Measuring COVID-19 economic and epidemiological countermeasures impact

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Abstract—We propose a novel framework that combines a state-of-the-art disease spreading model based on mobility data with an economic model. The goal of this simulation is to estimate how the application of various countermeasures can impact both the number of saved lives and the economy of every sectors. In this report we will present a limited set of countermeasures to keep it as simple as possible, but the framework can be easily extended to simulate additional countermeasures. We will then compare our results with the real data gathered during the SARS-CoV-2 pandemic.

I. Introduction

In the last year, the number of studies regarding the simulation of disease spreading has increased dramatically. These studies focus only on the epidemiological models that better fit the simulations, sometimes underlining some possible strategies that could limit the speed of the spread [4, 28]. These papers though neglect completely the economic impact that could be caused by the application of aggressive countermeasures.

Our framework tries to fill this gap by first extending Chang et al. state-of-the-art simulation model based on Safegraph mobility data to predict the diffusion of the COVID-19 virus [24, 4], then by correlating these results with a simulation of the Leontief input-output economic model [14]. This allows us to apply countermeasures and to compute their impact from both an epidemiological and an economic point of view.

The paper is organized as follows: the first part will describe some related work about disease spreading and economic simulation; we then describe the simulation methodology, including the epidemiological and the economic parts, along with some countermeasures; finally, we will then compare our simulation results with the real data and present some possible improvements and future work.

II. Related Works

In the first part of this section we describe some related works about disease spreading simulations, while in the second part we focus on the economic side.

A. *Disease spreading simulation*

In a sufficiently large group of people the spread of a disease can be formally described using mathematical models, as first proposed by Ross and Hudson and later refined by Kermack, McKendrick and Kendal [21, 22, 23, 11, 5]. This simple formalization is powerful enough to describe the spread of various diseases in different conditions [13, 26, 7].

One of these formalization is called SEIR model. In the SEIR model the population can be subdivided in four different states: susceptible, i.e. healthy individuals that have not been exposed to the virus yet; exposed people who have already been infected by the virus but can not infect others; infectious individuals that are capable of transmitting the disease; recovered people that have been removed from the simulation.

The parameters of disease spreading models like SEIR can be tuned in order to capture some sociological aspects of the disease (application of countermeasures, e.g. social distancing) and therefore are generally accurate [13, 7]. For this reason, a series of models based on mobility networks have been developed [15, 19, 4]. We choose to use as a starting point the Chang et al. work [4] and the changes that we made will be explained in detail later in section III.

B. *Economic model simulation*

To understand how our economic model is being simulated, we first need to mention some economic theories. These can be divided in two categories: one that focuses on the specific phenomena on a smaller scale called *microeconomics* and one that tries to describe and model an entire economic system called *macroeconomics* [16, 14, 12].

Since the goal of this part of the simulation is to represent an economic model from a high point of view, we focus only on the macroeconomics theories. Some of these are strictly theoretical [8] and therefore can not be directly applied to our model, while others are more empirical and use data released by the statistical state bureau, called I/O tables [14, 12, 3].

These I/O tables usually cover the economy of the whole state, bu they can be adapted to a smaller area using some linear scaling procedure or more advance techniques like IPFP [20]. In our model, a single input-output table is defined as 2D matrix, where each cell indicates the output of a specific industry and the input to another. This representation allows us to build a graph of relations among different sectors and to identify losses across different supply chains. Although this approach identifies the linear interrelationships among the economic actors, it fails to model non-linear ones.

III. METHODOLOGY

Our framework aims to understand how people interaction and SARS-CoV-2 spreading are correlated, to then apply countermeasures to reduce its diffusion and to observe how these strategies can impact both the economic and epidemiological aspects of the simulation.

The simulation has been implemented in three different steps: the first one involves the enactment of the epidemiological model, the second one focuses on the implementation of economic model, the third one consists of the creation of countermeasures to reduce the number of victims.

A. Epidemiological component

The environment of the epidemiological model is divided in two components: CBGs (Census Block Groups) where people live and POIs (Points of Interest) where people from different CBGs meet, mostly shops and offices.

The simulation is based on a bipartite graph that keeps track of the number of people visiting a specific POI from any CBGs. This graph needs to be computed by correlating data extracted from many different datasets, which will be the focus of the next section.

1) Data: The work presented in this paper is based mainly on data provided by SafeGraph. In particular, these are the datasets that have been used for its implementation:

- *Open Census Data*: data gathered by the United States Census Bureau (American Community Survey - 2016) and distributed freely by SafeGraph
- *Safegraph Core POI*: dataset containing information about POIs, such as IDs, categories, addresses, cities, regions and postal codes
- *Safegraph Home Summary*: weekly organized data about CBGs, such as IDs, origin states, number of devices residing
- *Safegraph Social Distancing*: daily organized data for correlating interactions between CBGs, such as whether people visited other CBGs or not
- *Safegraph POI Area*: dataset containing the area in square meters of each POI
- *Safegraph Weekly Pattern*: weekly organized data about POIs, such as IDs, hourly visits, median visit times, visitor home CBGs

2) Model parameters: We now describe the matrices we build for running the simulation. Most of the original Safegraph matrices are organized in weeks, and therefore many of obtained matrices maintained this division.

