

How can ABM models become part of the policy-making process in times of emergencies - The S.I.s.a.R. Epidemic Model

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Outline

Introduction

NetLogo model

- A static view

- A live view

Contagions

- The proposed technique

- An introductory example

- A significant sequence

Batches

- Batches

- Two heat-maps

Policies

Current situation

Current data

A new model

Final remarks

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 the susceptible one, plus those of the space in which contact occurs.
- ▶ The model includes the structural data of Piedmont, an Italian region, but it can be readily calibrated for other areas. The model reproduces a realistic calendar (e.g., national or local government decisions), via its script interpreter.
- ▶ S.I.s.a.R. is at <https://terna.to.it/simul/SISaR.html> with information on model construction, the draft of a paper also reporting results, and an online executable version of the simulation program, built using NetLogo.
- ▶ A short paper at <https://rofasss.org/2020/10/20/sisar/>.

The scale and the items

- ▶ 1 : 1000.
- ▶ Contagions are related to the characteristics of infected persons, the fragility of susceptible ones, the peculiarity of the different places, distances, probabilities.
- ▶ Houses.
- ▶ Schools.
- ▶ Hospitals.
- ▶ Nursing homes,
- ▶ Factories.

The screenshot displays the NetLogo 'epidemic' model interface. At the top, there is a toolbar with buttons for 'clear', 'setup', 'go', and various sliders. Below the toolbar, there are several monitors displaying statistics: 'total-population', 'total-infected', 'total-dead', 'total-susceptible', 'total-exposed', 'total-recovered', 'total-deceased', 'total-quarantined', 'total-vaccinated', 'total-treated', 'total-hospitalized', 'total-isolated', 'total-quarantined-dead', 'total-vaccinated-dead', 'total-treated-dead', 'total-hospitalized-dead', 'total-isolated-dead', 'total-quarantined-dead', 'total-vaccinated-dead', 'total-treated-dead', 'total-hospitalized-dead', 'total-isolated-dead'. Below these monitors are two large plots: 'stocks in each tick' and 'cumulative values'. The 'stocks in each tick' plot shows the number of individuals in different states (susceptible, infected, etc.) over time. The 'cumulative values' plot shows the total number of individuals in each state over time. The interface also includes a command area on the right for entering text and a 'help' button. The bottom status bar shows the current time and the number of ticks.

Figure 1: The interface

The interface and the information sheet

A live look to the running model, also in a 3D view.

Contagion representation

- ▶ The model allows analyzing the sequences of contagions in simulated epidemics, while taking in account the places where they occur.
- ▶ We represent each infecting agent as a horizontal segment with a vertical connection to another agent receiving the infection. We represent the second agent via a further segment at an upper layer.
- ▶ With colors, line thickness, and styles, we display multiple data.
- ▶ 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.

An introductory example

An example

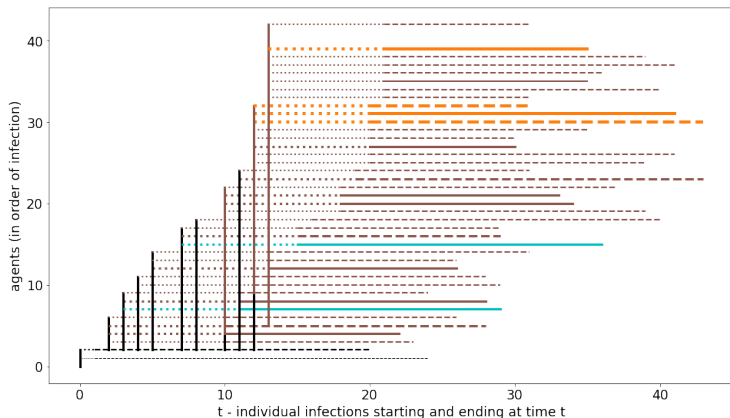


Figure 3: A case with containment measures, first 40 infections: workplaces (brown) and nursing homes (orange) strictly interweaving

