# Stochastic Modelling of Event-Based SARS-CoV-2 Superspreading

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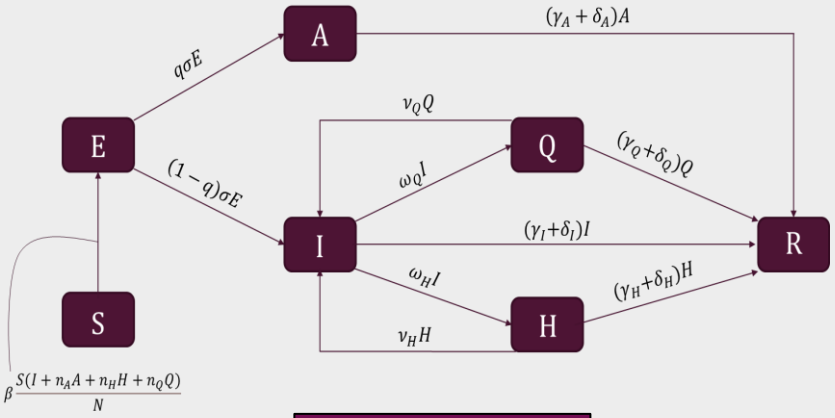
## Deterministic Model [1]

- Incorporates heterogeneities in transmission from and recovery of asymptomatic versus symptomatic individuals, as well as hospitalization, quarantine, hospital discharge, and quarantine violation
- System of deterministic equations corresponding to the following flow diagram:




## Stochastic Model [2,3]

- Assume early outbreak scenario with a large, completely susceptible population, so that:

$$\frac{S}{N}\approx 1 \Rightarrow \beta\frac{S(I+n_AA+n_HH+n_QQ)}{N} \approx \beta(I+n_AA+n_HH+n_QQ)$$

- Set of events and probabilities based on deterministic movement patterns and rates:

| | |
|---|---|
| $E_{SE}: \mathrm{S}\to \mathrm{S}-1, \mathrm{E}\to \mathrm{E}+1$ | $\mathrm{P}(E_{SE}) = \beta(I+n_AA+n_HH+n_QQ)\Omega^{-1}$ |
| $E_{EA}: \mathrm{E}\to \mathrm{E}-1, \mathrm{A}\to \mathrm{A}+1$ | $\mathrm{P}(E_{EA}) = q\sigma E\Omega^{-1}$ |
| $E_{AR}: \mathrm{A}\to \mathrm{A}-1, \mathrm{R}\to \mathrm{R}+1$ | $\mathrm{P}(E_{AR}) = (\gamma_A+\delta_A)A\Omega^{-1}$ |
| $E_{EI}: \mathrm{E}\to \mathrm{E}-1, \mathrm{I}\to \mathrm{I}+1$ | $\mathrm{P}(E_{EI}) = (1-q)\sigma E\Omega^{-1}$ |
| $E_{IQ}: \mathrm{I}\to \mathrm{I}-1, \mathrm{Q}\to \mathrm{Q}+1$ | $\mathrm{P}(E_{IQ}) = \omega_Q I\Omega^{-1}$ |
| $E_{IR}: \mathrm{I}\to \mathrm{I}-1, \mathrm{R}\to \mathrm{R}+1$ | $\mathrm{P}(E_{IR}) = (\gamma_I+\delta_I)I\Omega^{-1}$ |
| $E_{IH}: \mathrm{I}\to \mathrm{I}-1, \mathrm{H}\to \mathrm{H}+1$ | $\mathrm{P}(E_{IH}) = \omega_H I\Omega^{-1}$ |
| $E_{QI}: \mathrm{Q}\to \mathrm{Q}-1, \mathrm{I}\to \mathrm{I}+1$ | $\mathrm{P}(E_{QI}) = \nu_Q Q\Omega^{-1}$ |
| $E_{QR}: \mathrm{Q}\to \mathrm{Q}-1, \mathrm{R}\to \mathrm{R}+1$ | $\mathrm{P}(E_{QR}) = (\gamma_Q+\delta_Q)Q\Omega^{-1}$ |
| $E_{HI}: \mathrm{H}\to \mathrm{H}-1, \mathrm{I}\to \mathrm{I}+1$ | $\mathrm{P}(E_{HI}) = \nu_H H\Omega^{-1}$ |
| $E_{HR}: \mathrm{H}\to \mathrm{H}-1, \mathrm{R}\to \mathrm{R}+1$ | $\mathrm{P}(E_{HR}) = (\gamma_H+\delta_H)H\Omega^{-1}$ |

$\Omega$ = Sum of movement rates

## Overview

The novel coronavirus SARS-CoV-2 emerged in 2019 and subsequently spread throughout the world. Superspreading – both individual- and event-based – spurs SARS-CoV-2 spread. While individual-based superspreading involves individuals who cause disproportionately more infections over their infectious lifetime, event-based superspreading involves public events and/or social gatherings that result in multiple infections. Here, we adopt an event-based framework. Superspreading events (SSEs) are incorporated into a continuous-time Markov chain model in such a way that their influence on outbreak dynamics may be investigated relative to that of non-SSEs. We explore three versions of this model – two with hospitalization and quarantine and one without – by varying the SSE-related and non-SSE-related infection rates. Limited resources and human behavior are accounted for via discharge of and quarantine violate by infectious individuals. Results indicate that SSE-dominated outbreaks are more variable than non-SSE-dominated outbreaks, and minimizing premature hospital discharge and quarantine violation are crucial for controlling SARS-CoV-2 spread.

