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An Agent-Based Covid-19 Simulator:
Extending Covasim to the Polish Context

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Abstract

Governments all over the world make their best to fight with Covid-19 pandemic as effectively as possible. Therefore, we observed a growing need of trustworthy data-intensive systems supporting administration in validating their policy decisions. ProMES, the Covasim-based multiagent pandemic simulator, may serve as such a system, adjusted to the specificity of living, working and social conditions in Poland.

The main role of ProMES is to evaluate and compare strategies for reducing Covid-19 transmissions. The strategies include time- and region-dependent combinations of nonpharmaceutical coronavirus-related individual and state interventions, tests and vaccinations. Ultimately, ProMES is meant to serve as a part of data/knowledge intensive decision support system, enhancing administrative reactivity as well as pro-activity in preventing the spread of the coronavirus.

This paper reports a work in progress.

Keywords: Covid-19; multi-agent simulation; synthetic populations; epidemiology software; non-pharmaceutical interventions

1. Difficult Decisions During Pandemic

Governments all over the world try to mobilize their citizens, with the help of available resources, to fight the Covid-19 pandemic. ProMES - an agent-based pandemic simulator, based on Covasim [10], that we present in this paper - serves as a part of an advanced decision support system. The agent-based and multiagent paradigm is applicable in both knowledge- and data-intensive complex decision making systems that, from their very nature, exploit intelligence, communication, coordination, negotiation as well as mass parallel computing to realize their complex goals [6, 15]. In particular, multiagent simulations are of great importance in modeling complex behaviors and social interactions

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between people during pandemic. These simulations allow us to explicitly model individual decision processes of agents on a micro level, while the effects of the chosen actions, interactions with others and/or with the environment are visible on the macro level. Such a bottom-up approach that takes into account a whole variety of human individual and social attitudes permits to model heterogeneous groups and societies acting in various circumstances.

During the pandemic, from among a wide range of non-pharmaceutical interventions (NPI's) that can be deployed, the following ones help prevent the spread of Covid-19 and other coronaviruses and influenza. They address a basic question: what can I do to protect myself and others from Covid-19? Natural answers are pretty clear nowadays.

- Wear a face mask.
- Maintain at least six feet of distance between yourself and others.
- Avoid large gatherings.
- Socialize outdoors.
- Avoid close contact with people who are sick.
- Minimize touching your eyes, nose, and mouth.
- Stay home when you are sick.
- Cover your cough or sneeze with a tissue, then throw the tissue in the trash.
- Clean frequently touched objects and surfaces regularly.
- Wash your hands often with soap and water.

Next to individual interventions, state coronavirus-related ones include

- Quotas to places of worship, post offices, shops, bazaars.
- Quotas to public transportation.
- Domestic travel restrictions.
- Quarantine requirements.
- State reopen plans.

An analysis offered in ProMES intensively uses observational and retrospective data for understanding and predicting different types of behavior visible in complex systems with the ultimate goal of predicting various aspects of the development of pandemic. This goal is to be realized in the form of what-if scenarios for which the user specifies an initial situation, specific geographical location and a considered time horizon. Actually, a nuanced spatio-temporal scaling is among basic assumptions behind ProMES. As a result, a possibly detailed characteristics of the simulation is provided together a specific data on different aspects of the situation in question. Potential scenarios may deal with prediction of the pandemic development in a presence of diversity of restrictions, various testing and vaccination strategies, acting separately or together [2].

Ultimately, ProMES is supposed to enhance both administrative reactivity and pro-activity in preventing the spread of the coronavirus by helping to address the following, complex questions formulated in a form of what-if scenarios.

- What is the pandemic dynamics?
- When to resume various activities under certain sanitary conditions?
- When and how to apply lock-down in different phases of epidemics?
- What are the expected effects of lock-down depending on (the range of) dissemination of coronavirus?
- What are the effects of particular non-pharmaceutical interventions?
- What is a joint effect of large-scale NPIs?
- What are the effects of, potentially nuanced, strategy of testing?