Same example, more cases

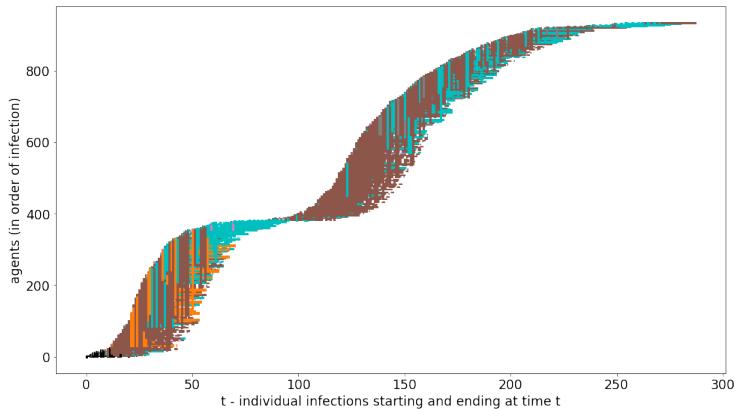


Figure 4: A Case with containment measures, the whole epidemics: workplaces (brown) and nursing homes (orange) and then houses (cyan), with a bridge connecting two waves

An introductory example

Other examples (i) on the left, an epidemic without containment measures; (ii) on the right, an epidemic with basic non-pharmaceutical containment measures

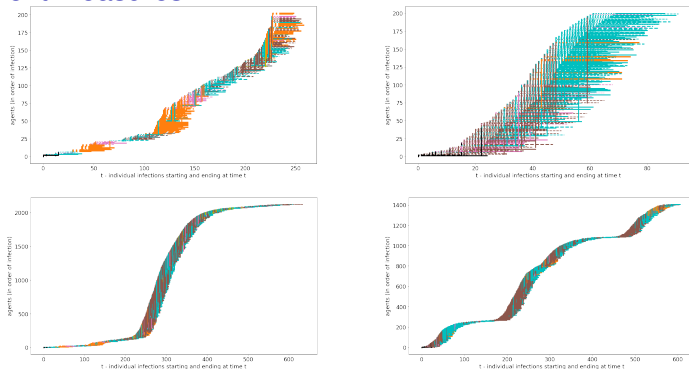


Figure 5: Two cases with initial and full periods

A significant sequence

A contagion sequence suggesting policies: in Fig. 6 we can look both at the places where contagions occur and at the dynamics emerging with different levels of intervention.

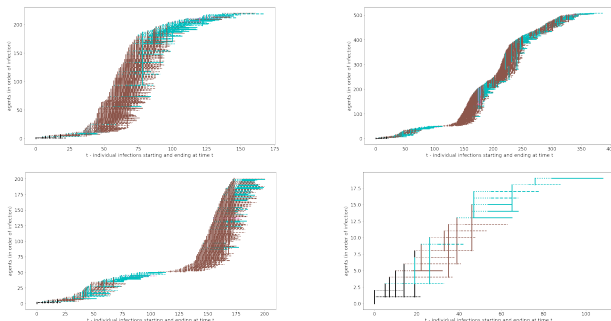


Figure 6: (*top left*) an epidemic with regular containment measures, showing a highly significant effect of workplaces (brown); (*top right*) the effects of stopping fragile workers at day 20, with a positive result, but home contagions (cyan) keep alive the pandemic, exploding again in workplaces (brown); (*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.

Batches

- ▶ We explore systematically the introduction of factual, counterfactual, and prospective interventions to control the spread of the contagions.
- ▶ Each simulation run—whose length coincides with the disappearance of symptomatic or asymptomatic contagion cases—is a datum in a wide scenario of variability in time and effects.
- ▶ Consequently, we need to represent compactly the results emerging from batches of repetitions, to compare each batch's basic assumption's consequences.
- ▶ We used blocs of one thousand repetitions. Besides summarizing the results with the usual statistical indicators, we adopted the technique of the heat-maps.

