

SNA Project

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⇒ CoronaVirus Pandemic Analysis

Models for the Spread of Disease

Case:-

Fully Mixed Model or Mass action Approximation.

→ def :- every individual has an equal chance per unit time of coming into contact with each other.

types of Models:-

① SI Model:

$S(t)$ = Susceptible cases

$I(t)$ = Infected cases.

$\beta \rightarrow$ each individual coming in contact to βS people per unit time at random.

$N \rightarrow$ total number of people.

prop. of being Susceptible = $\frac{S}{N}$

infected person has average βS contacts with Susceptible people per unit N time.

overall rate of new infection = $I \cdot \beta \frac{S}{N}$

$$\Rightarrow \frac{dI}{dt} = \beta \frac{SI}{N}, \quad \frac{dS}{dt} = -\beta \frac{SI}{N}$$
$$I + S = N$$

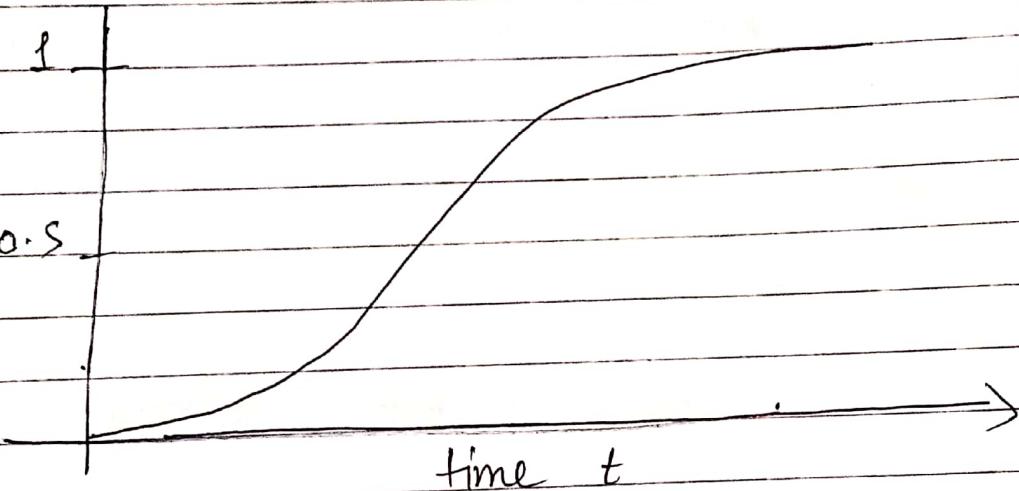
$$\text{Consider, } S = \frac{S}{N} + X = \frac{X}{N}$$

$$\frac{dS}{dt} = -\beta S X, \quad \frac{dX}{dt} = \beta S X$$

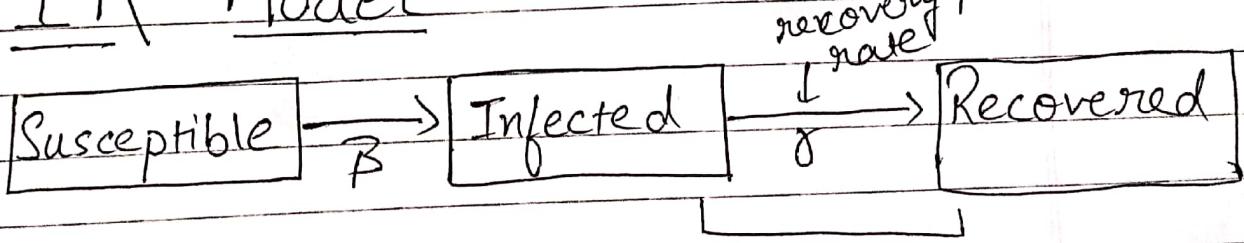
$$\Rightarrow \text{since, } S + X = 1, \quad \frac{dX}{dt} = \beta X(1-X) \quad \left. \begin{array}{l} \text{logistic} \\ \text{growth} \\ \text{equation} \end{array} \right\}$$

$$X = \frac{x_0 e^{\beta t}}{1 - x_0 + x_0 e^{\beta t}}$$

$$x_0 \text{ is } X \text{ at } t=0,$$



SIR Model



time T
"Recovery time".

Given γ , we can calculate the recovery time a person is likely to remain infected.

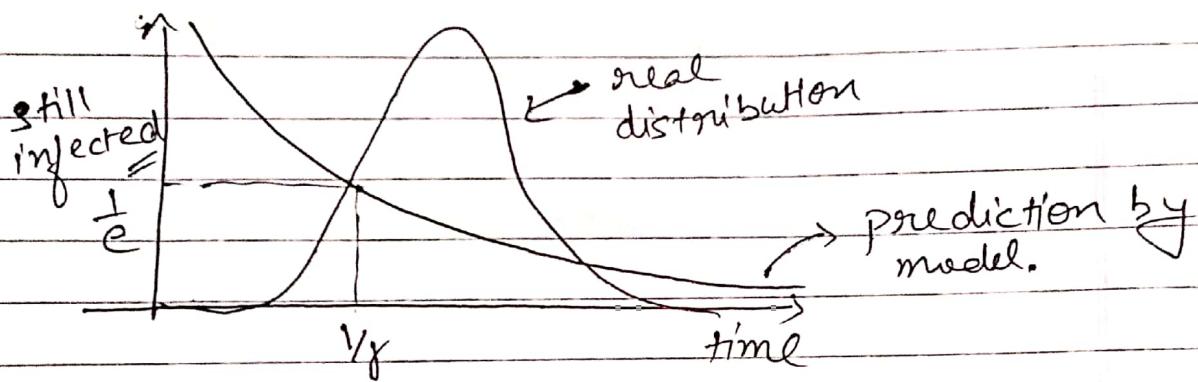
the probability of recovering in any time interval δt is $\gamma \delta t$.

$$p(n) = \gamma \delta t$$

$$1 - p(n) = \delta t$$

prob. that an individual is still infected after time t is

$$\lim_{\delta t \rightarrow 0} (1 - \gamma \delta t)^{t/\delta t} = e^{-\gamma t} \quad \text{mean time} = \frac{1}{\gamma}$$