ProMES was developed under the umbrella research project ProME that groups several initiatives for predictive modeling of Covid-19 epidemic, understanding the Covid-19 situation in Poland and optimal management of medical procedures during and after pandemic.
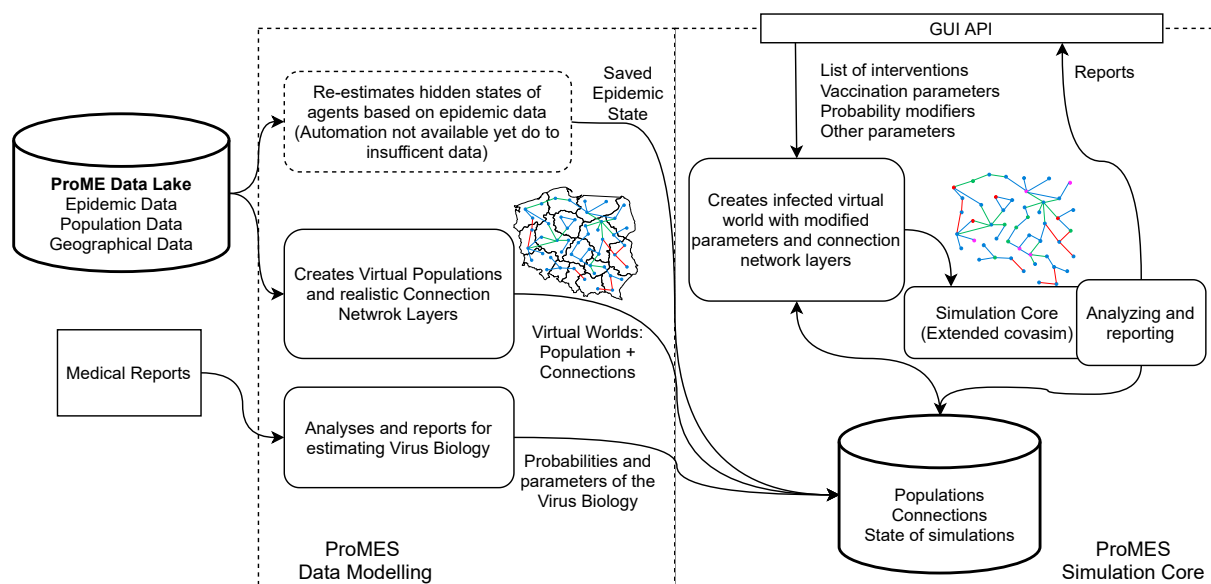
Fig. 1: The system architecture of ProMES agent-based pandemic simulator.

During initial phases of the project a comparative study of existing solutions was made [13]. We reviewed more than 50 projects worldwide as a potential inspiration or software base for developing ProMES. Among others, we reviewed the ASSOCC multi-agent simulator for Covid-19 from Europe [5], Covasim multi-agent simulator for Covid-19 from US [10], FRED multi-agent framework for reconstructing epidemic dynamics [8], pDYN influenza simulator with socstr virtual population generator from Poland [12] and STRIDE simulator adopted to Covid-19 [14]. After an in-depth analysis, we have chosen Covasim [10] as our reference solution. This simulator is highly modular, easy to extend, well documented and, most importantly, it contains a valuable model of virus biology adopted to SARS-Cov2. By using Covasim in ProMES simulation core we succeeded to speed up the project development while meeting the complex requirements and significantly extending the underlying simulator.

This paper, reporting a work in progress, is structured as follows. In Section 2 the system architecture is described. Section 3 guides the reader through selected elements of the data preparation process. Virus biology and its adjustments for the Polish specific case are described in Section 4. Then, in Section 5, we present experimental results. Finally conclusions and future work are discussed in Section 6.

2. The Architecture of ProMES

The design of ProMES system architecture was guided by the following design assumptions.

- The system should provide Graphical User Interface (a thin/web-based client and rich client for power users) and communication with GUI is organized by API. Moreover, GUI parameters should be widely understandable and close to the administrative reality of NPI's.
- ProMES needs to provide reporting along with the Poland administrative division over the levels of country, province, district and commune.
- The main database storage for external and internal data is a PostgreSQL database.

