Investigating the Evolution of the COVID-19 Pandemic in Germany Using Physics-Informed Neural Networks

Bachelor Thesis in Computer Science

submitted by

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Jena, den 14. September 2024 Phillip Rothenbeck

40 pages in total

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Überblick

German version of the abstract.
Hello, here is some text without a meaning. This text should show what a printed text will look like at this place. If you read this text, you will get no information. Really? Is there no information? Is there a difference between this text and some nonsense like "Huardest gefburn"? Kjift – not at all! A blind text like this gives you information about the selected font, how the letters are written and an impression of the look. This text should contain all letters of the alphabet and it should be written in of the original language. There is no need for special content, but the length of words should match the language.

Abstract

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Chapter 1

Introduction

1.1 Related work

Chapter 2

Theoretical Background

This chapter introduces the theoretical knowledge that forms the foundation of the work presented in this thesis. In Sections 2.1 and 2.2, we talk about differential equations and the underlying theory. In these Sections both the explanations and the approach are strongly based on the book on analysis by Rudin [Rud07] and the book about ordinary differential equations by Tenenbaum and Pollard [TP85]. Subsequently, we employ this knowledge to examine various pandemic models in Section 2.3. Finally, we address the topic of neural networks with a focus on the multilayer perceptron in Section 2.4 and physics informed neural networks in Section 2.5.

2.1 Mathematical Modelling using Functions

In order to model a mathematical problem, it is necessary to define a set of fundamental numbers or quantities upon which the subsequent calculations will be based. These sets may represent, for instance, a specific time interval or a distance. The term *domain* describes these fundamental sets of numbers or quantities [Rud07]. A *variable* is a changing entity living in a certain domain. In this thesis, we will focus on domains of real numbers in $\mathbb{R}$.

The mapping between variables enables the modeling of the process and depicts the semantics. We use functions in order to facilitate this mapping. Let $A, B \subset \mathbb{R}$ be to subsets of the real numbers, then we define a function as the mapping

$$f : A \to B. \tag{2.1}$$

In other words, the function f maps elements $x \in A$ to values $f(x) \in B$. A is the *domain* of f, while B is the *codomain* of f. Functions are capable of representing

the state of a system as a value based on an input value from their domain. One illustrative example is a function that maps a time point to the distance covered since a starting point. In this case, time serves as the domain, while the distance is the codomain.

2.2 Basics of Differential Equations

Often, the change of a system is more interesting than its current state. Functions are able to give us the latter, but only passively give information about the change of a system. The objective is to determine an effective method for calculating the change of a function across its domain. Let f be a function and $[a, b] \subset \mathbb{R}$ an interval of real numbers, the expression

$$m = \frac{f(b) - f(a)}{a - b} \tag{2.2}$$

gives the average rate of change. While the average rate of change is useful in many cases, the momentary rate of change is more accurate. To calculate this, we need to narrow down, the interval to an infinitesimal. For each $x \in [a, b]$ we calculate

$$\frac{df}{dx} = \lim_{t \to x} \frac{f(t) - f(x)}{t - x}, \tag{2.3}$$

if it exists. $\frac{df}{dx}$ is the *derivative*, or *differential equation*, it returns the momentary rate of change of f for each value x of f's domain. Repeating this process on $\frac{df}{dx}$ yields $\frac{d^2 f}{dx^2}$, which is the function that calculates the rate of change of the rate of change and is called the second order derivative. Iterating this n times results in $\frac{d^n f}{dx^n}$, the derivative of the n'th order. Another method for obtaining a differential equation is to create it from the semantics of a problem. This method is useful if no basic function exists for a system.

In the context of functions, it is possible to have multiple domains, meaning that function has more than one parameter. To illustrate, consider a function operating in two-dimensional space, wherein each parameter represents one axis or one that, employs with time and locations as inputs. The term *partial differential equations* (*PDE*'s) describes differential equations of such functions, which require a derivative for each of their domains. In contrast, *ordinary differential equations* (*ODE*'s) are the single derivatives for a function having only one domain. In this thesis, we only

need ODE's.

A *differential system* is the name for a collective of differential equations. The derivatives in a differential system each have their own codomain, which is part of the problem, while they all share the same domain.

Tenenbaum and Pollard [TP85] provides many examples for ODE's, including the *Motion of a Particle Along a Straight Line*. Newton's second law states that "the rate of change of the momentum of a body ($momentum = mass \cdot velocity$) is proportional to the resultant external force F acted upon it" [TP85]. Let m be the mass of the body in kilograms, v its velocity in seconds per meter and t the time in seconds. Then, Newton's second law translates mathematically to

$$F = m\frac{dv}{dt}. \tag{2.4}$$

It is evident that the acceleration, $a = \frac{dv}{dt}$, as the rate of change of the velocity is part of the equation. Additionally, is the velocity of a body the derivative of the distance traveled by that body. Based on these findings, we can rewrite the equation 2.4 to

