Comparison of Mathematical Models for Predicting

the Trend of the COVID-19 Pandemic

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Abstract

This is a research project carried out to make comparisons of widely using models for predicting the trend (including total deaths and total infected cases) of the COVID-19 pandemic. The research methods of this paper include literature summarization, comparative analysis, and induction. The three models compared in this paper include the Global Epidemic and Mobility (GLEAM) model, the DELPHI model, and the Institute for Health Metrics and Evaluation (IHME) model. It is concluded that the IHME model is the best performing model overall, especially in the accuracy, range of application, and timeliness of the model, while the DELPHI model is considered the best in the complexity of models. This research aims to provide a reliable reference for other people who are studying mathematical models and citizens who are curious about these models so that they can save time from looking at various models and thinking about which model is the most reliable one based on their focus.

Introduction

It is universally acknowledged that Coronavirus Disease 2019 (hereinafter referred to as COVID-19) (World Health Organization, 2020) is the most concerning global event from 2020 to 2021 (Lindsay, 2020). Both the governments and the citizens want to know when this pandemic will come to an end, and high-quality forecasting models are critical to these needs. The use of these mathematical models is crucial since there is the probability that we can turn the newly appeared virus predictable. Professional teams all over the world tried their best to establish all kinds of models, e.g., the SEIR-QD model (Peng et al., 2020) and the Imperial model (Imperial College London, 2020). However, people focus on different aspects of a model to judge whether its predictions are credible. Therefore, my work in this dissertation is to make comparisons of

widely used models and provide a reference for people who are curious about these prediction models and their results.

Up to now, a variety of prediction models are established. There was research by a team from China, who quantitatively evaluated eight empirical functions, four statistical inference methods and five dynamical models based on their Akaike information criterion, robustness index and root mean square error values (Yang et al., 2020). Although they compared plenty of models with rational methods, the evaluations are only based on the data from provinces in China, which is not comprehensive enough. Moreover, some of the models chosen in their dissertation are not the most widely-used ones, but models that few people know about. Most importantly, this evaluation of the seventeen models chosen was made in March 2020, still in the initial stage of COVID-19, so this comparison will become less meaningful over time since more accurate models are established with our increasing knowledge about the virus.

In this dissertation, the three models evaluated are The Global Epidemic and Mobility (GLEAM) model, the DELPHI model, and the IHME model. Surprisingly, the three models chosen are all American, which I did not expect while choosing them. It is of great importance to compare popular COVID-19 models. When the comparison is made, people get a reliable reference and they can save time from looking at different models and thinking about whether it is the most reliable one based on their focuses.

Methods

Choosing Models

To achieve the research objectives, the models compared in this dissertation were chosen based on the keyword "authoritative". They need to be prediction models from either authoritative organizations or authoritative scholars. These models are more credible since they are revised various times by professionals. Also, the chosen models should be popular enough since ordinary people have little chance to learn about unpopular ones. Based on the criteria explained above, three models are chosen for comparison in this dissertation.

The Global Epidemic and Mobility (GLEAM) model. GLEAM is a project in the United States directed by Alessandro Vespignani, the director of the Network Science Institute (Vespignani, 2021). The Network Science Institute is a multidisciplinary research community supporting studies in network science at Northeastern University (Network Science Institute at Northeastern University, 2021).

The DELPHI model. This model is created by a team from the Massachusetts Institute of Technology (MIT) in America, led by Dimitris Bertsimas, the Associate Dean of Business Analytics, Boeing Professor of Operations Research, and faculty director of the Master of Business Analytics at MIT (Bertsimas, 2021). The DELPHI model can be considered authoritative since MIT was ranked as one of the top universities in the world for several years by different organizations such as the QS World University Rankings (Massachusetts Institute of Technology, 2021). DELPHI is used by the Hartford Hospital, the Federal Reserve Bank of Philadelphia, and Janssen to aid their decision making (MIT Operations Research Center, 2021).

The Institute for Health Metrics and Evaluation (IHME) model. This is a model established by the Institute for Health Metrics and Evaluation in the United States. IHME is a research institute at the University of Washington founded in 2007 that works with global health statistics and

impact evaluation. It is funded by plenty of organizations such as the Bill & Melinda Gates Foundation (Paulson, 2021). The model was called "America's most influential coronavirus model" by The Washington Post in 2020. Also, its projections were cited during the White House briefings in April 2020 (Institute for Health Metrics and Evaluation, 2021).

