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Epidemics on networks I

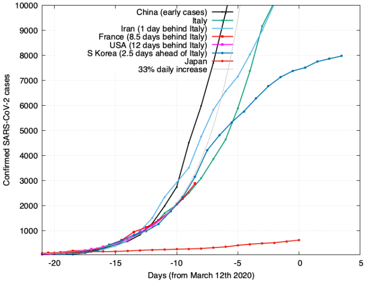
Network Science
Lecture 9

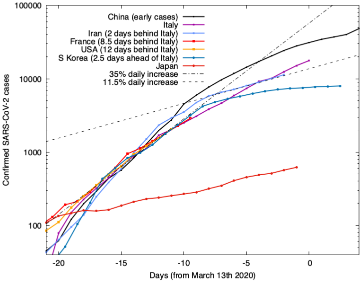
Leonid Zhukov

lzhukov@hse.ru
www.leonidzhukov.net/hse/2022/networks

National Research University Higher School of Economics
School of Data Analysis and Artificial Intelligence, Department of Computer Science

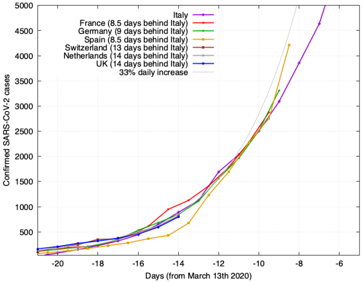
Coronavirus COVID-19

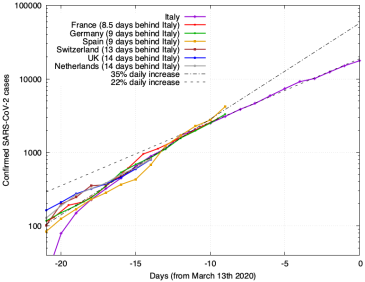




from Mark Handley, UCL

Coronavirus COVID-19





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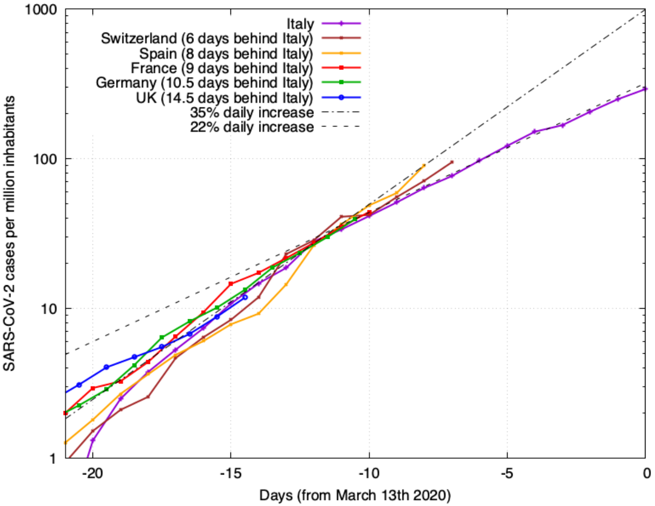
Coronavirus COVID-19



from Mark Handley, UCL

Simple model of contagion

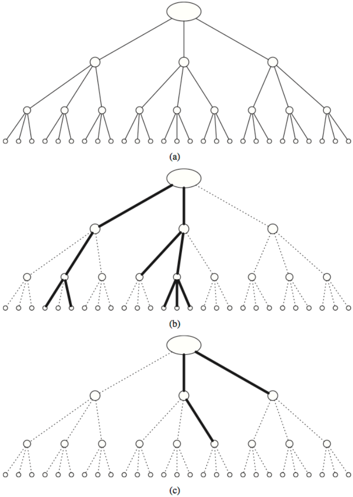
Simple model of contagion (decease transmission)

- 1st-wave: first infected person enters the population and transmits to each person he meets with probability p. Suppose he meets $\langle k \rangle$ people while contagious
- 2nd-wave: Each infected person from 1st wave meets $\langle k \rangle$ new people and independently transmits infection with probability p
- 3rd-wave: ....

