Remarks on the (mathematical) notation

Note 1: Plugging one equation into another one Frequently used over the course of this document is the practice of plugging in the definition of one quantity in the definition of another quantity. As an example, imagine as business in which the manager calculates their income I as the sum of income from sales in the store, denoted by S, plus sales on the web, denoted by W. This can be expressed in a mathematical equation as

$$I = S + W. \tag{0.1}$$

If the manager then calculates how much he has left after subtracting his costs, denoted by C, then this means the (pre-tax) win P is

$$P = I - C. \tag{0.2}$$

By using eq. (0.1) and replacing I in the equation that gives P, we can then express P as

$$P = S + W - C. \tag{0.3}$$

Regardless of what benefit the manager has from this, this shall demonstrate the common practice of replacing a variable in an equation by an equivalent (!) expression that depends on other variables.

When it is explained that "by using eq. 1.something", then usually something like this has been done. In this case, please take a look at the equation it has been referred to and try to see that this equation was used in the way illustrated above.

Note 2: Doing this iteratively In this light, one often does this procedure iteratively. Let us imagine the manager leads their company to be productive and increase its income every year by a factor α, which is bigger than 1. By denoting by I_t now the income in the t-th year, e.g., I_1 is the income in the first year of our counting, I_2 the year after etc., we can write the increase of the income as

$$I_{t+1} = \alpha \cdot I_t, \quad \text{e.g. } I_2 = \alpha \cdot I_1. \tag{0.4}$$

In order to look not one but an arbitrary number of years into the future, we can use this iteratively by noting that

$$I_{t+2} = \alpha \cdot \underbrace{I_{t+1}}_{= \alpha \cdot I_t} = \alpha^2 \cdot I_t, \tag{0.5}$$

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where α^2 means $\alpha \cdot \alpha$, and generally for an arbitrary number k of years

$$I_{t+k} = \alpha^k \cdot I_t. \tag{0.6}$$

Whenever a quantity I evolves over time in the form of eq. (0.6) we speak of exponential increase if $\alpha > 1$ and of exponential decay if $\alpha < 1$. Even if the notorious number e as from the e-function (exponential function) does not occur, if the evolution of a is governed by multiplying with a fixed factor, this means exponential behaviour.

Note 3: Symbols $\sum\limits_{i=0}^{t}$ denotes a sum of terms which have a numbering i that spans from 0 to s. An example is

$$\sum_{i=0}^{t} \alpha^t = \underbrace{\alpha^0}_{=1} + \underbrace{\alpha^1}_{=\alpha} + \alpha^2 + \alpha^3 + \cdots + \alpha^t. \tag{0.7}$$

The symbol $\sqrt[k]{x}$ represents the k-th root of a number x, which is the number so that when we multiply this number with itself k times, then we get x. An example is

$$\begin{aligned}
\sqrt[2]{4} &= 2 \quad \text{because } 2^2 = 2 \cdot 2 = 4 \\
\text{and } \sqrt[4]{16} &= 2 \quad \text{because } 2^4 = 2 \cdot 2 \cdot 2 \cdot 2 = 16.
\end{aligned} \tag{0.8}$$

A traditionally hostile-looking operation is the logarithm. The logarithm always has to be formulated in regard to a *basis* b and a target number x and is written as $\log_b(x)$. It denotes how often b has to be multiplied with itself to get x. As an example: We saw above that $2^4 = 16$. The logarithm turn this around and gives

$$log_2(16) = 4. \tag{0.9}$$

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1 Basics of the modelling of epidemics

In order to describe how the number of people within a population carrying a certain disease will evolve, there exists a commonly used class of models that encapsulates basic rules for the spread of an epidemic. This is the so-called **SIR-model**, where SIR stands for susceptible, infected and recovered, referring to the division of people into three groups that depend on their state in respect to the epidemic.

We will assume a discrete-time model which means that numbers of interest will be updated on a basis of fixed **time steps, e.g., days**. We will equip variables with an index t that represents that this variable has a certain value at time step t, e.q., on the t-th day.