Overall, the three models are all created and used by authoritative organizations and researchers.

Factors for Evaluating the Model

Based on the research of other researchers, some of the main factors to consider while evaluating a model are summarized below:

Accuracy of the model. The accordance between the predicted values and the true values is one of the most important factors to consider about. If a model can correctly predict the trend, it is sure to be considered a good model.

The complexity of the model. Complexity is needed for a COVID-19 model since the trend of the pandemic is something that cannot be predicted by a simple model. However, the model should not be over-complicated with too many variables which might make the actual predictions time-consuming and hard to achieve (Yang et al., 2020).

Range of application of the model. According to different needs, while making predictions, models with different ranges of application should be taken into consideration. For example, some models are better predictors of a small region like a province and others might give better predictions to a larger area such as the whole country.

Timeliness of the model. Mutation of the coronavirus might occur over time and more

accurate parameters needed for the prediction models are determined with our new understanding of the pandemic, so the COVID-19 models should have strong timeliness to make the best predictions.

Results

This section provides an overview of the three models chosen. However, only the basic methods and core principles are explained since these models are all complicated and there is no need to learn about every single detail for evaluating them. Note that different assumptions are also made in every model, which might affect the whole establishment process of the models.

The Global Epidemic and Mobility Model

The Global Epidemic and Mobility (GLEAM) model follows the basic principles of an agent-based model. Agent-based models give prediction results by creating a simulated community in which individuals follow specific rules about their behaviours (Michaud et al., 2021). These rules established in this "virtual world" are determined by various factors such as real-time data and policies.

In the GLEAM model, the whole world is divided into subsections with an area of 25*25 kilometres. These subpopulations are characterized by the available real-world data presented. The spread of COVID-19 between countries and states is therefore represented by this interaction between subsections. According to databases collected from the Offices of Statistics of 30 countries, this worldwide interaction network is established. As a reference, some possible ways of moving to another subpopulation include intercontinental flights (to further ones) and car travelling (to nearer ones).

The agent-based model introduced previously is superimposed on the global network modelled by

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subpopulations. Within each subsection, individuals move stochastically (a variable process where the outcome involves some randomness and has some uncertainty) based on given parameters and spread the virus via interactions with other people, following the basic SEIR compartmentalization (more detailed introduction in section 3.2). At the beginning of each day, travels between subsections proceed based on the worldwide network. The probability for individuals to travel varies each day or different age groups. Moreover, two important policies are also considered in this model: social distancing and staying at home. The settings of behaviours of each individual will also be adjusted when there are changes in policies.

Throughout this whole transmission process, GLEAM can track the number of people in each state across all subpopulations and record every individual's travelling pattern as shown in the pseudo-code below (The GLEAM Project, 2021).
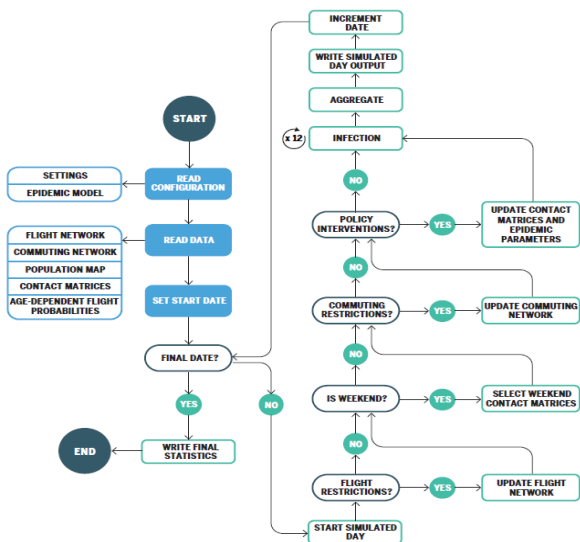

Figure 1. Pseudo-code of GLEAM's algorithm (The GLEAM Project, 2021)

The parameters needed for this model are similar to that of traditional epidemiological models. For example, the reproduction number R_0, detection rates, hospitalization time, and generation time (The GLEAM Project, 2021).