Mathematical Model of SIR:

$$\frac{ds}{dt} = -\beta sx, \quad \frac{dx}{dt} = \beta sx - \gamma x, \quad \frac{dr}{dt} = \gamma x$$

$$S + X + R = 1$$

$$-\beta r/\gamma$$

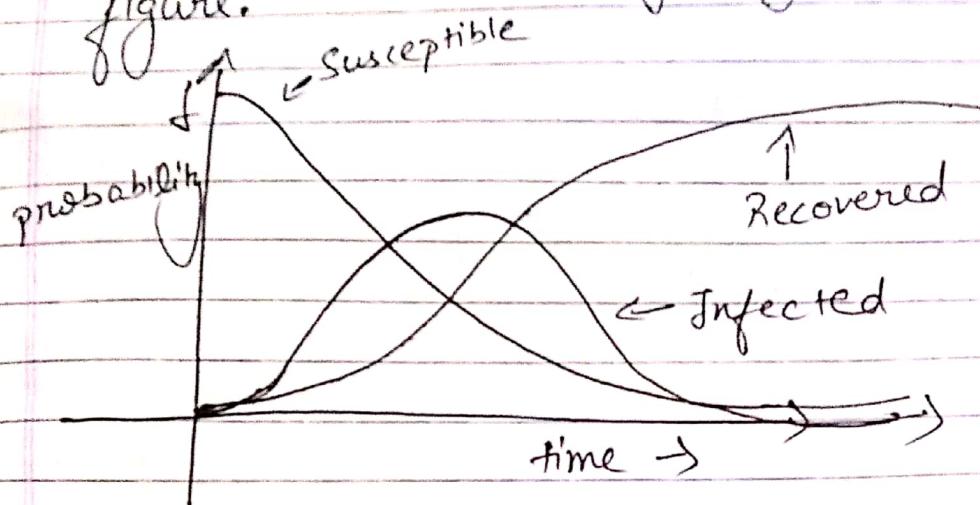
$$\Rightarrow \frac{1}{S} \frac{ds}{dt} = -\frac{\beta}{\gamma} \frac{dx}{dt} \Rightarrow S = S_0 e^{-\beta r/\gamma} \quad \Rightarrow x = 1 - r - S_0 e^{-\beta r/\gamma}$$

where, S_0 is the value at $t=0$.

$$\Rightarrow \frac{dr}{dt} = \gamma(x) = \gamma(1 - S - R) = \gamma(1 - S - S_0 e^{-\beta r/\gamma})$$

$$\Rightarrow dt = \frac{1}{\gamma} \int_0^{R_f} \frac{dr}{1 - R - S_0 e^{-\beta r/\gamma}}$$

This integral cannot be evaluated in closed form.
The Numerical analysis gives the following figure.



⇒ Proof for different time cases: (performed by us)

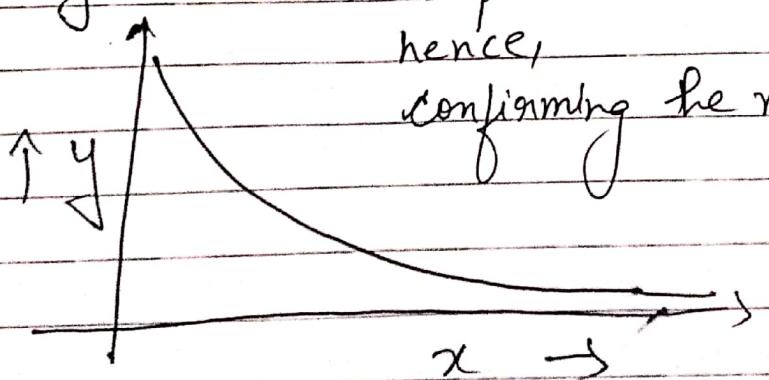
$S = S_0 e^{-\frac{\beta n}{\delta}}$, as σ is supposed to increase,
 S decreases gradually exponentially
as compliance with the figure.

$$S = S_0 e^{-\frac{\beta n}{\delta}}$$

$$\Rightarrow y = 1 \cdot e^{-\frac{\beta x}{\delta}}$$

→ as plotted on a graph gives,
hence,

confirming the numerical chart.



Infected cases,

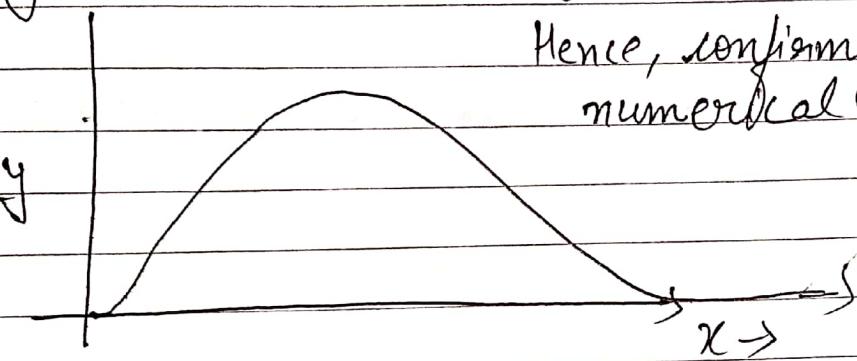
$$-\beta \pi / \gamma$$

$$x = 1 - \pi - S_0 e^{-\beta \pi / \gamma}$$

plotting it on a graph, with the equation,

$$y = 1 - x - e^{-2x}$$

gives,

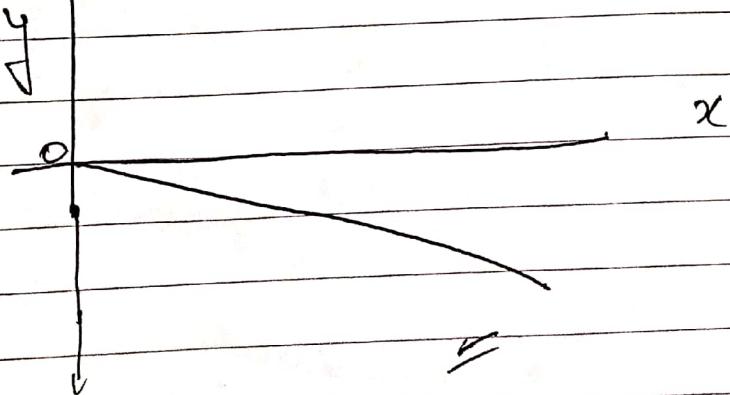


Hence, confirming the numerical graph,

pay attention that β should be greater than 0
 otherwise pandemic does not occur,
 consider the case,

$$y = 1 - x - e^{-0.5x}$$

we get which shows that prob. of infected never exceeds 0.



We plotted S and x as a variable of t
 but not with time,
 not we show how π varies with t .

we were given,

$$t = \frac{1}{\beta} \int_0^{\eta} \frac{du}{1 - u - s_0 e^{-\beta u/\delta}} \quad - \textcircled{1}$$

consider the initial time case,

we have, $s + \alpha t + x = 1$

and $s \rightarrow f$ and $x \rightarrow 0$ and $\alpha \rightarrow 0$.