Basically, ProMES consists of two parts: (i) the simulation core providing agent-based pandemic simulation components, and (ii) data modeling components, creating virtual worlds enabling one to run simulations (see Figure 1).

The simulation core takes user supplied specific scenario parameters from API and simulates what-if scenarios accordingly. It involves loading virtual population along with related connection layers from the database, constructing an initial simulation state and modifying both the virtual world and the virus biology parameters, respectively.
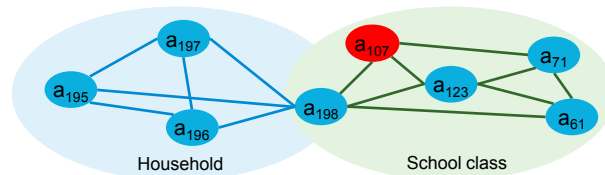
Fig. 2: The simulation requires detailed data about the population and social connection networks. All agents ($a_1 \ldots a_n$) have their internal properties like age, gender, social type and state of infection/disease. The connections between agents need to be explicitly given in a form of graph edges and grouped into layers corresponding to various contact types.

The simulation itself is executed by the Covasim simulator extended and adjusted to meet our requirements. In particular, the properties of agents are extended to include the commune of a domicile. A dedicated analyzer was implemented for reporting each simulation step on around 30 detailed metrics reported at the commune level, including the number of cases of each disease state as new, actual and cumulative numbers, both absolute as well as relative to the population size. Typical applications of Covasim simulator start from some initially specified infected agents according to a numerical parameter. Although such initialization is still possible at ProMES, it would not reflect realistic simulation scenarios. For a realistic starting point during epidemic agents should be distributed across all stages of the disease, including non-observable hidden parameters like a distribution of asymptomatic cases. Therefore, in ProMES the simulation initialization was implemented from scratch to enable the use of realistic predefined virtual populations. In addition, we implemented a functionality of saving a detailed state of simulation in the database and retrieving it as a starting point for the next simulation scenario.

After initialization the simulation runs in a day-steps. After each day the epidemic state is analyzed to provide detailed reporting at the commune level. These reports are stored in the database and are passed through the API to visualize them in GUI. All the core components have been wrapped in a module that provides API functionality for the GUI. Thanks to the object-oriented implementation of the extensions, ProMES runs successfully using Covasim 1.7.x and 2.0.x.

In order to test various epidemic scenarios one can choose specific parameters grouped as follows:

- Population and simulation options
  - Selection of one of the available populations from database
  - Selection of one of the available stored simulation states for that population
  - Simulation initialization parameters (if no simulation is selected as initial state)
  - Simulation length in days
- General nonpharmaceutical interventions
  - Quotas to stores, public transportation, places of worship
  - Distancing and hybrid education at schools, labor at workplaces
  - Domestic travel restrictions
  - Restrictions of leaving homes
  - Face mask obligation at stores, public transportation, closed spacesm open air
  - Information campaigns on sanitary means
- Vaccinations
  - Percentage of vaccinated population split down in age groups and vaccine efficacy
- Virus biology parameters
  - Scaling factor for virus transmission probability
  - Scaling factors for course of disease probabilities

All NPI's have also a corresponding numerical parameter representing the intensification of specific intervention (or effectiveness of policy enforcement). Importantly, the simulation core depends on data quality to produce realistic scenarios. The Figure 2 illustrates this need, namely the input data for the multi-agent simulation consist of precise population data and connections between agents on the detailed individual level. The data modeling part of ProMES ensures such data (see Fig. 1) in three streams: (i) creating the actual epidemic state, (ii) creating virtual populations,
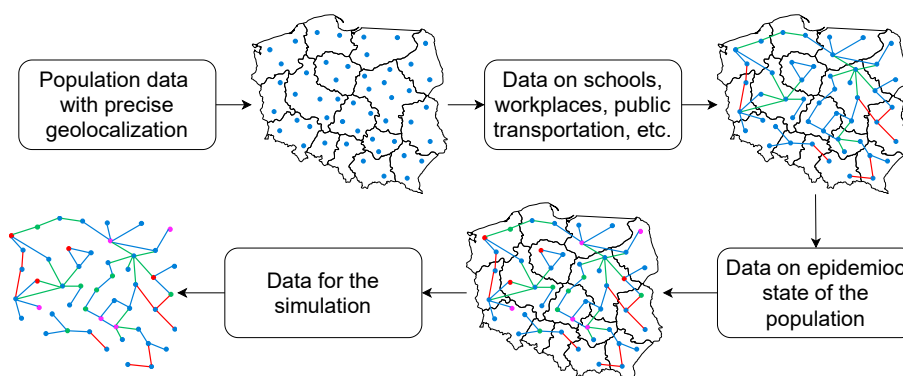
Fig. 3: Schematic diagram of generating data for simulation. From precise geographical information on population, data on connections in various social networks, data on epidemic state of population we generate abstract multi-layer network of agents that is used in the simulation.

