



EINDHOVEN UNIVERSITY OF TECHNOLOGY

COMPUTATIONAL BIOLOGY GROUP

## **Bachelor Eind Project SBMD Report Logs**

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# 1 Preface

The purpose of this **Report Log** is to keep track of the notes, tasks and every other information provided during the Bachelor Eind Project (BEP) meetings. The table of contents contains a list of many different dates. For each of the given date, with the name ***Notulen***, there is a description, notes or information received during the meeting. The dates named ***SSA***, contain a summary or listings of all the findings/information and tasks performed on that day as a self-study assignment. Lastly, the section ***Results*** contain the results of the performed SSA of the given date.

## 2 Introductory meeting 19-march-2020

This section contains information regarding the introductory meeting of this BEP.

### 2.1 Notulen

The introductory meeting was mainly focused on the different kind of topics regarding the **BEP SBMD**.

The different **topics** were:

1. **Hospital patient's data/clinical data regarding:**

- (a) Obesitas after gastric bypass surgery
- (b) Heart failure, monitoring Troponin
- (c) Liver transplantation template model

2. **Dynamic, biological data:**

- (a) Diabetic patients
- (b) Metabolism/reaction on different meals
- (c) Parameter estimation

3. **Sars-Cov-2, aka COVID-19:**

- (a) Epidemic models
- (b) estimation of the infected/exposed

### 2.2 SSA

The tasks to be completed for this self-study assignment are:

- Fill and sign BEP form
- Read the articles and give preferred topic

## 2.3 Results

After the given tasks, it was important to read and analyse the different articles and information, given by prof.dr.ir N.A.W. van Riel. All topics were interesting, but the topic of **COVID-19** is the most "recent and ongoing" topic and is a major concern for the global health.

**The obtained results or the completed tasks from this SSA are:**

1. The BEP form is signed and sent
2. Read all the given articles
3. The preferred topic is **Sars-Cov-2 aka COVID-19**

### 3 "Startbijeenkomst" 08-april-2020

The very first meeting after choosing the preferred subject.

#### 3.1 Notulen

The chosen subject for this BEP is **COVID-19**.

Interesting topics to research regarding the subject of COVID-19:

1. Kalman filter to predict the number of daily infection  
(<https://towardsdatascience.com/using-kalman-filter-to-predict-corona-virus-spread-72d91b74cc8>)
2. The main programming language to be used is Python
3. Public Data as resource for model training
4. John Hopkins map and data is useful  
(<https://coronavirus.jhu.edu/map.html>)
5. Using the SIR/SEIR model
6. Making a blogpost and Github as "final report"
7. Should focus on the Netherlands
8. Would be good to compare 2 or 3 models (Kalman vs Logistic fit vs SEIR model)

Furhtermore, there is an outreach of the TU/e regarding research of the COVID-19.

#### 3.2 SSA

The tasks to be completed for this self-study assignment are:

- Study the Kalman filter and its applications
- Take a look at the outreach of TU/e regarding research of the COVID-19
- Make a Github repositories for the codes of this BEP

### 3.3 Results

It was important to read the medium article regarding the modelling of COVID-19, using the **Kalman Filter**. The Kalman filter is combines system dynamics, (real-time) data and statistics/stochastics. Furthermore, since the spread of COVID-19 in the Netherlands can be seen as a system that is continuously changing and as a real-time problem, using the Kalman filter might be an ideal approach.

**The obtained results or the completed tasks from this SSA are:**

1. Kalman filter and its application is studied. Background information is obtained
2. Wrote a proposal for the application regarding the TU/e - outreach for the research of COVID-19.
3. Public repository, containing the codes and progress of the work, is available on Github at : <https://github.com/jiehaocao/BEP-SBMD-COVID19>.

## 4 Meeting on 16-april-2020

This time, dr. D. Bosnacki joined the team as a supervisor.

### 4.1 Notulen

It is difficult to use the SEIR model, since there are currently no available data regarding the **Recovered** patients of COVID-19 in the Netherlands. dr. Bosnacki suggested to use a model without the recovered, since the recovery at the beginning is almost negligible. Furthermore, it is difficult to know the **Exposed**, since it is difficult to track the amount of people who are actually exposed to this virus, due to lack of test kits.

It is still advisable to study the Kalman filter, and applying this to the data of RIVM, made available to the public. This way it is possible to check the performance of the Kalman filter on the data of the Netherlands. Another suggestion from dr. Bosnacki, was to use the data regarding the amount of patients taken in the hospital or ICU. This is more trustworthy and this data is also available. Furthermore, it would be possible to use the Kalman filter to predict the daily hospitalized patients due to COVID-19. Lastly, it is advisable to write a proposal for the TU/e innovation space, regarding the outreach and offering help to the research of COVID-19.

