Network Models to predict Influenza-like Illnesses

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***Abstract*—Infectious disease spread forecasting plays a crucial role in estimating the potential spread of diseases within a population, providing public health officials with an early warning system that enables them to prepare for and respond to potential outbreaks effectively. The flu has been a popular disease for forecasting in the United States due to the availability of data and recurrent flu seasons. However, a significant drawback of many existing forecasting systems is their season-dependence, meaning they primarily consider data from specific seasons. Our project introduces a comprehensive forecasting model consisting of two primary components. The first component is a machine learning-based approach that incorporates neural networks and an Agent-Based Model (ABM) to predict disease-specific parameters. The second component utilizes the output parameters from the ABM to solve the SEIRM model, an extension of the traditional Susceptible, Infectious, Recovered (SIR) epidemiological model that includes the Exposure and Mortality rates. We integrated training data from various sources, including search trends related to disease symptoms, hospitalization, case reports, and mortality reports across multiple flu seasons. The model was tested on unseen flu seasons (2021 - 2022) and evaluated using the Mean Absolute Error (MAE) and Coverage metrics.**

I. Introduction

Over the past few years, the field of epidemiology has witnessed substantial growth, largely driven by the global pandemic. A critical aspect of this discipline is understanding disease dynamics and transmission patterns, which necessitates the development of comprehensive and universally applicable models. Our research aims to take a step towards building such a model, specifically designed to be robust in the face of seasonal fluctuations. This approach allows for more accurate predictions and valuable insights into the spread of infectious diseases and the management of complex medical conditions.

Our methodology consists of a two-step process. The first step employs an Agent Based Model (ABM) to estimate the parameters for the modified Susceptible Exposed Infectious Recovered Mortality (SEIRM) model, taking into account disease-specific factors and parameters related to agent initialization. The ABM is a powerful tool for simulating individual interactions and their aggregate effects on the spread of diseases, providing a detailed and nuanced understanding of disease transmission. The second phase involves applying the SEIRM model, which uses conventional differential equations along with the parameters generated by the ABM. This combination allows for the estimation of disease spread within a specific region over a designated time period, offering insights into the possible trajectory of an outbreak.

A primary objective of our model is its adaptability across different seasons. To achieve this, it is essential to consider data collected throughout the entire year, independent of the flu season. This comprehensive approach enables the model to serve as an effective tool for informing policy decisions aimed at reducing widespread exposure and mitigating the impact of infectious diseases. To that end, we train our model using a variety of data sources, such as case and death records for each epiweek, symptom surveys, and ILI (Influenza-like Illness) values for each state in the United States. This wealth of data allows the model to account for various factors that influence disease transmission and provides a solid foundation for accurate predictions.

Focusing on predicting the spread of the flu, our training data set includes flu data from multiple seasons spanning from 2016 to 2019. Meanwhile, the test data consists of unseen seasons from 2021 and 2022, which allows us to evaluate the model's performance on novel data. This targeted approach ensures that our model is well-calibrated to provide accurate predictions and valuable insights into the transmission and impact of various infectious diseases. We evaluate the test data through n-week ahead forecasting ($n \in \{1, 2, 3, 4\}$) and looking at metrics like Mean Absolute Error (MAE) & Coverage.

Contributions

Our main contributions are the following:

- A modified Agent-Based Model (ABM) building upon [1] for forecasting seasonal variations of Influenza in the United States by incorporating data from multiple flu and non-flu seasons in the training dataset
- A Stochastic SEIRM (Sto-SEIRM) model into the DNN to account for the inherent randomness and uncertainty in the spread of infectious diseases*
- Loss functions to fine-tune predictions from each model individually
- Improvement over GradABM [1] approach to predict the mortality along with ILI (Influenza-like Illness).

In summary, our research introduces a robust and adaptable model that can account for seasonal variations while providing valuable insights into the spread of Influenza. By combining the strengths of Agent Based Modeling and the SEIRM model, we offer a powerful tool that can inform policy decisions and contribute to the ongoing efforts to control and mitigate the impact of infectious diseases on a global scale.

* A deviation from our original plan is the use of deterministic SEIRM model over Sto-SEIRM model when training. This has been necessitated due to computational constraints from the large population size when solving the SDEs, which is increasing the training time from our experiments.