Population is organized as a tree

This is Galton-Watson branching stochastic process

Branching process



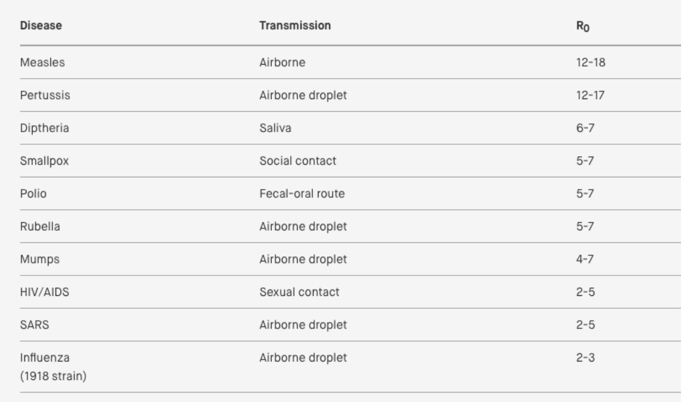
$p \cdot \langle k \rangle$ - average number of secondary infections from one node

Branching process

- $R_0 = p\langle k \rangle$ - the average number of new infected nodes/people on every step
- On the n step, the average number of infected people $R_0^n = (p\langle k \rangle)^n$
- if $R_0 > 1$, the average grows geometrically as R_0^n
- if $R_0 < 1$, the average shrinks geometrically as R_0^n
- when $n \to t$, geometric growth $\to$ exponential growth

R_0 - basic reproduction number, is the average number of secondary infections produced when one infected individual is introduced into a host population where everyone is susceptible
$R_0 = 1$ - is the threshold that determines when an infection can invade and persist in a new host population.

Basic reproductive number



Disease	Transmission	R_0
Measles	Airborne	12-18
Pertussis	Airborne droplet	12-17
Diptheria	Saliva	6-7
Smallpox	Social contact	5-7
Polio	Fecal-oral route	5-7
Rubella	Airborne droplet	5-7
Mumps	Airborne droplet	4-7
HIV/AIDS	Sexual contact	2-5
SARS	Airborne droplet	2-5
Influenza (1918 strain)	Airborne droplet	2-3

from Barabasi, 2016

Compartmental models in epidimiology

- Mathematical epidemiology
- W. O. Kermack and A. G. McKendrick, 1927
- Deterministic compartmental model (population classes) $\{S, I, R\}$
- $S(t)$ - susceptible, number of individuals not yet infected with the disease at time t
- $I(t)$ - infected, number of individuals who have been infected with the disease and are capable of spreading the disease.
- $R(t)$ - recovered, number of individuals who have been infected and then recovered from the disease, can't be infected again or to transmit the infection to others.
- Fully-mixing model
- Closed population (no birth, death, migration)
- Models: SI, SIS, SIR, SEIR,

SI model

- $S(t)$ -susceptible , $I(t)$ - infected

$$S \longrightarrow I$$

$$S(t) + I(t) = N$$

- β - transmission/infection rate, number of transmitting contacts per unit time; $T_c = 1/\beta$ - time between transmitting contact
- Infection equation:

$$I(t + \delta t) = I(t) + \beta \frac{S(t)}{N} I(t) \delta t$$

$$\frac{dI(t)}{dt} = \beta \frac{S(t)}{N} I(t)$$

SI model

- Fractions: $i(t) = I(t)/N, s(t) = S(t)/N$
- Equations

$$\begin{aligned} \frac{di(t)}{dt} &= \beta s(t) i(t) \\ \frac{ds(t)}{dt} &= -\beta s(t) i(t) \end{aligned}$$

$$s(t) + i(t) = 1$$

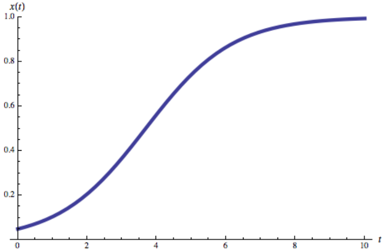
- Differential equation, $i(t=0) = i_0$

$$\frac{di(t)}{dt} = \beta(1 - i(t))i(t)$$

Logistic growth function

- Solution:

$$i(t) = \frac{i_0}{i_0 + (1 - i_0)e^{-\beta t}}$$



- Limit $t \to \infty$

$$i(t) \to 1$$
$$s(t) \to 0$$

in image $i_0 = 0.05, \ \beta = 0.8$

SIS model

- $S(t)$ -susceptable , $I(t)$ - infected,

$$S \longrightarrow I \longrightarrow S$$

$$S(t) + I(t) = N$$

- β - infection rate (on contact), γ - recovery rate; $T_r = 1/\gamma$ - average time to recovery
- Infection equations:

$$\begin{aligned} \frac{ds}{dt} &= -\beta si + \gamma i \\ \frac{di}{dt} &= \beta si - \gamma i \end{aligned}$$

