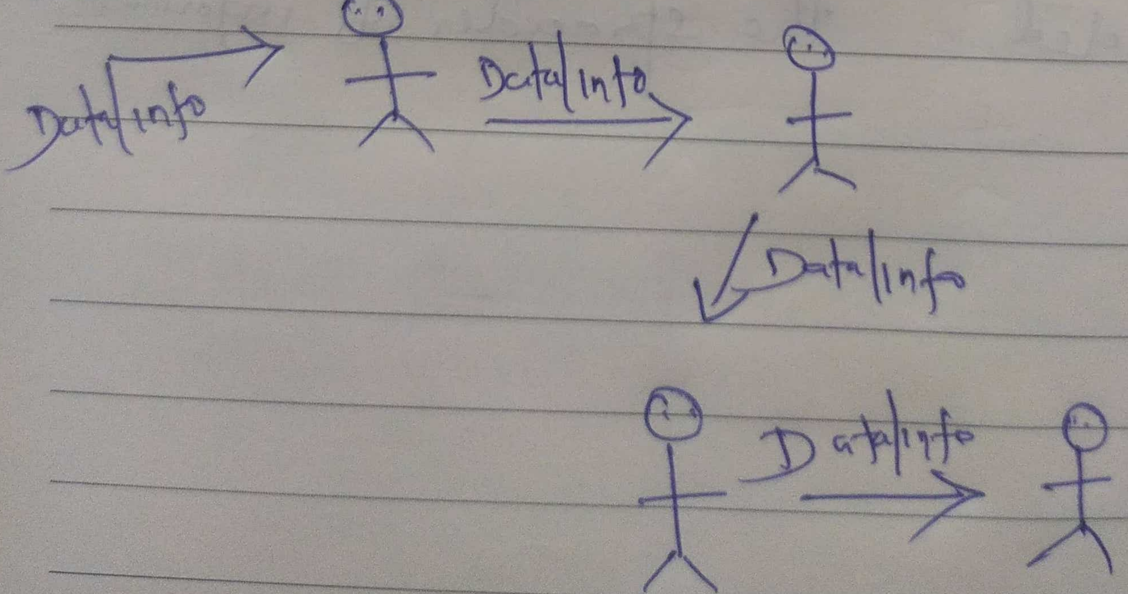
Lecture - 16

Contagion

Meaning: Spreading of diseases

in social networks:
information spreading from person to person.

otherwise called diffusion/ information diffusion.



- can be used to model infection, economic

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→ social networks are prominent tool for information diffusion in society.

→ modelling and predicting information diffusion is very important.

→ useful in predicting, marketing, advertising, political campaigns etc.

→ tie strength is very important in information diffusion.

Social Contagion:

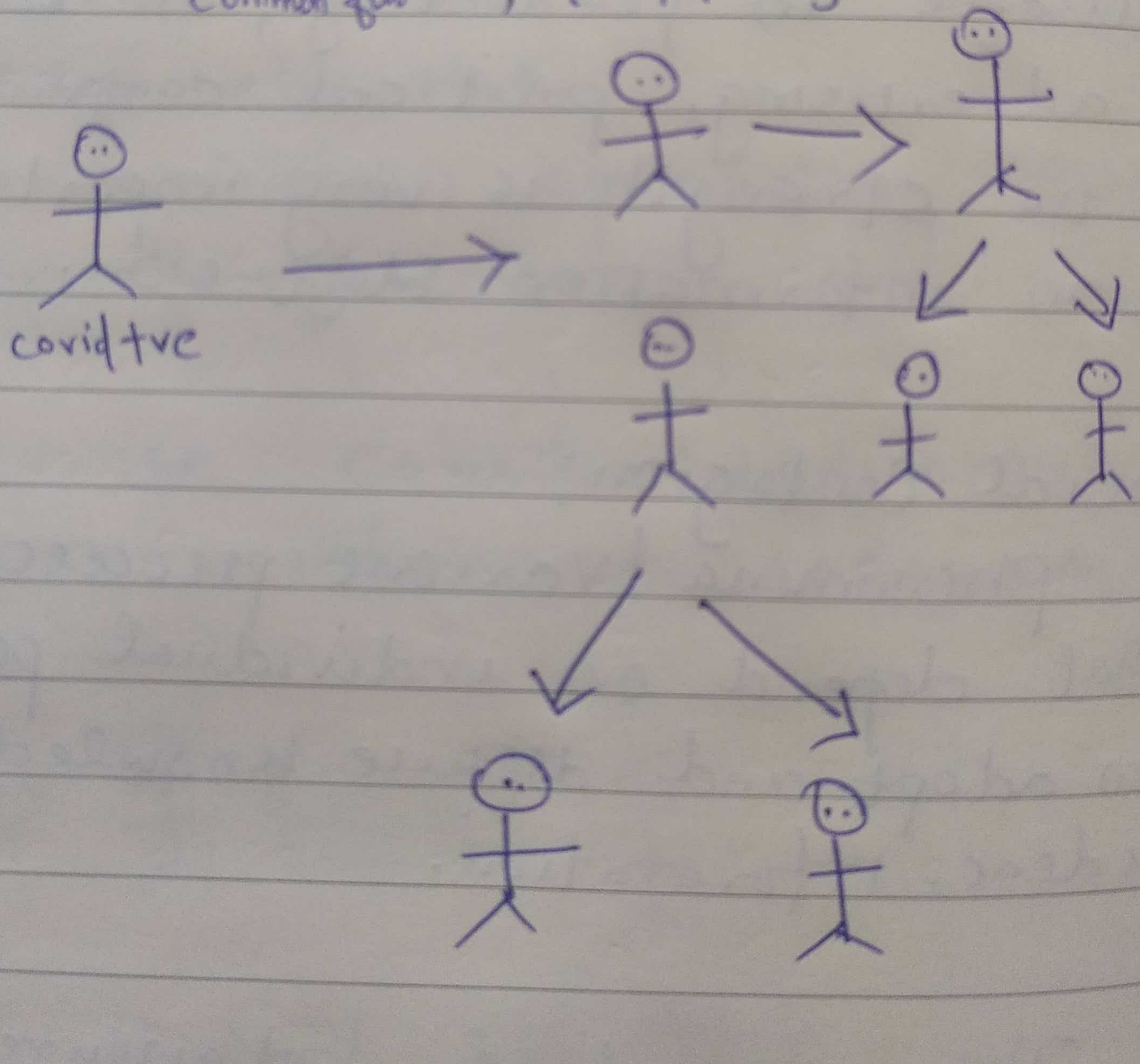
Phenomena | various processes that depend on individual propensity to adopt and diffuse knowledge, ideas, information.

→ The spread of behaviours, attitudes and affect through crowds and other types of social aggregates from one member to other.

- Simple contagion

  - Single exposure sufficient for transmission.

eg: disease, information etc
covid
common flu, traffic jam



- Complex contagion.