II. Related Works

Differential Equation based models (like the popular SIR model [2] or the Fisher-KPP model [3], built upon partial derivatives [4]) have been used to describe the temporal dynamics of infectious disease spread. An underlying assumption is that all infected individuals have been observed, which poses issues when there are cases of under-reporting, especially in evolving situations like the COVID-19 pandemic, which can have significant impact [5]. Directly modeling an SIR model on under-reported data would underestimate the transmission rate, giving false indications about the severity of disease spread.

Much research has been done to address this drawback. For example, [6] proposes a Distributed Infection model where the susceptible population is split into the observed and unobserved categories. But since the data from the unobserved category is not available, even this model can fail. More recently, other models propose extending the SIR framework to include the exposed [7] and other parameters to stratify the populations [8], [9], [10].

Given the algorithmic and computational simplicity of SIR-like models, they have also been used in hybrid models along with neural networks in various forecasting problems [11], and probabilistic Monte Carlo simulation based approaches [12]. One reason for this simplicity is due to the fact that the modeling makes assumptions of homogenous transmission and perfect mixing, which abstracts away the heterogeneity of contact graphs within a population. This led to the emergence of agent based models (ABMs), as further discussed in [1]. ABMs can be especially useful in modeling the micro-level interactions (for counterfactuals) like the effect of policy decisions. A major potential contribution includes an exploration of the interplay between ABM/ODEs at the micro-macro levels to better capture the dynamics & network effects of disease spread. This work has some limitations, which are discussed towards the end of this section.

As an extension of the hybrid models, approach to disease spread estimation using ensemble techniques has been widely popular among the community since the start of COVID-19. Starting from April 2020, US COVID Forecast Hub [13] collaborated with more than 90 research groups from academia, industry and as well as independent groups to collectively share the weekly or monthly COVID-19 predictions and used an ensemble model which took into account all the submissions and gave a better predictive model [14] This gave rise to so many ensemble techniques which could incorporate different models or predictions and improve the prediction of the model. One study showed that neural network based transfer learning can be used from previous pandemics to help predict multiple diseases occurring in the same timeline such as COVID-19 and the flu [15]. Although ensemble models work well in forecasting models, new approaches like Agent Based Models seem to model the simulation of the interaction in a population and forecast the disease spread based on this simulation better than existing traditional Machine Learning approaches.

Other proposed methods also include the use of Lyapunov functions to model the dynamics from a chaos theory perspective [16], the use of Markov Random Fields [17], and adopting stochastic models for SIR [18] and contact networks [19].

Our proposed approach builds upon the model in [1] by taking all discussed advantages and limitations into consideration. The proposed model makes use of agent interactions using ABM and forecasts the disease spread using the SEIRM to better account for the uncertainty in the disease spread. The applicability & advantages of the use of stochasticity has been well discussed in [18], and will be omitted here for brevity. We further extend the SIR model by including two compartments - Exposed and Mortality to include additional stages of disease progression mimicking the real world scenarios.

A. Data

The recent pandemic has underscored the critical importance of accurate disease spread forecasting, driven in large part by the availability of vast amounts of diverse data. This wealth of information, encompassing biological, social media, geographic, genomics, and satellite imagery data, has been leveraged extensively for modeling disease transmission at both micro and macro levels [20].

Data from the Centers for Disease Control and Prevention (CDC) of the United States [21], which includes hospitalization rates, testing data, infection rates, and death rates, has played a significant role in forecasting efforts. However, recent studies [20]. have demonstrated that incorporating macro-level data, such as mobility data, social media analysis, pharmaceutical data, and geographical factors like air quality or wastewater data, can lead to more accurate predictions. This is because the spread of a disease is influenced by a complex interplay of these interconnected components.

Our approach primarily focuses on utilizing data from the CDC for flu-related factors, such as deaths and cases for each epidemiological week. We also consider Google symptom survey data to gain further insight into the prevalence of flu-related symptoms. To generate agent parameters for each state in our model, we take into account several demographic factors, such as age distribution, occupation, and household size data for each US state, sourced from the US Census. By integrating this diverse range of data sources and carefully considering the various factors that contribute to disease spread, we aim to develop a more comprehensive and reliable model for forecasting the transmission and impact of infectious diseases.

B. Evaluation

Evaluating the performance of forecasting systems is a complex and often challenging task, with various metrics

employed to assess the accuracy and reliability of predictions. Historically, the logarithmic score has served as a benchmark for evaluating forecasting systems, but its use requires the availability of an entire predictive distribution [22]. As a result, alternative metrics have been developed and adopted by the forecasting community.