There will be several quantities of interest whose notation we introduce here:

- I_t: The number of people that are **currently infected** on day t

- n_t: The number of people that get **newly infected** between the t-th and the $t + 1$-st time step

- h_t: The number of **newly recovered** people, i.e., the number of people that recovers between the t-th und $t + 1$-st time step

- R_t: The number of total **recovered** people, i.e., the number of people who have been infected with the disease but are not any longer

- T_t: The **total number of infected** people until day t, meaning the number of all people who at any time have been infected

Plus, there will be several **parameters** that govern the play-out of the epidemic. With parameters we mean numbers who are variables of the governing equations of the epidemic but we assume to be fixed. For these, we use the symbols α, β and γ and they represent

- α: The **spread rate**, i.e., the speed in which the epidemic either spreads or declines

- β: The **infection rate** which denotes the portion of people that is added to the number of infected people per time step

- γ: The **recovery rate** which denotes the portion of currently infected people that recovers per time step.

Additional values that characterize the epidemic are

- The **doubling time** which denotes the time until the number of infected people has doubled itself. This value only exists, or makes sense, if the disease is spreading and not in decline

- The **reproduction factor** which quantifies the ratio of infection rate to recovery rate.

In the following, we will outline how all these quantities are precisely defined and how they are related.

1.1   Deriving the dynamics of the epidemic

Assumptions on the epidemic   We now motivate the following rule under which the number of infections evolves: Let the number of infected people on day t be denoted by I_t. We assume, that on average, every infected person has contact with K non-infected people every day and infects each of them with probability p. Let us denote the **infection rate**, i.e., average number of people an infected person infects per day, by

$$\beta = K \cdot p \tag{1.1}$$

This yields, that the number of newly infected people is given by

$$n_t = I_t \cdot \beta. \tag{1.2}$$

> **Example**: This means, if $\beta = 0.1$, then on average, 10 infected people cause 1 new infection per time step.

The assumptions made here are quite strong. They are immediately false if the number of people that an infected person meets per day on average or the infection probability p vary with time. This is likely if behaviour is different depending on the the day of the week, "random" events like the weather or people becoming more careful over time. Still, the framework we will lay here is basic in understanding more complex disease spreading models.

The governing equations   The number of infected people on day $t+1$ depends not only on the number of newly infected people but also on how many of the infected people on day t either recover or die. In both cases, they leave the class of infected people and move to the recovered group. We denote the portion of infected people that move to recovered per day as γ and the absolute number of those as

$$h_t = I_t \cdot \gamma \tag{1.3}$$

and call it the **recovery rate**.

We then obtain for the number of infected people on day $t + 1$

$$I_{t+1} = I_t + n_t - r_t = I_t \cdot (1 + \beta - \gamma). \tag{1.4}$$

Let us denote the **spread rate** α by

$$\alpha := 1 + \beta - \gamma \tag{1.5}$$

Then by iteratively using eq. (1.4) we get for the number of infected people

$$I_{t+k} = \alpha I_{t+k-1} = \alpha^2 I_{t+k-2} = \cdots = \alpha^k \cdot I_t \tag{1.6}$$

Additionally, for the evolution of the number of newly recovered people in every time step we get

$$h_{t+k} \stackrel{(1.3)}{=} \gamma \cdot I_{t+k} \stackrel{(1.6)}{=} \gamma \cdot \alpha^k \cdot I_t. \tag{1.7}$$

Eq. (1.6) and (1.7) are the governing equations for the evolution of the epidemic.