As a result, it projects weekly deaths and hospital beds in the U.S. and by state with an error range.
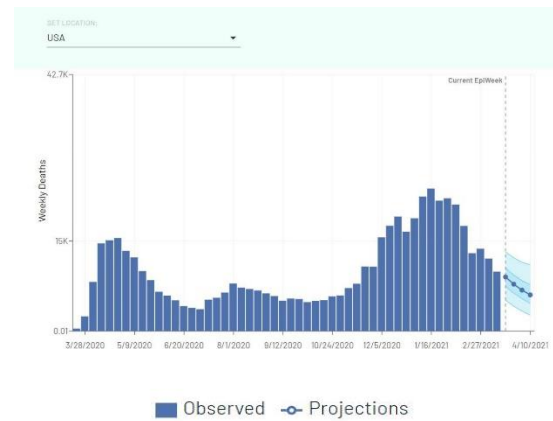

Figure 2. GLEAM projections of weekly deaths for the U.S. on March 20 (The GLEAM Project, 2021)
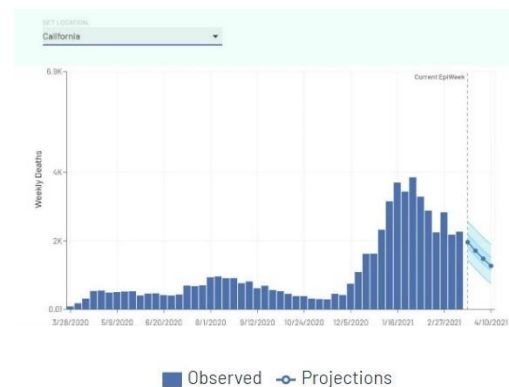

Figure 3. GLEAM projections of weekly deaths for California on March 20 (The GLEAM Project, 2021)

The first version of the GLEAM system was published in 2006, then it was used to predict the trend of the H1N1 pandemic in 2009 and has been validated using the actual data collected from 46 countries (GLEAMviz, 2021). Therefore, GLEAM is a very well-developed model since it has proven its validation in previous projections of other pandemics.

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The DELPHI Model

The DELPHI model is established based on the widely applied SEIR modelling approach. In the basic SEIR model, every human being is sorted into one of the for states:

-Susceptible (S): People that are not infected and also not immune to the virus.
-Exposed (E): The population who are currently infected but not contagious (i.e. in the incubation period).
-Infectious (I): People who are infected and contagious.
-Recovered (R): The population recovered and is immune to the virus (MIT Operations Research Center, 2021).
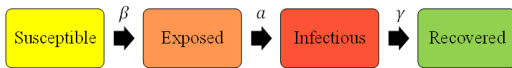

Figure 4. Flow chart of the SEIR model (Wikipedia, 2021)

The DELPHI model adds case-specific parameters to the basic SEIR approach so that the whole model will be more appropriate for the COVID-19 pandemic. By considering two crucial factors that might affect the natural spread of the virus: underdetection and governmental response, the population is sorted into 11 different states. Except for the four basic states in the SEIR model, the rest of the states are:

-Undetected (AR) and (AD): The population that is infected and self-quarantined themselves. However, due to insufficient testing, they are not reported as confirmed cases. It is assumed that some of them recover (AR) and the rest of them die (AD).

-Detected, Hospitalized (DHR) and (DHD): People who are infected, confirmed, and hospitalized. Some recover (DHR) and some die (DHD).

-Detected, Quarantined (DQR) and (DQD): People who are detected but quarantined. As above, it is modelled that some people recover (DQR) and some of them die (DQD).

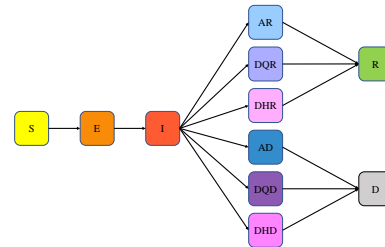-Death (D): The population died because of the virus.