and (iii) estimating virus biology parameters. Currently the initial simulation state is semi-automatically prepared and stored in the database. However, we plan to develop fully automated processes of daily/weekly system's data lake updates together with the corresponding updates of the initial simulation state to reflect the most recent epidemic course.

Creating realistic virtual populations together with their connection network layers requires some pre-processing as described in Section 3. The simulation rules regarding virus biology and related medical parameters were estimated based on the scientific reports focused on Poland epidemic specificity, as described in Section 4.

3. Data-Driven Cross-Country Modeling

Multi-agent simulation is executed on a population of agents meeting one another during different types of social activities and/or contacts represented by different layers of connection networks (see Fig.2). Figure 3 illustrates how the relevant data is structured. Actually, we apply real data to reconstruct the realistic population of agents on individual level, while encoding information about the agents, their location and social type in the connection network. As no explicit geolocalization is involved, a proper level of anonymity is ensured.

3.1. Virtual Population in ProMES

In order to run the simulations, we need data about the Polish population and relevant social relations as realistic as possible. Administratively, Poland is divided into 16 provinces, 380 districts and 2477 communes. The size of communes varies a lot, but in average they have around 15k inhabitants and area of 120 square kilometers. For the sake of simulation, we've received a great amount of data from national registries and Central Office of Statistics. However, these data sets turned out to be differently aggregated, therefore we had to reconstruct them in a randomized manner, using a realistic probability distribution. All in all, the corresponding datasets ware reconstructed from three sources:

- a detailed data of all buildings in Mazovian province including their precise geolocalization and split in apartments (around 1M buildings with 2.2M apartments),
- an aggregated data on age and gender at the level of commune, and
- an aggregated data on size of household at the level of district.

We've got the number of people at a particular age (precisely up to 20 and in groups of 5 years above) and gender in each commune what permitted us to construct a list of commune residents what enabled us to create virtual households. The number of households of with 1 and 2 inhabitants was given explicitly per each district, while the bigger ones were grouped in 3+ category. We used average household size along with the number of 1,2,3+ households to fit exponential
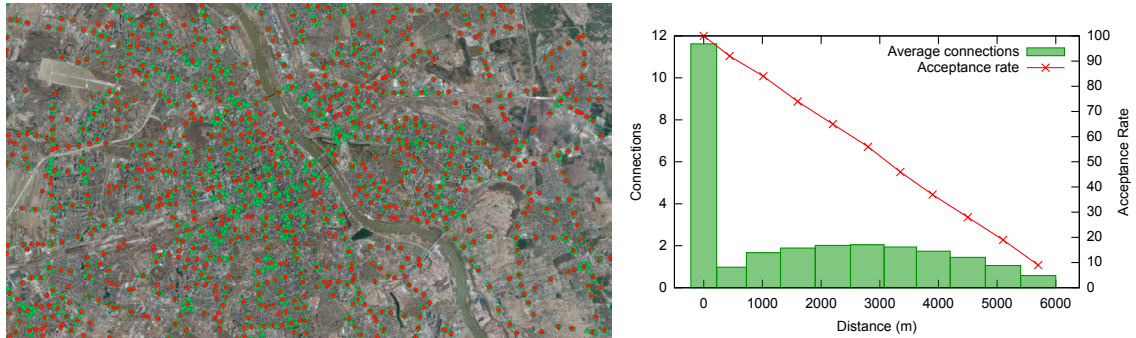
Fig. 4: Reconstructing the connection network in the public transportation. On the left clustering of public transportation stops in the center of Warsaw. Green points are all public transportation stops as from topographical information. Red points are clustered stops with radius of around 150 meters. On the right, the outcome of the connections drawing between the agents measured by distance from the travel initial node.

estimation of the households of size $3, 4, 5, 6, \ldots$. Agents have been assigned to the households accordingly, which have been randomly settled in apartments.