We can derive a similar identity for the evolution of the number of newly infected people

$$n_{t+k} \stackrel{(1.2)}{=} I_{t+k} \cdot \beta \stackrel{(1.6)}{=} I_1 \cdot \alpha^{t+k} \cdot \beta. \tag{1.8}$$

Example: Let us assume $\beta = 0.6$ and $\gamma = 0.1$. Then $\alpha = 1.5$. We assume, at the start of the epidemic, 100 people are infected so that $I_1 = 100$. Then we get

$$
\begin{aligned}
I_2 &= 1.5 \cdot I_1 = 150, & n_1 &= \beta \cdot I_1 = 60 \\
I_3 &= 1.5 \cdot I_2 = 225, & n_2 &= \beta \cdot I_2 = 90 \\
I_4 &= 1.5 \cdot I_3 = 337.5 \approx 338, & n_3 &= \beta \cdot I_3 = 135 \\
I_5 &= 1.5 \cdot I_4 = 506.25 \approx 506, & n_4 &= \beta \cdot I_4 = 202.5 \approx 203
\end{aligned}
\tag{1.9}
$$

Total number of infected people   Another interesting property is the number of people, that are not only infected at day t but have been at any point in time, which we denote by T_t. These are given by summing up the numbers of newly infected people until the t-th time step plus I_1, the number of people infected on the first day.

For $\alpha \neq 1$, we obtain a rather complicated expression in

$$T_t = I_1 + \sum_{s=1}^{t-1} n_s \stackrel{(1.2)}{=} I_1 + \sum_{s=1}^{t-1} I_s \cdot \beta \stackrel{(1.8)}{=} I_1 + \sum_{s=0}^{t-2} I_1 \cdot \alpha^s \cdot \beta = I_1 + I_1 \cdot \beta \sum_{s=0}^{t-2} \alpha^s$$

$$\stackrel{\text{Geometric series}}{=} I_1 \cdot (1 + \beta \cdot \frac{1 - \alpha^{t-1}}{1 - \alpha})$$

$$(1.10)$$

In the last step we used the identity of the so-called Geometric series that states that $\sum_{s=0}^{t-2} \alpha^s = \frac{1-\alpha^{t-1}}{1-\alpha}$.

If $\alpha = 1$, then n_t stays constant because

$$n_t = I_t \cdot \beta,$$

$$\text{and } I_t = \underbrace{\alpha}_{=1} \cdot I_{t-1} = I_{t-1}. \tag{1.11}$$

We then get

$$T_t = I_1 + \sum_{s=1}^{t-1} n_s = I_1 + n_1 \cdot (t - 1) \tag{1.12}$$

because the number of totally (not currently) infected people on day t is equal to the sum of the numbers of people who were newly infected on all days until day t. In this case we say that T_t **grows linearly** because in every time step the same number of newlyinfected people is added to the total number.

Example: From the example above where $\beta = 0.6$, $\gamma = 0.1$ and $I_1 = 100$ the first five time steps of the epidemic yielded the following values for I_t and n_t:

$$I_2, \ldots, I_5 = 150, 225, 338, 506, \quad n_1, \ldots, n_4 = 60, 90, 135, 203.$$

How many people now have been infected in total within the first five time steps? The answer is: The 100 that were infected in the beginning plus the $60, 90, 135$ and 203 newly infected people in the first time steps. This amounts to

$$T_5 = I_1 + n_1 + n_2 + n_3 + n_4 = 588.$$

As it should, this is equivalent to the formula we derived in eq. (1.10), which is given by

$$I_1 \cdot (1 + \beta \cdot \frac{1 - \alpha^4}{1 - \alpha}) = 100 \cdot (1 + 0.6 \cdot \frac{1 - 7.59}{1 - 1.5}) = 587.5 \approx 588. \tag{1.13}$$

Total number of recovered people Similarly, we can calculate how many people are recovered in total up to time step t. For this we have to sum up the numbers of recovered people per time step until the t-th time step, i.e.,

$$R_t = \sum_{s=1}^{t-1} h_s \overset{(1.7)}{=} \sum_{s=1}^{t-1} \gamma \cdot I_s = \sum_{s=1}^{t-1} \gamma \cdot \alpha^{s-1} \cdot I_1 = \gamma \cdot I_1 \cdot \sum_{s=1}^{t-1} \alpha^{s-1} \overset{\text{Geometric series}}{=} \gamma \cdot I_1 \cdot \frac{1-\alpha^{t-1}}{1-\alpha}$$

(1.14)

