**USING Repast4Py AND GHOSTS IN MULTIRANK ABMs WITH FULL AGENTS’ INTERACTION**

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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 asset of the model is the development of a tool that allows analyzing the contagions' sequences in simulated epidemics and identifying the places where they occur.

**The characteristics of the S.I.s.a.R. model**

S.I.s.a.R. can be found 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. 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 a dedicated script interpreter.

Why another model? The starting point has been the need to model the pandemic problem in a multi-scale way. This was initiated a few months before the publication of new frontier articles, such as Bellomo *et al*. (2020), so when equation-based S.I.R. models, with their different versions, were predominating.

As any model, also this one is based on some assumptions: time will tell whether these were reasonable hypotheses. Modeling the Covid-19 pandemic requires a scenario and the actors. As in a theatre play, the author defines the roles of the actors and the environment. The characters are not real, they are pre-built by the author, and they act according to their peculiar constraints. If the play is successful, it will run for a long time, even centuries. If not, we will rapidly forget it. Shakespeare’s Hamlet is still playing after centuries, even if the characters and the plot are entirely imaginary. The same holds for our simulations: we are the authors, we arbitrarily define the characters, we force them to act again and again in different scenarios. However, in our model, the *micro-micro* assumptions are not arbitrary but based on scientific hypotheses at the molecular level, the *micro* agents’ behaviors are modeled in an explicit and realistic way. In both plays and simulations, we compress the time: a whole life to 2 or 3 hours on the stage. In a few seconds, we run the Covid-19 pandemic spread in a given regional area.

With our model, we move from a macro compartmental vision to a meso and microanalysis capability. Its main characteristics are:

* scalability: we take in account the interactions between virus and molecules inside the host, the interactions between individuals in more or less restricted contexts, the movement between different environments (home, school, workplace, open spaces, shops, in a second version, we will add transportations and long trips between regions/countries; discotheques; other social aggregation events, as football matches); the movements occur in different parts of the daily life, as in Ghorbani *et al.* (2020);

the scales are:

* *micro*, with the internal biochemical mechanism involved in reacting to the virus, as in Silvagno *et al.* (2020), from where we derive the critical importance assigned to an individual intrinsic susceptibility related to the age and previous morbidity episodes; the model incorporates the medical insights of one of its co-authors, former full professor of clinical biochemistry, signing also the quoted article; a comment on Lancet (Horton, 2020) consistently signals the syndemic character of the current event: «Two categories of disease are interacting within specific populations—infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and an array of non-communicable diseases (NCDs)»;
* *meso*, with the open and closed contexts where the agents behave, as reported above;
* *macro,* with the emergent effects of the actions of the agents; this final analysis is a premise to evaluate the costs and benefits of the different intervention policies;
* granularity: at any level, the interactions are partially random and therefore the final results always reflect the sum of the randomness at the different levels; changing the constraints at different levels and running multiple simulations should allow the identification of the most critical points, i.e., those on which the intervention should be focused.

**Contagion sequences as a source of suggestions for intervention policies**

All the previous considerations are not exhaustive. The critical point that makes helpful the production of a new model is creating a tool that allows analyzing the contagions' sequences in simulated epidemics and identifying 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.

As an example, look at Fig.4: we start with two agents coming from the outside, with black as color code (external place), the first one–regular, as reported by the thickness of the segment, starting at day 0 and finishing at day 22–is asymptomatic (dashed line) and infects five agents; the second one–robust, as reported by the thickness of the segment, starting at day 0 and finishing at day 15–is asymptomatic (dashed line) and infects no one; the first of the five infected agents received the infection at home (cyan color) and turns to be asymptomatic after a few days of incubation (dotted line), and so on. Solid lines identify symptomatic agents; brown color refers to workplaces, orange to nursing homes; yellow to schools; pink to hospitals; gray to open spaces. Thick or extra-thick lines refer to fragile or extra-fragile agents, respectively.

This technique 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. In Figs. 1-4, we can look both at the places where contagions occur and at the dynamics emerging with different levels of intervention. In Fig. 1 we find evidence of the role of the workplaces in diffusing the infection, with a relevant number of infected fragile workers. In Fig. 2, by isolating fragile workers at home, the epidemics seems to finish, but in Fig. 3, we see a thin event (a single case of contagion) that creates a bridge toward a second wave. Finally, in Fig. 4, we see that the epidemic is under control by isolating the workers and any kind of fragile agents. (Please enlarge the on-screen images to see more details).

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| Figure 1 - An epidemic with regular containment measures, showing a highly significant effect of workplaces (brown) | Figure 2 - 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) |
| Figure 3 – Same, analyzing the first 200 infections with evidence of the event around day 110 with the new phase due to a unique asymptomatic worker | Figure 4 - Stopping fragile workers plus any case of fragility at day 15, also isolating nursing homes |

**Batches of simulation runs**

The sequence in the steps described by the four figures is only a snapshot, a suggestion. We need to 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 the consequences of each batch's basic assumptions.

For this purpose, we used blocks of one thousand repetitions. Besides summarizing the results with the usual statistical indicators, we adopted the technique of the heat-maps. In this perspective, with Steinmann *et al.* (2020), we developed a tool for comparative analyses, not for forecasting. This consideration is consistent with the enormous standard deviation values that are intrinsic to the problem.

Figs. 5-6 provide 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.

The actual data for 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. 6. In the Fall, a second wave seems possible, jumping into one of the events of the range of events on the right side of the same figure.

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| Figure 5 - Epidemics without containment measures | Figure 6 - Epidemics with basic non-pharmaceutical containment measures, no school in September 2020 |

In Table 1 we have a set of statistical indicators related to 1,000 runs of the simulation with the different initial conditions. Cases 1 and 2 are those of Fig. 5 and 6. Then we introduce Case 4, excluding from the workplace workers with health fragilities, so highly susceptible to contagion, with smart work when possible or sick pay conditions. The gain in the reduction of affected people and duration is relevant and increases – in Case 5 – if we leave at home all kinds of fragile people.

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| Scenarios | Total symptomatic | Total symptomatic, asymptomatic, 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) |
| 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 fragile workers & fragile people, nursing-homes isolation, no schools in Sep 2020 | 105.63  (134.80) | 302.62  (382.14) | 174.39 (12.82) |
| 7. basic controls, stop f. workers & fragile people, nursing-homes isolation, open factories, schools in Sep 2020 | 116.55  (130.91) | 374.68  (394.66) | 195.28 (119.33) |

Table 1 – Statistical indicators, limited to the mean and to the standard deviation, reported in parentheses, for a set of experiments; the row numbers are consistent with the paper at <https://terna.to.it/simul/SIsaR.html> where we report a larger number of simulation experiments

In Case 7, we show that keeping the conditions of Case 5, while opening schools and factories (work places in general), increases in a limited way the adverse events.

**A second version**

A second version of the model is under development, using <https://terna.github.io/SLAPP/>, a Python shell for ABM prepared by one of the authors of this note, referring to the pioneering proposal <http://www.swarm.org> of the Santa Fe Institute.

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