  - If the behaviour is risky or technology requires coordination

then

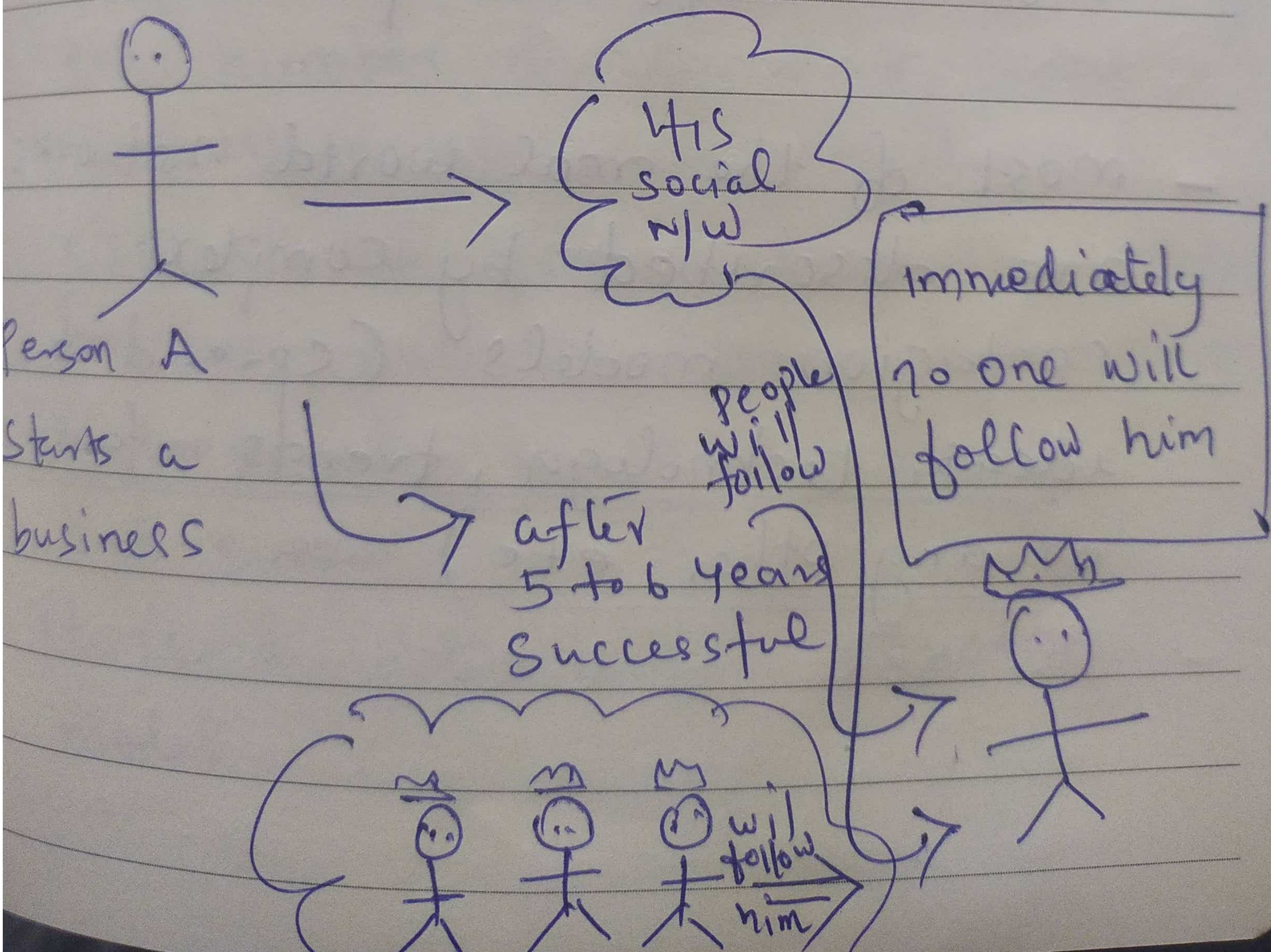
single exposure is not enough

ie; simple contagion not sufficient.

There comes

- Complex contagion

  - Repeated exposure is needed for tranmission.



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To analyse contagion we need to use some mathematical models.

- Simple contagion mainly inspired by disease spreading.
- various epidemic models such as SIR, SIS are examples.

- Complex contagion can be modelled using threshold model, generalized epidemic models, diffusion percolation etc.

- Most of the real world networks are described by complex contagion models (spread of ideas, technology, trends in fabric or any other etc)

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simple epidemic model / simple contagion model.

S-I-R model.

S — Susceptible (people/nodes capable of spreading a disease/info)

I — Infected (people infected/or done with what they can)

R — Recovered (People recovered ~~from an affect~~/ disease)

- SIR model capable of predicting the number of S, I, R. people (illness or information impact etc)
- SIR is a compartmental model means can be separated into groups.
- Introduced in 1927, popular and simple.
- It is a differential equation model.

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- There will be dependent variables and independent variables to model a disease situation

- Dependent variables.
  - people in each group
  - total population (fraction of population in each category)

- Independent variable.
  - Time t. (measured) in days/hrs/etc

Other parameters.