One such metric is the Weighted Interval Score (WIS), which assesses the consistency of prediction intervals in relation to the ground truth [14]. WIS can be interpreted as a generalization of absolute error for probabilistic forecast models, allowing for a more nuanced understanding of model performance [22]. This metric has gained popularity due to its ability to provide meaningful insights into the accuracy of interval forecasts and probabilistic predictions.

Another widely used metric is the Mean Absolute Error (MAE), which has increasingly been favored over the Mean Squared Error (MSE) in recent years. The reason for this preference lies in the fact that MSE tends to penalize outliers more heavily than MAE, which can lead to an overestimation of a model's performance. By contrast, MAE provides a more balanced assessment, taking into account both the magnitude and direction of errors, making it a more suitable choice for evaluating forecasting models in various scenarios.

In summary, the selection of appropriate evaluation metrics is crucial for understanding the effectiveness and reliability of forecasting systems. Metrics such as WIS and MAE have gained prominence due to their ability to provide meaningful insights into model performance, allowing researchers and practitioners to make informed decisions when developing and refining their forecasting methodologies.

III. Methodology

Our approach is a combination of the below three components. We derive & build upon the work done in [1].

Our initial idea has been to utilize Stochastic SEIRM for reporting all our results, but given the population times and the inherent nature of the SDE solvers, we encountered longer training times. This led to a decision to only report evaluation results for the deterministic version of SEIRM.

We use the ODE component only during the training part so that it can regularize the short-term predictions.

A. Caliberation Networks (CalibNN)

The primary interface between our model and the real-world data (discussed in Experiments) is the Caliberation Network (CalibNN).

As can be seen in the figure 1, we use three variations of the CalibNN to feed in parameters to our model.

The ABM-CalibNN & ODE-CalibNN have a similar architecture, as defined in the original work:

- Gated Recurrent Unit (GRU) based encoder-decoder, which is fed in a time-series data from various sources to obtain a condensed representation for each time step
- Self Attention layer, which is used to capture long-term relations and prevent over-emphasis on last terms of sequence
- Fully connected layer to obtain a single embedding of the time series.

The first network (ODE-CalibNN) deals with the ODE part of our model. The outputs of this network are:

- SEIRM parameters β, α, γ, μ
- Boundary conditions defining the initial state of the SEIRM model

These are fed into SEIRM model along with the population and time-interval to obtain the compartmentalized predictions of disease progression, the specifics of which are further discussed in the upcoming sections.

Similarly, the second network (ABM-CalibNN) deals with the ABM part of our model. The outputs of this network are the disease reproduction rate R_0, initial infections percentage, and a transmissibility for the infection.

These parameters are fed to the ABM to model network interaction effects, further discussed in the upcoming sections.

The third network takes the output from ABM - exposures, infections, deaths per day - and parameterize it into real-world like data to allow us to calculate the loss functions, further discussed in upcoming sections.

B. Agent Based Models (ABM)

Primarily, our approach modifies the Agent Based Model introduced in [1], and most details are from that work. It designs the ABM using tensor operations in such a way that it is end-to-end differentiable.

The micro-interactions between the agents are modeled through a network graph, and by introducing a deterministic message-passing system to capture disease transmission, progression & update stages for a given population. As with typical epidemiological research, the ABM uses the standard Transmission Model and a Progression Model. These two recursively update the state of all agents.

Given a state population N, our model currently considers the number of agents N_a as

$$N_a = 20\sqrt{N} \tag{1}$$

For each agent $j \in \{1, ..., n\}$, Agent States are denoted by a 3D tensor $X_j^t = (a_j, d_j^t, e_j^t)$, at time step $t \in \{0, ..., K\}$. Here, $a_j \in \{0-10, 11-20, ..., 71-80, 80+\}$ is the age of the agent, d_j^t is the current disease state of the agent, $e_j^t \in \{-1, ..., t-1\}$ is the time step of the last exposure.

The Transmission Model is a parameterized model that computes the probability of infection transmission as a result of an interaction between Susceptible and Exposed individuals. Interaction networks are generated here to represent the sites of contact between agents that transmit infection, and takes into account location based proximity as well (household, work, etc). For every interaction between agents i and j, the graph evolves at each time step, bound to the parameters of infectiousness of the pathogen R^t, susceptibility of infectee i (S_i) to transmission, transmissibility of the infector j (T_j), and the time since exposure of the infector.

