Compartmental models in epidemiology
or
The emergence of a global pandemic

Journal Club, 3rd of April 2020

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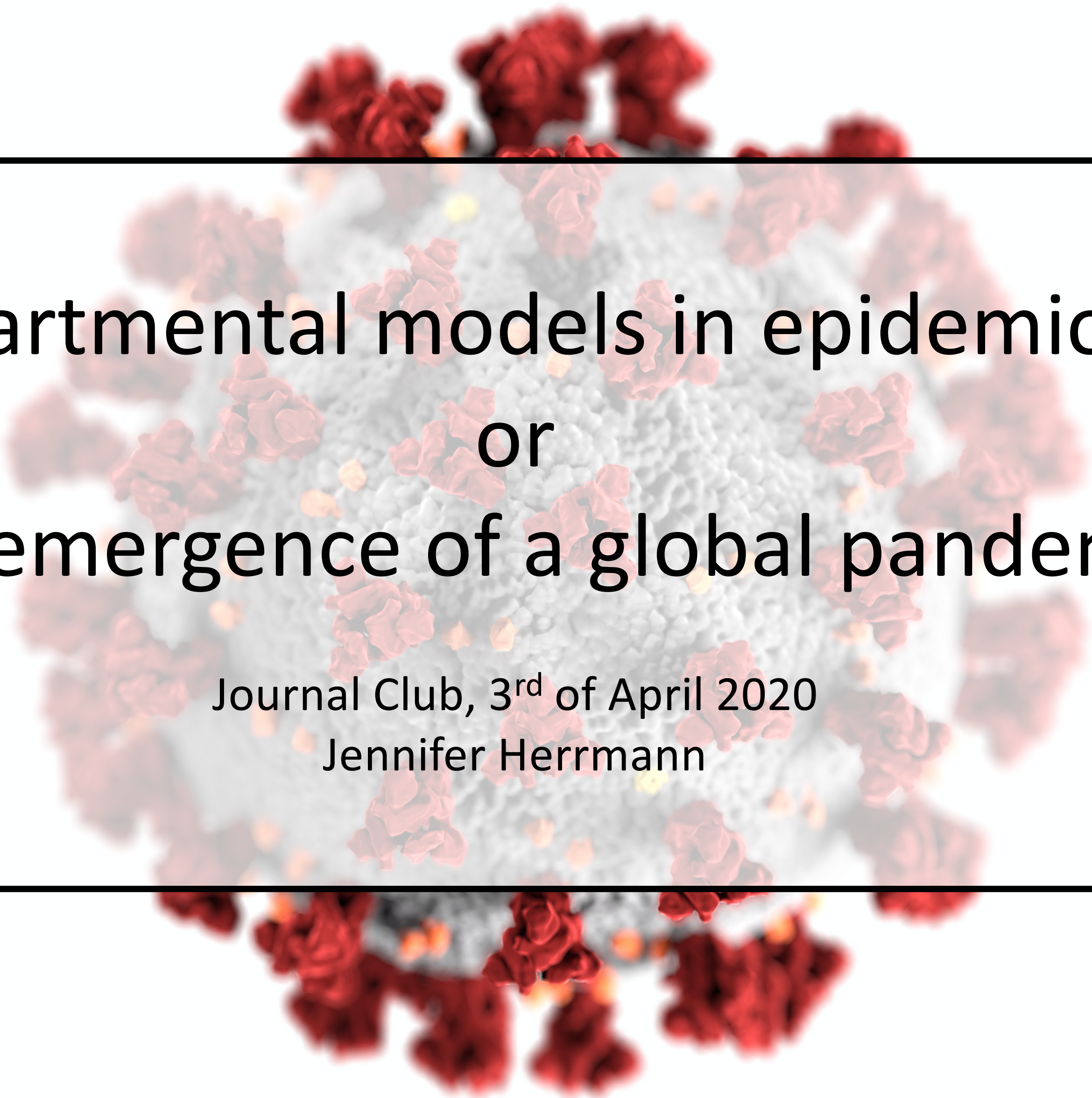


Ultrastructural morphology of 2019-nCoV (CDC / Alissa Eckert, MS; Dan Higgins, MAM / public domain)

The emergence of a global pandemic

31/12/19	Multiple cases of pneumonia of unknown cause reported from Wuhan, China.
11/01/20	First death following infection confirmed in Wuhan, China.
20/01/20	First cases confirmed outside mainland China (Japan, South Korea, Thailand, …).
30/01/20	Outbreak declared "public health emergency of international concern" by WHO.
02/02/20	First death following infection confirmed outside mainland China.
14/02/20	First death following infection confirmed in Europe (France).
26/02/20	First case reported in Latin America (Brazil).
28/02/20	Number of reported cases in Europe increased sharply (Italy, Germany, France, …). First case reported in Sub-Saharan Africa (Nigeria).
26/03/20	Number of infections in United States surpassed China.
…	

Taylor, D. B. (2020). A Timeline of the Coronavirus Pandemic, *NYT* (URL: www.nytimes.com/article/coronavirus-timeline.html)

Back in time…

- 1760: Model for smallpox (D. Bernoulli)
- 1906: Discrete time model for measles (W. H. Hamer)
- 1911: Differential equation models for malaria (R. Ross)
- 1927: Epidemic models (W. O. Kermack and A. G. McKendrick)
- 1975: Book on "The Mathematical Theory of Infectious Diseases" (N. T. J. Bailey)
- [Many more articles and books on mathematical models for epidemiology]

Hethcote, H. W. (2000). The Mathematics of Infectious Diseases. *SIAM Review*, 42(4):599-653.

