

Towards an Epidemiological Model for the Spread of an Infectious Disease with Quarantine



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Senior project in Wash U ESE department:

R. Agrawal, M. Balchan, M. Lambros

Standard SIR Model

$$\dot{S} = \nu N - \beta IS - \nu S - \kappa \omega S$$

$$\dot{I} = \beta IS - \nu I - \alpha \tau I$$

$$\dot{R} = \alpha \tau I + \kappa \omega S - \nu R$$

Assumptions:

- constant population $N = S + I + R = \text{const}$
- no “deaths” from disease / **deaths from disease are “removed”**

Standard SIR Model

$$\dot{S} = \nu N - \beta IS - \nu S - \kappa \omega S$$

$$\dot{I} = \beta IS - \nu I - \alpha \tau I$$

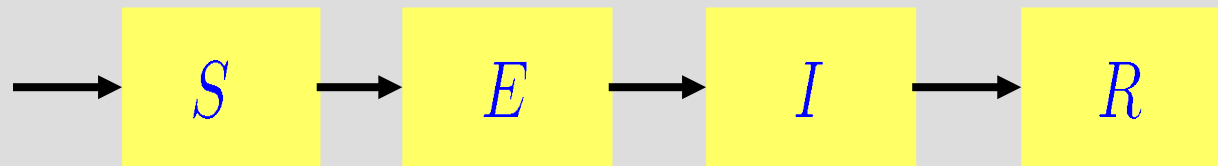
$$\dot{R} = \alpha \tau I + \kappa \omega S - \nu R$$

Assumptions:

- constant population $N = S + I + R = \text{const}$
- no “deaths” from disease / deaths from disease are “removed”

If there are significant deaths from the disease, this should be accounted for and population is really time varying

An SEIR Model with Time-Varying Populations



Sun and Hsieh,
Appl Math Mod,
2010

$$\dot{S}(t) = \gamma N(t) - \beta \frac{I(t)}{N(t)} S(t) - \nu S(t) - \kappa \omega S(t)$$

$$\dot{E}(t) = \beta \frac{I(t)}{N(t)} S(t) - (\delta + \nu) E(t)$$

$$\dot{I}(t) = \delta E(t) - (\mu + \nu) I(t) - \alpha \tau I(t)$$

$$\dot{R}(t) = \alpha \tau I(t) + \kappa \omega S(t) - \nu R(t)$$

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

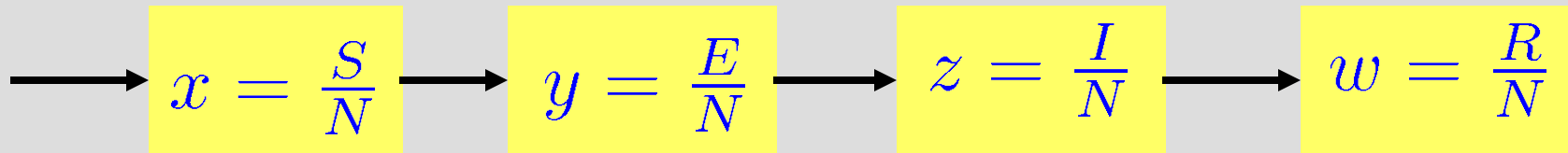
$$\Rightarrow \dot{N} = (\gamma - \nu)N - \mu I$$

no equilibria

Model for Proportions

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

“occupancy measure”



$$\dot{x} = (\mu - \beta) x z - (\gamma + \kappa \omega) x + \gamma$$

$$\dot{y} = (\beta x + \mu y) z - (\gamma + \delta) y$$

$$\dot{z} = \mu z^2 + \delta y - (\gamma + \mu + \alpha \tau) z$$

$$\dot{w} = \mu w z - \gamma w + \kappa \omega x + \alpha \tau z$$

**Sun and Hsieh,
Appl Math Mod, 2010**

- **disease free ratio at**

$$(x_0, y_0, z_0, w_0) = \left(\frac{\gamma}{\gamma + \kappa\omega}, 0, 0, \frac{\kappa\omega}{\gamma + \kappa\omega} \right)$$