- susceptible individuals may ~~be~~ become infected.
- This measures rate of transfer from susceptible to infected.
- The rate of transfer depends on number of individuals in each compartments. and frequent contacts.

- The rate of contact which converts susceptible to infected is β.

- This β value may be reduced through quarantines, lockdowns etc.

- Next value, rate of recovery (γ) (mortality)
(infected to recovered status)

- R_0 → Basic reproduction no.
the mean number of infections caused by a single infected individual over the course of their illness.

- R_0 is the ratio between β and γ
  R_0 → contacts per infection
- a decrease in β reduces R_0.
- if $R_0 > 1$ spread will be increased ~~in upcoming days~~.
  $R_0 < 1$ spread will be reduced.

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- Expressing S, I, & R values in terms of t.

- $S(t)$
  $I(t)$
  $R(t)$
- we know total population N is the sum of $S(t)$, $I(t)$ & $R(t)$

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

- To form defferential equations.

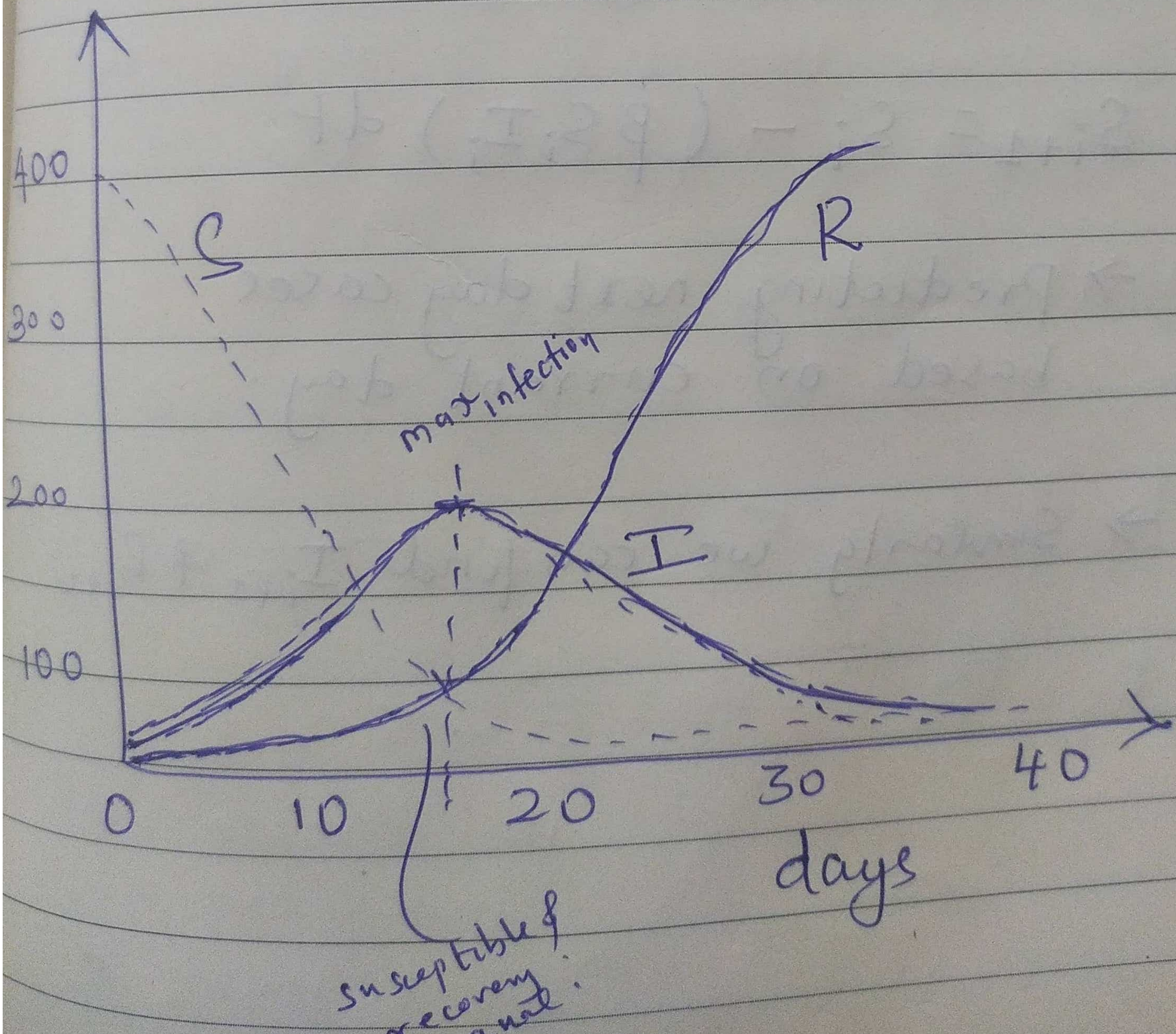
$$\left.\begin{array}{l} \dfrac{dS}{dt} \\ \\ \dfrac{dI}{dt} \\ \\ \dfrac{dR}{dt} \end{array}\right\} \text{Rate of change of } S, I \,\&\, R \text{ w.r.t time } t$$