3.2. Contact Network Layers

The SARS-Cov2 transmission holds during contacts between infectious and susceptible persons. Moreover, different contacts cause different risk of transmission. To properly simulate these transmissions, it is necessary to explicitly model contacts between the agents. The possibilities of contacts and their types are recognized thanks to dedicated contact networks, organized in layers (see Fig.2), representing numerous contacts: in the household, during shopping, in public transportation, at workplace, etc. For the sake of realistic simulation we created the most important parts of this network: household and close neighborhood, public transportation, schools kindergartens, workplaces, shops and places of religious worship.

3.2.1. Households and Neighborhood

The biggest risk of virus transmission is related to the household contacts. In ProMES they were directly derived from the information about the household. Additionally, the local neighborhood represent possibility of virus transmission in the case of shared communication paths and facilities. Currently, the connection network layer of the local neighborhood consists of residents of the same building, while in the future we intend to extend this aspect.

3.2.2. Public Transportation

For all kinds of public transportation (buses, trams, subways, trains) we used a detailed topographical data of stops. However, this information turned our to be more fragmented than expected (c.f. Fig.4). Therefore, to reconstruct the paths of travel we clustered the stops into communication nodes. Experiments showed that optimal clustering radius is around 150 meters to group stops from one communication node. The sample of the clustering outcome is shown in the Fig.4.

From the general statistical data it follows that 26.1% of population uses public transportation regularly. Accordingly, the same fraction of agents are randomly chosen as public transportation users. For each of the agents, the nearest communication node has been identified and we have randomized paths of potential trips in a circle of at most 6km from the starting point. During traveling, agents can meet others with probability decreasing with distance (see Figure 4). On average, during their trips the agents were contacting 27.0 other agents (in the range between 7 and 127). Around 11.6 of connections were made at the starting point while around 15.4 contacts took place later.

3.3. School, Workplace, Shop, Church

Similarly we generated contact network layers for schools and kindergartens, workplaces, shopping centers and individual shops, churches and other religious worship places. Typically, we used detailed topographical information

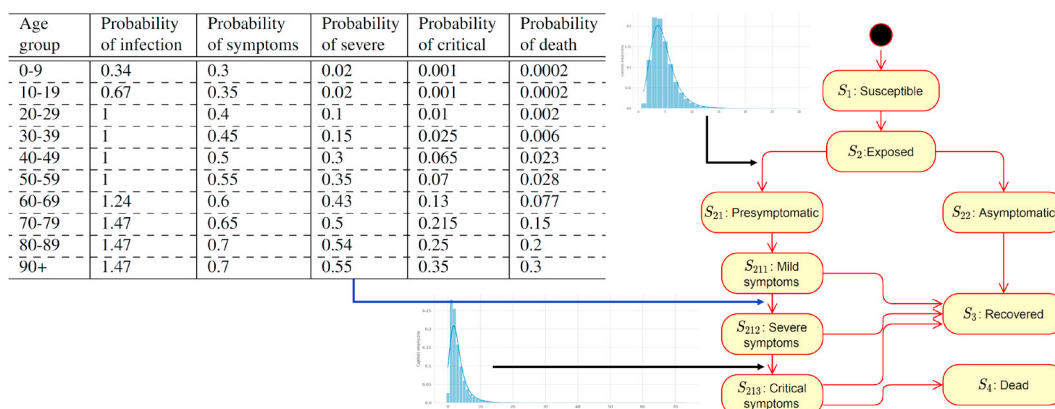| Age group	Probability of infection	Probability of symptoms	Probability of severe	Probability of critical	Probability of death
0-9	0.34	0.3	0.02	0.001	0.0002
10-19	0.67	0.35	0.02	0.001	0.0002
20-29	1	0.4	0.1	0.01	0.002
30-39	1	0.45	0.15	0.025	0.006
40-49	1	0.5	0.3	0.065	0.023
50-59	1	0.55	0.35	0.07	0.028
60-69	1.24	0.6	0.43	0.13	0.077
70-79	1.47	0.65	0.5	0.215	0.15
80-89	1.47	0.7	0.54	0.25	0.2
90+	1.47	0.7	0.55	0.35	0.3