- **disease free ratio at**

$$(x_0, y_0, z_0, w_0) = \left(\frac{\gamma}{\gamma + \kappa\omega}, 0, 0, \frac{\kappa\omega}{\gamma + \kappa\omega} \right)$$

- **basic reproduction number**

$$R_0 = \frac{\gamma}{\gamma + \kappa\omega} \cdot \frac{\delta}{\gamma + \delta} \cdot \frac{\beta}{\gamma + \mu + \alpha\tau}$$

identical with formula for SEIR model with constant population

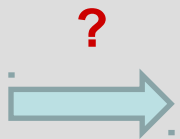
- disease free ratio at

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- basic reproduction number

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identical with formula for SEIR model with constant population



- if $R_0 < 1$ then the DFR is globally asymptotically stable
- if $R_0 > 1$ there exists a unique, globally stable endemic equilibrium point

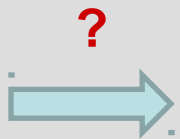
- disease free ratio at

$$(x_0, y_0, z_0, w_0) = \left(\frac{\gamma}{\gamma + \kappa\omega}, 0, 0, \frac{\kappa\omega}{\gamma + \kappa\omega} \right)$$

- basic reproduction number

$$R_0 = \boxed{\frac{\gamma}{\gamma + \kappa\omega}} \cdot \frac{\delta}{\gamma + \delta} \cdot \frac{\beta}{\gamma + \mu + \alpha\tau}$$

identical with formula for SEIR model with constant population

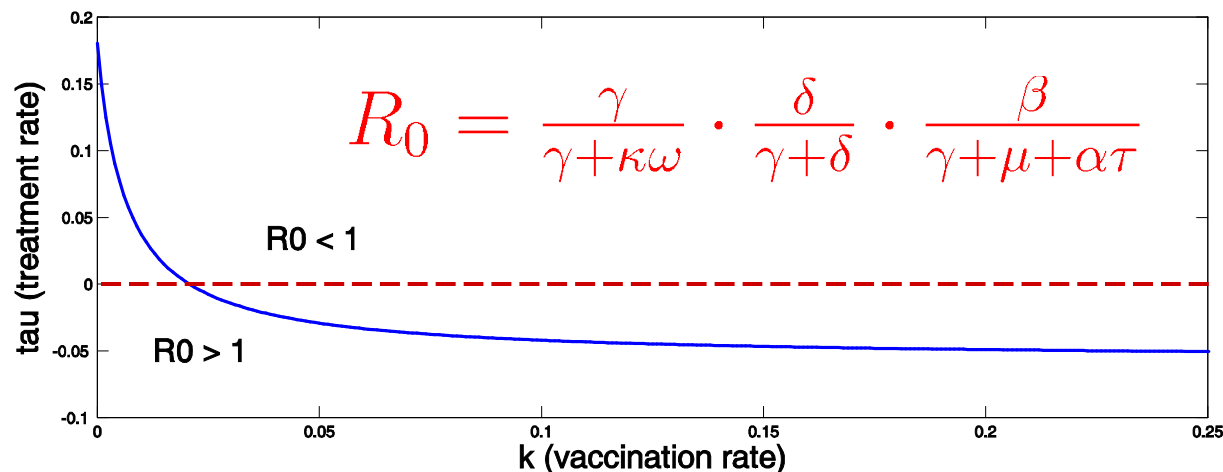


- if $R_0 < 1$ then the DFR is globally asymptotically stable
- if $R_0 > 1$ there exists a unique, globally stable endemic equilibrium point

partial results in **Sun and Hsieh, Appl Math Mod, 2010**

Parameters related to the recent Ebola outbreak in Westafrica (R. Agarwal, M. Balchan and M. Lambros)

parameter	estimated value	interpretation	Reference
γ	0.00683	birth rate of the population	[13]
ν	0.00188	natural death rate of the population	[13]
μ	0.059	disease induced death rate in the population	[11, 12]
β	0.2426	rate of infectiousness of the disease	[11, 12]
δ	0.50	rate at which exposed individuals become infectious	[11, 12]



