Easy Epidemic<superscript>*</superscript>

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1. A Simple Discrete Model

We model our little(?) epidemic as a simple Markov process. Supposed are three classes of people: Those who are **S**usceptible to the infection are in class **S**, the already **I**nfected ones are in class **I**, and the **R**emoved ones are in class **R**. Class **R** comprises the ones recovered from the infection as well as the deceised ones. We do not consider birthes or deaths from other causes than the infectuous disease we are dealing with.

We set up a matrix of transition propabilities between the classes,

$$M = \begin{pmatrix} 1 - p_{S2I} & 0 & 0 \\ p_{S2I} & 1 - p_{I2R} & 0 \\ 0 & p_{I2R} & 1 \end{pmatrix}. \tag{1}$$

There can be no transfers from class **S** directly to class **R**, as can be no transfers from class **I** back into class **S**. Once a person has entered class **R**, she can luckily or sadly never escape it again. All transition propabilities refer to a fixed time period T. Here is an example matrix:

$$M = \begin{pmatrix} 0.99 & 0 & 0 \\ 0.01 & 0.96 & 0 \\ 0 & 0.04 & 1 \end{pmatrix}.$$

This means that during each period T, one percent of the S-persons will be infected, and from the infected persons four percent will recover or die. We also determine an initial state of our system,

$$v_0 = (\ S_0\ \ I_0\ \ R_0\ )^T,$$

and give an example for this too:

$$v_0 = (\ 99.9\ \ 0.1\ \ 0\ )^T.$$

In that way the chosen numbers can easily be interpreted as percentages. The dynamics can now be stated straightforwardly.

$$v_n = M.v_{n-1}, \quad n = 1, 2, \ldots \tag{2}$$

and we see the resulting time behaviour in the plot below.

With this simple framework, one may play around and compare the curves to available empirical data.

2. Further Musings

Explicit functions for $S(n) = v_{n,0}$, $I(n) = v_{n,1}$, and $R(n) = v_{n,2}$ can be derived from the difference equations (2) using z-transform. Time continuous funtions can then be formulated by using $t = nT$, and the time-derivatives may be used to establish a standard dynamic system in continuous time, f.i. to be compared to established epidemiological models[1]. Additional classes may be introduced, transitions may be allowed that were excluded in §1 etc. This and more is left to the reader.

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*. Of course it should read *Easy epidemiology*. Anyhow at the same time we wish all readers that they may live through the current coronavirus epidemic without troubles.

1. See f.i. https://de.wikipedia.org/wiki/SIR-Modell.
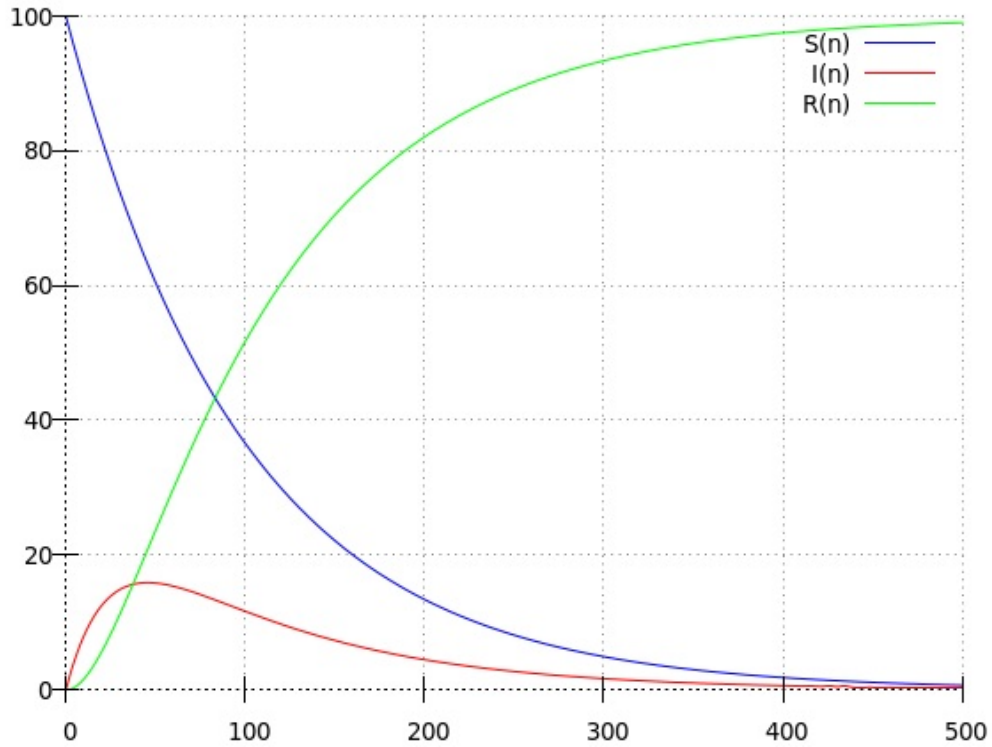
2.1. Extensions

In plots from real data[2] or from other models we often observe exponential growth in the **I**nfected class particularly at the early stages. But we do not see this from our model - the slope of I(n) is decreasing from the onset. The cause is to be found in our *static transition propabilities* in (1), and we may conclude that in reality we do not have these constant transition rates throughout the devolution of an epidemic. We would have to dynamise the propabilies e.g. by feeding back the actual values of infected and susceptible portions of a populace[3].

$$p_{S2I}(n) = f(S(n-1), I(n-1)), \quad p_{I2R}(n) = g(S(n-1), I(n-1)),$$

thus creating a second "layer" of our model. This too is, for the time being, left to the inclined reader.