### 4.2 SSA

The tasks to be completed for this self-study assignment are:

- Try to model and find a parameter for **Exposed**
- Model the hospital intake
- Try to implement the codes of Kalman filter, specifically on the data of the Netherlands (predicting the daily infected people)
- Proposal for TU/e innovation space (Offer help)
- Study the potential SEIR model



### 4.3 Results

The number of **Exposed** can be estimated from the SEIR model, if and only if the estimated parameters are accurate. Since the SEIR model, is a dynamic model and consists of differential equations, it is really sensitive to outliers, thus the different parameters. By changing of the parameters, the graph and model would have a complete different output. It would also be possible to add "Hospital" as an extra compartment to the SEIR model, since these models are compartmental models.

The implementation of the Kalman filter was unsuccessful. There were many errors when converting the R script to Python. Therefore, it was better to focus on the SEIR model and implement this in Python for to try to model the epidemic in the Netherlands.

**The obtained results or the completed tasks from this SSA are:**

1. **Exposed** can be estimated with the SEIR model, but is highly dependent on the estimated parameters (for the differential equations of the different compartments).
2. Extra compartment can be added to model the hospital intake.
3. Proposal is written and sent.
4. The SEIR model is implemented and available on Github repository.
5. Attempt was made to implement the Kalman filter, but it was not successful. z

## 5 Meeting on 23-april-2020

### 5.1 Notulen

It is quite difficult to estimate the parameters using the SIR or SEIR models, since this is a dynamic model. Therefore, one would have to estimate the parameters and solving the differential equations, simultaneously.

It is interesting to apply the SEIR model on the hospital admissions or ICU admissions. Furthermore, it is also possible to add extra compartments to this model, taking hospital and ICU admissions into account.

Instead of estimating the parameters, since these are sensitive (sensitivity can be tested by taking the derivative of these parameters function as time). One can also use **parameter sweep**. However, it might be better to use values obtained from literature or the ongoing research on COVID-19.

It is recommended to focus on the **Logistic Growth Curve (Verhulst)** and using this function to estimate the parameters (less complicated), with the help of *Maximum Likelihood Estimation*. With these estimations, the SEIR model can be tweaked and a simulation can be performed on the SEIR model. Finally, the combination of the information obtained from the SEIR and Verhulst model, can be applied on the Kalman Filter.

**From now on, prepare the work and questions on a Powerpoint Presentation, same as OGO computational biology (recap, work done, upcoming, questions for supervisors)**

### 5.2 SSA

The tasks to be completed for this self-study assignment are:

- Implement Logistic Growth Curve on Python
- Use Logistic Growth Curve to estimate the parameters using MLE
- Tweak and improve the Logistic Growth Curve
- (Optional) Implement these estimated parameters in the SEIR model

### 5.3 Results

The **logistic growth curves** are successfully implemented in Python and on the data of COVID-19 in the Netherlands. This logistic growth is applied on:

1. Number of confirmed cases (daily) in the Netherlands
2. Hospital Admissions (daily) in the Netherlands
3. ICU Admissions (daily) in the Netherlands

Furthermore, a **exponential growth trajectory** is also implemented in Python, regarding the data of COVID-19 in the Netherlands.

The detailed results and explanations are shown in the README.md on Github.

#### 5.3.1 Logistic Growth

After estimating the parameters and fitting the model, it is possible to get an idea of the predicted maximum number of cases in the Netherlands. These models can also be used to simulate and check whether a lockdown had any effect, by fitting a model with data before the strict measurements and a model with data during these strict measurements. A difference in the **predicted maximum** can be a sign that there the measurements are effective.

Furthermore, this is important, because it can be predicted what the **maximum intake** is and when is "peak" is achieved. With this information, it is possible to take preventive measurements (such as necessary lockdowns, making sure that there are enough medical supplies and/or that the hospitals and ICU are not overloaded).

Lastly, it is possible that the actual data passes the predicted maximum, but these models are still valid, meaning that there exist a chance that the actual admissions can pass the predicted maximum. Therefore, it is important use these models to achieve insights when taking preventive measurements.

***Note: detailed explanation and results are available on Github***

### 5.3.2 Exponential growth trajectory

Eventhough exponential growth function are quite abstract and difficult to tell when the peak is reached, by plotting the **log-scale**, a straight line is obtained. This represents the trajectory of confirmed COVID-19 cases. By plotting the actual data (in the Netherlands), it can be seen whether the actual data deviates from the trajectory.

A downward deviation, would mean that things are getting better, but a upward deviation is a sign that more preventive measurements should be taken.

## **6 Meeting on 30-april-2020**

### **6.1 Notulen**

### **6.2 SSA**

### **6.3 Results**