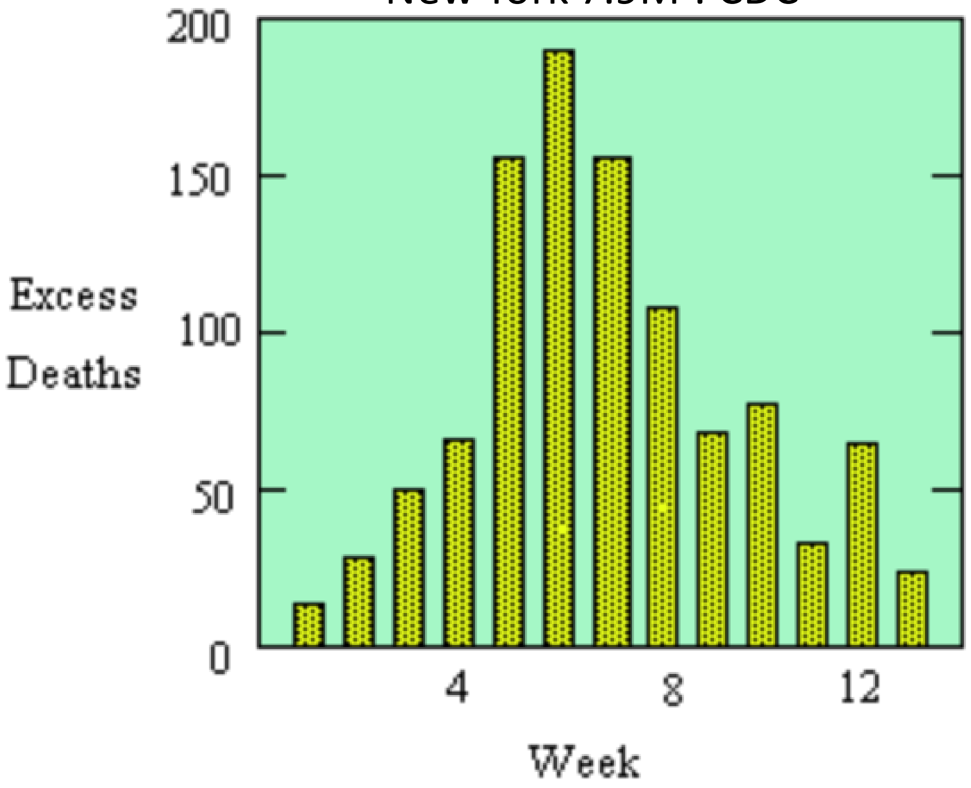
Hong Kong Flu (US, winter 1969-69)

virulent new strain of influenza, named *Hong Kong flu* for its place of discovery

Week	Flu-related deaths	Week	Flu-related deaths
1	14	8	108
2	28	9	68
3	50	10	77
4	66	11	33
5	156	12	65
6	190	13	24
7	156		

new cases $\propto$ deaths 3 weeks ago

New York 7.9M : CDC



MAA - mathematical association of america

14.10.2020

SIR MODEL - FOR SPREAD OF DISEASE

independent variable

$S(t)$ = susceptible individuals

$I(t)$ = infected "
active cases

$R(t)$ = removed " (recovered + dead)
total - active cases

dependent variables

$s(t)$, $i(t)$, $r(t)$ = fraction of population.

PROVE: $s(t) + i(t) + r(t) = 1$

assuming, births = 0 ⇒ susceptible cant ~~decrea~~ increase
immigration = 0 ∴ susceptibles can only become infected.

∴ s(t) is decreasing

assuming, each infected individual has "b" contacts per day.
not all of them are susceptible.

∴ no. susceptible = $b.s(t)$ per infected.
got infected.

∴ total susceptible $\Delta S(t) = b.s(t).I(t)$
got infected

$$\frac{dS}{dt} = -b.s(t).I(t)$$

contacts

$$\frac{ds}{dt} = -b.s(t).i(t)$$

assuming, probability of an infected individual recovering (or removed) is "k"

$$\Delta R(t) = k.I(t)$$

$$\frac{dR}{dt} = k.I(t)$$

$$\frac{dr}{dt} = k.i(t)$$

probability of removal.