Figure 5. Flow chart of the DELPHI model (Li et al., 2020)

This model can be expressed as the following set of differential equations:

$$\frac{dI}{dt} = r_i E(t) - r_d I(t) \qquad (1)$$

$$\frac{dDHR}{dt} = r_d(1 - p_{dth}(t))p_a p_h I(t) - r_{rh}DHR(t) \quad (2)$$

$$\frac{dDQR}{dt} = r_d(1 - p_{dth}(t))p_a(1 - p_h)I(t) - r_{ri}DQR(t) \quad (3)$$

$$\frac{dAD}{dt} = r_d p_{dth}(t)(1 - p_a)I(t) - r_{dth}AD(t) \qquad (4)$$

$$\frac{dDHD}{dt} = r_d p_{dth}(t)p_a p_h I(t) - r_{dth}DHD(t) \qquad (5)$$

$$\frac{dDQD}{dt} = r_d p_{dth}(t)(1 - p_h)I(t) - r_{dth}DQD(t) \qquad (6)$$

$$\frac{dTH}{dt} = r_d p_a p_h I(t) \qquad (7)$$

$$\frac{dDD}{dt} = r_{dth}\big(DHD(t) + DQD(t)\big) \qquad (8)$$

$$\frac{dDT}{dt} = r_d p_a I(t) \qquad (9)$$

$$\frac{dR}{dt} = r_{ri}\big(AR(t) + DQR(t)\big) + r_{rh}DHR(t) \qquad (10)$$

$$\frac{dD}{dt} = r_{dth}\big(AD(t) + DHD(t) + DQD(t)\big) \qquad (11)$$

The parameters used in the differential equation

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above are defined as the following (Li et al., 2020):

Table 1. Parameters used and definition (Li et al., 2020)

Parameter	Definition
α	infection rate (differs with the region)
$\gamma(t)$	measurement of government response
r_d	rate of detection
r_i	rate of infection leaving the incubation phase
r_{ri}	rate of recovery not under hospitalization
r_{rh}	rate of recovery under hospitalization
r_{dth}	rate of death (differs with the region)
$p_{dth}(t)$	measurement of the mortality percentage over time
p_d	percentage of infection cases detected
p_h	percentage of infection cases hospitalized

By plugging in the needed parameters calculated by regional data, the code of the set of differential equations above can be run in Matlab. This model gives results of total detected cases, total detected deaths, active cases, active hospitalized cases, and cumulative hospitalized cases for two months. These predictions can be plotted as graphs to show the trend more clearly.
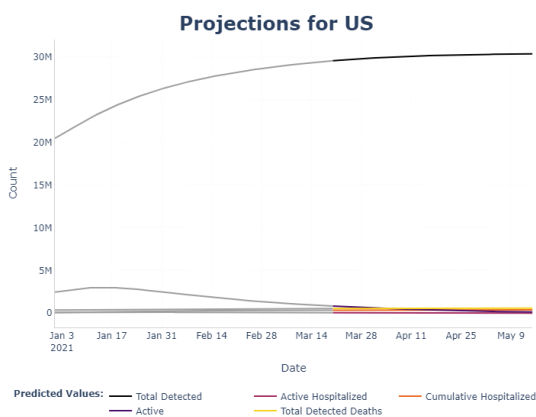

Figure 6. DELPHI projections for the U.S. on March 20 (MIT Operations Research Center, 2021)
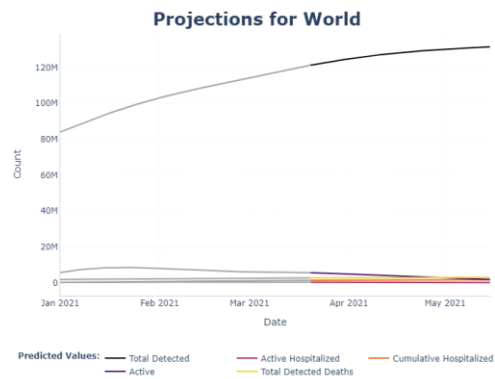

Figure 7. DELPHI projections for the world on March 20 (MIT Operations Research Center, 2021)