\Rightarrow putting $u \rightarrow 0$ in eq. $\textcircled{1}$.

$$t = \frac{1}{\beta} \int_0^{\eta} \frac{du}{1 - s_0 e^{-\beta u/\delta}} \quad s_0 \rightarrow 1$$

$$t = \frac{1}{\beta} \int_0^{\eta} \frac{du}{1 - e^{-\beta u/\delta}} \Rightarrow \frac{1}{\beta} \int_0^{\eta} \frac{e^{\frac{\beta u}{\delta}}}{e^{\frac{\beta u}{\delta}} - 1} du$$

$$\text{let } e^{\frac{\beta u}{\delta}} = z, \frac{d}{dz} e^{\frac{\beta u}{\delta}} = \frac{d}{du} z = \frac{\beta}{\delta} z$$

$$\Rightarrow t = \frac{1}{\beta} \times \frac{1}{\beta} \int_{z_0}^{\eta} \frac{z}{z-1} \times \frac{dz}{z} \Rightarrow \frac{1}{\beta} \int_{e^{\frac{\beta z_0}{\delta}}}^{e^{\frac{\beta \eta}{\delta}}} \frac{dz}{z-1}$$

$$\beta t = \left[\log(z-1) \right]_{e^{\frac{\beta z_0}{\delta}}}^{e^{\frac{\beta \eta}{\delta}}}$$

$$\Rightarrow \beta t = \log \left(\frac{e^{\frac{\beta \eta}{\delta}} - 1}{e^{\frac{\beta z_0}{\delta}} - 1} \right) \Rightarrow e^{\frac{\beta \eta}{\delta}} - 1 = e^{\beta t} \left[e^{\frac{\beta z_0}{\delta}} - 1 \right]$$

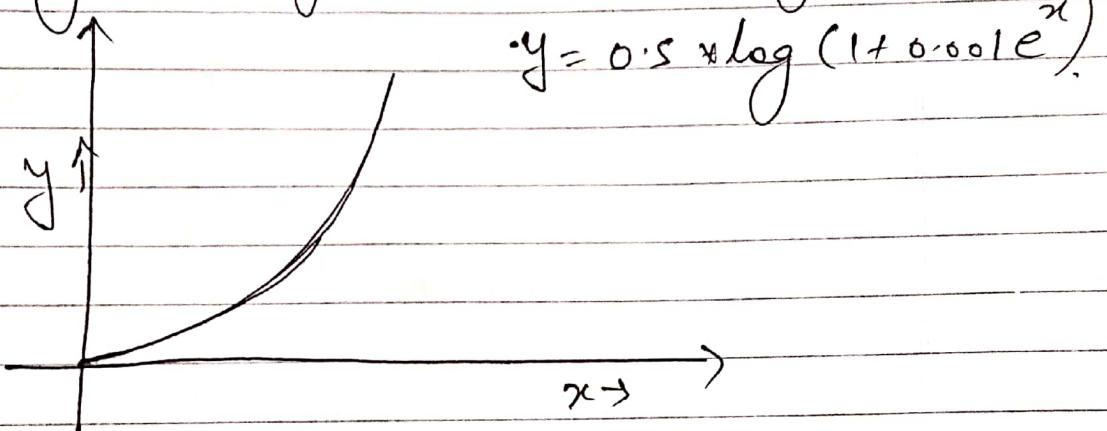
$$\Rightarrow \frac{\beta \eta}{\delta} = \log \left(1 + e^{\beta t} \left[e^{\frac{\beta z_0}{\delta}} - 1 \right] \right) \Rightarrow \eta = \frac{\delta}{\beta} \log \left(1 + e^{\beta t} \left[e^{\frac{\beta z_0}{\delta}} - 1 \right] \right)$$

which is a curve,

$$y = a \log(1 + b e^x).$$

$$a < 1, \quad \cancel{b} \rightarrow 0.$$

On plotting it on a graph plotter, we get,



which is in compliance with our original graph
for initial time $t \rightarrow 0$.

for case $s \rightarrow 0$ and $\alpha \rightarrow 1$,

we can similarly find relation of α with t .

given,

$$t = \int_{\alpha_0}^{\alpha} \frac{du}{1 - u - s_0 e^{-Bu/\alpha}}, \quad U \rightarrow 1$$

$$t = \int_{\alpha_0}^{\alpha_1} \frac{du}{1 - 1 - s_0 e^{-Bu/\alpha}} \Rightarrow t = \int_{\alpha_0}^{\alpha_1} \frac{du}{-s_0 e^{-Bu/\alpha}}$$

$$t = \frac{1}{s_0} \int_{\alpha_0}^{\alpha_1} du \cdot e^{Bu/\alpha} = \frac{1}{s_0} \times \frac{B}{\alpha} \left[e^{Bu/\alpha} \right]_{\alpha_0}^{\alpha_1}$$

$$t = \frac{1}{\beta s_0} \left[e^{\frac{\beta \eta_1}{\delta}} - e^{\frac{\beta \eta_0}{\delta}} \right]$$

$$+ \beta s_0 t = e^{\frac{\beta \eta_1}{\delta}} - e^{\frac{\beta \eta_0}{\delta}}$$

$$e^{\frac{\beta \eta_1}{\delta}} = e^{\frac{\beta \eta_0}{\delta}} + \beta s_0 t$$

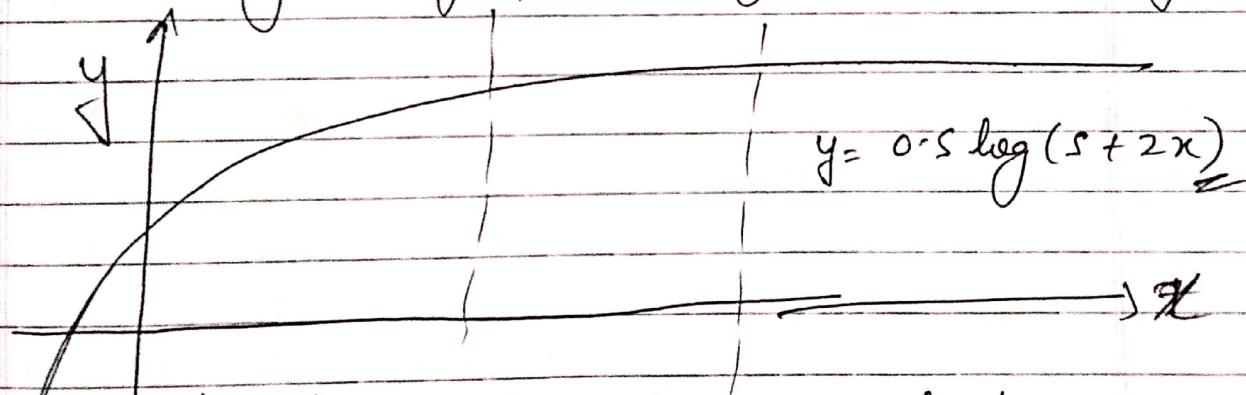
$$\frac{\beta \eta_1}{\delta} = \log \left(e^{\frac{\beta \eta_0}{\delta}} + \beta s_0 t \right)$$

$$\eta_1 = \frac{1}{\beta} \log \left(e^{\frac{\beta \eta_0}{\delta}} + \beta s_0 t \right)$$

\Rightarrow which follows the formula,

$$y = a \log(b + cx)$$

on plotting this graph with graph plotter we get,



for large value of x , graph almost saturated,
which is in compliance with our original graph

Hence,

η_1, s, x are almost approximately correctly plotted for SIR model.