Fig. 5: A state machine of agent epidemic state is based on SEIR epidemic modeling adopted to SARS-Cov2 case with parameters fit to the specificity of the epidemic in Poland. Probability of reaching a state is controlled by a probability table shown on the left. Each transition between states can take different amount of time and this is modeled by individual duration distributions. Two of them, are for example, visualized in this figure with a blue histograms.

about those objects, so an initial clustering, similar to that for public transportation, was necessary. Moreover we had to estimate the size of the object (e.g. the size of workplace) based on its type and features in topographical register. In the case of schools and kindergartens we collected a precise data split into classes with number of children, their age and gender.

Based on geolocalized objects and their estimated sizes we started to generate contacts induced by those places. For schools and churches, a simplifying assumption was made that the agents meet at the closest location. As for shopping, we assumed that an agent visits stores in a range of 12km and on average they meet 28.88 agents where 11.92 connections take place at the nearest store, while the remaining 16.96 connections at more distant ones. For the workplaces we assumed that the agents travel to work at most 20km, while the distance is less important for traveling agents employed at bigger workplaces. In average an agent meets 32.7 agents at work in range from 2 to 1860. All connection network layers were drawn accordingly and are stored in PostgreSQL database.

4. Virus Biology

Multi-agent simulation of the Covid-19 epidemic is grounded in well established SEIR model in epidemiology [1]. Each autonomous agent has allocated its epidemic state as shown in Figure 5. An agent starts from a state of being susceptible (S_1) to virus transmission. After successful transmission it becomes exposed (S_2) and may develop symptoms of different severity. Severe symptoms (S_{212}) correspond to a patient state that requires hospitalization with oxygen therapy, while critical symptoms (S_{213}) correspond to a patient state that requires ICU with mechanical ventilation. Finally, the agent can become recovered (S_3) from the Covid-19 or is dead (S_4). There is no path in the model to return from recovered to susceptible state ($S_3 \rightsquigarrow S_1$) because humoral and cellular responses to the SARS-Cov2 last many times longer (if not permanent) then planned simulation time horizon.

Transitions between states are conditional and based on dedicated probability distributions. For example the transition $S_{211} \rightsquigarrow S_{212}$ is conditional and depends on the probability of developing severe symptoms (see Fig.5 where the corresponding column and transition are marked with a blue arrow). The duration of a transition may take different number of days for different agents, so it is also modeled by a probability distribution (see the duration distributions corresponding to e.g. $S_2 \rightsquigarrow S_{21}$ transition in Fig.5). Every transition has its own probability of transition (if there are more than 2 possible paths) and a probability of the duration of that transition measured in days (for all transitions).

Within the umbrella project ProME, there is also a stream of in-depth the medical analyses [9, 11]. Importantly, we have verified with medical experts that the Covasim model of virus biology fits the epidemic situation in Poland. In particular, it turned out that probability distributions of transition duration presented in [10] are applicable to the Polish situation. However, the probabilities of developing the disease symptoms needed to be updated.

The detailed report based on Chief Sanitary Inspectorate data revealed the mortality rates for all age groups in Poland [9]. Moreover, based on SARSTer research in Poland [7] we received recent data for second and third wave of Covid-19. This study also shows the conditional probability of mortality depending on the disease state. In particular, adults that have severe symptoms have mortality rate in range between 8.3% and 17.6%, while for adults with critical symptoms the mortality rate is 66.7%. As usual, the more difficult part of the analysis was to estimate the asymptomatic rates. It is not so easy to collect reliable data according to the correct definition of asymptomatic cases, understood as cases with no symptoms in the course of the whole disease, and not only during first 1-2 weeks where most of the tests and examinations are performed. Actually, the paper [3] that aggregates conclusions of many medical research studies states that a proper estimation is nearly impossible, but suggests that the asymptomatic course of Covid-19 is in the range between 20% and 31% of infected patients while relative transmission of asymptomatic cases is 35% of the symptomatic ones. In contrast, the authors of [4] provide estimations that asymptomatic cases reach 79% for age groups 10-19 and drops to 31% for 70+. Moreover, the relative transmission of asymptomatic cases was estimated to 75%.