$$R_0 = 3.67$$

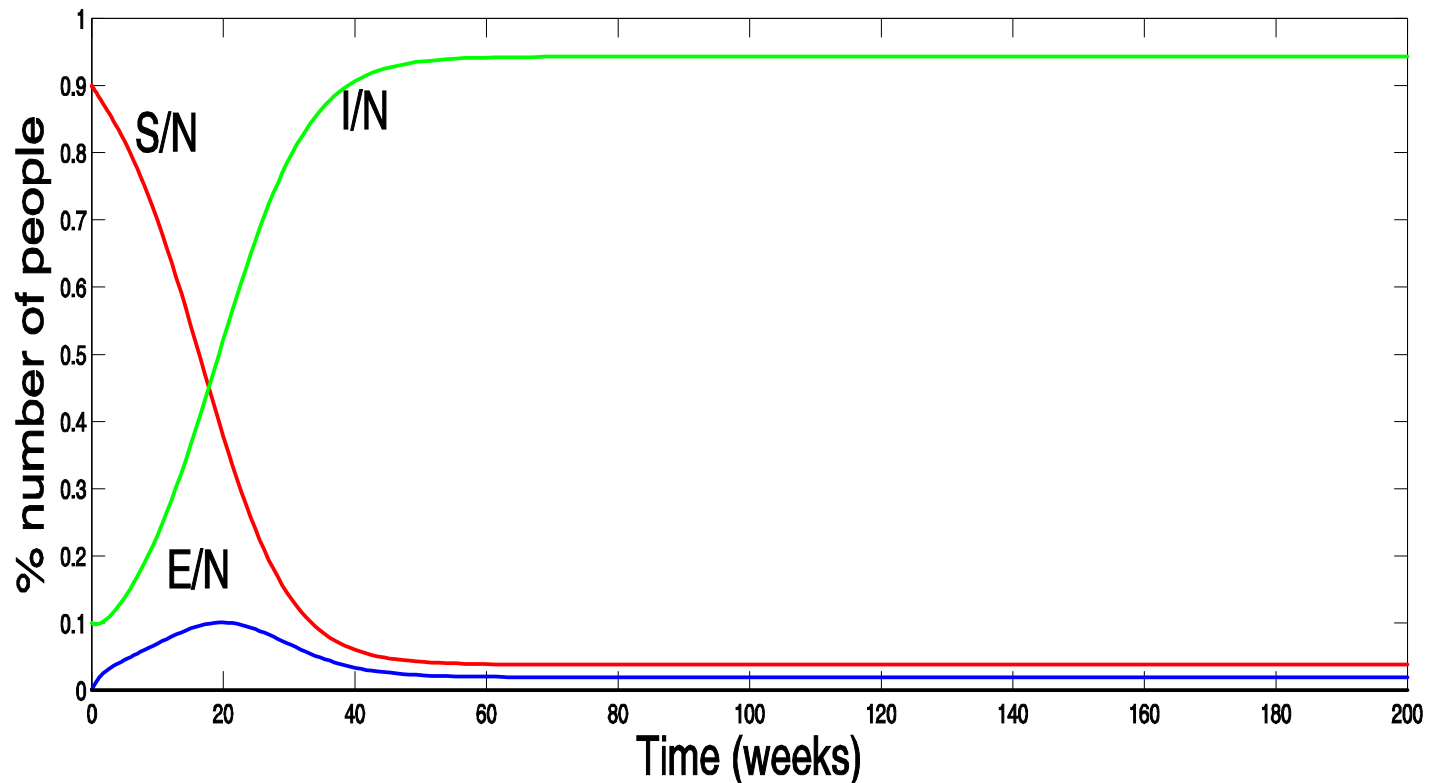
$$R_0 = 2.49$$

NIH-pub

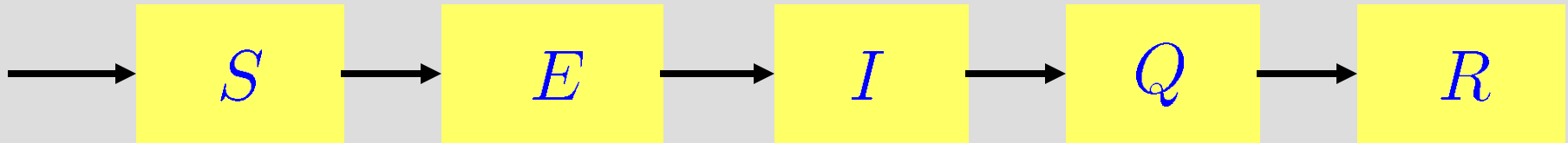
treatment/vaccination would not be effective to control outbreak