Equilibrium Transition & Reproduction Number

for the case of SIR model,

equilibrium comes when $\beta = \gamma$,

in this case,

there is no outbreak and the number $I(t)$ tends to 0.

for SI case, epidemic always happens because $\gamma = 0$.

Reproduction number is the number of susceptible people to which the infected person passes before he recovers.

If $R = \frac{1}{2}$ means 2 infected people passes disease to 1 person before recovering and the situation is under control.

If $R = 2$, 1 infected person passes disease to 2 person and the situation is not under control.

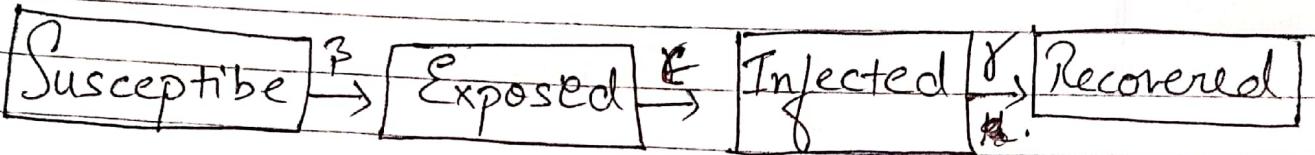
R is an important criteria to determine the severeness of pandemic.

$$R_0 = \beta/\gamma$$

proof: $R_0 = \beta\gamma \int_0^\infty e^{-\gamma t} dt = \frac{\beta}{\gamma}$

More Realistic model for Pandemic [Covid-19]

SEIR model



$\beta \rightarrow$ rate from $S \rightarrow E$

$\gamma \rightarrow$ rate from $E \rightarrow I$.

$\mu \rightarrow$ rate from $I \rightarrow R$.

Similar to SIR model,

Equations for SEIR model can be written,

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$

$$\frac{dE}{dt} = \beta \frac{SI}{N} - (\gamma + \mu)E$$

$$\frac{dI}{dt} = \gamma E - \mu I$$

$$\frac{dR}{dt} = \gamma I$$

This Equation is similar to SIR model and can be plotted similarly.

Also considering a constant birth and death rate, we get:

$$S = \Delta - \mu S - \frac{\beta S I}{N}$$

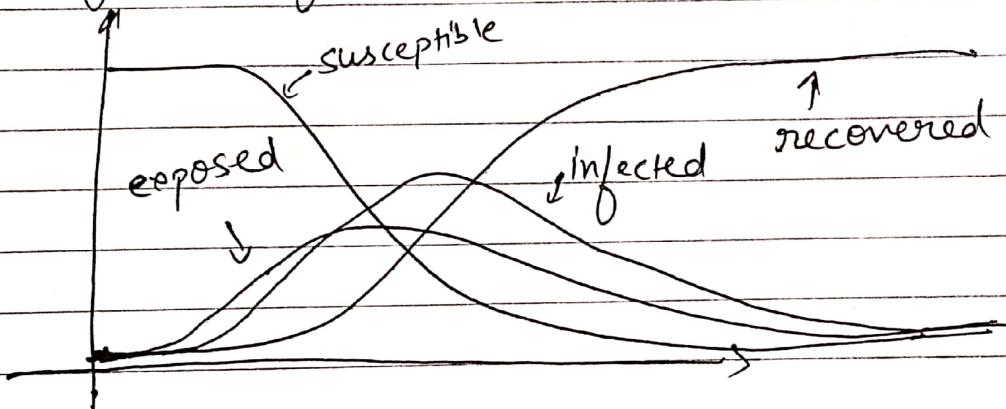
$$E = \frac{\beta S I}{N} - (\mu + \epsilon) E$$

$$I = \epsilon E - (\gamma + \mu + \alpha) I.$$

$$R = \delta I - \mu R$$

where. $N = S + E + I + R$

the graph for this condition is plotted as:



Reproduction Ratio for this case,

$$R_0 = \frac{\beta \epsilon}{(\epsilon + \mu)(\gamma + \alpha + \mu)}$$

This model is more relatable to Real life situation.

But still, there is something wrong with all these models.
What is that?

Epidemic Modelling on Contact Graphs

⇒ till now we saw the full mixing of the population where each person has equal chance to infect any other person in the network.

However, in real world this is not true as a person can only infect people present in its neighbours.

In contact graphs, transmission rate is the probability per unit time that infection will transmit from one transmitter to susceptible who are connected by an edge.

Dynamics of epidemic on a contact graph

① SI Model:

here the probability $S_i(t)$ and $x_i(t)$ is defined for each node separately because each node is different from each other.

To become infected an individual must catch the disease from its neighbours which happens with prob. x_j .

and the time period is Δt , prob = $B \Delta t$, we should also satisfy the condition that i is susceptible, which is prob. S_i .

the total prob. of a susceptible node becoming infected is thus

$$\beta S^i \sum_{j=1}^n A_{ij} x_j^i \quad \text{where } A_{ij} \text{ is the adjacency matrix.}$$

$$\Rightarrow \frac{dS_i^i}{dt} = -\beta S^i \sum_{j=1}^n A_{ij} x_j^i$$

$$S^i + x_i^i = 1$$

$$\frac{dx_i^i}{dt} = \beta (1 - x_i^i) \sum_{j=1}^n A_{ij} x_j^i$$

for the initial case,

$$S^i \rightarrow 1,$$

$$x_i^i \rightarrow 0.$$

$$\frac{dx_i^i}{dt} = \beta \sum_{j=1}^n A_{ij} x_j^i$$

which can be written as,

$$\frac{dx}{dt} = \beta Ax$$

also,

A is a symmetric matrix of size $n \times n$, it means its eigenvectors are the basis vectors of dim. n .