> **In summary, we obtain the following equations for the evolution of the epidemic**
>
> $$\text{Currently infected:} \quad I_{t+1} = \alpha \cdot I_t$$
> $$\text{Newly infected:} \quad n_t = \beta \cdot I_t$$
> $$\text{Total infected:} \quad T_t = I_1 \cdot (1 + \beta \cdot \frac{1-\alpha^{t-1}}{1-\alpha})$$
> $$\text{Total recovered:} \quad R_t = \gamma \cdot I_1 \cdot \frac{1-\alpha^{t-1}}{1-\alpha}$$
>
> (1.15)

Of course, the real rules under which the epidemic evolves can easily be more complex. Still, in the following we will see how to infer characteristics of the epidemic from its dynamical rules.

1.2 Inferring properties of the epidemic

Recovering the spread rate from data In order to identify the value of α from data $I_0, \ldots, I_T$ about the numbers of infected people on each day, one can select two arbitrary days t and $t + k$ and obtain

$$\alpha^k = \frac{I_{t+k}}{I_t} \Leftrightarrow \alpha = \sqrt[k]{\frac{I_{t+k}}{I_t}}$$

(1.16)

as a direct consequence of eq. (1.6).

Note that we get an equivalent relation for the numbers of newly infected people per day which we denoted by n_t:

$$n_{t+k} = I_{t+k} \cdot \beta, n_t = I_t \cdot \beta \quad \Rightarrow \frac{n_{t+k}}{n_t} = \frac{I_{t+k} \cdot \beta}{I_t \cdot \beta} = \frac{I_{t+k}}{I_t} = \alpha^k$$
$$\Rightarrow \alpha = \sqrt[k]{\frac{n_{t+k}}{n_t}}.$$

(1.17)

We can thus deduce the spread rate α from data about both the numbers of currently infected and newly infected people each day.

Example: If the values for $I_1, \ldots I_5$ are given by $100, 150, 225, 338, 506$, and the newly infected people per day sum up to $n_1, \ldots, n_4 = 60, 90, 135, 203$, then this yields that

$$\alpha = \sqrt[4]{\frac{I_4}{I_1}} = \sqrt[4]{\frac{506}{100}} \approx 1.5, \quad \alpha = \sqrt[4]{\frac{n_5}{n_1}} = \sqrt[4]{\frac{51}{10}} \approx 1.5. \tag{1.18}$$

By the way, we can compute β from eq. (1.2) by

$$\beta = \frac{n_t}{I_t} = \frac{n_1}{I_1} = \frac{60}{100} = 0.6. \tag{1.19}$$

Duplication time   Eq. (1.6) immediately yields how many days it takes for I_t to reach a certain value. e.g. how long it takes to duplicate itself, i.e., to reach a value that is at least c times as high, for example how long it takes for the number of infected people to double itself. We are then interested in how to set k so that

$$\frac{I_{t+k}}{I_t} \geq c. \tag{1.20}$$

Since $\frac{I_{t+k}}{I_t} = \alpha^k$ from eq. (1.6), this means

$$\alpha^k \geq c \Leftrightarrow k \geq \log_\alpha(c)(= \frac{\log_{10}(c)}{\log_{10}(\alpha)}). \tag{1.21}$$

We denote the value for k so that the last inequality becomes an equality by k_c, i.e.,

$$k_c = \log_\alpha(c). \tag{1.22}$$

This means that the value of I_{t+k_c} is c times higher than the value of I_t.
Eq. (1.21) automatically yields a connection between k_c and the spread rate, given by