The Institute for Health Metrics and Evaluation Model

The Institute for Health Metrics and Evaluation (IHME) uses a hybrid modelling approach to make projections, which includes elements of statistical models and epidemiological models (Institute for Health Metrics and Evaluation, 2021). The primary model of IHME is also the compartmental model SEIR. However, in this model, symptomatic and asymptomatic patients are not distinguished, thus the "Infectious" state is further divided into I_1 and I_2, representing the pre-symptomatic and symptomatic state respectively. This new model is presented as:

$$\frac{dS}{dt} = -\beta(t)\frac{S(I_1 + I_2)^\alpha}{N} - \theta^+ S \qquad (12)$$

$$\frac{dE}{dt} = \beta(t)\frac{S(I_1 + I_2)^\alpha}{N} - \sigma E + \theta^+ S - \theta^- E \qquad (13)$$

$$\frac{dI_1}{dt} = \sigma E - \gamma_1 I_1 \qquad (14)$$

$$\frac{dI_2}{dt} = \gamma_1 I_1 - \gamma_2 I_2 \qquad (15)$$

$$\frac{dR}{dt} = \gamma_2 I_2 + \theta^- E \qquad (16)$$

In the differential equations above, α is a coefficient accounting for imperfect mixing in each area, σ is the rate at which infected people become infectious, γ_1 is the rate of

transitioning out of the pre-symptomatic state, γ_2 is the recovery rate.

As you can see, some parameters are not part of the traditional SEIR model presented. Different from other SEIR-based models, the IHME model includes a time-varying parameter $\beta(t)$ that captures temporal variations in past transmission intensity. And the association between $\beta(t)$ and some covariates (including both time-varying and non-time varying ones such as altitude and population density) are assessed by a multivariate mixed-effects regression using a solving tool called SLIME. The regression model and forecast covariate values are used to give an estimation of the future transmission intensity $\beta_p(t)$. Moreover, to ensure continuity of the parameter after some time, $\beta_p(t)$ is adjusted into the final parameter $\beta_F(t)$.

θ^+ and θ^- are two corrections made to the model: the importation correction and the small location correction. The importation correction factor increases the number of additional infections besides the interactions between individuals in "Susceptible" and "Infectious" states. This can be explained easier by the fact that some people become infected outside the modelled area and come back as individuals in the "Exposed" state. The small location correction transfers some individuals in the "Exposed" state to the "Recovery" state. Note that for every location, only one of these two corrections is received.

With all these parameters determined from the data available, the differential equations can be solved by using the Runge-Kutta 4 algorithm (Barber et al., 2020).

This model incorporates predictions four months into the future, mainly focusing on deaths and hospitalization (Institute for Health Metrics and

Evaluation, 2021). For each projection, several prediction results with different scenarios are given. For example, in the graph of predicted total deaths shown below, three projection curves are provided: The purple dashed line represents a current projection, while the red dashed line indicates the worst case and the green dashed line shows the scenario in which people all over the world wear masks.
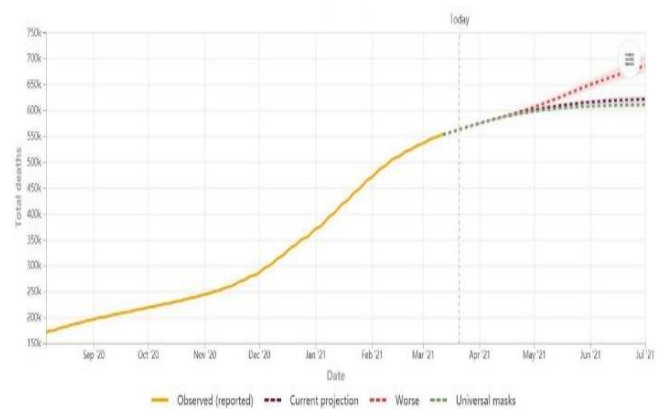

Figure 8. IHME projections of total deaths for North America on March 21(Institute for Health Metrics and Evaluation, 2021)

Comparisons

The three models chosen are evaluated from the four aspects: accuracy, complexity, range of application, and timeliness, respectively. "Accuracy" and "Timeliness" are rated by scores from 1 to 5, in which the highest score 5 represents the greatest accuracy and timeliness, and the lowest score 1 indicates the worst accuracy and timeliness. "Complexity" is evaluated by three levels: complex, moderate, and simple. The range of applications is summarized as global, national, or regional (provinces or states). Note that this comparison is based on the author's personal opinions concerning available information.