It means x can be written as a linear combination of eigenvectors of A .

$$\Rightarrow x(t) = \sum_{n=1}^{\infty} a_n(t) v_n \quad \begin{matrix} \uparrow \\ \text{eigenvectors of } A \end{matrix}$$

constant

$$\Rightarrow \frac{dx}{dt} = \sum_{n=1}^m \frac{d\alpha_n(t)}{dt} v_n = \beta A \sum_{n=1}^m \alpha_n(t) v_n \\ = \beta \sum K_n \alpha_n(t) v_n$$

$$[A v_n(t) = K_n v_n(t)]$$

In comparison,
we get,

$$\frac{d\alpha_n}{dt} = \beta K_n \alpha_n$$

$$\Rightarrow \alpha_n(t) = \alpha_n(0) e^{\beta K_n t}$$

$$\therefore x(t) = \sum_{n=1}^m \alpha_n(0) e^{\beta K_n t} v_n$$

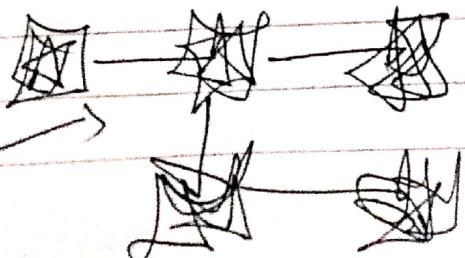
the $x(t)$ is a ~~linear~~ combination of exponential of eigenvalues of A and hence, the largest eigenvalue of A contributes the most.

$$\Rightarrow x(t) \underset{\approx}{\sim} e^{\beta K_1 t} v_1$$

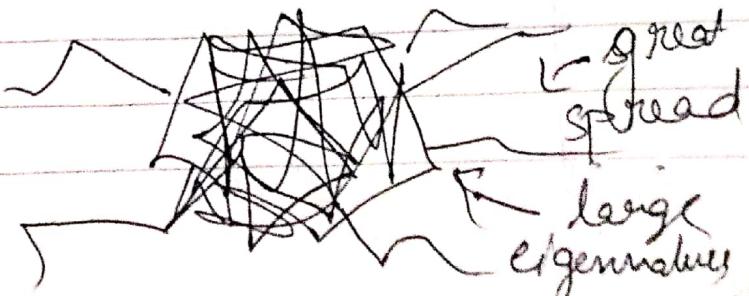
hence, the infected people grows exponentially in SI model but the difference is that it also depends on β as well as eigen value K .

~~Case 1~~, n nodes

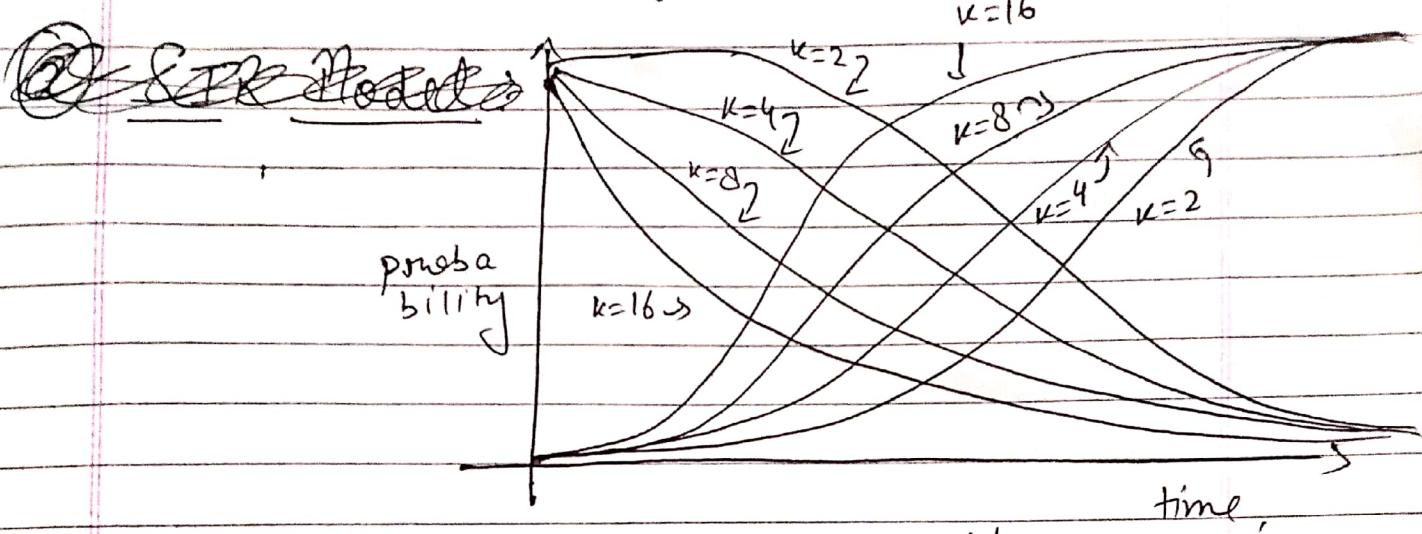
small eigenvalue
slow spread



~~Case 2~~, n nodes



SI model for contact graphs shows the same end result as that of fully mixed version but the vertex with high eigen value are likely to get infected faster.



- SI model for different degree vertices : degree: 16, 8, 4, 2.

(2) SIR Model:

the previous technique can be applied to SIR model with some modification.

for each node, we define

$$S_i^o, x_i^o, r_i^o$$

susceptible injected recovered.

$$\frac{dS_i^o}{dt} = -\beta S_i^o \sum_j A_{ij} x_j$$

$$\frac{dx_i^o}{dt} = [\beta S_i^o \sum_j A_{ij} x_j - \gamma x_i^o]$$

$$\frac{dx_i}{dt} = \gamma x_i$$

for case, $c \ll n$, $s_i^0 \rightarrow 0$ initially,

$$\begin{aligned}\frac{dx_i}{dt} &= \beta \sum A_{ij} x_j - \gamma x_i \\ &= \sum_j (\beta A_{ij} - \gamma s_{ij}) x_j\end{aligned}$$

where $s_{ij}=1$ when $i=j$

for a $n \times n$ matrix,

S becomes a identity matrix.

\Rightarrow in vector notation,

$$\frac{dx}{dt} = \beta M x$$

where, $M = A - \frac{\gamma}{\beta} I$ [a symmetric $n \times n$ matrix].

Once again,

We can write x as a linear combination of eigenvectors of M which will have the same eigenvectors as A and eigenvalues shifted by γ/β .

On solving we get,

$$M v_n = A v_n - \frac{\gamma}{\beta} I v_n = \left(\lambda - \frac{\gamma}{\beta} \right) v_n$$

$$\Rightarrow x(t) = \beta M \sum a_n(t) v_n$$

$$\Rightarrow \beta \sum \left(\lambda - \frac{\gamma}{\beta} \right) v_n$$

$$x(t) = \sum_{n=1}^N a_n(t) v_n$$

$$\Rightarrow \frac{dx}{dt} = \sum_{n=1}^N \frac{da_n(t)}{dt} v_n$$

$$\Rightarrow \frac{da_n}{dt} = \beta a_n(t) \left(k - \frac{\gamma}{\beta} \right)$$

$$\Rightarrow a_n(t) = a_n(0) e^{(\beta k - \gamma)t}$$

$$\Rightarrow x(t) = \sum_{n=1}^N a_n(0) v_n e^{(\beta k_n - \gamma)t}$$

now, the exponential depends now not only on the eigenvalue and growth rate but also on recovery rate.