The POIs Area matrix $\mathcal{A}$ is obtained by extracting the necessary data from the *Safegraph POI Area* dataset and by limiting the values at the 5 and 95 percentile for each category. The N_c matrix represents the estimated population of each CBG and it is created by filtering the original *Open Census* dataset (N_{c_i} represents the estimated population of the i-th CBG). We define the daily $\hat{h}_c^{(t)}$ matrices as the estimated fraction of people in CBG c_i who left their home in the t-th day of the week, obtained by processing the *Social Distancing* dataset. The $\hat{\delta}_p$ matrices represent the median visit length to

each POI (expressed in fractions of hours) and are extracted from the *Weekly Pattern* datasets.

The bipartite visit graph mentioned before, indicated with $\hat{W}^{(r)}$ (where r indicates a particular week) is represented as a matrix and its computation involves many different steps. First, we need to compute the aggregate visit matrix $\bar{W}$ as:

$$\bar{W} = \frac{1}{R} \sum_r \hat{W}^{(r)} \tag{1}$$

Each entry $\bar{w}_{ij}$ represents the estimated number of people that left their home CBG_i and visited a POI_j (averaged over each hour).

The next step is to estimate the POI marginals $V^{(t)}$, where $V_{p_j}^{(t)}$ represents the number of people from any CBGs visiting the j-th POI. However, this is an underestimate of the real value since SafeGraph only covers a fraction of the overall population. To adjust this estimate, we multiply this data by a correction factor computed by dividing the New York Metropolitan Area population by the total number of SafeGraph devices in this area (approximately 7).

One of the final steps is now to estimate the CBG marginals $U^{(t)}$, where $U_{c_i}^{(t)}$ is the estimate number of people in CBG_i who are out visiting a POI at hour t. These matrices have been computed using the following formula:

$$U_{c_i}^{(t)} = N_{POIs}^{(t)} \cdot \frac{\hat{h}_{c_i}^{(t)} N_{c_i}}{\sum_{k=1}^{m} \hat{h}_{c_k}^{(t)} N_{c_k}} \tag{2}$$

where $N_{POIs}^{(t)}$ is the total number of people who are out visiting any POIs from any CBGs at hour t, and can be computed as follows:

$$N_{POIs}^{(t)} = \sum_{j=1}^{n} V_{p_j}^{(t)} \tag{3}$$

with n representing the total number of POIs. The multiplication $\hat{h}_{c_i}^{(t)} \cdot N_{c_i}$ represents the estimate of the total number of people from each CBG_i who are not at home at hour t. Note now that the construction of POI and CBG marginals should match the following relationship:

$$N_{POIs}^{(t)} = \sum_{j=1}^{n} V_{p_j}^{(t)} = \sum_{i=1}^{m} U_{c_i}^{(t)} \tag{4}$$

The final step before starting the simulation is to adjust the aggregate visit matrix $W^{(t)}$ using the CBG and POI marginals. We need to construct a non-negative matrix $W^{(t)}$ whose rows sum up to the CBG marginals $U^{(t)}$ and whose columns sum up to the POI marginals $V_{p_j}^{(t)}$ [6]. Therefore, we can draw the following relationships:

$$U_{c_i}^{(t)} = \sum_{j=1}^{n} w_{ij}^{(t)} \tag{5}$$

$$V_{p_j}^{(t)} = \sum_{i=1}^{m} w_{ij}^{(t)} \tag{6}$$

This can be achieved using the iterative proportional fitting procedure (IPFP), which is an iterative algorithm that alternates between scaling each row to match the target $U^{(t)}$ and scaling each column to match the target $V^{(t)}$. This procedure has been run for $\tau_{max} = 100$ times.

3) Model: The SEIR model can be described from a mathematical point of view by the following relationships:

$$N_{c_i} = S_{c_i}^{(t)} + E_{c_i}^{(t)} + I_{c_i}^{(t)} + R_{c_i}^{(t)} \tag{7}$$

$$\Delta S_{c_i}^{(t)} = -N_{S_{c_i} \to E_{c_i}}^{(t)} \tag{8}$$

$$\Delta E_{c_i}^{(t)} = N_{S_{c_i} \to E_{c_i}}^{(t)} - N_{E_{c_i} \to I_{c_i}}^{(t)} \tag{9}$$

$$\Delta I_{c_i}^{(t)} = N_{E_{c_i} \to I_{c_i}}^{(t)} - N_{I_{c_i} \to R_{c_i}}^{(t)} \tag{10}$$

$$\Delta R_{c_i}^{(t)} = N_{I_{c_i} \to R_{c_i}}^{(t)} \tag{11}$$

where N_{c_i} is the total number of people in the i-th CBG. Also, from each state it is only possible to transition forward to the next state, therefore assuming that if a person has been infected and recovered from the disease, it can not be exposed to the virus anymore.