$$k_c = \log_\alpha(c) \Leftrightarrow \alpha = \sqrt[k_c]{c}. \tag{1.23}$$

Note that, if $c \geq 1$ and $\alpha < 1$ or $c < 1$ and $\alpha \geq 1$, there is no positive solution for k. This is intuitive because if the spread rate is smaller than 1 than I_t gets smaller over time and it cannot duplicate itself. If $\alpha > 1$ and one asked for the time until I_t has, e.g., halved itself, this time is infinite since the number of infected people is not getting smaller but bigger.
The **doubling time** is a special case of this where $c = 2$. We denote it by k_2. Figure 1 illustrates the relation between α and k_2.
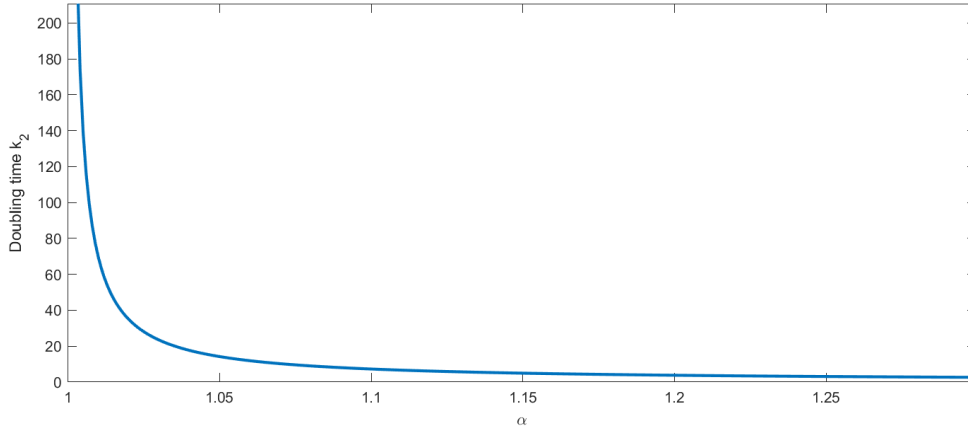
Figure 1: Relation between spread rate α and doubling time. Note that when the spread rate is small, small changes to the spread rate have a strong effect on the doubling time.

Example: Using the values from the example above where $I_1, \ldots I_5$ are given by $100, 150, 225, 338, 506$, we inferred that $\alpha = 1.5$. The doubling time thus is

$$k_2 = \log_{1.5}(2) \approx 1.71. \tag{1.24}$$

Looking at $I_1, \ldots, I_5$, we see that after two days the number of currently infected people rises from 100 to 225, i.e., more than doubles. Again from time step 3 to 5 it incrases from 225 to 506. It thus becomes visible that the doubling time has to be slightly less than 2 time steps.

Reproduction factor An important value for the long-term behaviour of the epidemic is the **reproduction factor**. We define it by

$$r_0 = \frac{\beta}{\gamma}. \tag{1.25}$$

This suggests the distinction of three cases:

1. $r_0 > 1$. This means that more people are infected than recover per day. Since $\frac{\beta}{\gamma} > 1$ means that $\beta > \gamma$, we get that $\alpha > 1$. Following eq. (1.6), I_t increases over time. We say that the number of totally infected people **grows exponentially** with rate α.

2. $r_0 = 1$. This means that $\beta = \gamma$ and thus $\alpha = 1$. Hence, I_t stays constant over time. As a consequence, the number of newly infected people per day stays constant, too. This means, the number of totally infected people T_t **grows linearly** because of eq. (1.12).

3. $r_0 < 1$. This means that $\beta < \gamma$ so that $\alpha < 1$. In this case I_t **decays exponentially** over time. The number of totally infected people converges to the value $\frac{I_0 \cdot \beta}{1-\alpha}$.

Duplication time of total number of infected people   Regarding the duplication time of the total number of infected people T_t, we find another quite complex expression:

$$
\frac{T_{t+k}}{T_t} \geq c \overset{(1.10)}{\Rightarrow} \frac{I_1 \cdot (1 + \beta \cdot \frac{1 - \alpha^{t+k-1}}{1-\alpha})}{I_1 \cdot (1 + \beta \cdot \frac{1-\alpha^{t-1}}{1-\alpha})} \geq c
$$

$$
\Rightarrow 1 + \beta \cdot \frac{\alpha^{t+k-1} - 1}{\alpha - 1} \geq c \cdot (1 + \beta \cdot \frac{1 - \alpha^{t-1}}{1 - \alpha})
$$

$$
\Rightarrow \frac{\alpha - 1}{\beta} + \alpha^{t+k-1} - 1 \geq c \cdot (1 + \beta \cdot \frac{1 - \alpha^{t-1}}{1 - \alpha}) \cdot \frac{\alpha - 1}{\beta} \tag{1.26}
$$

