**On the SIR model**

byi H. Mahasedra Ratsimbarison, notes taken from the Institute for Disease Modeling website, EMOD modeling for general disease: <https://idmod.org/docs/general/index.html>

The SIR model was introduced Kermack and McKendrick in 1927 and is still used to analyse the evolution of various diseases. It considers the following concepts:

Susceptible (S): Individual is able to become infected.

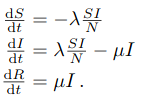
Infectious (I) : Individual is infected with a pathogen and is capable of transmitting the pathogen to others.

Recovered (R): Individual is either no longer infectious or “removed” from the population.

Equations highlighted in white were taken from the research paper of interest cited in the remarks below.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Time |  | ... | t | t+ δt |
| R |  |  | R(t) | R(t+δt) = R(t) + [μI(t) - vR(t)]δt (for v= 0) |
| μ: rate of recovery , v: rate of death  μI(t)δt : number of recovered among I during the interval [t; t+δt]  vR(t)δt: number of deaths among R during the interval [t; t+δt] | | | | |
|  | | | | |
| S |  |  | S(t) | S(t+δt) = S(t) + [mN - λS(t)I(t) - vS(t)]δt  (for v=m=0) |
| λ: spread of infection , m : rate of birth  N: the total population, N = S+ I + R,  : dependance on the size N (by inverse proportionality (linear approx.))  λI(t)S(t)δt: number of future infected among S during the interval [t; t+δt]  mNδt : number of born among N during the interval [t; t+δt]  vS(t)δt: number of deaths among S during the interval [t; t+δt]  (linear dependance with rapport to S and/or I for small interval) | | | | |
|  | | | | |
| I |  |  | I(t) | I(t+δt) = I(t) + [λS(t)I(t) - μI(t) - vI(t)]δt (for v = m = 0) |
| μY(t)δt : number of recovered among I during the interval [t; t+δt]  vY(t)δt: number of deaths among I during the interval [t; t+δt] | | | | |

then the ordinary differential equation (ODE) of SIR model:

 (for v = m = 0)

**Remarks:**

1/ A team work on estimating the central epidemiological parameters and forecasting about Covid-19 uses the SIR model combined with statistical methods:

Inferring COVID-19 spreading rates and potential change points for case number forecasts <https://arxiv.org/pdf/2004.01105.pdf>. See the simplified explanation given in the file **Replicable research (Mahasedra).docx.**

2/ There are SIR-like models: SIRS, SIER and SIERS.

The SIER model adds the function Exposed (E) “Individual has been infected with a pathogen, but due to the pathogen’s incubation period, is not yet infectious”.

Models with names ending in -S (SIRS sy SIERS) consider the case in which individuals in R may get re-infected and moved to Susceptible S.