Since we assumed the total population to be constant,

$$\frac{ds}{dt} + \frac{di}{dt} + \frac{dr}{dt} = 0$$

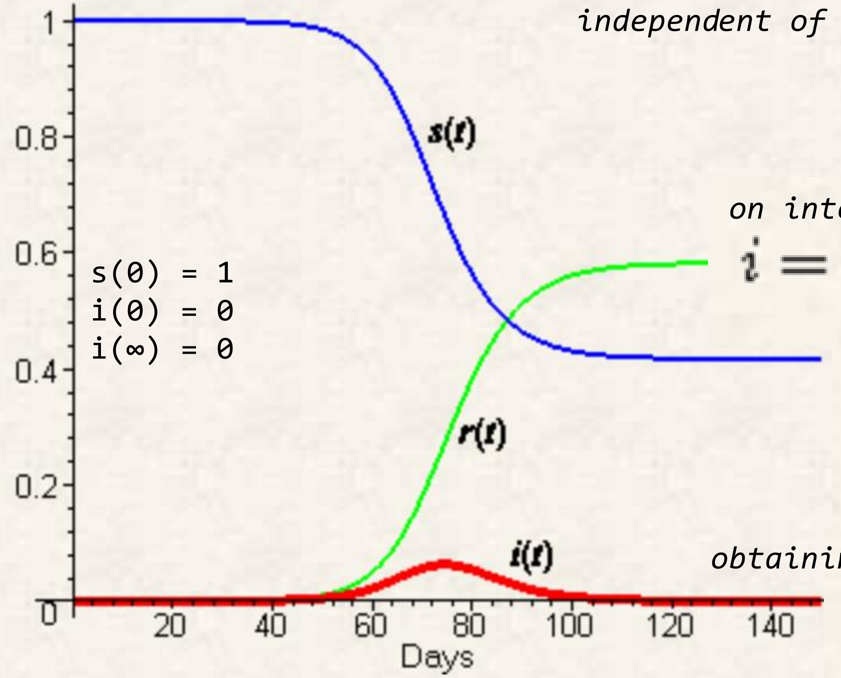
or, equivalently, any increse in infected is due to decrease in susceptible and less than recovered.

$$\frac{di}{dt} = -\frac{ds}{dt} - \frac{dr}{dt}$$

epidemic can't develop if:
- i'(t) < 0
- s(0) < 1/c

$$\frac{di}{dt} = b\,s(t)\,i(t) - k\,i(t)$$

$$i'(0) = (b\,s_0 - k)\,i_0$$



independent of time

$$\frac{di}{ds} = -1 + \frac{1}{cs}$$

on integration

$$i = -s + \frac{1}{c}\ln s + q$$

is constant

$$i + s - \frac{1}{c}\ln s$$

obtaining parameter

$$c = \frac{\ln s_\infty}{s_\infty - 1}$$

what initial conditions we know.

S(0) = population, everyone susceptible

I(0) = some infected people

R(0) = no one removed yet

S(0)	7,900,000
I(0)	10
R(0)	0

now we can guess the parameters

b: if an infecting contact happens once every 2 days,
b = 1/2

k: if avg. period of infectiousness is 3 days D
k = 1/3 (exponential decay)

contact number /infected

c = b.D
  = b/k

basic reproductive number
R0 = b.D

effective reproductive number
R = b.D.s(t)

R0

1.4-1.6:	2009 flu H1N1, swine
1.4-2.8:	1918 flu H1N1, influenza
12.8:	1918-28 measles (US)
4.9:	1955 poliomyelitis (US)
5.7:	COVID-19