## Superspreading Events [4]

- Assume that SSEs involve a single infected individual and otherwise susceptible individuals so that may incorporate as follows:

$\psi$: SSE Rate
$K$: Poisson r.v. w/ param. $\phi$
$\phi$: Expected # infections
$k$: Some val. of $K$

$E_{SSE}: \mathrm{S}\to \mathrm{S}-\mathrm{k}, \mathrm{E}\to \mathrm{E}+\mathrm{k}$

$P(E_{SSE}) = \frac{\psi(n_AA+I)}{\Omega}$

## Constancy Condition [4]

- Require that the expected number of infections (SSE and non-SSE combined) following the first change in state be the same as when $\beta^* = \beta$ (no SSEs) for different values of $\beta^*$
- Hold $\phi$ constant for different values of $\beta^*$ and use the above requirement to obtain $\psi$ as a function of $\beta, \beta^*, \phi, I_1, I_2$, and $\Omega'$:

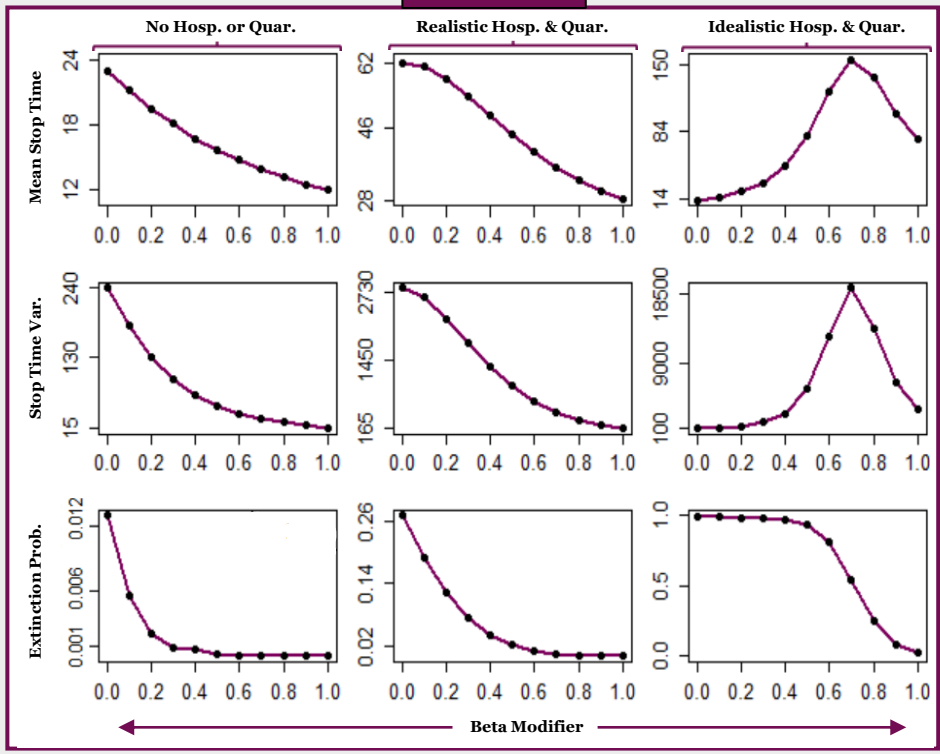
$$\psi = \frac{I_1(\beta-\beta^*)\Omega'}{I_2(\phi\Omega'+\beta I_1(\phi-1))}$$

$$I_1 = n_AA + \mathrm{I} + n_QQ + n_HH$$
$$I_2 = n_AA + \mathrm{I}$$
$$\Omega' = \sigma E + (\gamma_A+\delta_A)A + (w_Q+\omega_H+\gamma_I+\delta_\mathrm{I})I + (\nu_Q+\gamma_Q+\delta_Q)Q + (\nu_H+\gamma_H+\delta_H)H$$

## Simulation

- Model simulated model using Gillespie's direct algorithm
- Simulations ended once 50 current infections or extinction occurs

## Results




## Conclusions

- The greater the incidence of SSEs, the greater the variability in outbreak profiles
- The greater the incidence of SSEs, the longer it takes on average to attain a given number of current infections, but it may still happen more quickly than when there is lower incidence of SSEs
- The disease easily establishes itself in NHQ but struggles more in RHQ and IHQ
- The disease much more easily establishes itself in RHQ compared to scenario IHQ

## References

1. F. B. Agusto, I. V. Erovenko, A. Fulk, Q. Abu-Saymeh, D. D. Romero-Alvarez, J. Ponce, S. Sindi, O. Ortega, J. M. Saint Onge, and A. T. Peterson. "To isolate or not to isolate: The impact of changing behavior on COVID-19 transmission."
2. I. Oluwatobilloba. "Markov Chain Epidemic Models and Parameter Estimation."
3. J. C. Miller. "A primer on the use of probability generating functions in infectious disease modeling."
4. A. James, J. W. Pitchford, and M. J. Plank. "An event-based model of superspreading in epidemics."