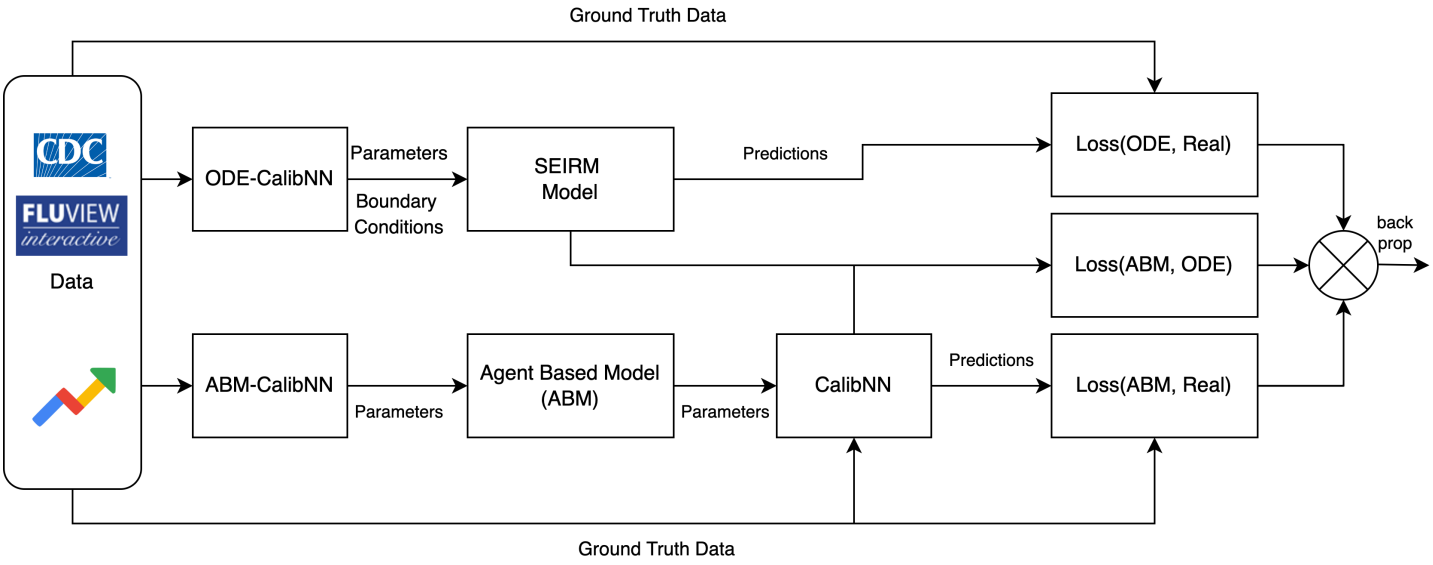

Fig. 1. High level model architecture, showing the ABM and the SEIRM model, and the flow of data into the three caliberation networks, and its further flow into the ABM and SEIRM modules. Details are explained in the Methodology section.

Once exposed, the agent enters the hierarchy of disease progression, as defined in the Progression Model which triggers subsequent changes in the state of the individual to the other compartments. While this part also uses the SEIRM model, it is different from our ODE component, and is fully internal to the ABM. This is parameterized by stage transition times and mortality rate.

Overall, the interaction networks better inform the $S \rightarrow E$ transitions, which make the model better suited for real-world applications.

In the forward simulation for ABM, we combine the parameters discussed above to simulate the disease dynamics over a time horizon. The details are similar to the original work, and are being omitted here for brevity.

C. ODE Component

Given the inherent randomness of disease progression, we expand upon the SIR compartmental model to include two additional compartments for Exposure and Mortality, and look into adding stochasticity to better mimic the real-world scenarios. This led to the Sto-SEIRM model. The model is based on five compartments: Susceptible (S), Exposed (E), Infected (I), Recovered (R), and Deceased (M).

We explain the Sto-SEIRM model in terms of drift and diffusion terms. The drift term represents the deterministic part of the system, while the diffusion term introduces the stochastic component.