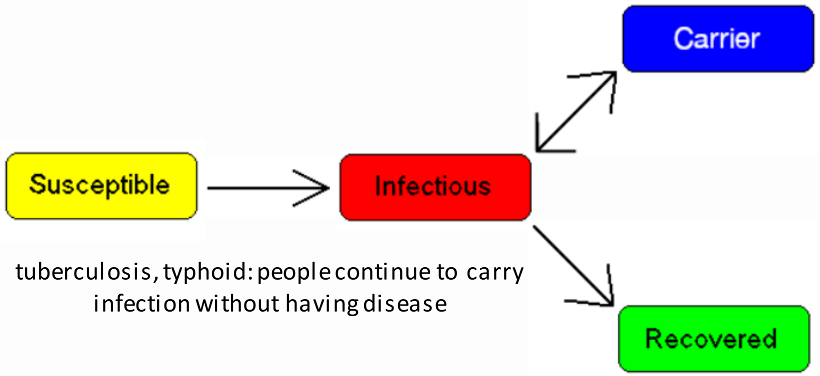
For halting epidemic, R ≤ 1
R = R0.s(t)
∴ s(t) = 1/R0
= 0.175

90% vaccine efficacy?

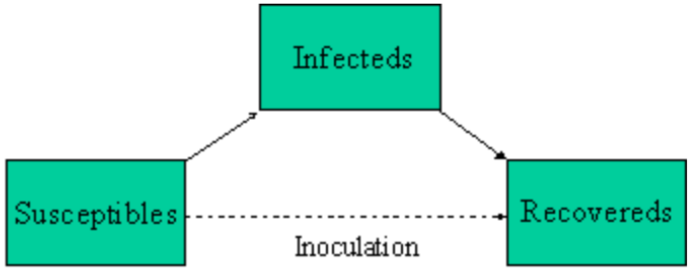
82.5% herd immunity needed

measles: babies are immune due to maternal antibodies

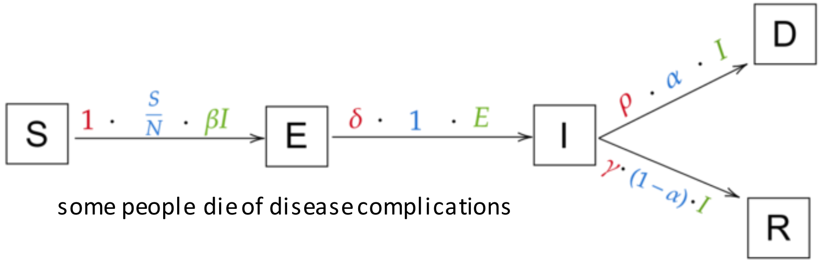
COVID-19: disease has significant incubation period



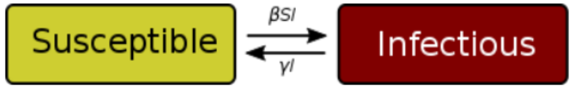
tuberculosis, typhoid: people continue to carry infection without having disease



immunization: for avoiding epidemic



some people die of disease complications



common cold, influenza: no long-lasting immunity

$$\mathcal{S} \rightarrow \mathcal{E} \rightarrow \mathcal{I} \rightarrow \mathcal{S}$$

recovered people don't acquire immunity

$$\mathcal{M} \rightarrow \mathcal{S} \rightarrow \mathcal{E} \rightarrow \mathcal{I} \rightarrow \mathcal{R}$$

diseases with passive immunity and latency

$$\mathcal{M} \rightarrow \mathcal{S} \rightarrow \mathcal{E} \rightarrow \mathcal{I} \rightarrow \mathcal{R} \rightarrow \mathcal{S}$$

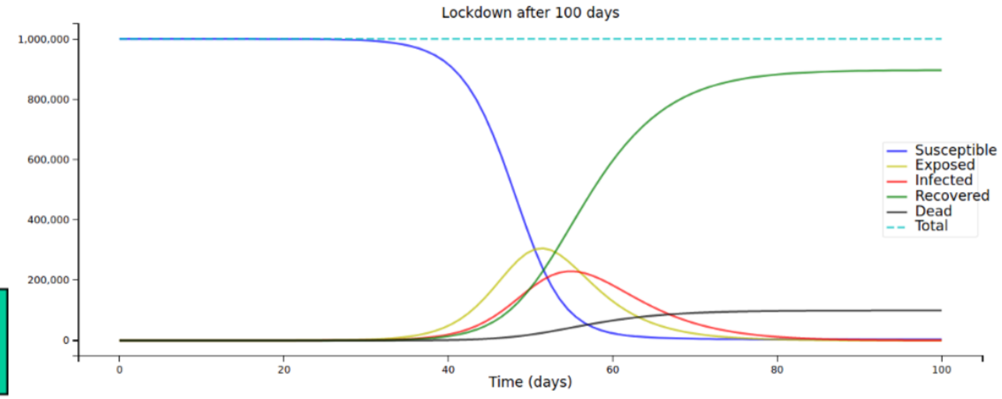
recovered people acquire temporary immunity

