Neural Networks as Surrogates for Changing Dynamics in Epidemics

Lukas Stelz *Frankfurt Institute for Advanced Studies, Osnabrück University*
stelz@fias.uni-frankfurt.de
Jan Fuhrmann *Heidelberg University* fuhrmann@math.uni-heidelberg.de
Pascal Nieters *Osnabrück University* pascal.nieters@uos.de

Abstract

Traditional epidemiological models struggle to capture how disease transmission evolves due to policy interventions, behavioral shifts, and changing testing strategies. We developed a hybrid AI modeling framework that uses neural networks to automatically discover these time-varying patterns from routine surveillance data alone. Applied to Germany's COVID-19 data, our method successfully reconstructed how transmission rates responded to lockdowns and holidays, while simultaneously uncovering the hidden number of undetected infections as testing capacity evolved. Our AI system works with just reported cases and deaths, making it broadly applicable for real-time epidemic analysis. This approach offers public health officials an interpretable ex-post tool to evaluate interventions and understand outbreak dynamics.

Keywords: Universal Differential Equations, Hybrid Models, Epidemiology

1 Introduction

Epidemiological transmission parameters evolve in response to public health interventions, behavioral adaptations, and pathogen mutations. These external forces challenge traditional epidemiological models which assume fixed parameters. Classical compartmental mean-field models, such as the SIR model [Kermack and McKendrick, 1927], can only capture short periods with constant parameters: Multi-month analyses therefore require explicit modeling of temporal parameter variation.

Existing approaches to time-dependent epidemiological modeling fall into two broad categories. Agent-based models incorporate individual behaviors but require extensive, and often unavailable, data on population mobility and interaction patterns, restricting them to small-scale outbreaks (e.g. [Truszkowska et al., 2021]). Statistical methods can estimate varying reproduction numbers from case data, but lack mechanistic grounding and thus cannot distinguish true transmission changes from observation artifacts (e.g. [Xiao et al., 2023, Cori et al., 2013]).

We present a universal differential equations [Rackauckas et al., 2020] approach that embeds neural networks into the differential equations of the SEIRD model (see Fig. 1) to infer time-dependent parameters in the early COVID-19

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epidemic in Germany. Using ensemble methods (see next section), we were able to handle noisy surveillance data and quantify the uncertainty of predictions. In addition to reconstructing the temporal evolution of the transmission rate, we also recovered the detection probability for all cases, revealing the true number of hidden infections. Unlike approaches that require external behavioral datasets (e.g. [Núñez et al., 2023]), our method relies solely on reported cases and deaths, making it broadly applicable across different epidemiological contexts and data availability scenarios.

2 Method

Our approach uses the universal differential equations framework, incorporating neural networks as surrogates for time-dependent epidemiological parameters in a mechanistic compartmental SEIRD model that includes a pre-death compartment (UDE-SEIRD+, see Fig. 1). The time-dependent transmission rate $\beta(t)$ and case detection probability $p(t)$ are modeled by the output of a single ANN (2 hidden layers, 5 nodes each). Other model parameters were fixed following standard epidemiological practices.

The combined UDE-SEIRD+ model[1] was optimized to fit observed COVID-19 case and death data from Germany in the first 17 months of the epidemic, minimizing the mean squared error between predicted and observed cases and deaths. To statistically validate individual fits, we selected one random day per week as holdout, and performed training on the remaining 86% of the dataset. We used an ensemble of $n = 100$ members fit on different neural network initializations. This ensemble method allows us to quantify uncertainty in our predictions [Schmid et al., 2025]. Reported results represent the ensemble median and 95% confidence interval of the ensemble. Individual ensemble members, even with a moderately small ANN, can overfit the data. This method reliably fitted the data and prevented overfitting of the final ensemble fit.

3 Results

We validated the UDE-SEIRD+ model on German COVID-19 surveillance data from January 27, 2020 to June 30, 2021, encompassing the pandemic's initial phase including multiple surges and policy interventions. The dataset included daily reported cases and deaths, preprocessed using 7-day moving averages to remove weekly reporting artifacts.