Evolution of proportions from

$$(x_0, y_0, z_0, w_0) = (0.90, 0, 0.10, 0)$$



An SEIQR Model with Quarantine



$$\dot{S}(t) = \gamma N(t) - \beta \frac{I(t)}{N(t) - Q(t)} S(t) - \nu S(t) - \kappa \omega S(t)$$

$$\dot{E}(t) = \beta \frac{I(t)}{N(t) - Q(t)} S(t) - (\delta + \nu) E(t)$$

$$\dot{I}(t) = \delta E(t) - (\mu + \nu) I(t) - \rho I(t)$$

$$\dot{Q}(t) = \rho I(t) - (\mu + \nu) Q(t) - \alpha \tau Q(t)$$

$$\dot{R}(t) = \alpha \tau Q(t) + \kappa \omega S(t) - \nu R(t)$$

$$N = S + E + I + Q + R$$

$$\Rightarrow \dot{N} = (\gamma - \nu) N - \mu(I + Q)$$

$$N = S + E + I + Q + R$$

Model for Proportions

$$\longrightarrow x = \frac{S}{N} \longrightarrow y = \frac{E}{N} \longrightarrow z = \frac{I}{N} \longrightarrow v = \frac{Q}{N} \longrightarrow w = \frac{R}{N}$$

$$\dot{x} = -\beta \frac{xz}{1-v} + \gamma - (\gamma + \kappa\omega) x + \mu(z+v)x$$

$$\dot{y} = \beta \frac{xz}{1-v} - (\gamma + \delta) y + \mu(z+v)y$$

$$\dot{z} = \delta y - (\gamma + \mu + \rho) z + \mu(z+v)z$$

$$\dot{v} = \rho z - (\gamma + \mu + \alpha\tau) v + \mu(z+v)v$$

$$\dot{w} = \kappa\omega x + \alpha\tau v - \gamma w + \mu(z+v)w$$

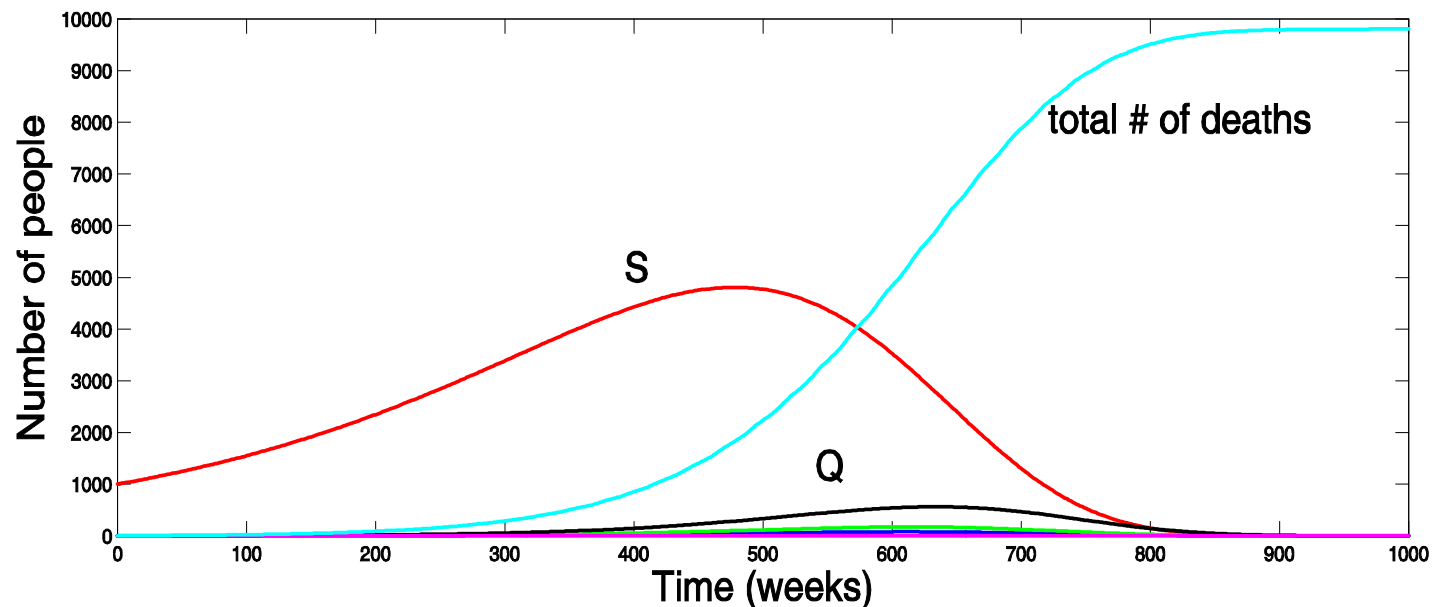
disease free ratio at $(x_0, y_0, z_0, v_0, w_0) = \left(\frac{\gamma}{\gamma + \kappa\omega}, 0, 0, 0, \frac{\kappa\omega}{\gamma + \kappa\omega} \right)$