Again, mode having highest eigenvalue has higher chance of getting infected first.

the threshold for equilibrium where the pandemic dies out burst is,

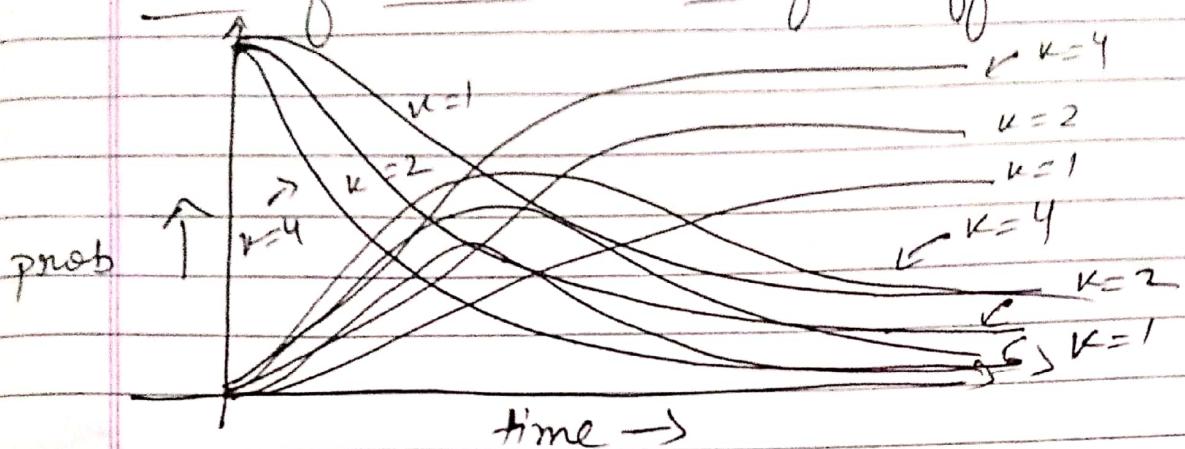
$$\beta k_f - \gamma = 0$$

$$\beta k_1 = \gamma \Rightarrow \left[\frac{1}{k_1} = \frac{\beta}{\gamma} \right]$$

hence,

pandemic outburst depends on the highest eigenvalue in SIR model.

Curve for SIR model for different degrees.



→ node with highest degree k has the fastest growing number of infected and recovered (case.)

③ SEIR Model: [Derived by US].

$S_i^0, E_i^0, X_i^0, R_i^0$

↓ ↑ ↑ ↑
susceptible excited infected recovered.

$$\frac{dS_i^0}{dt} = -\beta S_i^0 \sum A_{ji} E_j^0$$

$$\frac{dE_i^0}{dt} = \beta S_i^0 \sum A_{ij} E_j^0 - \gamma E_i^0$$

$$\frac{dX_i^0}{dt} = \gamma E_i^0 - \lambda X_i^0$$

$$\frac{dR_i^0}{dt} = \lambda X_i^0$$

$$S_i^0 + E_i^0 + X_i^0 + R_i^0 = 1$$

≡.

\Rightarrow we can write,

$$e = \sum a_n(t) v_n(t)$$

where, v_n are the eigenvectors of Adj matrix A .

on solving we get,

~~$$\frac{de}{dt} = \sum a_n(0) e^{(\beta K_n - \gamma)t} v_n$$~~

$$\Rightarrow \frac{ds}{dt} = -\beta A e$$

$$\Rightarrow -\beta \sum_{n=1}^{\infty} a_n(0) K_n e^{(\beta K_n - \gamma)t} v_n.$$

$$s = -\beta \sum_{n=1}^{\infty} a_n(0) K_n \frac{e^{(\kappa_i \beta - \gamma)t}}{(\beta K_n - \gamma)} v_n + C.$$

$$s = \beta \sum_{n=1}^{\infty} a_n(0) K_n v_n - \beta \sum_{n=1}^{\infty} \frac{a_n(0) K_n}{(\beta K_n - \gamma)} e^{(\kappa_i \beta - \gamma)t} v_n$$

$$\frac{dx}{dt} + \lambda x = \gamma e$$

$$\frac{dx}{dt} + \lambda x = \gamma \sum a_n(0) e^{(\beta K_n - \gamma)t} v_n$$

$$\frac{dx}{dt} + \lambda x = \gamma \sum a_n(0) e^{(\beta K_n - \gamma)t} v_n$$

$$A = -\lambda$$

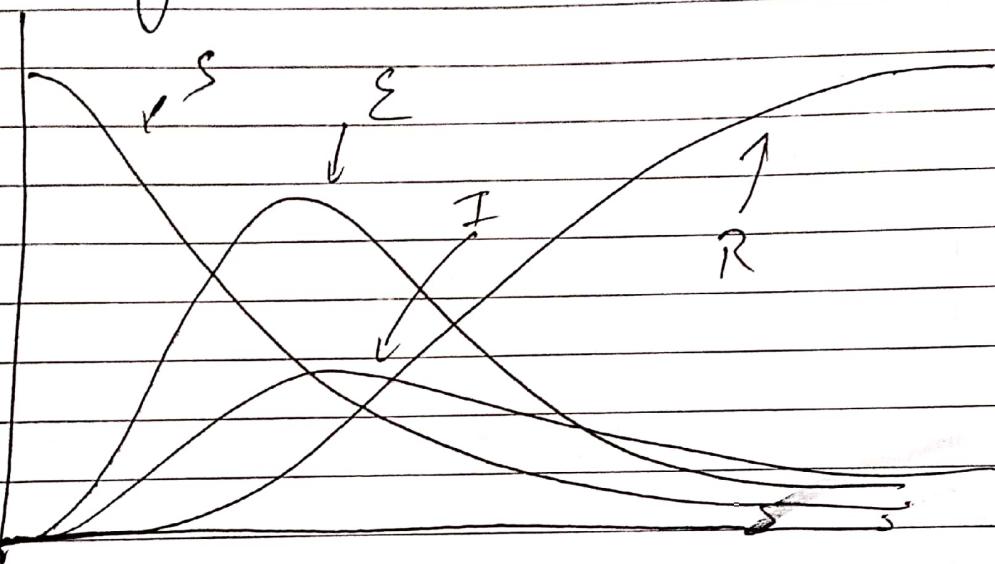
$$\beta = \gamma \sum a_n(0) e^{(\beta K_n - \gamma)t} v_n$$

$$x(t) = K e^{-\lambda t} + e^{-\lambda t} \int_0^t e^{\lambda \tau} \gamma \sum a_n(0) e^{(\beta K_n - \gamma)\tau} v_n d\tau$$

By integration of non-homogeneous linear eq.

$$\Rightarrow X(t) = K e^{-\lambda t} + \gamma \sum_{n=1}^{\infty} a_n(0) e^{\frac{(\beta K n - \gamma)t}{\beta K n - \gamma}} \quad \text{Vn} \\ - \frac{\gamma \sum a_n(0)}{(\beta K n - \gamma)} \quad \text{Vn}$$

Probable Graph.