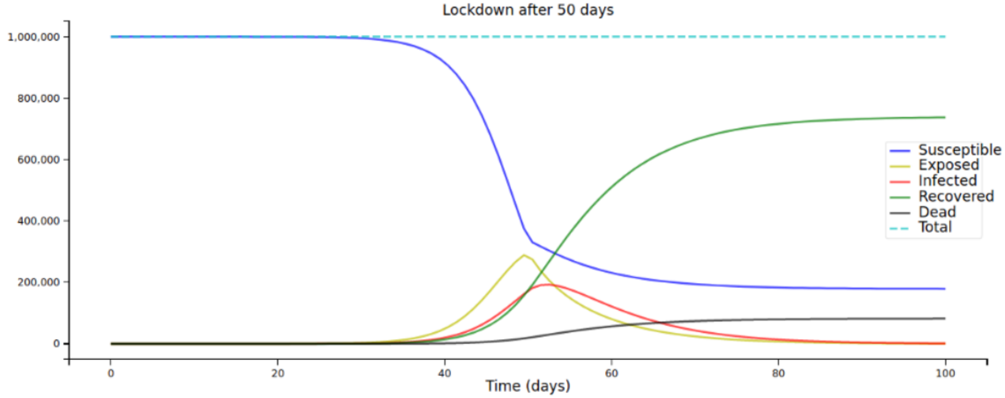
$$\frac{dS}{dt} = -\beta \cdot I \cdot \frac{S}{N}$$
$$\frac{dE}{dt} = \beta \cdot I \cdot \frac{S}{N} - \delta \cdot E$$
$$\frac{dI}{dt} = \delta \cdot E - (1-\alpha) \cdot \gamma \cdot I - \alpha \cdot \rho \cdot I$$
$$\frac{dR}{dt} = (1-\alpha) \cdot \gamma \cdot I$$
$$\frac{dD}{dt} = \alpha \cdot \rho \cdot I$$

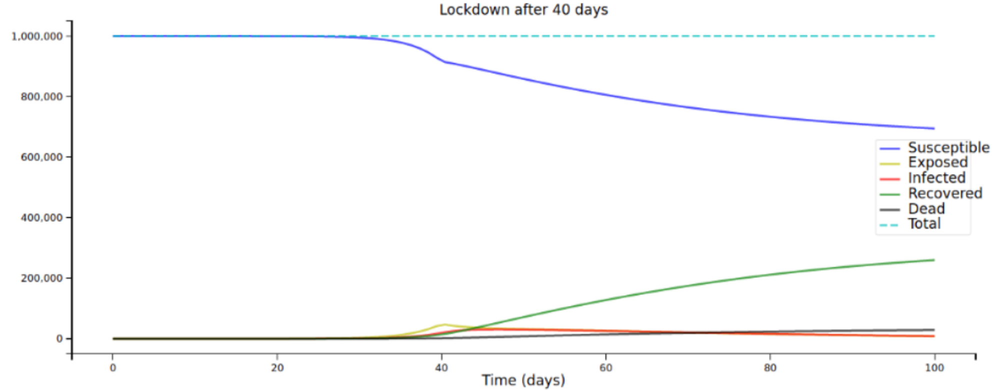
```
resource and age dependent recovery and fatality rates
- no. of ICU beds, ventilators available
- high risk groups, like elderly, diabetics
- change in population structure due to fatality
```