Our ensemble approach successfully fitted both reported cases and deaths with a high degree of agreement between ensemble members (see Fig. 2 A). We achieved this by recovering an interpretable time-dependent effective reproduction number $R_t = \frac{S(t)\beta(t)}{N\gamma}$ (see Fig. 2 B), showing clear signatures of policy interventions: sharp decreases coincided with lockdown implementations, gradual increases during reopening phases, and distinct spikes around holidays

[1] https://github.com/SirLukeSchande/time-dependent-epidemiological-models.git

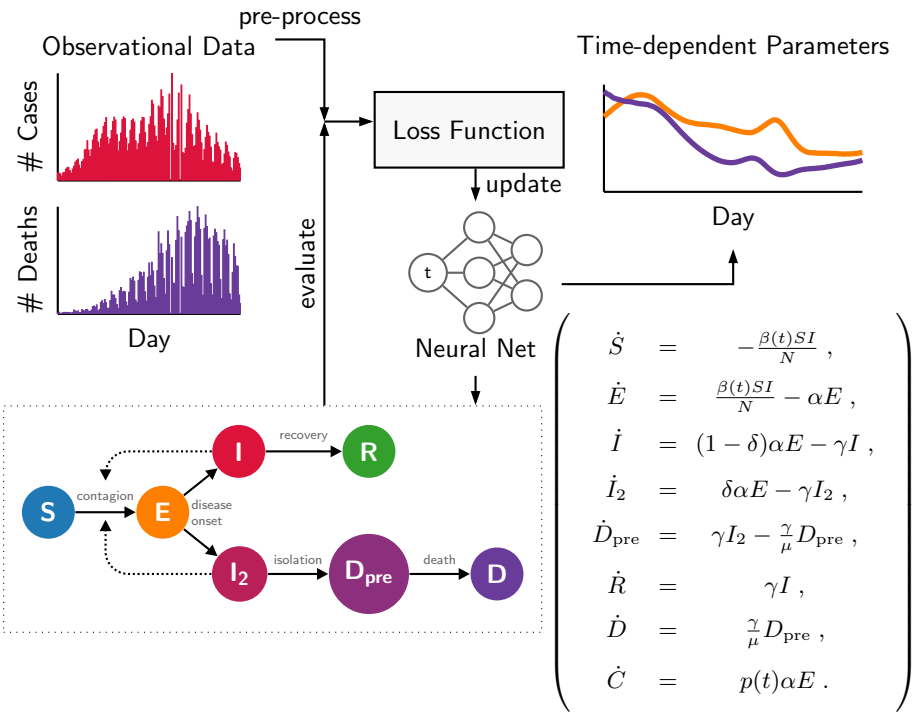

Figure 1: **Modeling approach.** We use an artificial neural network (ANN, center) to fit time-dependent parameters in a classical ODE-based compartmental model(the SEIRD model, bottom). The population is divided into **S**usceptible, who on contact with **I**nfectious individuals get **E**xposed to the disease, subsequently turn infectious themselves, before either becoming **R**ecovered or being isolated (pre-death) and afterwards **D**eceased. Cumulative **C**ases are discovered when entering the I_i compartments (rate αE) with a certain probability. Parameters of the model are transition rates between compartments, we fit time-dependent transitions from **S** to **E**, $\beta(t)$, and time-dependent detection probability $p(t)$. The ANN is trained by comparing reported cases and deaths to real data and backpropagating through the hybrid UDE-SEIRD+ model.

when contact restrictions were temporarily relaxed or ignored. Strikingly, our estimated reproduction number R_t decreased slightly before lockdown measures were imposed. Consistent with other analyses, this suggests that the public was broadly decreasing contacts before policy makers were convinced to mandate this behavior.