$$\frac{dS}{dt} = -\beta S I$$ (Negative because susceptible changes to Infected)

$$\frac{dI}{dt} = \beta S I - \gamma I$$ (Balanced)

$$\frac{dR}{dt} = \gamma I$$ (recovered)

$1/\gamma$ = days to recover



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$$dS = -(\beta S I)\, dt$$

$$dI = (\beta S I - \gamma I)\, dt$$

$$dR = \gamma I\, dt$$

change in $\underset{(i-\text{day})}{dS} = S_{i+1} - S_i$

$$S_{i+1} - S_i = -(\beta S_i I_i)\, dt$$

$$S_{i+1} = S_i - (\beta S_i I_i)\, dt$$

→ Predicting next day cases based on current day.

→ Similarly we can find I_{i+1} & R_{i+1}

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Limitations of SIR.

- Not including any other parameters other than S, I, R. (carrier, vaccinated, etc)
- assumes homogeneous mixing of population ($S \times I$). in reality, human networks are highly local.

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Consider the statistics of an epidemic in country X.

$S = 1000, \quad I = 10, \quad R = 0$

The time t is measured in days. Each infected person would make infecting contacts every two days. The average recovery period is 3 days.

Calculate S, I & R on the 2nd day of epidemic.

Solution:

Day 0

$S_0 = 1000 \quad I_0 = 10 \quad R_0 = 0$

$\beta = 1/2 = 0.5, \quad \gamma = 1/3 = 0.33$

$R_0 = \beta / \gamma = 1.51 > 1$

$\therefore$ The epidemic will spread

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We know that

$S_{i+1} = S_i - (\beta S_i I_i)dt$

$I_{i+1} = I_i + (\beta S_i I_i - \gamma I_i)dt$

$R_{i+1} = R_i + \gamma I_i dt$

<u>Day 1</u> $dt = 1$ day (change in time)

$S_1 = S_0 - (\beta S_0 I_0)dt$

$= 1000 - (0.5 \times 1000 \times 10)$

$= -4000$

$I_1 = I_0 + (\beta S_0 I_0 - \gamma I_0)dt$

$= 10 + (5000 - 3.3)$

$= 5006.7$

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$R_1 = R_0 + \gamma I_0 dt$

$= 0 + 3.3$

$= 3.3$

Day 2

$S_2 = S_1 - (\beta S_1 I_1) dt$

$= -4000 - (0.5 \times -4000 \times 5006.7)$

$= -4000 + 10,013,400$

$= 10,009,400$

$I_2 = I_1 + (\beta S_1 I_1 - \gamma I_1) dt$

$= 5006.7 + (-10,013,400 - 0.33 \times 5006.7)$

$= 5006.7 + (-10,013,400 - 1652.211)$

$= 5006.7 - 10,015,052.2$

$= -10,010,045.5$

$R_2 = R_1 + r I_1$

$= 3.3 + 0.33 \times 5006.7$

$= 1655.511$