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Table 2. Comparison of three models

	Accuracy	Complexity	Range of application	Timeliness
GLEAM	3	complex	regional/national	3
DELPHI	4	moderate	national/global	3
IHME	5	moderate	regional/national/global	5

Discussions

Accuracy of the Model

Different models give projections of different periods into the future based on the teams' understanding of the pandemic. GLEAM makes predictions for four future weeks in total, the DELPHI model gives predictions for six future weeks, and the IHME model provides forecasting results for four future months. These predicted periods should not be too short, making the model unable to show the trend of the pandemic; also, not too long, giving less accurate results. So, the developers should strike a balance between the time in which results are provided and the accuracy of the model. However, this balance is more crucial to policymakers, who require both accurate and prospective forecasting results. If we merely compare the accuracy of models, the length of this projection period taken should not be taken into consideration. Thus, it becomes a control variable: under the same time range, which model has the most accurate results.

Generally, all three models give good results in the first one or two weeks of projection, while The GLEAM model shows a higher value of MAPE (less accurate) than DELPHI in most of the evaluated weeks and showed lower robustness since there is one big fluctuation of its MAPE value (MIT Operations Research Center,

2021). Note that the mean absolute percentage error is a measure of the accuracy of a model. The DELPHI team claims that the trends predicted by DELPHI are shown to be 3-5% more accurate than other models. It performs well on per-state predictions, having an average mean absolute percentage error (MAPE) below 7%, being accurate and robust (MIT Technology Licensing Office, 2021). However, in an evaluation of models by the IHME team, the results turned out to be that the IHME model gives the best results in MAPE with a long projection period, especially when the prediction time range is extended to 12 weeks (Friedman et al., 2020). These two teams seemed to provide some contradictory results, demonstrating the accuracy of their models. After comparing these two pieces of evaluations, I tend to believe more in the results provided by the IHME team since they presented detailed data and evidence to support their conclusions, while the DELPHI team did not introduce how their results are concluded.

The accuracy results concluded from projections of some regions might be a little different from the results provided in the previous paragraph since this is a general result and the quality of data might vary with region.

Complexity of the Model

The complexity of a model is not a factor considered by most people since they tend to pay greater attention to actual forecasting results, but not the process of establishing these models. However, whether a model is complex or not is an important factor to consider if one tries to learn this model and use it for further predictions by him/herself.

The GLEAM model is a combination of agent-based models and epidemiological dynamic models, thus carrying out a complicated process

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while setting up the model. As this model is established, a huge worldwide network is set up at first, and this requires a great number of calculations and large amounts of data worldwide. Moreover, the SEIR model is superimposed on this network, which gives even larger amounts of calculations. So, this model requires a complicated coding process due to its principle of creating a simulation of the world.

The DELPHI model is an improved version of the SEIR model. Concerning the set of differential equations shown in section 3.2., it is obvious that a large number of new parameters are defined and added to the original model. It agrees with our common sense that the code produced and data needed would become much more complicated when each new parameter is added. Although the forecasting process involves a huge workload of coding, the underlying logic is not hard to understand. The basic principles are almost the same as the SEIR model, which is the transfer of individuals from one compartment into the other when time passes. Also, the team which created this model shortens the algorithm design process, which might take a human team a whole year to develop (MIT Technology Licensing Office, 2021).

The IHME model is an SEIR-based model involving multiple parameters. It seems similar to the DELPHI model and has even fewer parameters. However, it involves various fitting processes and a regression model is also used. Therefore, it is not as simple as it seems to be.

To sum up, none of these three models consists of simple modelling and calculations. It is easy to understand since the transmission of COVID-19 is a complicated process itself, thus various parameters, assumptions, and codes are used. However, within these three models compared, the DELPHI model presented the simplest logic

and the easiest operating process.

Range of Application of the Model
Since all the three models chosen in this dissertation are established mainly by teams from the United States, it is understandable that every model includes forecasting results of America and its states, regardless of the range of application of the model itself.

Up to now, the GLEAM model is only used to forecast the pandemic in America and its states. GLEAM may perform well in the prediction of other regions in the world. However, forecasts outside the United States have not been carried out yet, so we have no idea whether it would still be a good model when dealing with data from different countries. Also, it does not provide any prediction results in larger regions such as continents and the world.

DELPHI gives prediction results of 166 countries, five continents including Asia, North America, South America, Africa, and Europe, and the world. It mainly focuses on the prediction of large areas and only provides regional forecasting results within the United States.

IHME also provides national, continental, and worldwide forecasting results, similar to that of DELPHI. Besides, it also predicts the trends in different states or provinces in some countries, not only the United States. So, compared to DELPHI, it is a more widely used model.