basic reproduction number

$$R_0 = \frac{\gamma}{\gamma + \kappa\omega} \cdot \frac{\delta}{\gamma + \delta} \cdot \frac{\beta}{\gamma + \mu + \rho}$$

Evolution of the dynamics from

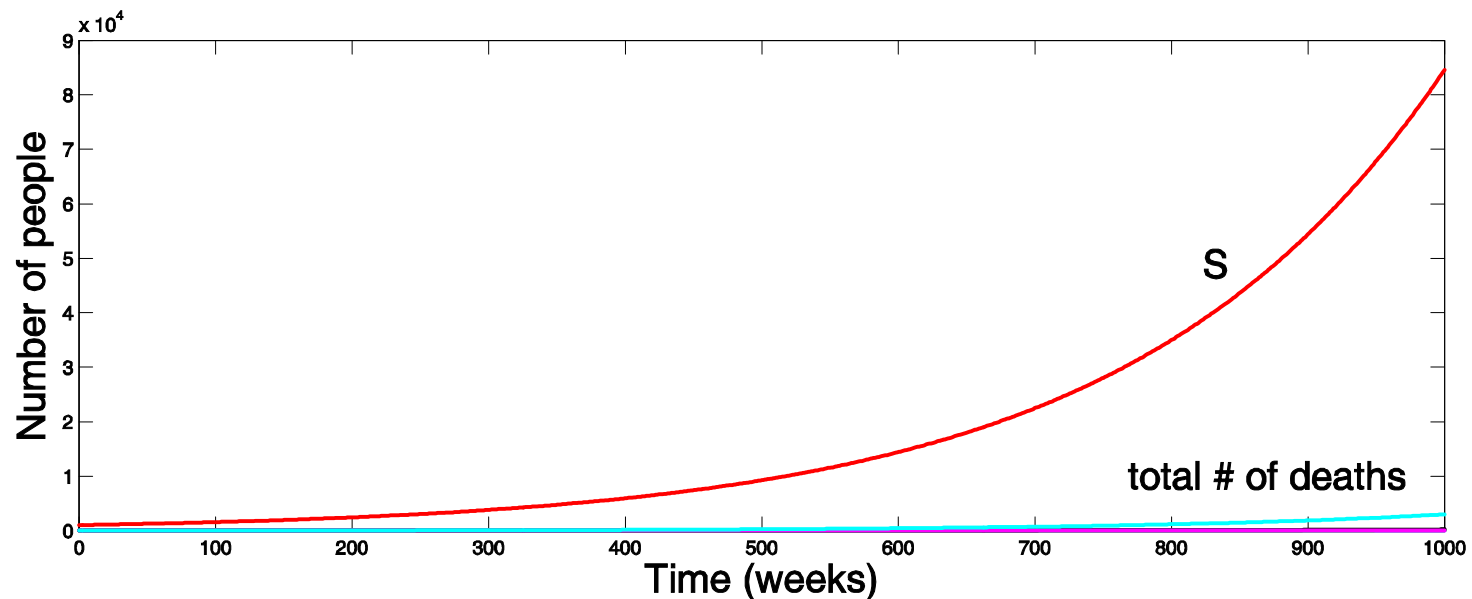
$$(S_0, E_0, I_0, Q_0, R_0) = (999, 0, 1, 0, 0)$$



without vaccination and treatment and quarantine rate $\rho = 0.17$

Evolution of the dynamics from

$$(S_0, E_0, I_0, Q_0, R_0) = (999, 0, 1, 0, 0)$$



without vaccination and treatment and quarantine rate $\rho = 0.182$

- in the model above, individuals are quarantined as they are recognized to have the disease
- individuals who were in contact and possibly exposed are not
- try to include contact/spatial aspects