$$F = ma = m\frac{d^2s}{dt^2}. \tag{2.5}$$

2.3 Epidemiological Models

After a pandemic like *COVID-19*, which has resulted in a significant number of fatalities, the question remains: How should we fight a pandemic correctly. Also, it is necessary to study whether the employed countermeasures efficacious in combating the pandemic. In the light of the unfavorable public responce to measures such as lockdowns, it is imperative to investigate that their efficacy remains commensurate with the costs incurred to those affected. In the event that alternative and novel technologies were in use, such as the mRNA vaccines in the context of COVID-19, it is needful to test the effect and find the optimal variant. In order to conduct the aforementioned investigations we need to develop a method to quantize the pandemic and its course of progression. The real world is a highly complex system, which presents a significant challenge attempting to describe it fully in a model. The model must therefor reduce the complexity while retaining the essential information. Furthermore, it must address the issue of limited data availability. For instance,

during COVID-19 institutions such as the Robert Koch Institute (RKI) were only able to collect data on infections and mortality cases. Consequently, we require a model that employs an abstraction of the real world to illustrate the events and relations that are pivotal to understanding the problem.

2.3.1 SIR Model

One of the most influential epidemiological models is the *SIR Model* introduced by Kermack and McKendrick [KM27] in 1927. The book *Mathematical Models in Biology* [EK05] re-iterates the model and the following explanation will be based on it.

The SIR Model is able to depict diseases, which are transferred by contact or close proximity of an individual carrying the illness and a healthy one. This is possible due to the distinction between infected beings carrying the disease and the group if people that are healthy but can be infected. In the model the mentioned are able to change, by healthy individuals getting infected. In the real world the size of a population has many causes to change. Births increase the population, while deaths make it decease. There are different reasons for people dying, for instance old age, or another disease. To omit this factor of complexity, the model assumes the size N of the population is constant across the duration of the epidemic. Three groups make up the population N: the *susceptible* group S, the *infectious* group I and the *removed* group R (hence SIR Model). For S, I, R and N applies:

$$N = S + I + R. \tag{2.6}$$

The model makes another assumption by stating that recovered people are immune to the illness and infectious individual can not infect them. The individuals in the R group are either recovered and dead, which both cannot carry the disease anymore. As visualized in the Figure 2.1 the individuals can traverse from one group to another on the bases of rates. The transmission rate β is responsible for people being infected, while the rate of removal or recovery rate α (in literature also δ or ν) moves people from I to R.

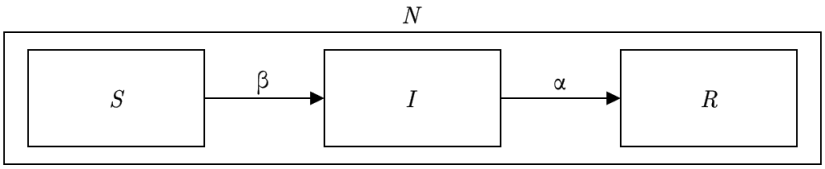


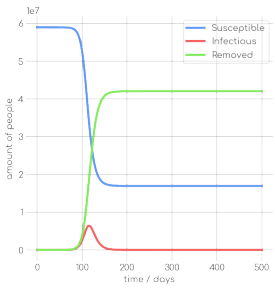
Figure 2.1: SIR Model

2.3.2 reduced SIR Model

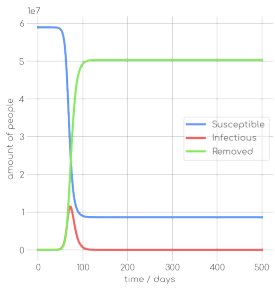
2.4 Multilayer Perceptron

2.5 Physics Informed Neural Networks

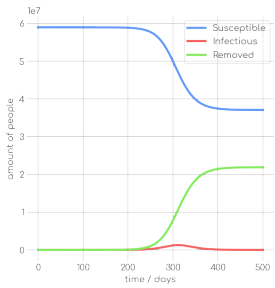
2.5.1 Disease Informed Neural Networks



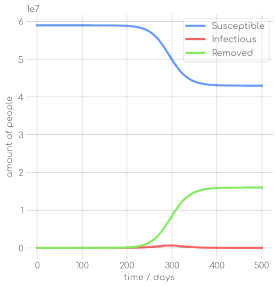
(a) Basic configuration, $\alpha = 0.35$, $\beta = 0.2$



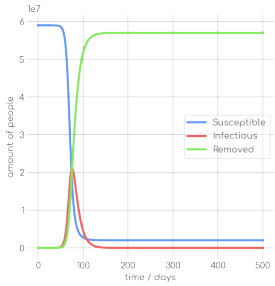
(b) High α configuration, $\alpha = 0.45$, $\beta = 0.2$



(c) Low α configuration, $\alpha = 0.25$, $\beta = 0.2$



(d) High β configuration, $\alpha = 0.35$, $\beta = 0.3$



(e) Low β configuration, $\alpha = 0.35$, $\beta = 0.1$

Figure 2.2: Synthetic data with different sets of parameters.

Chapter 3

Methods

3.1 Data Preprocessing

3.1.1 RKI Data

3.1.2 Recovery Queue

3.2 PINN for the SIR Model

3.3 PINN for the reduced SIR Model

Chapter 4

Experiments

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4.1.1 Setup

4.1.2 Results

4.2 Reduced SIR Model

4.2.1 Setup

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Chapter 5

Conclusions

5.1 Further Work

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