All of these models considered static network.

Let's consider a simple case for dynamic graphs where the adjacency matrix evolves with time randomly.

We cannot get a definite equation for solving this because the evolution of adjacency matrix with time t is random.

Our Derivation

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⇒ Time varying Contact Graph following SI model

In case the adjacency matrix is time varying.

for the SI case model,
we write,

$$\frac{dx_i}{dt} = \beta \sum A_{ij} x_j$$

$$\frac{dx}{dt} = \beta Ax$$

also,

$$x(t) = \sum a_n(t) v_n(t)$$

since, a and v both varies with time.

$$\frac{dx}{dt} = \sum \left(a_n(t) \frac{dv_n}{dt} + v_n \frac{da_n}{dt} \right) \quad \text{--- (1)}$$

$$\text{also, } \frac{dx}{dt} = \beta A \sum a_n(t) v_n(t)$$

$$\Rightarrow \frac{dx}{dt} = \beta \sum_{n=1}^m a_n(t) K_n(t) v_n(t) \quad \text{--- (2)}$$

On comparison b/w (1) and (2),
we get,

$$\beta a_n(t) K_n(t) v_n(t) = a_n(t) \frac{dv_n(t)}{dt} + v_n(t) \frac{da_n(t)}{dt}$$

$$\beta K_n(t) = \frac{dv_n(t)/dt}{v_n(t)} + \frac{da_n(t)/dt}{a_n(t)}$$

$$\int \beta K_n(t) dt = \int \frac{dv_n(t)}{v_n(t)} + \int \frac{da_n(t)}{a_n(t)}$$

$$\Rightarrow \beta K_n(t) = \log(v_n) + \log(a_n) + \dots$$

$$\Rightarrow \beta K_n(t) = \log\left(\frac{v_n \cdot a_n}{v_{n(0)} a_{n(0)}}\right).$$

Since, we don't know the dynamics of adjacency matrix with time, we cannot directly find a relation between eigenvalues and t .

In case, adjacency matrix is a defined function of t , we can find the eigenvalue variation with t and hence the integral $K(t)$.

$$A = \begin{bmatrix} f_{11}(t) & f_{12}(t) & \dots & f_{1n}(t) \\ f_{21} & f_{22}(t) & \dots & f_{2n}(t) \\ \vdots & & & \\ f_{n1}(t) & f_{n2}(t) & \dots & f_{nn}(t) \end{bmatrix}$$

$$|A - \lambda I| = 0$$

$$\lambda = K_1(t), K_2(t), K_3(t) \dots K_n(t)$$

\equiv

Eigenvalues as a function of time.

$$\beta K_n(t)$$

$$V_n a_n = v_{n(0)} a_{n(0)} e^{\beta K_n(t)}$$

~~$$d\eta = \beta K_n(t) v_{n(0)} a_{n(0)} e^{\beta K_n(t)} dt$$~~

~~$\beta K_n(t)$~~

since,

$$x = \sum a_n(t) v_n(t)$$

$$x = \sum a_n(0) v_n(0) e^{\beta K_n(t)}$$

where $K_n = \int k_n dt$

Hence,

if the time dynamics of adjacency matrix J is given,
we can define the growth of x and s
as a function of t .

$$x_i = \sum a_n(0) v_n(0) e^{\beta K_n(t)}$$

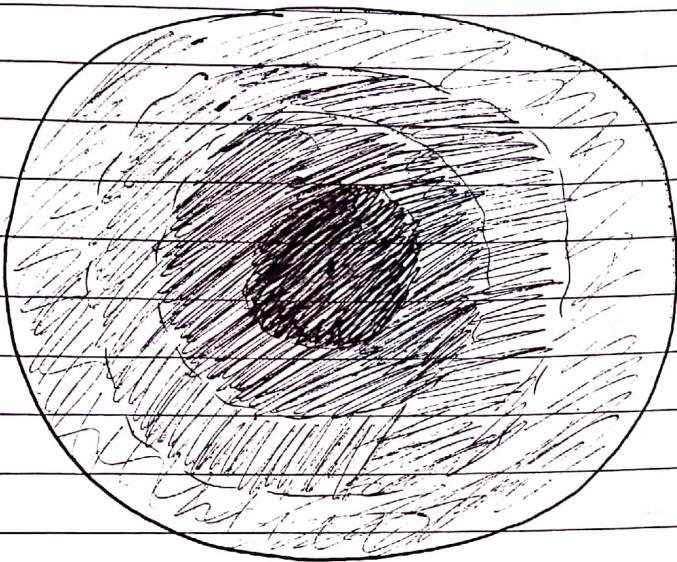
$$s_i = 1 - \sum a_n(0) v_n(0) e^{\beta K_n(t)}$$

Similarly,

time variant contact graph mathematical models can be generated for other models such as SIR or SEIR

~~but~~ given the dynamics of adjacency matrix with time.

Case for a Spatial Gaussian Distribution SIR model



consider a spatial region where the density of nodes varies with radius r as

$$f = f_0 e^{-\frac{r^2}{r_0^2}}$$

Now,

we have three states :

$$S_i^0, \quad g_i^0, \quad x_i^0$$

$$\frac{dS_i^0}{dt} = -\beta S_i^0 \sum_{j=1}^{g_i^0} A_{ij} x_j^0 \quad \text{summation of neighbours. infected nodes.}$$

$$\frac{dx_i^0}{dt} = \beta S_i^0 \sum_{j=1}^{g_i^0} A_{ij} x_j^0 - \gamma x_i^0$$

$$\frac{dg_i^0}{dt} = f x_i^0$$

$-n^2$ open density ρe

we consider a contact when two nodes comes less than ϵ distance.

Consider a node,
all the number of nodes in its contact are,

$$(\rho e^{-x^2}) \left(\frac{4\pi \epsilon^3}{3} \right) = N_n$$

$$\Rightarrow \cancel{\frac{dS_i}{dt}} = -\beta S_i \sum_{j=1} A_{ij} x_j$$

$$\frac{dx_i}{dt} = \beta S_i \sum_{j=1}^{N_n} A_{ij} x_j - \gamma x_i$$

$$\frac{dS_i}{dt} = \cancel{S_i}$$

the growth rate of infected nodes at center is much faster due to summation from larger neighbour nodes.