Two heat-maps

Two quite different heat-maps for the Piedmont region

In Fig. 7 we have two heat-maps reporting the duration of each simulated epidemic in the x axis and the number of the symptomatic, asymptomatic, and deceased agents in the y axis. 1,000 runs in both cases.

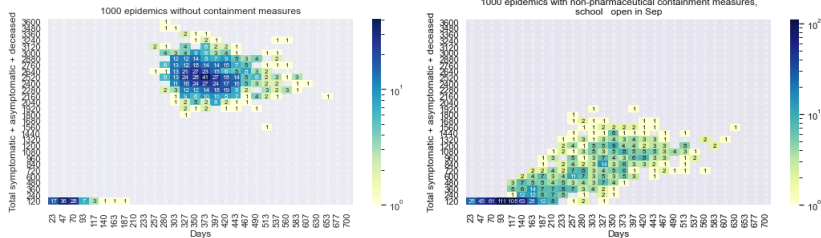


Figure 7: (on the left) Epidemics without containment measures; (on the right) Epidemics with basic non-pharmaceutical containment measures, schools open in September 2020

The actual Piedmont, where the curve of the contagions flattened with the end of May, with around 30 thousand subjects, is included in the cell in the first row, immediately to the right of the mode in Fig. 7, right side.

Different Intervention: policies and results

Scenarios	total sym.	total sym., asympt., deceased	days
1. no control	851.12 (288.52)	2253.48 (767.58)	340.10 (110.21)
2. basic controls, no school in Sep 2020	158.55 (174.10)	416.98 (462.94)	196.97 (131.18)
3. basic controls, <i>schools open</i> in Sep 2020	153.71 (168.55)	409.73 (454.12)	199.35 (129.00)
4. basic controls, stop fragile workers , no schools in Sep 2020	120.17 (149.10)	334.68 (413.90)	181.10 (125.46)
5. basic controls, stop f. workers & f. people & n. h. isol. , no sch. Sep.	105.63 (134.80)	302.62 (382.14)	174.39 (121.82)
6. b. controls, stop f. workers & f. people & nur. h. isol., & factories op. , no sch. Sep.	124.10 (132.42)	397.05 (399.64)	200.31 (121.46)
7. b. controls, stop f. workers & f. people & nur. h. isol., & factories op. , sch. open Sep.	116.55 (130.91)	374.68 (394.66)	195.28 (119.33)

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

Where we were

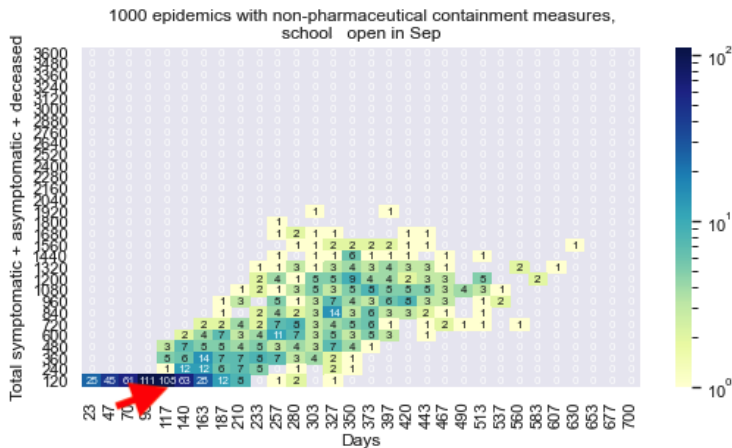


Figure 8: → the cell of epidemics concluded in May (less than 120k symptomatic+asymptomatic)