2.2. The Long End

Equation (2) describes a linear transformation of the three-dimensional vector space of the v_n onto itself (an *endomorphism*). It has an *eigenvector* $v_\infty = M.v_\infty$ (with an *eigenvalue* of 1). With matrix M from equation (1) we get

$$v_\infty = \begin{pmatrix} 0 & 0 & A \end{pmatrix}^T,$$

where constant $A = \Sigma_{j=0}^{2} v_{0,j}$ stands for "All". v_∞ describes a (*attractive*) *fixpoint* of the mapping formed by equation (2). Though reached only in infinite time, once reached the system will never leave that state. Intuitively that is easily seen too. A class receiving propabilty weight from the other classes but never feeding back to them, will finally gather the total weight available. All individuals will finally find themselves in the **R** class, and the epidemic will have passed through all of them, leaving them immune to the same infection for all future.

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2. See f.i. https://coronavirus.jhu.edu/map.html.

3. The SIR model mentioned in footnote (1) lets $\dot{I}(t)$ depend on the product $S(t)I(t)$.

Can there be other such distributions that once arrived at, will persist? By consequence of what was just said above, we will need a $p_{R2R} = 1 - p_{R2S} < 1$ for that. So let's change the transition matrix from equation (1) to

$$\boldsymbol{M} = \begin{pmatrix} 1 - p_{S2I} & 0 & p_{R2S} \\ p_{S2I} & 1 - p_{I2R} & 0 \\ 0 & p_{I2R} & 1 - p_{R2S} \end{pmatrix},$$

or in numbers, to have an example again,

$$\boldsymbol{M} = \begin{pmatrix} 0.99 & 0 & 0.002 \\ 0.01 & 0.96 & 0 \\ 0 & 0.04 & 0.998 \end{pmatrix}.$$

0.2 % of the **R**emoved populace will get **S**usceptible to the infection again. - We keep v_0 and equation (2). Over time our $S(n)$, $I(n)$, and $R(n)$ now look like
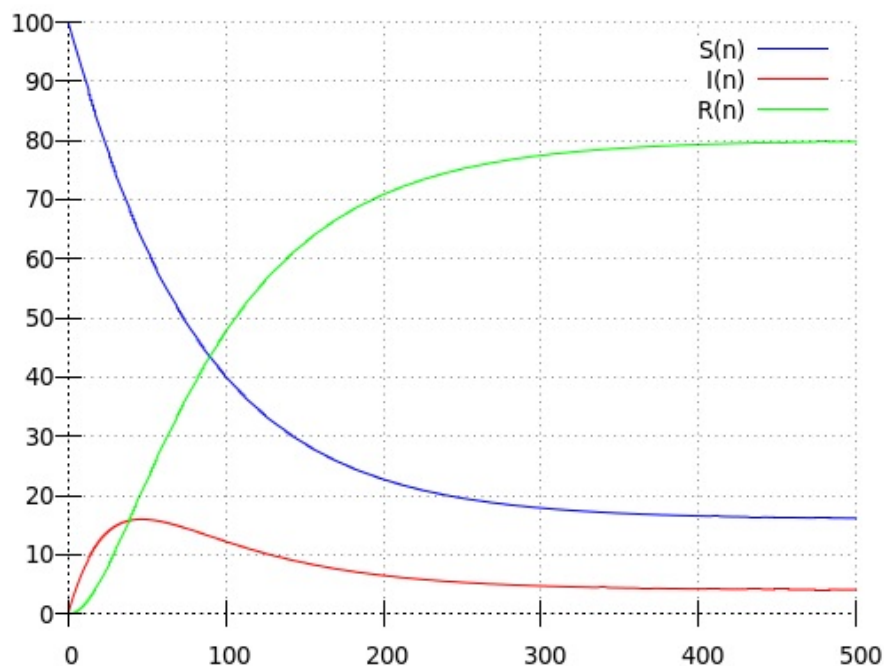
and our

$$v_\infty = \frac{A}{(p_{R2S} + p_{I2R}) \, p_{S2I} + p_{I2R} \, p_{R2S}} \begin{pmatrix} p_{I2R} \, p_{R2S} \\ p_{R2S} \, p_{S2I} \\ p_{I2R} \, p_{S2I} \end{pmatrix},$$

or again in the numbers of our example

$$v_\infty = \begin{pmatrix} 16.0 \\ 4.0 \\ 80.0 \end{pmatrix}.$$

A constant portion of 4 % of infected population is thus generated by only 0.2 % of already recovered people getting endangered to be hit again by the infection - all other weights being the same as in the first model, where the infection completely vanished.