If an infected node is placed at center,
we can see that

the rate of change of infected nodes is very high as compared to outer shell because of high eigenvalue contribution by the center nodes.

$$x(t) = \beta \sum_{i=1}^N \alpha_i e^{(\lambda_i - \frac{\beta}{\lambda_i}) t}$$

the center where nodes are dense leading to high eigenvalues leading to more intense spread as compared to outer sparse nodes.

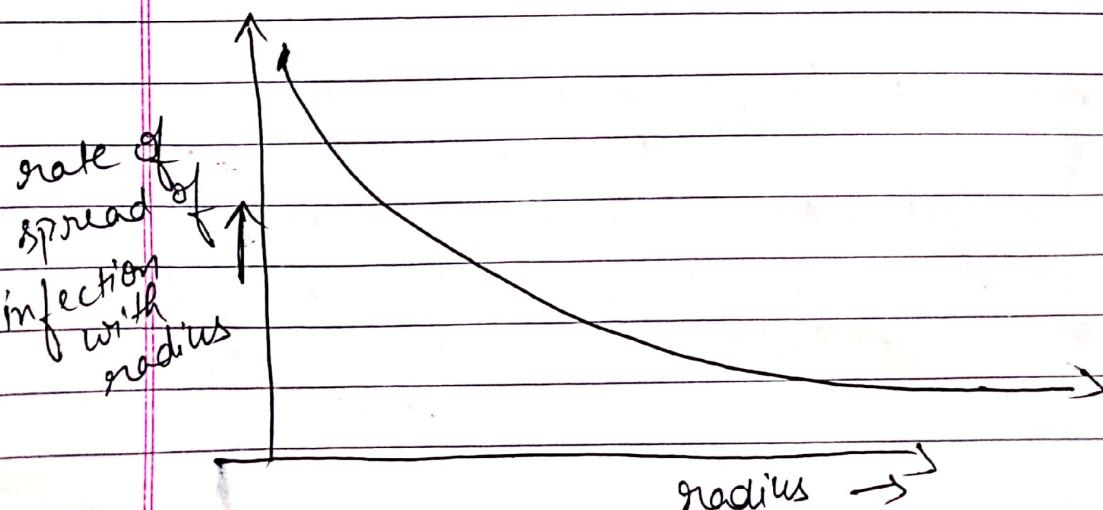
considering, λ_n eigenvalue & number of neighbours

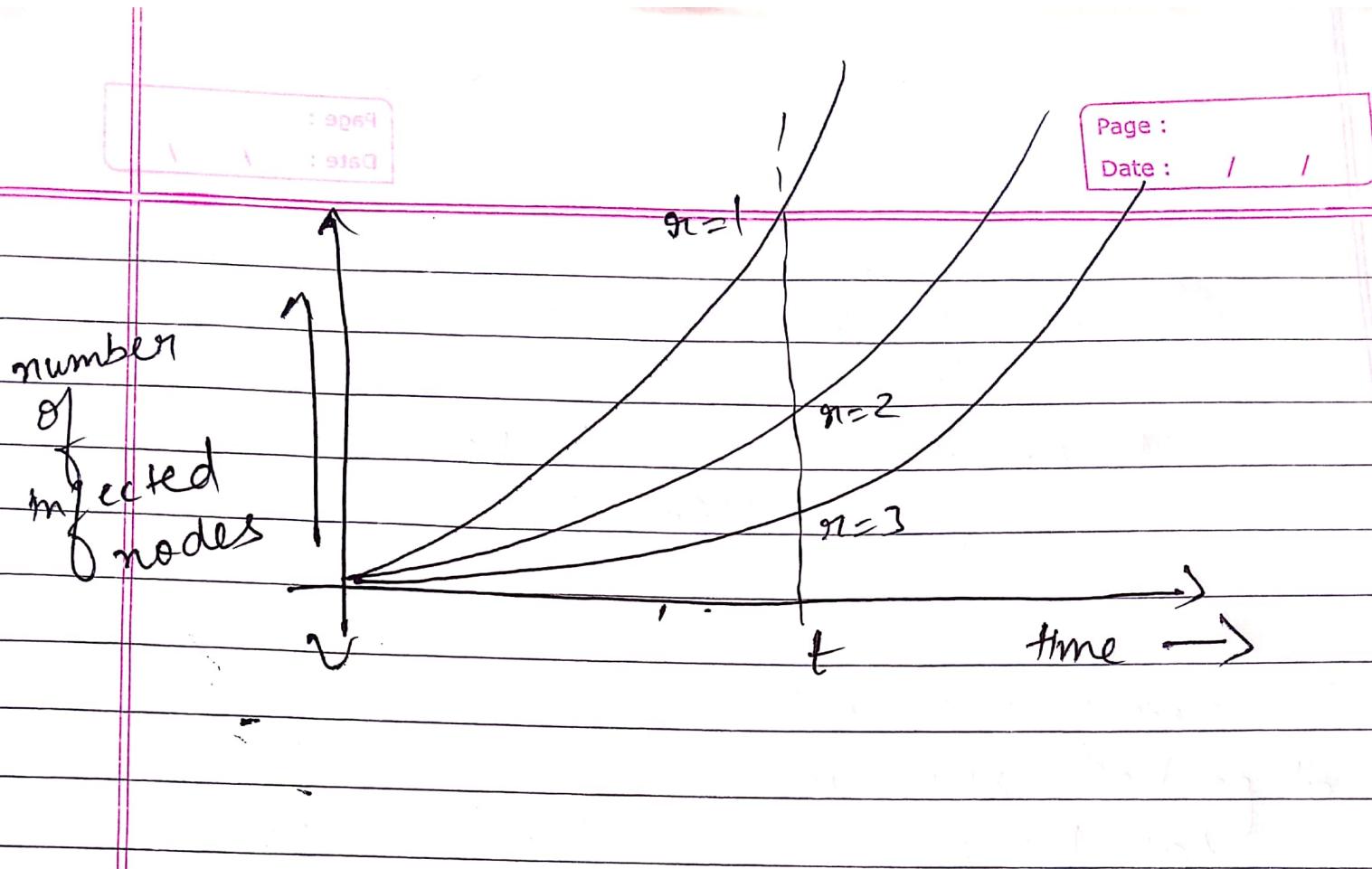
$$\frac{dx}{dt} = \beta M x \text{ originally.}$$

$$\frac{dx}{dt} = \beta M \left[\frac{4\pi r^3}{3} \right] \left[\int_0^r p e^{-\lambda_i r} \right] \left[\frac{dx}{dt} \right]$$

prob that neighbour is infected.

which reduces with radius.





Contributions

- (1) Mathematical insight to all existing models for pandemic modelling.
- (2) Derived a mathematical model for SEIR model in case of a contact graph.
- (3) Derived a time varying graph SI model which can be extended to SIR, SEIR and other models.
- (4) Derived a model on Gaussian distribution SIR model and plotted the graph.