The overall process is framed as a Stochastic Differential Equation (SDE) as given below:

$$dy(t) = f(t, y)dt + g(t, y)dW(t), \tag{2}$$

where $y(t) = [S(t), E(t), I(t), R(t), M(t)]^T$ represents the state of the system at time t, $f(t, y)$ is the drift term representing the deterministic dynamics of the system, and $g(t, y)$ is the diffusion term representing the effect of the noise. $dW(t)$ is the vector of independent Wiener processes.

The drift term ($\boldsymbol{f}$) represents the deterministic differential equations, which also is a part of the SEIRM model:

$$f(t, y) = \begin{bmatrix} -\frac{\beta SI}{N} \\ \frac{\beta SI}{N} - \alpha E \\ \alpha E - \gamma I - \mu I \\ \gamma I \\ \mu I \end{bmatrix}. \tag{3}$$

where β is the transmission rate, α is the rate of progression from Exposed to Infected (inverted incubation), γ is the recovery rate, μ is the death rate, and $N = S+E+I+R+M$ is the total population.

The diffusion term ($\boldsymbol{g}$) represents the stochastic component, corresponding to the independent Wiener processes for each compartment. The diagonal elements represent the noise intensities (standard deviations) for the respective compartments, and the off-diagonal elements are zeros, indicating no correlation between the noise in different compartments. This can be given by:

$$g(t, y) = \begin{bmatrix} \sigma_S & 0 & 0 & 0 & 0 \\ 0 & \sigma_E & 0 & 0 & 0 \\ 0 & 0 & \sigma_I & 0 & 0 \\ 0 & 0 & 0 & \sigma_R & 0 \\ 0 & 0 & 0 & 0 & \sigma_M \end{bmatrix}. \tag{4}$$

$dW(t)$ represents a vector of independent Wiener processes (also known as Brownian motion), one for each compartment in the model. In the case of the Stochastic SEIRM model, we have 5 compartments: S, E, I, R, and M. Thus, $dW(t)$ can be written as:

$$dW(t) = \begin{bmatrix} dW_S(t) \\ dW_E(t) \\ dW_I(t) \\ dW_R(t) \\ dW_M(t) \end{bmatrix}, \quad (5)$$

where $dW_S(t)$, $dW_E(t)$, $dW_I(t)$, $dW_R(t)$, and $dW_M(t)$ are independent increments of Wiener processes associated with each compartment. These increments represent the random fluctuations in the model due to stochastic effects. The increments $dW_i(t)$, for $i \in S, E, I, R, M$, are typically small random variables with mean 0 and variance proportional to the time step Δt. In a discrete time setting, one can approximate the Wiener process increments using normally distributed random variables, i.e., $dW_i(t) \sim \mathcal{N}(0, \sqrt{\Delta t})$.

Given these SDEs, the goal is to generate time-series data for the given time period $\boldsymbol{t}$. Since they are inherently non-differentiable due to the randomness parameter, we employ approximations to ensure that the overall model remains differentiable end-to-end to allow gradient updates. We explored several approaches for this:

- Stochastic Simulation (Gillespie) Algorithm [23]
- Differentiable SDE solvers with backprop [24]
- RNN based Surrogate models [25]
- Physics Informed VAEs [26]

We found the work by [24] to be most compatible with our overall approach, and we adopted it using the PyTorch based library the authors provide.

However, as mentioned earlier, we decided to primarily report our results using the deterministic version of the SEIRM model (without the drift & noise terms), given the longer training times due to the population size & computational constraints. We intend to include these results in a future revision.

D. Combining...

The overall architecture has been shown in Figure 1, and the individual components have been discussed in detail in the previous sections. This section ties these components together.

We consider three loss functions, for ILI (subscript i) and deaths (subscript d), and aggregate them to inform our overall loss. The loss functions (MAE) are generally of the form

$$\mathcal{L}(\mathbf{y}, \hat{\mathbf{y}}) = \frac{1}{n} \sum_{i=1}^{n} |\hat{y}_i - y_i| \quad (6)$$

with comparisons happening between the following ($Real_x$ is the real world ground truth data):

- (ABM_i, ODE_i), (ABM_d, ODE_d)
- $(ABM_i, Real_i)$, $(ABM_d, Real_d)$
- $(ODE_i, Real_i)$, $(ODE_d, Real_d)$

These losses are further used to backprop over the network, and update the gradients of the entire model, specifically to CalibNN which contain the components building the parameters that drive the model.