$$
\Rightarrow \frac{\alpha - 1}{\beta} + \alpha^{t+k-1} - 1 \geq c \cdot (\frac{\alpha - 1}{\beta} + \alpha^{t-1} - 1)
$$

$$
\Rightarrow \alpha^{t+k-1} \geq -\frac{\alpha - 1}{\beta} + 1 + c \cdot (\frac{\alpha - 1}{\beta} + \alpha^{t-1} - 1)
$$

$$
\Rightarrow k \geq \log_\alpha(\frac{1 - \alpha}{\beta} + 1 + c \cdot (\frac{\alpha - 1}{\beta} + \alpha^{t-1} - 1)) - (t - 1)
$$

We see that the duplication time now actually is time-dependent because in the lower bound for k the terms α^t and t occur. In fact, the more people are already infected, the more time it takes for the total number of infected people to duplicate itself.

Moreover, we obtain that even for $\alpha < 1$, a duplication can happen depending on the relation of c to α. In other words, even if the number of currently infected people decreases so that the epidemic is on the decline, the total number of infected people still grows and can duplicate itself. This cannot happen indefinitely: For $\alpha < 1$, T_t converges to

$$
I_1 \cdot (1 + \frac{\beta}{1 - \alpha}). \tag{1.27}
$$

We denote k such that the last row of eq. (1.26) is an equality for a given t by $k_{Tc}(t)$.

Using the infection time as the time step   Assuming that an infected person automatically recovers after a period of D days, e.g. 14 days, it can be of interest, how many non-infected people an infected person infects within D days. We can simply augment the tools we have at hand already in the equations derived until this point: So far, we have assumed a day-by-day model that stemmed from the assumptions in eq. (1.2) that every infected person has contact to K people per day. Let us replace the assumption of "K people per day" by "K_D people per D days". Then every time step in the equations denotes not one but D days. For coefficients α, β, γ and r_0, we now write $\alpha_D, \beta_D, \gamma_D$ and $(r_0)_D$ since these coefficients should have different values now

if $D \neq 1$. Naturally, we then find that

$$\gamma_D = 1 \tag{1.28}$$

because we assumed that all infected people are recovered after D days and thus none of these people is infected at time step D. Then we are left with

$$I_{t+k} = \alpha_D^k I_t = (1 + \beta_D - \gamma_D)^k I_t = \beta_D^k I_t. \tag{1.29}$$

β_D **then denotes the average number of people an infected person infects within the time span in which this person is infected. Moreover, it holds that $r_0 = \beta_D$ in this case. This, in contrast to the day-by-day parameter for r_0, is the value Angela Merkel refers to when she mentions the reproduction factor!**

Connection between doubling time and reproduction factor if time step is equal to infection time Eq. (1.21) and the relation $(r_0)_D = \beta_D$ if $\gamma_D = 1$ automatically yield a connection between the doubling time and the reproduction factor. With $\alpha_D = 1 + \beta_D - \gamma_D = \beta_D$, we get for the doubling time from eq. (1.22)

$$k_2 = \log_\alpha(c) = \log_{\beta_D}(c) \Leftrightarrow \beta_D = \sqrt[k_2]{c}. \tag{1.30}$$

This means that the two numbers that are publicly discussed, namely the reproduction factor r_0 for time steps of 14 days, and the doubling time are directly connected to each other so that, when given one of these values we can immediately compute the respective other one if the number of currently infected people I_t is increasing. Since this is currently not the case, I_t is decreasing and cannot double itself. For this reason, in public, more focus is on the reproduction factor currently.