Based on the collected data and findings, we decided to build from the scratch the probability table of the course of SARS-Cov2 (see Fig.5). This table contains the probabilities of symptoms and mortality consistent with the epidemic data observed in Poland. Regarding the duration of the state transition, we confirmed that probability distributions estimated in Covasim are similar enough to the course of disease observed in Poland, so we can use them with no changes. Additionally, unlike Covasim, we set the virus transmission parameter for asymptomatic cases to 75% compared to symptomatic cases.

5. Experimental Results

The experiments were held at the data center of CDS&T of Cardinal Stefan Wyszyński University on a computing cluster CATO composed out of IBM AC922 nodes. Each node has 1TB of RAM, two Power9 CPU with 16 cores and 64 threads and two NVidia Tesla V100 GPU.

First, we tested if the simulation of the whole Poland is feasible. The execution of ProMES on random data of 38 millions of Polish citizens with different number of connection network layers required around 140 minutes for one layer and five more minutes per each additional layer. The RAM memory consumption was around 16.5GB to run the simulator with population alone and then additional 20GB per each connection network layer. It is clearly visible that the execution time depends mostly on the population size (what implies the number of infectious agents), while memory consumption is dominated by the connection layer data.

The execution of ProMES on realistic data for Mazovian province (with 5.4 millions of agents and 6 connection network layers) takes on average 24 minutes of execution time and run on single connection layer gives execution time in range between 17 and 22 minutes. The memory consumption was in total 32GB of RAM for all connection network layers, but we estimate that the simulator and the population itself consumes around 2.5GB of RAM, while connection network layers consume between 1GB and 9GB of RAM each.

From the execution time perspective, the real-world data scales similarly to random data and it is quite predictable based on a population size and a number of days. However, the memory consumption on realistic data is slightly higher than for the random data and depends on the connection network layer specificity. The existing infrastructure with 1TB of RAM per each node should allow us to run simulations on realistic data for the countries of the size up to 150 millions of population.

Further experiments were concentrated on calibrating many transmission parameters that reflect a realistic epidemic behavior, like the reference β for the simulation, β for each layer of contact network and the intensity of transmission reduction resulting from sanitary interventions, etc. Actually, we focused mostly on the mortality data, because the positive Covid-19 diagnoses are strongly dependent on testing strategy which happens to be a subject of frequent changes in Poland. Daily Covid-19 related mortality was fairly stable between November 2020 and April 2021, with an average of 340 deaths per day ranging from 200 to 600 (7-days moving average). For Mazovian province it corresponds to about 50 deaths daily. We tested many approaches to be as close to real mortality as possible, but regardless of the detailed parameters and initial scenario one interesting observation was common for the perceived epidemic dynamics. Figure 6 shows the example of two different 120-day simulation runs with different initial parameters. They both meet a criterion to not exceed mortality by 500 deaths daily and don't fall below 30 deaths daily once this level is
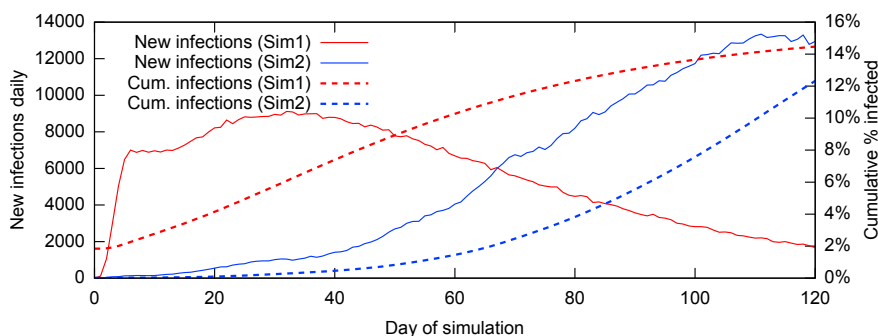
Fig. 6: Example of two different simulation runs with different initial parameters. Regardless of the exact parameters, for all simulation that maintain daily mortality rate at realistic level we observed a slowdown of epidemic after reaching prevalence at level of 10% or less.