One distinction is that the loss between ODE & real world data is only backprop'd over the ODE network, and not over the entire model. This has been done since the ABM model is already informing the parameters of ODE.

This approach is an improvement over the existing work.

IV. Experiments

Our primary goal has been to show that the modified approach we took gives better results than the existing models, even when not using the stochastic component as originally planned. This section describes the experiments we did, and the data used, along with some results.

A. Data

Our model uses various data sources for flu forecasting in the United States, focusing on state-level and region-level information. The first key data source is ILINET [27], which gathers data from a network of medical care providers outside of the hospital setting across the country. These providers collect and share crucial data on the number of patients visiting them due to Influenza-Like-Illnesses (ILI) categorized by age groups. This extensive ILI dataset offers valuable insights into the prevalence and spread of flu-like symptoms within different regions and states, contributing to the accuracy of our model.

The second primary data source is the Google Search Symptom Dataset [28], which contains symptom-related search queries from users. By analyzing search trends for common influenza symptoms such as fever, cough, sore throat, headaches, fatigue, shortness of breath, weakness, and diarrhea, we can better understand the relationship between search history and disease spread. This information helps facilitate the study of disease dynamics and improves the model's ability to forecast flu outbreaks in specific areas.

Lastly, our model incorporates data from the National Center of Health Statistics (NCHS) Mortality Surveillance system and the United States CDC in collaboration with WHO/NREVSS [29]. The NCHS system collects and shares weekly influenza mortality data for the United States, providing a clear picture of the impact of flu on the nation's population. The CDC, working with WHO/NREVSS, offers another major state and region-level data source for influenza cases reported per variant (Influenza A and Influenza B). By combining these comprehensive data sources, our model strives to provide accurate and reliable flu forecasts, ultimately supporting public health efforts to mitigate the impact of influenza outbreaks.

B. Evaluation Metrics

We use the following metrics to evaluate our performance:

1) Mean Average Error (MAE): Given by the equation

$$MAE = \frac{1}{N} \sum_{k=1}^{N} |\hat{y}_k - y_k| \quad (7)$$

where N is the total number of samples being tested, y_k is the target output value, and $\hat{y}_k$ is the predicted output value.

2) Coverage:

$$Coverage = \frac{\sum_{K=1}^{N} lowerbound \leq y_k \leq upperbound}{N} \quad (8)$$

Given N as the total number of data points, with y_k representing the target output and with , the indicator function, we calculate the lower bound of the confidence interval (CI) using the (0.5 - CI/2) quantile prediction, while the upper bound is determined by the (0.5 + CI/2) quantile prediction.

C. Baseline

Vector Autoregression (VAR) and Seasonal AutoRegressive Integrated Moving Average with eXogenous regressors (SARIMAX) are two powerful time series forecasting techniques that are widely used in the field of econometrics, finance, and other domains with time-dependent data.

VAR is a multivariate time series model that captures the linear interdependencies among multiple time series variables. It extends the univariate autoregressive (AR) model to a system of equations, wherein each variable's future values are predicted based on its own lagged values and the lagged values of other variables in the system. This allows for a more comprehensive understanding of the relationships among variables and enables better forecasting of their joint behavior over time.

SARIMAX, on the other hand, is an extension of the AutoRegressive Integrated Moving Average (ARIMA) model, a univariate time series model. It incorporates seasonality by adding seasonal differencing and seasonal autoregressive and moving average components to the base ARIMA model. Moreover, SARIMAX allows for the inclusion of exogenous variables, which are external variables that may influence the target time series but are not predicted by the model. This feature makes SARIMAX particularly useful when there is a need to account for external factors or covariates that could impact the target variable's behavior.Both models offer valuable forecasting capabilities, with VAR being well-suited for multivariate time series and SARIMAX tailored for univariate time series with seasonal patterns and exogenous factors.

D. Results

The model was evaluated for each states and with 1, 2, 3 and 4-week ahead period and the results in tables I and II are the average performance over all these targets. The baseline models have a better coverage but very low MAE score. A low MAE indicates that the model's point predictions are accurate and close to the true values, while a high coverage means that the model's confidence intervals are capturing the true values most of the time.

We can observe that our model improves on MAE but the coverage is less than other baseline model. An ideal combination would be a low MAE with high coverage, but we see both values are low, indicating that while the model has relatively accurate point predictions, the confidence intervals are narrow, which means that it is underestimating the uncertainty in the predictions.