Let $\Omega \subset \mathbb{R}^k$ model different “locations” and set $P = N - Q$

$$\begin{aligned}\dot{S}(t, x) = & \gamma N(t, x) - \left(\int_{\Omega} \beta(x - y) \frac{I(t, y)}{P(t, y)} d\mu(y) \right) S(t, x) \\ & - \left(\int_{\Omega} \varphi(x - y) \frac{I(t, y)}{P(t, y)} d\mu(y) \right) S(t, x) \\ & + \xi Q_p(t, x) - \nu S(t, x) - \kappa S(t, x)\end{aligned}$$

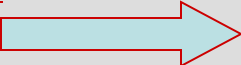
SIR Model with Constant Population

Let $\Omega \subset \mathbb{R}^k$ model different “locations”/compartments

$$\begin{aligned}\dot{S}(t, x) = & A(x) - \left(\int_{\Omega} \beta(x - y) I(t, y) d\mu(y) \right) S(t, x) \\ & + \eta R(t, x) - \nu S(t, x)\end{aligned}$$

$$\dot{I}(t, x) = \left(\int_{\Omega} \beta(x - y) I(t, y) d\mu(y) \right) S(t, x) - (\tau + \nu) I(t, x)$$

$$\dot{R}(t, x) = \tau I(t, x) - (\eta + \nu) R(t, x)$$


$$\dot{N}(t, x) = A(x) - \nu N(t, x)$$

Let $\Omega \subset \mathbb{R}^k$ model different “locations”/compartments

$$N(t, x) = \frac{A(x)}{\nu} + e^{-\nu t} \left(N(0, x) - \frac{A(x)}{\nu} \right) \rightarrow \frac{A(x)}{\nu}$$

total population:

$$\widehat{N}(t) = \int_{\Omega} N(t, x) d\mu(x) \rightarrow \frac{1}{\nu} \int_{\Omega} A(x) d\mu(x) = \frac{A^*}{\nu}$$

SIR Model with Constant Population

Let $\Omega \subset \mathbb{R}^k$ model different “locations”/compartments

$$\dot{S}(t, x) = A(x) - (\beta * I)(t, x)S(t, x) + \eta R(t, x) - \nu S(t, x)$$

$$\dot{I}(t, x) = (\beta * I)(t, x)S(t, x) - (\tau + \nu)S(t, x)$$

$$\dot{R}(t, x) = \tau I(t, x) - (\eta + \nu)R(t, x)$$

Aggregated populations: $\hat{S}(t) = \int_{\Omega} S(t, x) d\mu(x)$

$$\hat{I}(t) = \int_{\Omega} I(t, x) d\mu(x) \quad \hat{R}(t) = \int_{\Omega} R(t, x) d\mu(x)$$

$$\Rightarrow \left\{ \begin{array}{l} \dot{\hat{S}} = A^* - \int_{\Omega} (\beta * I)(t, x) S(t, x) d\mu(x) + \eta \hat{R} - \nu \hat{S} \\ \dot{\hat{I}} = \int_{\Omega} (\beta * I)(t, x) S(t, x) d\mu(x) - (\tau + \nu) \hat{S} \\ \dot{\hat{R}} = \tau \hat{I} - (\eta + \nu) \hat{R} \end{array} \right.$$

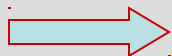
to be continued ...

Conclusion

- epidemiological models with time varying populations and **significant disease induced death rates** are not just a straightforward mathematical extensions of the typical SIR-type models

there already exists some substantial work (e.g., Sun and Hsieh), but has gaps

- quarantine probably is the most effective means to control a highly infectious disease



models should include these aspects



attempt to model spatial aspects of spread