Within these relationships, we need to care about other parameters, such as the probability of being infected at time $t = 0$, the mean latency period δ_E (time between exposure and infectivity), the mean infectious period δ_I (time between infectivity and recovery) and other simulation-dependent parameters.

Additionally, in our model we separate recovered people in $R_{c_i dead}$ and $R_{c_i alive}$, which represent the number of people who transitioned from I_{c_i} to R_{c_i} by death or by healing, respectively.

4) Simulation: The model is first initialized using the following formulae:

$$S_{c_i}^{(0)} = N_{c_i} - E_{c_i}^{(0)} \tag{12}$$

$$E_{c_i}^{(0)} = Binom(N_{c_i}, p_0) \tag{13}$$

$$I_{c_i}^{(0)} = 0 \tag{14}$$

$$R_{c_i}^{(0)} = 0 \tag{15}$$

We assume that initially ($t = 0$) there are neither infectious nor removed individuals in any CBGs and that the number of exposed people is drawn from a Binomial distribution $\mathcal{B}(n, p)$, where $n = N_{c_i}$ and $p = p_0$ (the probability of being exposed at time $t = 0$). In order to respect the first rule of the SEIR model (equation 7), we need to set $S_{c_i}^{(0)} = N_{c_i} - E_{c_i}^{(0)}$.

The model is being updated for each time unit t of the simulation (in hours) and the matrices representing the states of the simulation are being computed with the following rules. First of all, the computation of new exposed $N_{S_{c_i} \to E_{c_i}}^{(t)}$ is divided in two separate cases: one representing the possibility

of being infected while visiting a particular POI and one representing the possibility of being infected in a certain CBG.

For what regards the computation of how a person is being infected in a certain POI, we need to consider many different variables, such as the number of infectious people already present in the POI $I_{p_j}^{(t)}$, the average time spent in that POI dp_j and the area in square meters of the POI a_{p_j}. All these factors are gathered under the infection rate at POI$_j$ λ_{p_j} at time t and computed as follows:

$$\lambda_{p_j}^{(t)} = \psi dp_j^2 \cdot \frac{I_{p_j}^{(t)}}{a_{p_j}} \tag{16}$$

where ψ is a transmission constant (shared across all POIs) that we will fit to data (explained later in this section).

On the other hand, to represent the possibility of being infected in CBG$_i$, we need to compute a similar λ_{c_i} at time t, such that:

$$\lambda_{c_i}^{(t)} = \beta_{base} \frac{I_{c_i}^{(t)}}{N_{c_i}} \tag{17}$$

where β_{base} is another transmission constant (shared across all CBGs) that we will fit to data.

Finally, having these two rates it is possible to compute the number of new exposures for each time unit t in the following way:

$$N_{S_{c_i} \to E_{c_i}}^{(t)} = Binom(w_{ij}^{(t)} \cdot \frac{S_{c_i}^{(t)}}{N_{c_i}}, \lambda_{p_j}^{(t)}) + Binom(S_{c_i}^{(t)}, \lambda_{c_i}^{(t)}) \tag{18}$$

Note that $Binom(w_{ij}^{(t)} \cdot \frac{S_{c_i}^{(t)}}{N_{c_i}}, \lambda_{p_j}^{(t)})$ can be approximated using $Poisson(w_{ij}^{(t)} \cdot \frac{S_{c_i}^{(t)}}{N_{c_i}} \cdot \lambda_{p_j}^{(t)})$, therefore saving computation time.

To compute the number of new infectious individuals, we need to take into account the mean latency period δ_E (in our simulation $\delta_E = 96h$), therefore assuming a constant and time-independent probability of becoming infectious computed as

$$N_{E_{c_i} \to I_{c_i}}^{(t)} = Binom(E_{c_i}^{(t)}, 1/\delta_E) \tag{19}$$

A similar procedure has been applied to compute the number of removed individuals, using in this case the approximated mean infectious period δ_I (in our simulation $\delta_I = 84h$), therefore having

$$N_{I_{c_i} \to R_{c_i}}^{(t)} = Binom(I_{c_i}^{(t)}, 1/\delta_I) \tag{20}$$

From the number of removed individuals, we can obtain the number of dead people by computing $R_{c_i dead} = \mathcal{B}(R_{c_i}, p_{dead})$, where p_{dead} is the probability of dying (2% [2]) and therefore $R_{c_i alive} = R_{c_i} - R_{c_i dead}$.