$$s + i = 1$$

- Differential equation, $i(t = 0) = i_0$

$$\frac{di}{dt} = (\beta - \gamma - \beta i)i$$

SIS model

- Solution

$$i(t) = (1 - \frac{\gamma}{\beta})\frac{C}{C + e^{-(\beta-\gamma)t}}$$

where

$$C = \frac{\beta i_0}{\beta - \gamma - \beta i_0}$$

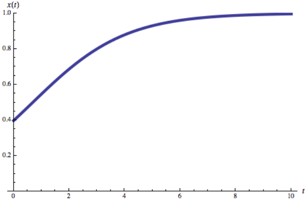
- Limit $t \to \infty$

$$\beta > \gamma \quad , \quad i(t) \to (1 - \frac{\gamma}{\beta})$$

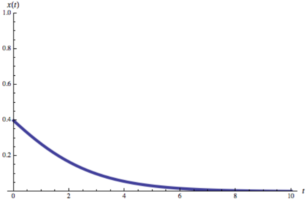
$$\beta < \gamma \quad , \quad i(t) = i_0 e^{(\beta-\gamma)t} \to 0$$

Logistic function

- $\beta > \gamma, \quad i(t) \to (1 - \frac{\gamma}{\beta})$



- $\beta < \gamma, \quad i(t) = i_0 e^{(\beta-\gamma)t} \to 0$



SIR model

- $S(t)$ -susceptable , $I(t)$ - infected, $R(t)$ - recovered

$$S \longrightarrow I \longrightarrow R$$

$$S(t) + I(t) + R(t) = N$$

- β - infection rate, γ - recovery rate
- Infection equation:

$$\begin{aligned} \frac{ds}{dt} &= -\beta s i \\ \frac{di}{dt} &= \beta s i - \gamma i \\ \frac{dr}{dt} &= \gamma i \end{aligned}$$

$$s + i + r = 1$$

SIR model

- Equation

$$\frac{ds}{dt} = -\beta s \frac{dr}{dt}\frac{1}{\gamma}$$

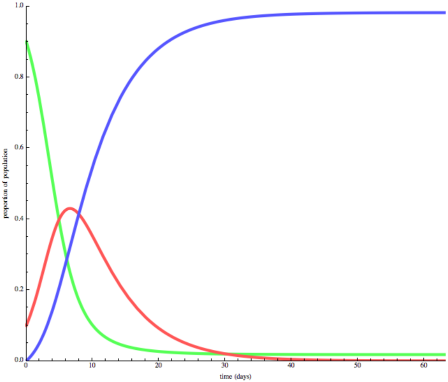
$$s = s_0 e^{-\frac{\beta}{\gamma} r}$$

$$\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\frac{\beta}{\gamma} r})$$

- Solution

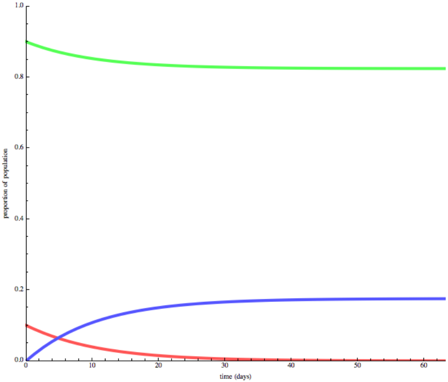
$$t = \frac{1}{\gamma}\int_0^r \frac{dr}{1 - r - s_0 e^{-\frac{\beta}{\gamma} r}}$$

SIR model



- $\frac{\beta}{\gamma} = 4$
- $i_0 = 0.1$

SIR model



- $\frac{\beta}{\gamma} = 0.5$
- $i_0 = 0.1$

SIR model

- Equation

$$\frac{dr}{dt} = \gamma(1 - r - s_0 e^{-\frac{\beta}{\gamma} r})$$

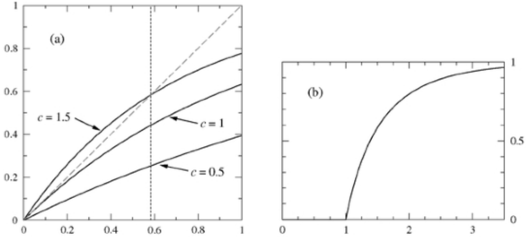
- Limits: $t \to \infty$, $\frac{dr}{dt} = 0, r_\infty = const,$

$$1 - r_\infty = s_0 e^{-\frac{\beta}{\gamma} r_\infty}$$

- Initial conditions: $r(0) = 0, i(0) = c/N, s(0) = 1 - c/N \approx 1$

$$1 - r_\infty = e^{-\frac{\beta}{\gamma} r_\infty}$$

SIR model



$$r_\infty = 1 - e^{-R_0 r_\infty}, \quad R_0 = \frac{\beta}{\gamma}$$

$$(r_\infty)'|_{r_\infty=0} = (1 - e^{-R_0 r_\infty})'|_{r_\infty=0},$$

critical point: $R_0 = 1$

SIR model

- r_∞ - the total size of the outbreak
- Epidemic threshold

$$\begin{array}{rl} \text{Epidemics:} & R_0 > 1, \quad \beta > \gamma \quad , \; r_\infty = const > 0 \\ \text{No epidemics:} & R_0 < 1, \quad \beta < \gamma \quad , \; r_\infty \to 0 \end{array}$$