reached. In every scenario that tried to match the realistic daily mortality we observed a slowdown of epidemic at the prevalence level around 10% or less. It is a very interesting, because Polish medical surveys done in showed that the prevalence as 18.7% as for end of November 2020. Moreover, the proportion of vaccinated people as for the end of April 2021 exceeds 7% of population fully vaccinated and 20% of population vaccinated with first dose. We consider several hypotheses on how we can uncover the mechanism behind this phenomenon starting from explicit modeling of different virus variants (i.e. explicit model of spreading B.1.1.7 variant in late 2020) ending with better modeling of disregarding sanitary means (i.e. by re-implementation connection network modeling in the simulation).

6. Conclusions

A significant success factor of this project was a conclusive cooperation with the Medical Centre of Postgraduate Education in Warsaw [9, 11]. We gained an in depth insight into the SARS-Cov2 virus biology, its transmission in various social groups, as well as to the epidemic situation in Poland, including estimation for Covid-19 disease stages (see Fig.5). Even though we observed that a higher risk of Covid-19 severity correlates with increasing age, comparing to other countries, the risk trajectory for Poland is flattened.

In ProMES we succeeded to run simulations on realistic data sizes, even though many multi-agent simulators tend to scale down their simulations. However, we faced some difficulties with obtaining fine-grained data. According to the initial assessment, we counted on detailed data regarding the population of Poland, like including place of living, mobility and employment data, etc., at an appropriate anonymization level. Unfortunately, some of the obtained datasets contain partially aggregated data. Therefore, the reconstruction at the individual level was needed and has been implemented by sampling and generating data according to realistic marginal frequencies and probability distributions. This process has been described in Section 3.

ProMES can still be improved by using more refined transmission parameters estimation for various virus mutations as well as for different contact types. Regardless the fine parameter tuning, we already made some interesting observations. Our experimental results show that deceleration of epidemic should become visible when at least 10% of population is recovered or vaccinated. However, the actual Polish immunity is estimated to be within the range 30%-40% and still such a deceleration is not observed in reality. We therefore consider several hypotheses how to proceed with further research to clarify this issue. They include, in particular, explicit modeling of different virus mutations with varied virus biology parameters, improved stochastic models of contact layer and intervention modeling as well as changing the state machine of the SARS-Cov2 to explicitly include limited immunity (i.e. $S_3 \rightsquigarrow S_1$ in the Fig. 5).

We also considered different testing and quarantining scenarios. However, in real life the testing strategies applied in Poland were subject to numerous and frequent changes, so became rather fragmented. Moreover, a part of the population consciously and systematically avoided testing, therefore for the time being we deliberately abandoned related functionality in the GUI. The computational core including Covasim is still capable of performing test-trace-quarantine at later stages.

In the future, we plan to concentrate on social aspects of pandemic: modeling social behaviors together with tracking both information flow and evolution of motivational attitudes in the Polish population. It is easy observable that all these aspects are highly dynamic. In particular, an evolution of societal attitudes towards vaccination turned out to be age-correlated and strongly evolved over time. Such social phenomena should find its place in ProMES, intended to serve as an administrative decision-support system. In order to address this aspect, a more complex model of agency, for example, BDI (Belief, Desire, Intention) architecture [6] could be applied. We also acknowledge the necessity of constant monitoring of up-to-date medical knowledge on SARS-Cov2 and (a spread of) its new variants.

Technically, there is still room for a performance improvements by both enriching the contact network layer and reducing computation time. The future work assumes exploration of most promising parallelization approaches including the choice of a MIMD-CPU parallelization or a SIMD-GPU vectorization.

Acknowledgment

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