As mentioned before, it is necessary to compute some parameters to adjust the initial configuration of the simulation: p_0, ψ and β_{base}. In order to estimate the best possible values for these parameters, we compare the results obtained by running the simulation with different combinations of these values with the real data provided by the New York Times,

using a procedure called grid-search. Each simulation has been run 10 times (in batch) to avoid inaccuracies due to probability, testing the following values:

- β_{base}: 10 values in the range 0.0012 - 0.024;
- ψ: 9 values in the range 0.001 - 50
- p_0: these 10 values: $1 \cdot 10^{-2}$, $5 \cdot 10^{-3}$, $2 \cdot 10^{-3}$, $1 \cdot 10^{-3}$, $5 \cdot 10^{-4}$, $2 \cdot 10^{-4}$, $1 \cdot 10^{-4}$, $5 \cdot 10^{-5}$, $2 \cdot 10^{-5}$, $1 \cdot 10^{-5}$

The estimated data has been compared with the real data using the root-mean-square error (RMSE) measure and the best parameters have been selected by taking the minimum averaged error among all the results of the simulation.

B. Economic component

This part of the simulation is based on the input-output economics theory [14]. Even though there are other more comprehensive and sophisticated empirical economic theories [8], there is no available data to simulate them.

1) Data: The economic simulation requires as input the input-output table (I/O table) that is generally provided by the government [3, 10, 9]. This data explains the correlation among economic sectors and their relationship with the final demand, describing yearly the costs of each sector (e.g. acquisition of raw materials) and their incomes (i.e. sales of refined products).

2) Simulation: To implement the economic loss simulation, we have to make some strong assumptions. The first one regards the fact that the input-output table is measured on annual scale and therefore needs to be scaled down to match the time unit of the epidemiological data.

A second assumption has been made to take into account the possibility of simulating a period of time of only few months, meaning that the yearly economic data needs to be scaled down even more.

The third assumption that needs to be made is due to the impossibility of distinguishing POIs at a finer level than the POI categories. In this case we need to assume that all the POIs under the same category earn, on average, the same amount of money in each period of the year and in each hour of the day.

As mentioned before, these are strong assumptions, but they are needed to avoid the introduction of randomness in the simulation or pollution of other data.

We build a graph of dependencies among sectors using the I/O table: each entry v_{ij} is considered as an input from sector i to sector j and as an output from sector j to sector i. In this model, each sector can be seen as a node of the dependency graph, while each input/output relationship can be seen as a weighted edge between nodes (note that there is the possibility of having intra-sector relationships).

We can now simulate an economic loss by providing an origin (e.g. the final demand), a target sector (e.g. real estate) and a monetary loss. Since we adopt a graph as data structure, the propagation of this economic loss among all the sectors can be computed as simple depth first search (DFS), where each visit to a certain node causes a new economic evaluation of its incomes. To avoid infinite loops, we do not take into account losses that are smaller that some input value δ.

In particular, the propagation of the economic loss among all the sectors can be explained with few simple steps. First of all, we directly apply the economic loss to the output relationship between the target sector (provider) and the origin sector (buyer). We then compute how this loss impacts the other input edges of the provider sector by calculating the percentage of its overall economic loss. If this percentage is greater than the parameter δ, it is applied to each input of the provider sector and the process is repeated for each input sector.

Once the algorithm has finished propagating losses, the total economic loss can be computed by first summing all the sectors initial values v_{init_i} and all the sectors final values v_{fin_i}, and then by computing $\frac{v_{init} - v_{fin}}{v_{init}}$.

C. Countermeasures component

Each countermeasure is implemented as a separate module that can be enabled at the start of the simulation and it is used to compute the number of saved lives and the possible economic damages. Each countermeasure can impact the economic graph by adding losses and the visit matrix by limiting the number of people who visit certain POI categories.

Since each countermeasure reduces the number of people visiting certain POI categories (i.e. targeting the final demand), once decided the categories to close and the hours involved in the closure, we compute the total number of affected customers while setting all the necessary entries in the estimate visit matrix $W^{(t)}$ to 0. By computing the percentage of lost visits for a certain POI category, we can estimate an final demand economic loss and therefore we can start its propagation.

Using this procedure, the following countermeasure have been implemented:

- Allow only takeaway from food venues after 18 pm
- Allow only takeaway from food venues
- Closure of cinemas and theaters
- Closure of religious organization

Note that it is possible to add other countermeasures by simply creating new modules and that it is possible to test any combination of the implemented countermeasures.

IV. RESULTS

In this section we will first briefly describe the implementation of the simulation and the data used to run it, and then we will discuss the results obtained in our scenario.

A. Implementation and testing data

The model has been implemented in Python and it adopts PyTorch as a vectorization library to leverage on GPUs computational power [18]. In our current implementation we decide to manage some of the matrices as sparse matrices (such as the aggregate visits matrix), mainly because they contain large areas that are equal to zero that can be easily clustered.