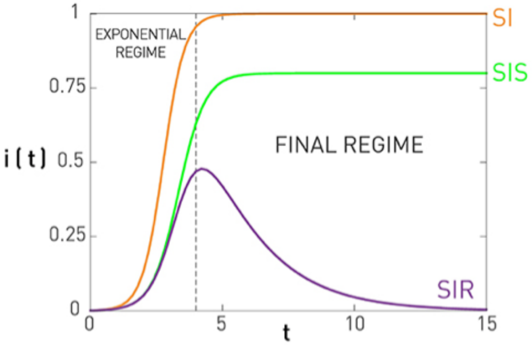
- β - infection rate, γ - recovery rate $\to$
- Basic reproduction number

$$R_0 = \frac{\beta}{\gamma} = \frac{T_r}{T_c}$$

It is average number of people infected by a person before his recovery

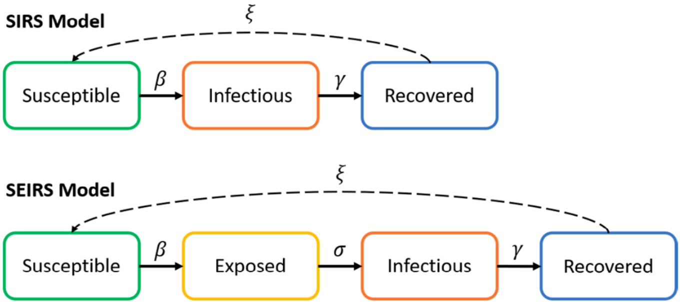
$$R_0 = E[\beta\tau] = \beta \int_0^\infty \gamma\tau e^{-\gamma\tau} d\tau = \frac{\beta}{\gamma}$$

Compartmental models summary



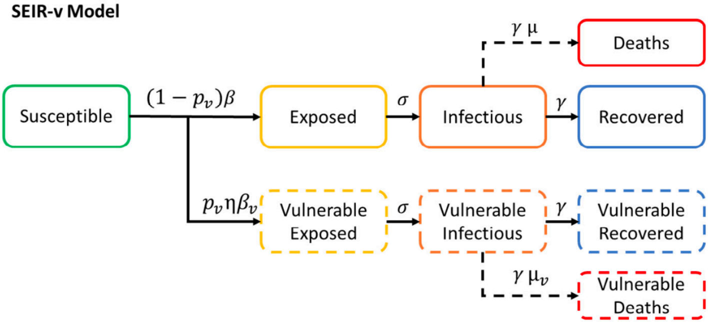
Model	early time	late time	Epidemic threshold
SI	$i_0 e^{\beta t}$	1	-
SIS	$(1-\frac{\gamma}{\beta})e^{(\beta-\gamma)t}$	$1-\frac{\gamma}{\beta};0$	$R_0=1$
SIR	exponential	0	$R_0=1$

More models: SIRS and SEIRS



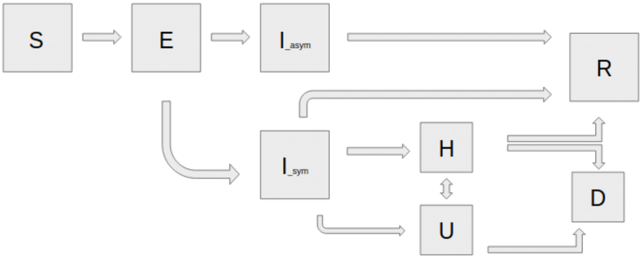
D. Anderez et.al, 2020

More models: SEIR-v



D. Anderez et.al, 2020

More models: SEIIHURD



8-compartamental model:
S - susceptible, E - exposed, I -infectious,
H - hospitalised, U - ICU units, R - recovered

Juliane F. Oliveira et.al, 2020

References

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- The Mathematics of Infectious Disease, Herbert W. Hethcote, SIAM Review, Vol. 42, No. 4, p. 599-653, 2000
- Network Science, Chapter 10, Albert-Laszlo Barabasi, Cambridge University Press, 2016