Where we are

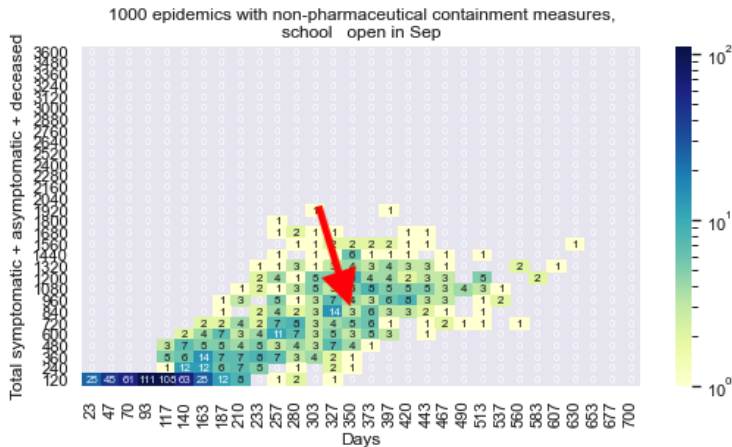


Figure 9: → where (and when) the second wave will end?

Raw data

Sources: <https://terna.to.it/datiProtezioneCivile.html> based on
<http://www.protezionecivile.gov.it> data, daily updated.

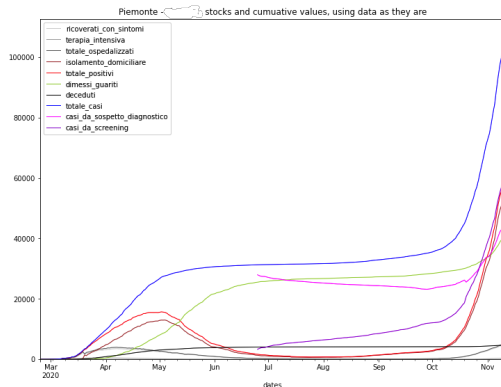


Figure 10: Raw data introduces the cases of screening analysis, making tests

Comparable current data

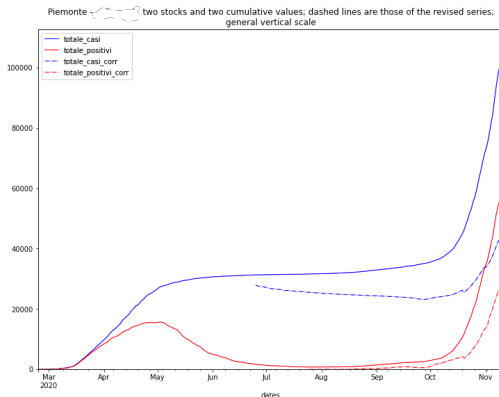


Figure 11: Dashed lines (cumulative values and daily stocks) are corrected deducing the number of screening cases (as cumulative values or 14 days differences)

A new model: the map

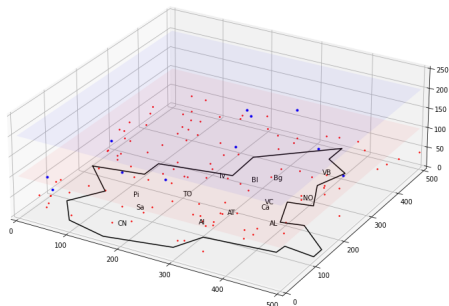
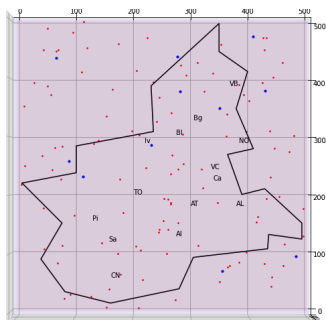


Figure 12: 3D Piedmont

A new model: the scale and the items

- ▶ 1 : 100.
- ▶ Contagion engine.
- ▶ Houses.
- ▶ Schools.
- ▶ Hospitals.
- ▶ Nursing homes,
- ▶ Factories.
- ▶ **Transportations.**
- ▶ **Aggregation places: happy hours, night life, sport stadiums, discotheques, ...**

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

This project is maintained by [terna](#)

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



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.

Figure 13: Swarm-Like Agent Protocol in Python

A few considerations

- ▶ The model is a tool for comparative analyses, not forecasting (the enormous standard deviation values are intrinsic to the problem).
- ▶ *How can your work be adapted to (or is relevant/useful for) another disease, crisis, context, ...*
- ▶ 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.