For maintaining the simulation as general and reusable as possible, all the parameters described before can be passed in the simulation upon initialization, providing the possibility of studying multiple scenarios under the same basic assumptions.

We run the simulation to tune the epidemiological parameters (β_{base}, ψ and p_0) on a period that spans between 2 March 2020 and 3 May 2020. Once these parameters have been computed, we run the simulation on a period the spans between 7 January 2019 and 31 March 2019.

Although Safegraph data is available for the entire United States, for performance reasons we consider only the New York Metropolitan Area, which includes New York City, Long Island, and the Mid and Lower Hudson Valley in New York State, part of the New Jersey and Connecticut [29]. This area includes around $14'000$ CBGs and $203'000$ POIs.

To test the accuracy of our simulation, we compare our results with the real SARS-CoV-2 pre-lockdown data, which is freely downloadable from the New York Times GitHub [17].

For the economic data, we adopt the publicly available I/O table released by the U.S. Bureau of Labour statistics [10]. However, since this dataset contains the data of all the States, it needs to be linearly scaled down to only the New York Metropolitan Area based on its GDP.

B. Results

In Fig. 1 we present the comparison between the distribution of real cases with the distribution of simulated cases. While both curves follow the same pattern, the simulated one diverges with respect to the real data at the start of the simulation (estimating more cases) and at the end of the simulation (estimating less cases). This could be explained by the fact that the input parameters of our simulation have been obtained by testing largely spread values during the grid-search procedure.

In Fig. 5 and Table I it can be noticed how the closure of the food venues results in being the best countermeasure in terms of disease spreading limitation. However, by comparing the number of saved lives with the economic losses caused by the application of the countermeasure, it can be derived that the closure of the religious organizations is the most effective way to slow down the spread of the infection while limiting the economic damage.

Countermeasure	Economic losses (in B$)	People saved	Cases avoided
Closure of cinemas and theaters	4.95	336	10365
Closure of religious organizations	2.14	443	17393
Only takeaway from food venues	24.19	1389	66837
Only takeaway from food venues after 18	9.14	682	30629

Fig. 3 and 4 represent the economic impact of each countermeasure. Despite the strong assumptions about the input-output economic theory, we are able to predict the economic loss of some sectors with a 5% precision.

As an example, we estimate a loss of 38.25% from the fishing, hunting and trapping industries, while according to a FAO report the USA experienced a reduction of 40% in terms of fishing [27]. In other cases like in the motion picture, video and sound recording industries the difference is larger but still relative small. According to the analysts, these sectors have lost 71.5% in 2020, while we predict a loss of 60.29% [1].
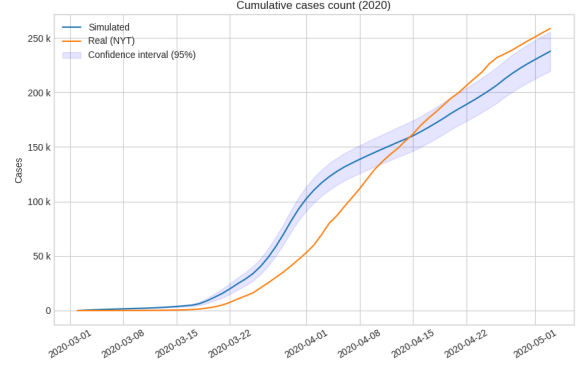

Figure 1. The graphs show the difference between the simulated cumulative cases and the real cases provided from the New York Times dataset
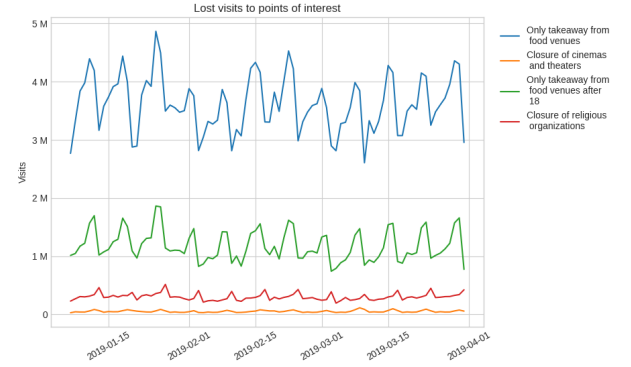

Figure 2. The graph shows the amount of visits each countermeasure avoided over the simulation time

This result is remarkable if we consider the fact that these are sectors where the assumption about linearity is challenged by the $1+$ years required to produce a movie [25].

V. CONCLUSIONS

Our epidemiological simulation combines AI-like workloads (characterized by the use of large quantities of data) with the classic simulation world (that usually requires lower amount of data while producing large quantities of data). This model in our opinion fills the gap between agent-oriented simulations that are characterized by scalability issues and high-level simulations where it is difficult to obtain meaningful insights other than the spreading speed of the disease. This model is able to predict accurately the actual cases [4], but it can probably be improved by correlating the virus transmission mechanisms with the people social behaviour inside different POI categories. As a quick example, we consider the difference between the quantity of emitted droplets in restaurants and supermarkets.

