
	std	167.4	424.3	246.4	599.7	118.9
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 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

Planning a vaccination campaign

- Exploring vaccination sequences, using *genetic algorithms*. A detailed note, frequently updated, is at `https://terna.to.it/simul/GAresultPresentation.pdf`.
- We compare the effect of choosing vaccination quotas via GAs with two predetermined strategies.
- 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*).

Vaccination quotas, *plain* strategy

Considering the *plain* option adopted in Table 2 and remembering that the time-sequence in daily actions is the winner, we will primarily vaccinate the left column groups to move gradually to other columns: (*g1*) extra fragile people, (*g2*) teachers, (*g3*) fragile workers, (*g4*) regular workers, (*g5*) fragile people, (*g6*) regular people, (*g7*) young people.

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							

Table 2: From the day of the first column, considering the quantity of the second column (000), the vaccination of each group follows the quota of the related columns

(000)	*g1*	*g2*	*g3*	*g4*	*g5*	*g6*	*g7*
Susc. at t = 0	133	84	240	1560	1179	254	900

Table 3: Susceptible persons at the beginning of the simulation

Vaccination quotas, *wise* strategy

Considering the *wise* option adopted in Table 4 and remembering that the time-sequence in daily actions is the winner, we will primarily vaccinate the left column groups to move gradually to other columns, but postponing group *g4* (regular workers), *g6* (regular people), and *g7* (young people).

From day	Q. of vaccines (000)	*g1*	*g2*	*g3*	*g4*	*g5*	*g6*	*g7*
373	5	0.1	0.1	0.1	0.0	0.1	0.0	0.0
433	10	0.1	0.1	0.1	0.0	0.1	0.0	0.0
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							

Table 4: From the day of the first column, considering the quantity of the second column (000), the vaccination of each group follows the quota of the related columns

(000)	*g1*	*g2*	*g3*	*g4*	*g5*	*g6*	*g7*
Susc. at t = 0	133	84	240	1560	1179	254	900

Table 5: Susceptible persons at the beginning of the simulation

Two cases

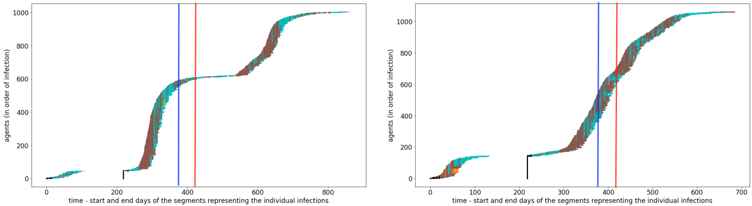

Figure 19: Case I Case II
Crucial dates: blue line for the starting point of the vaccination campaign and red line for the start of the effectiveness of the initial vaccinations

GAs quotas, an example in case I, with vaccinated people still spreading the infection

	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

Table 6: Case I: susceptible persons at the beginning of the simulation and when the vaccination campaign starts, day 373, Feb. 12th, 2021

Groups: (*g1*) extra fragile people, (*g2*) teachers, (*g3*) fragile workers, (*g4*) regular workers, (*g5*) fragile people, (*g6*) regular people, (*g7*) young people.

From day	Q. of vaccines (000)	*g1*	*g2*	*g3*	*g4*	*g5*	*g6*	*g7*
373	5	0.01	0	0	0.79	0.18	0.38	0.19
433	10	0.94	0.06	0.32	0.54	0.19	0.83	0.5
493	10	0.97	0.97	0.74	0.79	0.2	0.14	0.52
553	10	0.98	0.83	0.02	0.39	0.99	0.04	0.48
613	20	0.52	0.01	0.83	0.6	1	0.27	0.9
738	end							

Table 7: GAs best strategy in case I, with ***vaccinated people still spreading the infection***: from the day of the first column, considering the quantity of the second column, the vaccination of each group follows the quota of the related columns

GAs quotas, an example in case II, with vaccinated people still spreading the infection

	g1	g2	g3	g4	g5	g6	g7
Susc. at t = 0	116	108	244	1530	1216	250	886
Susc. when vacc. starts	92	105	170	1300	1104	245	878

Table 8: Case II: susceptible persons at the beginning of the simulation and when the vaccination campaign starts, day 373, Feb. 12th, 2021

Groups: (*g1*) extra fragile people, (*g2*) teachers, (*g3*) fragile workers, (*g4*) regular workers, (*g5*) fragile people, (*g6*) regular people, (*g7*) young people.

