**On the SIR model**

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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.

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| --- | --- | --- | --- | --- | --- |
| Time |  | ... | t | t+ δt | |
| R |  |  | R(t) | R(t+δ) = R(t) + [gI(t) - vR(t)]δt | |
| g: rate of recovery , v: rate of death  δgI(t) : number of recovered among I during the interval [t; t+δt]  δvR(t): number of deaths among R during the interval [t; t+δt] | | | | | |
|  | | | | | |
| S |  |  | S(t) | S(t+δt) = S(t) + [μN - bS(t)I(t) - vS(t)]δt | |
| b: rate of infection , μ : rate of birth  N: the total population, N = S+ I + R,  : dependance on the size N (by inverse proportionality (linear approx.))  bI(t)S(t)δt: number of future infected among S during the interval [t; t+δt]  (force of infection λ = bI(t) )  μNδt : 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+δ) = I(t) + [bS(t)I(t) - gI(t) - vI(t)]δt | |
| δgY(t) : number of recovered among I during the interval [t; t+δt]  δvY(t): number of deaths among I during the interval [t; t+δt] | | | | | |

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

\begin{aligned}
\frac{dS}{dt} & = \mu N -\frac{\beta S I}{N} - \nu S\\
\frac{dI}{dt} & = \frac{\beta S I}{N} - \gamma I - \nu I\\
\frac{dR}{dt} & = \gamma I - \nu R
\end{aligned}

**Remarks:**

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

Research Article Summary:Inferring COVID-19 spreading rates and potential change points for case number forecasts <https://arxiv.org/pdf/2004.01105.pdf>. See the simplified explanation on file **Fikarohana misy.**

2/ There are SIR-like models: SIRS, SIER ary ny 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.