From the economic point of view, one of the largest difficulties is represented by the unavailability of data. The model also accurately predicts the economic impact in some sectors while showing its limitations in others, where the input-output relationships are not linear. A future work can be represented
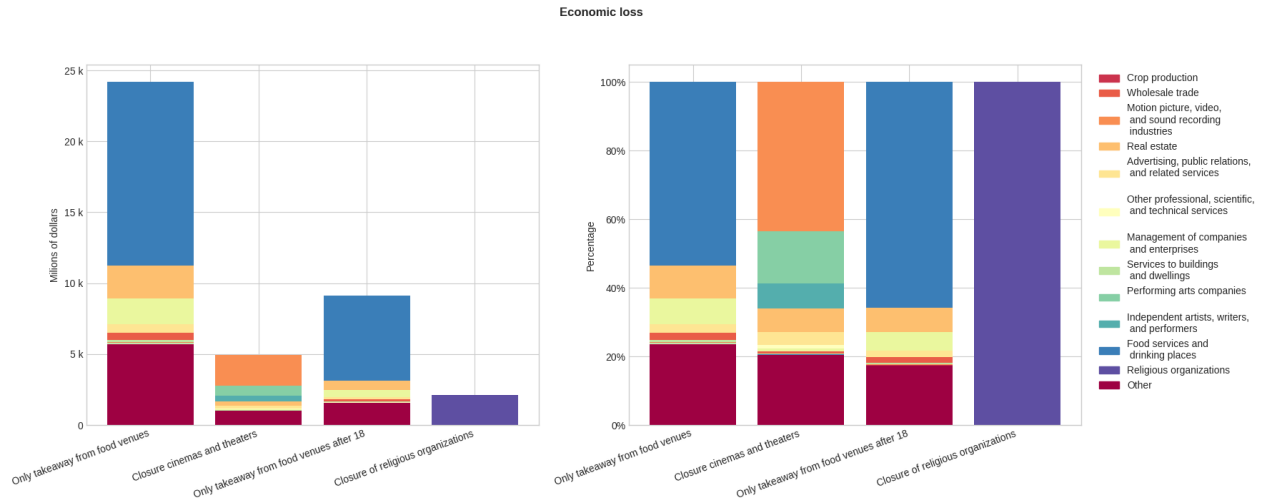
Figure 3. The graphs show for each countermeasure the five most hit sectors in monetary terms
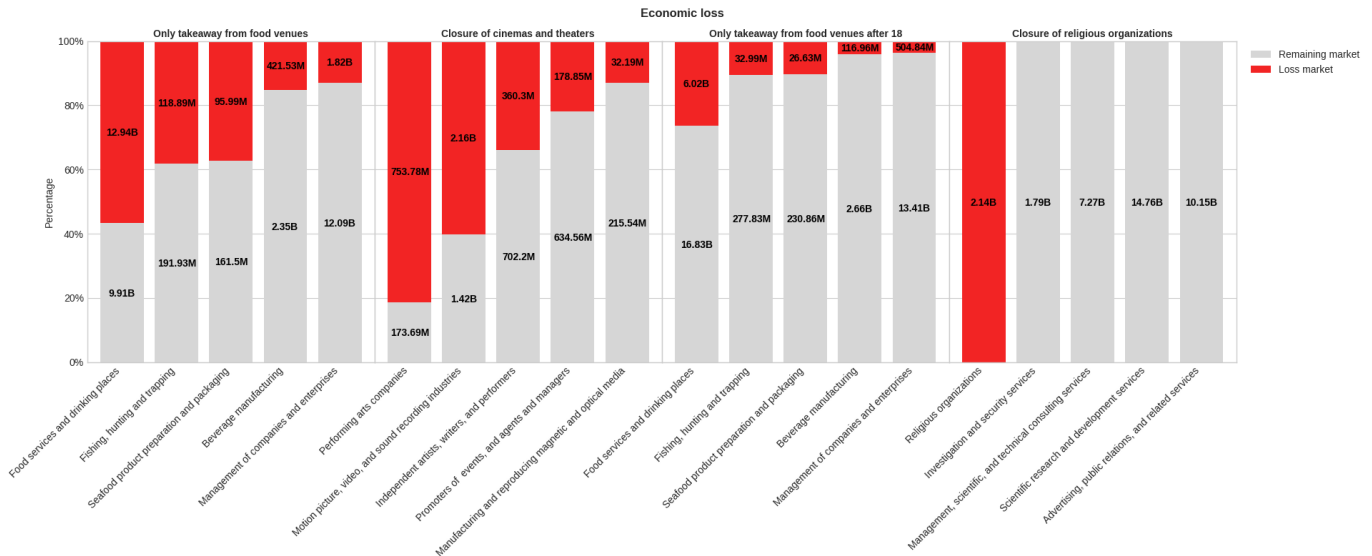

Figure 4. The graph shows for each countermeasure the five most hit sectors in terms of percentage economic loss. Each percentage is associated with its monetary value (in $)

by the introduction of sector specific functions that better model the input-output relationships.