From day	Q. of vaccines (000)	g1	g2	g3	g4	g5	g6	g7
373	5	0.03	0	0.97	0.75	0.89	0.59	0.9
433	10	0.97	0.97	0.45	0.78	0.22	0.82	0.8
493	10	0.35	0.37	0.07	0.63	0.04	0.41	0.03
553	10	0.45	0	0.9	0.29	0.01	0.07	0.12
613	20	0.31	0.22	0.35	0.41	0.52	0.22	0.68
738	end							

Table 9: GAs best strategy in case II, with ***vaccinated people still spreading the infection***: from the day of the first column, considering the quantity of the second column, the vaccination of each group follows the quota of the related columns

Synopsis

Three hypotheses about contagion transmission from vaccinated people, if infected: 100%, never, 50%.

Case (1000)	At day 413	Final no vaccin.	Final plain vaccin. infect. 100%	Final wise vaccin. infect. 100%	Final GAs vaccin. infect. 100%	Final plain vaccin. infect. 0%	Final wise vaccin. infect. 0%	Final GAs vaccin. infect. 0%	Final plain vaccin. infect. 50%	Final wise vaccin. infect. 50%	Final GAs vaccin. infect. 50%
I	197	325	236	263	**200**	203	211	199	204	229	203
	-	128	39	66	**3**	6	14	2	7	32	6
II	233	375	355	344	**305**	340	334	**297**	356	344	**288**
	-	142	122	111	**72**	107	101	**64**	123	111	**55**

Table 10: Results of the campaigns in the two cases, only symptomatic people (second row in each case: minus day 413)

A new model: the map

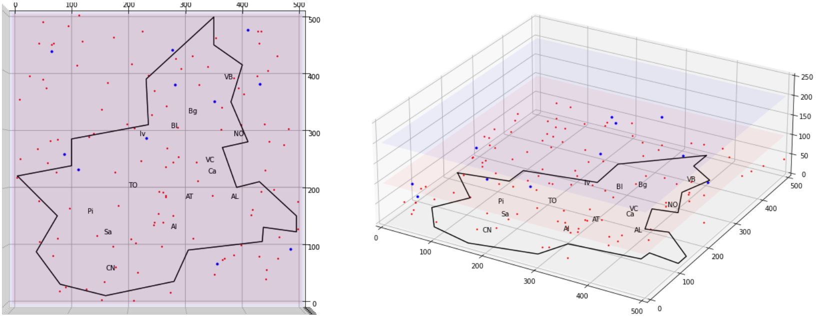

Figure 20: 3D Piedmont

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, . . .
- 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/`

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.

The new book of Mazzoli, M., Morini, M., and Terna, P., Rethinking Macroeconomics with Endogenous Market Structure, is deeply based on SLAPP.

This project is maintained by terna

Hosted on GitHub Pages — Theme by orderedlist

Figure 21: Swarm-Like Agent Protocol in Python

Some final considerations

- The importance of High Performance Computing.

- The S.I.s.a.R. model is a tool for comparative analyses, not for forecasting (the enormous standard deviation values are intrinsic to the problem).
- The model is highly parametric and more it will be.
- New crisis calling for immediate simulation could take a substantial advantage from the parametric structure of the model.

The slides are at `https://terna.to.it/simul/TernaCCA20210329.pdf`.
My homepage `https://terna.to.it` and my mail address `pietro.terna@unito.it`.