Time-Dependent R_0

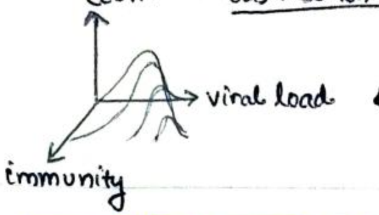
```
def R_0(t):
    return 5.0 if t < L else 0.9
```







distribution:



population = virus

components vs. compartments

multiple particles
S, I, R, a, x, y

viral load > immunity
→ infected

viral load < Lo
immunity > viral load
→ recovered.

possible compartments:

- 5 medicines affect different parts of life cycle.
- immune system effect
- medicine side effects.
- mutations (antiviral effect)
- presence of other viruses

damaged
inactive
within cell
replicating proteins
replicating capsule
discharged

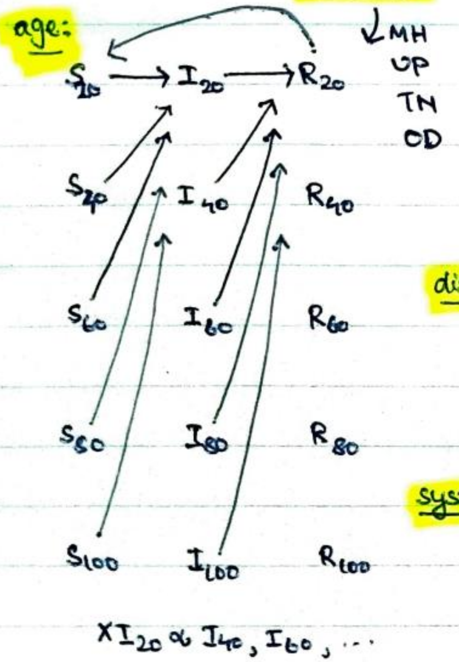
Separate compartments for hospital rooms? mall? road?

Compartments with

Other concerns:
- economics
- ethics

location?

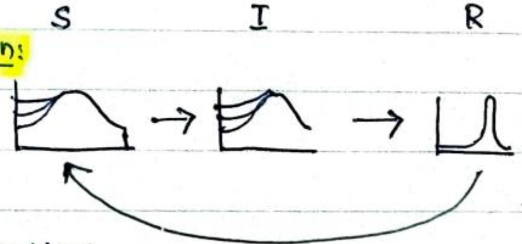
age:



automatically generating model parameters / structure with state-space search (ML, GA)

finding optimal solution(s) through right interventions, by adjusting model parameters / structure.

distribution:



system:

Circuit simulation
(reducing to simpler)

IDM Heterogeneous computing for epidemiological model fitting and simulation

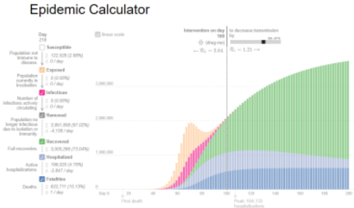
Thomas Kovac[1,2*†], Tom Haber[2†], Frank Van Reeth[2] and Niel Hens[1,3]

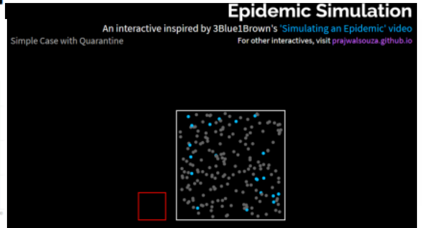
Spread of Infectious Disease Modeling and Analysis of Different Factors on Spread of Infectious Disease Based on Cellular Automata

Sheng Bin [1,*], Gengxin Sun [1] and Chih-Cheng Chen [2,*]

Application Of Heterogeneous Computing Techniques To Compartmental Spatiotemporal Epidemic Models

Grant Donald Brown
University of Iowa





A Simulation of a COVID-19 Epidemic Based on a Deterministic SEIR Model

José M. Carcione[1], Juan E. Santos[2,3,4], Claudio Bagaini[5] and Jing Ba[2]*

Hybrid Multi-threaded Simulation of Agent-Based Pandemic Modeling using Multiple GPUs

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CAS: computer algebra system

function dependent on n variables
s(a, t), i(a, t), r(a, t)
b(a, t), k(a, t)?

levels of parallelism
- multiple parameters values (sir)
- separate graph nodes
- per-node distribution
- multiple time steps