REFERENCES

[1] *2020 in Review: How Much Money Did the Film Industry Lose?* https://www.gobankingrates.com/money/business/2020-review-much-money-did-film-industry-lose/, Accessed: Jul, 2021.

[2] Anirban Basu. "Estimating The Infection Fatality Rate Among Symptomatic COVID-19 Cases In The United States". In: *Health Affairs* 39.7 (July 2020), pp. 1229–1236. DOI: 10.1377/hlthaff.2020.00455.

[3] *BEA: Input-Output Accounts Data.* https://www.bea.gov/industry/input-output-accounts-data, Accessed: Jul, 2021.

[4] Serina Chang et al. "Mobility network models of COVID-19 explain inequities and inform reopening". In: *Nature* 589 (2020), pp. 82–87. DOI: 10.1038/s41586-020-2923-3.

[5] Kendal D.G. "Deterministic and stochastic epidemics in closed populations". In: *Proceedings of the Third Berkeley Symposium on Mathematical Statistics and Probability: Contributions to Biology and Problems of Health* 4 (1956), pp. 149–165. DOI: 10.1525/9780520350717-011.

[6] W. Edwards Deming and Frederick F. Stephan. "On a Least Squares Adjustment of a Sampled Frequency Table When the Expected Marginal Totals are Known". In: *The Annals of Mathematical Statistics* 11.4 (1940), pp. 427–444. ISSN: 00034851.
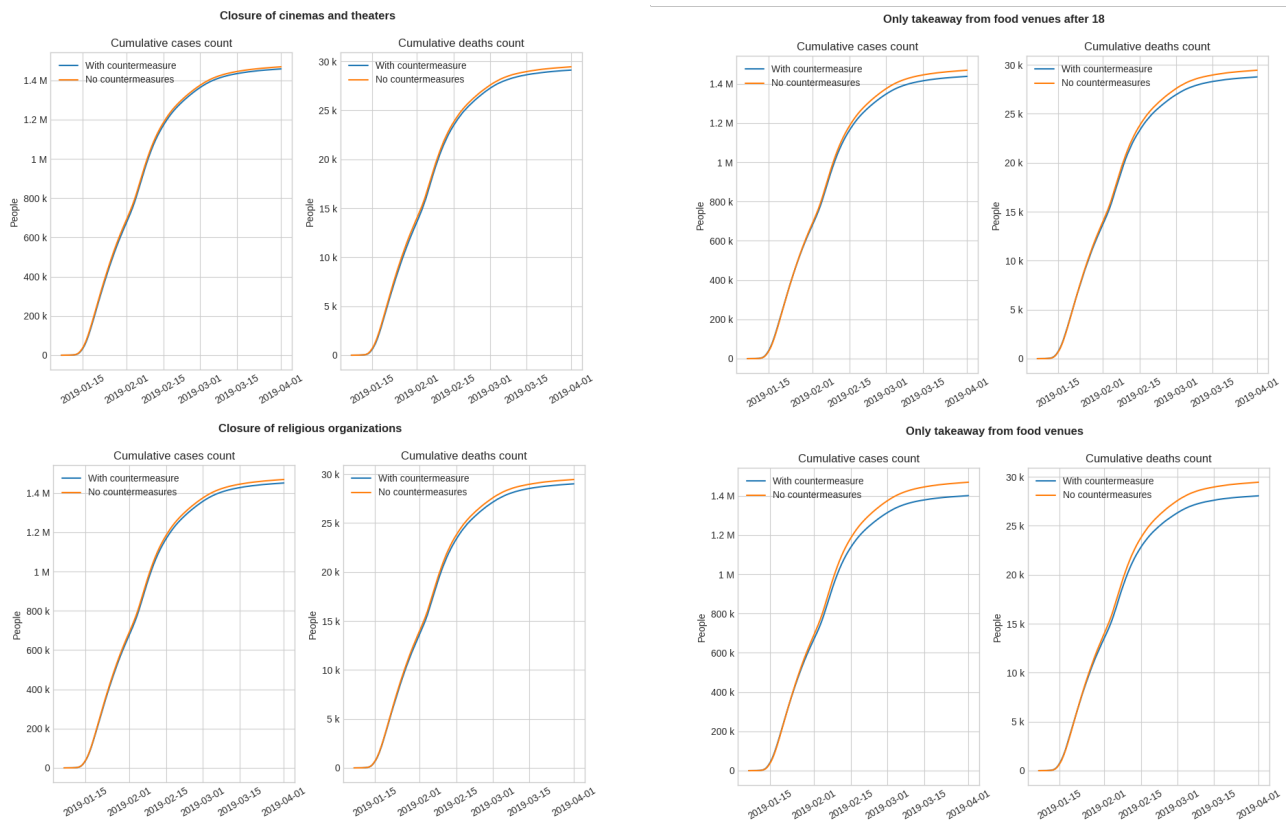
Figure 5. The graphs show the epidemiological impact of each countermeasure on the number of cases

[7] Davide Faranda and Tommaso Alberti. "Modeling the second wave of COVID-19 infections in France and Italy via a stochastic SEIR model". In: *Chaos: An Interdisciplinary Journal of Nonlinear Science* 30.11 (2020), p. 111101.