1.3   Examples

Exponential increase An example of the evolution of an epidemic is shown in Figure 2. For this example, we have set $\beta = 0.1$ and $\gamma = \frac{1}{14}$. Then $\alpha = 1 + \beta - \gamma \approx 1.029$ so that the number of infected people increases. The initial value of I was $I_1 = 100$, i.e., we assumed 100 people to be infected at day 1. We can observe the exponential increase of I_t. Also depicted are doubling times for I_t and T_t. As we derived analytically, the doubling time for I_t, which is independent of t, here has the value

$$k_2 = \log_\alpha(2) \approx 24.6 \tag{1.31}$$

The doubling time of T_t, which depends on t, is given by

$$k_{T2}(t) = \log_\alpha(2 \cdot \alpha^{t-1} - 1 - \frac{1-\alpha}{\beta}) - (t-1)$$

$$k_{T2}(1) \approx 8.92 \Rightarrow \ 200 \text{ people is reached after } \approx 10 \text{ days}$$

$$k_{T2}(10) \approx 13.08 \Rightarrow \ 400 \text{ people is reached after } \approx 23 \text{ days}$$

$$k_{T2}(23) \approx 17.02$$

$$k_{T2}(40) \approx 20.11$$

(1.32)

The reproduction factor is

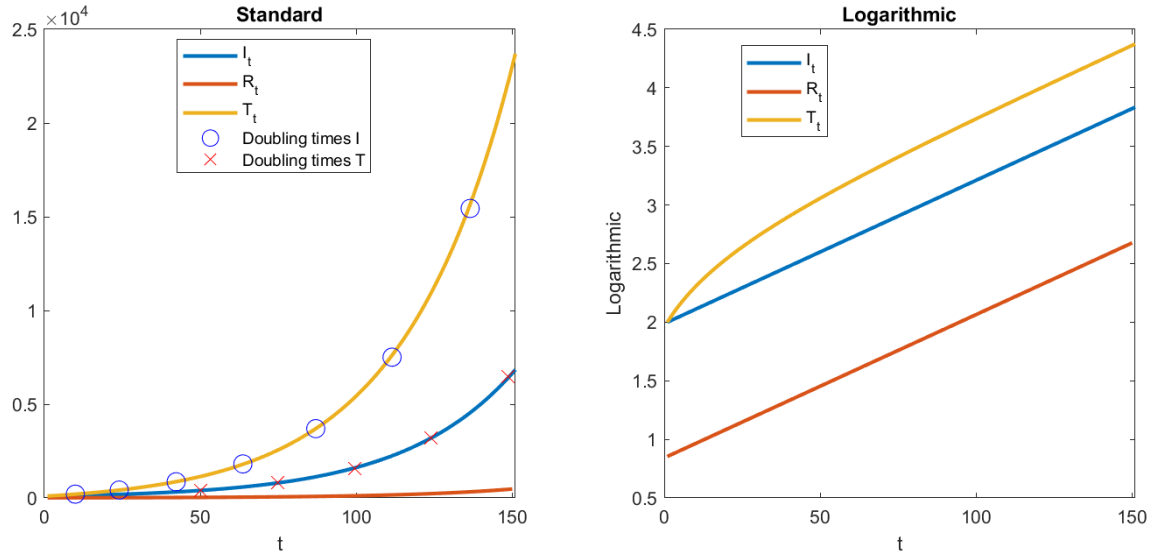$$r_0 = \frac{\beta}{\gamma} = \frac{0.1}{\left(\frac{1}{14}\right)} = 1.4. \tag{1.33}$$

Figure 2: Example trajectories of an epidemic with $\beta = 0.1, \gamma = \frac{1}{14}, I_1 = 100$. Note that the doubling times for I_t are equidistant while the doubling times for T_t increase, as observed from eq. (1.26).

Exponential decay   Let now $\beta = 0.1$ and $\gamma = 0.13$. Then more people recover per time step than get newly infected and $\alpha = 1 + 0.1 - 0.13 = 0.97 < 1$. With I_1, we get the following evolution of I_t, T_t and R_t, depicted in Figure 3.

Doubling times for I_t do not exist, resp. are infinite because the number of currently infected people does not get more but less. I_t shows exponential decay. T_t, on the other hand, still increases because although the number of newly infected people gets smaller over time, it is still positive, i.e., still the total number of infected people T_t increases but more and more slowly. In this case we speak of **logarithmic increase**.