In summary, GLEAM mainly provides regional predictions, especially within the United States, while DELPHI and IHME forecast larger regions up to a worldwide range. On the regional level, IHME gives results for more areas than DELPHI, which only forecasted the trends of states in America.

Timeliness of the Model

The team claims that GLEAM is regularly updated as new data and policies become available (The Gleam Project, 2021), but no specific date of update is stated on their website. Therefore, regardless of its prediction results, the timeliness of this model is still questionable.

The most recent update of the DELPHI model is on the 19th of November 2020 (MIT Operations Research Center, 2021). Although this time of update seems recent (only four months to now), it is a little bit outdated since policies and corresponding situations change rapidly. A small policy change might cause a great change in the results presented.

IHME updates its model when new information about the virus comes out and the most recent update is on March 2021. The team also improves their modelling methods based on feedback they receive (Institute for Health Metrics and Evaluation, 2021). Almost every week, the team provides results briefings of the areas they forecasted, which include the newest updates to the model, the current situation, and the projection results. Therefore, it has great timeliness since updates based on new situations are frequently made.

In a nutshell, all three models compared in this dissertation are still actively producing forecasts and making updates based on new information about the virus and new policies. Among these models, IHME is the most frequently updated model.

Although some models perform better than other models on specific aspects, it would be better not to rely on a particular model if you want a comprehensive and reliable forecasting result. In this case, combining the results of multiple models might be a more rational choice.

However, if you tend to value a specific factor of a model much greater than others based on your perceptions, the results presented in this dissertation would be a useful reference.

Possible Disadvantages

Attempts to model the spread of diseases were carried out since 1766. During the following centuries, more scientists made contributions to modern epidemiological models, with A. G. McKendrick and W. O. Kermack being the most acclaimed ones (Atkins, 2008). Along with the development of thoughts on modelling diseases, the SEIR model and similar compartmental models such as the SIR model were formed gradually and used to predict other epidemics and pandemics in the past. For example, various models were established based on the SEIR model to predict deaths from Ebola and Zika outbreaks.

Already mentioned in the previous sections, the three models chosen in this dissertation are all based on the SEIR model. Whether this is an advantage or disadvantage should be discussed. From my perspective, there must be a reason for different teams to choose the same model to start with. As introduced in the previous paragraph, it took a long time for the SEIR model to develop and many scientists contributed to this development, so the underlying mathematical logic is believed to be correct. This means that the newly established models also have reliable basic logic since they are all modifications of the SEIR model. Meanwhile, this might also be the point where a breakthrough is needed. There might be a more appropriate and flawless way of modelling the spread of diseases, which is not developed yet.

Normally, a model takes a long time to be established. However, for the emergency use of governments to make new policies due to the

COVID-19 pandemic, prediction models were created at a rapid speed. Inevitably, some assumptions made and parameters created are not the most appropriate ones since there is not enough time given to developers to consider them comprehensively as we gain more knowledge about the virus. Therefore, these models will possibly perform better projection results when the coronavirus is fully studied. More information will be provided to the developer teams and they would establish more accurate models. Anyhow, they already did their best to give the most accurate results under the current knowledge and situation.

Some critics question the reliability and accuracy of the IHME model since it was much concern due to its cited contents during the White House briefings. It does not mean that a model is unreliable when it is questioned by others. No models can be accepted by every single person in the world. It only represents the fact that every model created at such a rapid speed has defects. Less criticism on other models might indicate better models- that is what we are looking for, but at the same time, maybe they just simply gain less attention from people, leading to fewer discussions.

Conclusion

Focusing on the accuracy of the model, the IHME model gives more accurate forecasting results. Considering the complexity of the model, the DELPHI model turns out to be the simplest one among all three models. For the range of application of models, the IHME model has a wider range of use which includes predictions regionally, nationally, and globally. The IHME model is the model with the best timeliness.

On the whole, IHME is the model with the best performance in forecasting the trend of the COVID-19 pandemic.

All three models can be considered reliable since they are based on the SEIR model, while a breakthrough in basic models might give better models and results. When more knowledge about the pandemic and more time is provided, models will have better performances on projecting the trend of the pandemic.

Conflict of Interests: the author has claimed that no conflict of interests exists.

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