Our method simultaneously identified the time-dependent detection probability $p(t)$ from reported data alone, reflecting the evolution of Germany's testing strategy (see Fig. 2 C). During the first wave (March—May 2020), the detection probability remained below 15%, indicating substantial underestimation of true

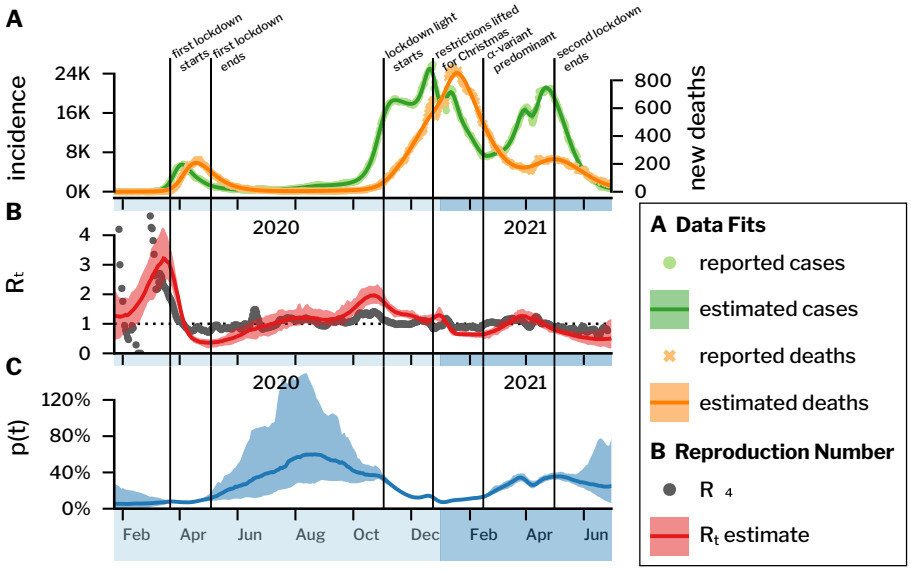

Figure 2: **Reconstructed model. A:** The model fits reported case and death data to very high precision and ensemble member agreement, which is indicated by narrow confidence intervals. **B:** The estimated reproduction number R_t follows the overall trend of the data-derived reproduction number $R_{t,4} = \frac{\Delta C_t}{\Delta C_{t-4}}$, while showing greater coincidence with countermeasures. **C:** The model simultaneously estimated detection probability $p(t)$ shows very low variability in periods with high incidence and high variability when incidences were low.

cases when testing was limited to symptomatic cases. Over the summer of 2020, $p(t)$ increased as testing capacity expanded, but the upper bounds of confidence intervals exceeding 100% indicate higher false positive rates during periods of low-incidence.

The ensemble members demonstrate a high degree of agreement in the model output and loss on the holdout dataset did fall in parallel to the training loss. Beyond this statistical validation, the close temporal alignment of changes in the inferred time-dependent parameters and the timing of lockdown measures (see Fig. 2 at the top) offers qualitative support for our model.

4 Discussion and Conclusion

We have demonstrated that neural networks in a hybrid modeling approach can serve as effective surrogates for time-dependent epidemiological parameters, enabling data-driven discovery of disease dynamics from routine surveillance data, as well as the analysis of derived metrics, such as the reproduction number and the average contact rate. Our ensemble approach addresses key challenges in epidemiological modeling: handling noisy, incomplete data while providing

uncertainty quantification and estimates of transmission rate changes dependent on surveillance reliability grounded-in-data.

The framework's ability to jointly estimate transmission rates and detection probabilities represents a significant advance over existing methods that typically assume one parameter is fixed and constant [Kharazmi et al., 2021]. However, parameter identification becomes challenging towards the end of the fitting period, because we do not know how many of the current infections in this period will lead to deaths. This increases variability in the model and limits direct application to forecasting. Future extensions may address this by including predictors for the recovered transmission and detection rates.

While classical assessment of epidemic outbreaks relies on reported incidence, this metric lags behind the actual changes in human behavior. In contrast, our approach estimates the real-time transmissibility of a pathogen, which enables more accurate temporal linking between observed changes in disease spread, real-world events and interventions. As an ex-post analytical tool our approach is also suited to compare these dynamics across different countries [2].

This work establishes universal differential equations as a powerful tool for data-driven epidemiological modeling, providing a new method to identify underlying, context-specific, and time-specific variations in the transmission and observation processes.

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