For the doubling time of the total number of infected people, we get

$$k_{T2}(t) = \log_\alpha(2 \cdot \alpha^{t-1} - 1 - \frac{1-\alpha}{\beta}) - (t-1)$$

$$k_{T2}(1) \approx 11.71$$

$$k_{T2}(10) \approx 67.91$$

(1.34)

Apparently, it takes quite long for T_t to double itself twice compared to the example above which had exponential increase. In fact, in this example, T_t does not double itself more than twice. In Figure 3, we can see how it converges to a value of ≈ 430. This in accordance to eq. (1.27) which gives us the value that T_t converges to if $\alpha < 1$. The reproduction factor is

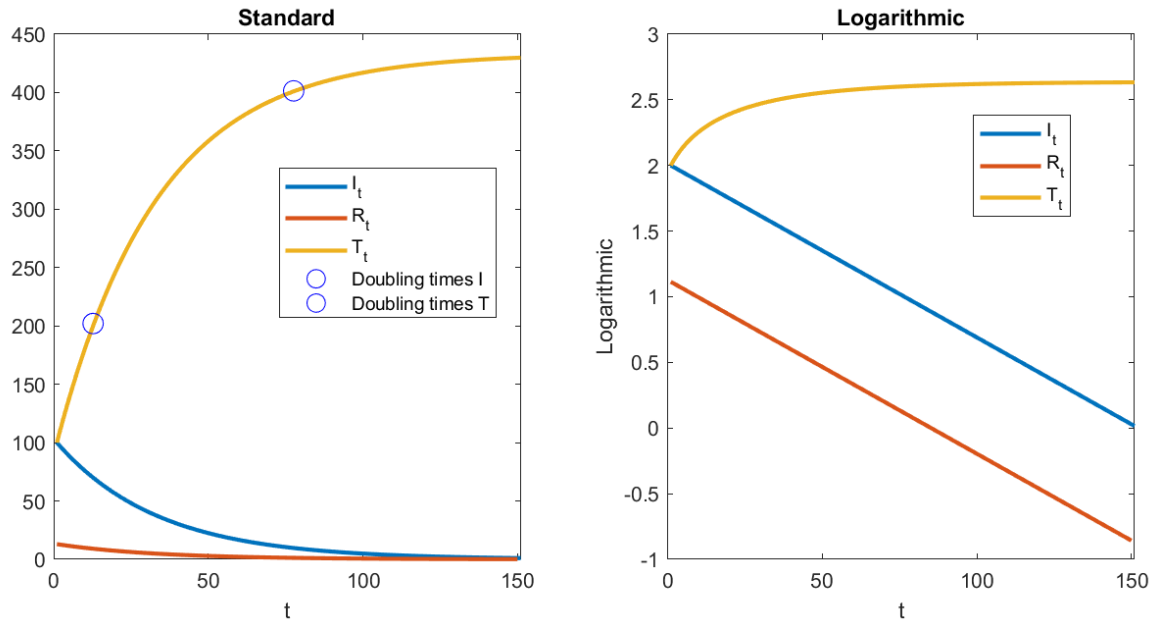$$r_0 = \frac{\beta}{\gamma} = \frac{0.1}{0.13} \approx 0.77.$$

(1.35)

Figure 3: Example trajectories of an epidemic with $\beta = 0.1, \gamma = 0.13, I_1 = 100$. We can see exponential decay in I_t and a logarithmic increase in T_t.

Table 1 summarizes the epidemic for three different cases regarding the spread rate α:

Spread rate α	relation btw. β and γ	reproduction factor r_0	doubling time of I_t	Currently infected I_t	Newly infected n_t	Total infected T_t
> 1	$\beta > \gamma$	> 1	$\log_\alpha(2)$	exponential increase	exponential increase	exponential increase
$= 1$	$\beta = \gamma$	$= 1$	infinite	constant	constant	linear increase
< 1	$\beta < \gamma$	< 1	infinite	exponential decay	exponential decay	logarithmic increase

Table 1: Characteristics of the epidemic dependent on the sprad rate α.