We are assuming that fully integrating the stochastic version of SEIRM would expand the coverage and better account for uncertainties, but other options such as hyperparameter tuning (especially for the ODE & other parameters) could help. This will be explored in future work.

V. Discussion

This section discusses our general approach. Using the data mentioned earlier, we did the following train-val-test split:

- **Train**: Epiweeks 201734 to 202049
- **Validation**: Epiweeks 202050 to 202112
- **Test**: Epiweeks 202201 - 202240

where the last two digits of the epiweeks represent the week in a given year.

During training, we observed the aggregate loss to exponentially decrease, as shown in the figure, resulting in a final loss of around 5.2.

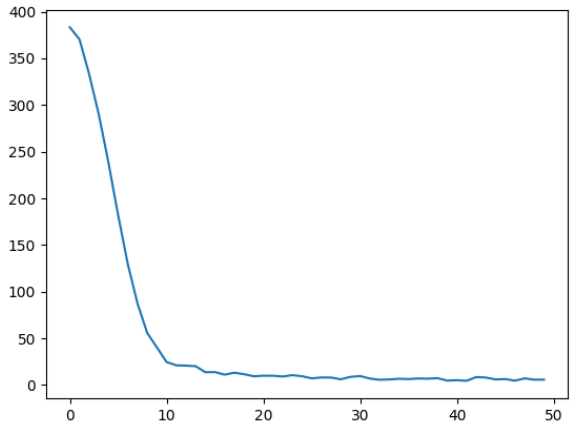

Fig. 2. Train Loss: MAE vs epoch

A main detraction from our initial approach has been adopting the deterministic SEIRM model instead of the stochastic one for final result showcase. This is primarily because for a population of around 5,000 and a time-period of 10 days the stochastic SEIRM doesn't converge even after 1 hour in our experiments. Considering that we are using the ABM networking model in conjunction with the ODE during training, the overall time per epoch goes out of hand. We intend to explore faster solvers to improve this for future work.

VI. Conclusion

Our research has successfully developed a comprehensive and adaptable forecasting model for Influenza-like Illnesses, combining the strengths of Agent-Based Modeling (ABM) and the modified Susceptible Exposed Infectious Recovered Mortality (SEIRM) model. By incorporating data from multiple flu and non-flu seasons, the model has been trained to be robust against seasonal variations, offering more accurate predictions and insights into disease spread and management.

TABLE I
2022 MEAN EVALUATIONS FOR ILI FORECASTING AND COMPARISON OF OUR APPROACH WITH SOME OTHER APPROACHES.

Model	**1 week**		**2 week**		**3 week**		**4 week**	
	MAE	**Coverage**	**MAE**	**Coverage**	**MAE**	**Coverage**	**MAE**	**Coverage**
Ours	**0.48**	0.78	**0.46**	0.79	**0.46**	0.74	**0.48**	0.74
VAR	9.13	**0.95**	9.31	**0.95**	9.02	**0.93**	9.6	**0.89**
SARIMAX	1.14	0.32	1.14	0.3	1.02	0.28	1.18	0.27

TABLE II
2022 MEAN EVALUATIONS FOR MORTALITY FORECASTING AND COMPARISON OF OUR APPROACH WITH SOME OTHER APPROACHES.

Model	**1 week**		**2 week**		**3 week**		**4 week**	
	MAE	**Coverage**	**MAE**	**Coverage**	**MAE**	**Coverage**	**MAE**	**Coverage**
Ours	**0.35**	0.29	**0.42**	0.295	**0.34**	0.31	**0.37**	0.26
VAR	2.51	**0.85**	2.54	**0.83**	2.62	**0.82**	2.62	**0.8**
SARIMAX	1.92	0.14	1.89	0.14	1.85	0.13	1.91	0.14

The integration of neural network training with the SEIRM model accounts for the inherent randomness and uncertainty in infectious disease transmission. Our methodology includes tailored loss functions to fine-tune the predictions from each model individually, providing a significant improvement over previous approaches, such as GradABM [1], by predicting both mortality and ILI rates. By evaluating the model on unseen data from the 2022, we demonstrate the improvement in existing Agent Based approach and its potential as a valuable tool for public health officials and policymakers to effectively prepare for and respond to future disease outbreaks.

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