[8] Mohammad Gani. *Foundations of economic science*. Scarborough, ON: Scholars, 2003. ISBN: 978-9843206558.

[9] *Il sistema di tavole input-output*. https://www.istat.it/it/archivio/225665, Accessed: Jul, 2021.

[10] *Inter-industry relationships (Input-Output matrix)*. https://www.bls.gov/emp/data/input-output-matrix.htm, Accessed: Jul, 2021.

[11] Kermack and McKendrick. "A Contribution to the Mathematical Theory of Epidemics". In: *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character* 115.772 (1927), pp. 700–721. DOI: 10.1098/rspa.1917.0015.

[12] John Maynard Keynes. *The general theory of employment, interest, and money*. Springer, 2018.

[13] Phenyo E Lekone and Bärbel F Finkenstädt. "Statistical inference in a stochastic epidemic SEIR model with control intervention: Ebola as a case study". In: *Biometrics* 62.4 (2006), pp. 1170–1177.

[14] Leontief Wassily. *Input-output economics*. New York: Oxford University Press, 1986. ISBN: 978-0195035278.

[15] Leonardo López et al. "An influenza epidemic model with dynamic social networks of agents with individual behaviour". In: *Ecological Complexity* 41 (2020), p. 100810. ISSN: 1476-945X. DOI: https://doi.org/10.1016/j.ecocom.2020.100810. URL: https://www.sciencedirect.com/science/article/pii/S1476945X19301084.

[16] John F Nash. "Equilibrium points in n-person games". In: *Proceedings of the national academy of sciences* 36.1 (1950), pp. 48–49.

[17] New York Times. *Coronavirus (Covid-19) Data in the United States*. https://github.com/nytimes/covid-19-data, Accessed: Jul, 2021.

[18] *PyTorch*. https://pytorch.org, Accessed: Jul, 2021.

[19] Alessandro Rizzo, Biagio Pedalino, and Maurizio Porfiri. "A network model for Ebola spreading". In: *Journal of theoretical biology* 394 (2016), pp. 212–222.

[20] Mínguez Roberto, Oosterhaven Jan, and Escobedo Fernando. "CELL-CORRECTED RAS METHOD (CRAS) FOR UPDATING OR REGIONALIZING AN INPUT–OUTPUT MATRIX". In: *Journal of Regional Science* 49.2 (2009), pp. 329–348. DOI: https://doi.org/10.1111/j.1467-9787.2008.00594.x.

[21] Ross Ronald. "An application of the theory of probabilities to the study of a priori pathometry.—Part I". In: *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character* 92.638 (Feb. 1916), pp. 204–230. DOI: 10.1098/rspa.1916.0007.

[22] Ross Ronald and Hudson Hilda. "An application of the theory of probabilities to the study of a priori pathometry.—Part II". In: *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character* 93.650 (May 1917), pp. 212–225. DOI: 10.1098/rspa.1916.0007.

[23] Ross Ronald and Hudson Hilda. "An application of the theory of probabilities to the study of a priori pathometry.—Part III". In: *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character* 89.621 (May 1917), pp. 225–240. DOI: 10.1098/rspa.1917.0015.

[24] *SafeGraph*. https://www.safegraph.com, Accessed: Jul, 2021.

[25] *Stages of Production*. https://www.filmtraining.mb.ca/resources/industry-info/stages-of-production/, Accessed: Jul, 2021.

[26] Juliette Stehlé et al. "Simulation of an SEIR infectious disease model on the dynamic contact network of conference attendees". In: *BMC medicine* 9.1 (2011), pp. 1–15.

[27] *The impact of COVID-19 on fisheries and aquaculture food systems, possible responses*. FAO, Feb. 2021. DOI: 10.4060/cb2537en. URL: https://doi.org/10.4060/cb2537en.

[28] Gianpaolo Scalia Tomba and Jacco Wallinga. "A simple explanation for the low impact of border control as a countermeasure to the spread of an infectious disease". In: *Mathematical Biosciences* 214.1-2 (July 2008), pp. 70–72. DOI: 10.1016/j.mbs.2008.02.009.

[29] Wikipedia. *New York metropolitan area*. 2021. URL: https://en.wikipedia.org/wiki/New_York_metropolitan_area.