Classic endemic/epidemic SIR model

$$\text{Susceptible S}(t) \xrightarrow{\beta \frac{I}{N} S} \text{Infectious I}(t) \xrightarrow{\gamma I} \text{Recovered R}(t)$$

$\boldsymbol{\beta}$: avg. number of contacts sufficient for transmission

$\boldsymbol{\gamma}$: inverse of infectious period ($\mathrm{T}_{\mathrm{inf}} = \frac{1}{\gamma}$)

$\boldsymbol{R_0}$: basic reproduction number ($R_0 > 1$)

$\boldsymbol{\sigma}$: contact number ($\sigma = \frac{\beta}{\gamma}$)

$\boldsymbol{R}$: replacement number ($R = Rt$)

$R_0 \geq \sigma \geq R$ (equal at time of invasion)

$$\frac{dS}{dt} = -\beta \frac{I}{N} S = -\frac{R_t}{T_{inf}} IS \quad \text{with } S(0) = S_0 \geq 0$$

$$\frac{dI}{dt} = \beta \frac{I}{N} S - \gamma I = \frac{R_t}{T_{inf}} IS - \frac{1}{T_{inf}} I \quad \text{with } \mathrm{I}(0) = I_0 \geq 0$$

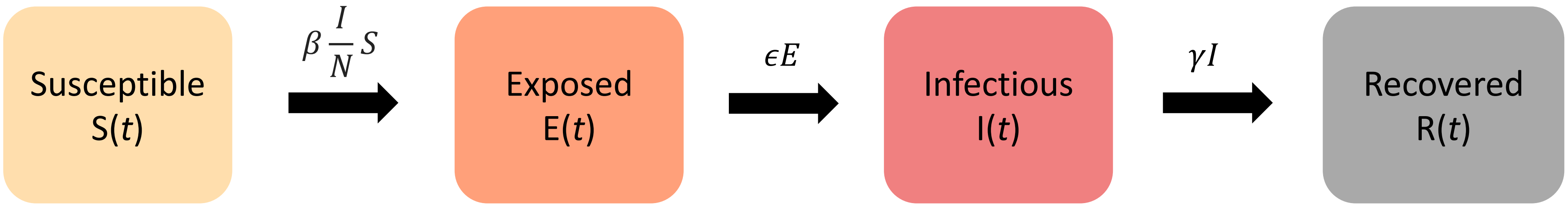
$$\frac{dR}{dt} = \gamma I = \frac{1}{T_{inf}} I \quad \text{with } R(0) = R_0 \geq 0$$

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

Goh, G. (2020). Epidemic calculator. Github (URL: gabgoh.github.io/COVID/index.html)

Hethcote, H. W. (2000). The Mathematics of Infectious Diseases. *SIAM Review*, 42(4):599-653.

Classic endemic/epidemic SEIR model



$\boldsymbol{\beta}$: avg. number of contacts sufficient for transmission

$\boldsymbol{\epsilon}$: inverse of latent period ($\mathrm{T}_{\mathrm{inc}} = \frac{1}{\epsilon}$)

$\boldsymbol{\gamma}$: inverse of infectious period ($\mathrm{T}_{inf} = \frac{1}{\gamma}$)

$\boldsymbol{R_0}$: basic reproduction number ($R_0 > 1$)

$\boldsymbol{\sigma}$: contact number ($\sigma = \frac{\beta}{\gamma}$)

$\boldsymbol{R}$: replacement number ($R = Rt$)

$R_0 \geq \sigma \geq R$ (equal at time of invasion)

$$\frac{dS}{dt} = -\beta \frac{I}{N} S = -\frac{R_t}{T_{inf}} IS$$

$$\frac{dE}{dt} = \beta \frac{I}{N} S - \epsilon E = \frac{R_t}{T_{inf}} IS - \frac{1}{T_{inc}} E$$

$$\frac{dI}{dt} = \epsilon E - \gamma I = \frac{1}{T_{inc}} E - \frac{1}{T_{inf}} I$$

$$\frac{dR}{dt} = \gamma I = \frac{1}{T_{inf}} I$$

$$S(t) + E(t) + I(t) + R(t) = N = const.$$

Goh, G. (2020). Epidemic calculator. Github (URL: gabgoh.github.io/COVID/index.html)

Hethcote, H. W. (2000). The Mathematics of Infectious Diseases. *SIAM Review*, 42(4):599-653.

R_0 estimates for SARS-CoV-2:

Study	Location	Method	R_0 estimate	95% CI
Joseph et al.	Wuhan	Stochastic MCMC methods	2.68	2.47-2.86
Shen et al.	Hubei province	Compartmental mathematical model	6.49	6.31-6.66
Liu et al.	China and overseas	Statistical exponential growth model	2.90	2.32-3.63
Liu et al.	China and overseas	Statistical maximum likelihood estimation	2.92	2.28-3.67
Read et al.	China	Mathematical transmission model	3.11	2.39-4.13
Majumder et al.	Wuhan	Mathematical IDEA model	2.0-3.1 (2.55)	-
WHO	China	-	1.4-2.5 (1.95)	-
Cao et al.	China	Compartmental mathematical model	4.08	-
Zhao et al.	China	Statistical exponential growth model	2.24	1.96-2.55
Zhao et al.	China	Statistical exponential growth model	3.58	2.89-4.39
Imai (2020)	Wuhan	Compartmental mathematical model	1.5-3.5 (2.5)	-
Julien and Althaus	China and overseas	Stochastic simulations of early trajectories	2.2	-
Tang et al.	China	Compartmental mathematical model	6.47	5.71-7.23
Qun Li et al.	China	Statistical exponential growth model	2.2	1.4-3.9
AVERAGE	**-**	**-**	**3.28**	**-**

Liu et al. (2020). The reproductive number of COVID-19 is higher compared to SARS coronavirus. *Journal of Travel Medicine*, 2020, 1–4.

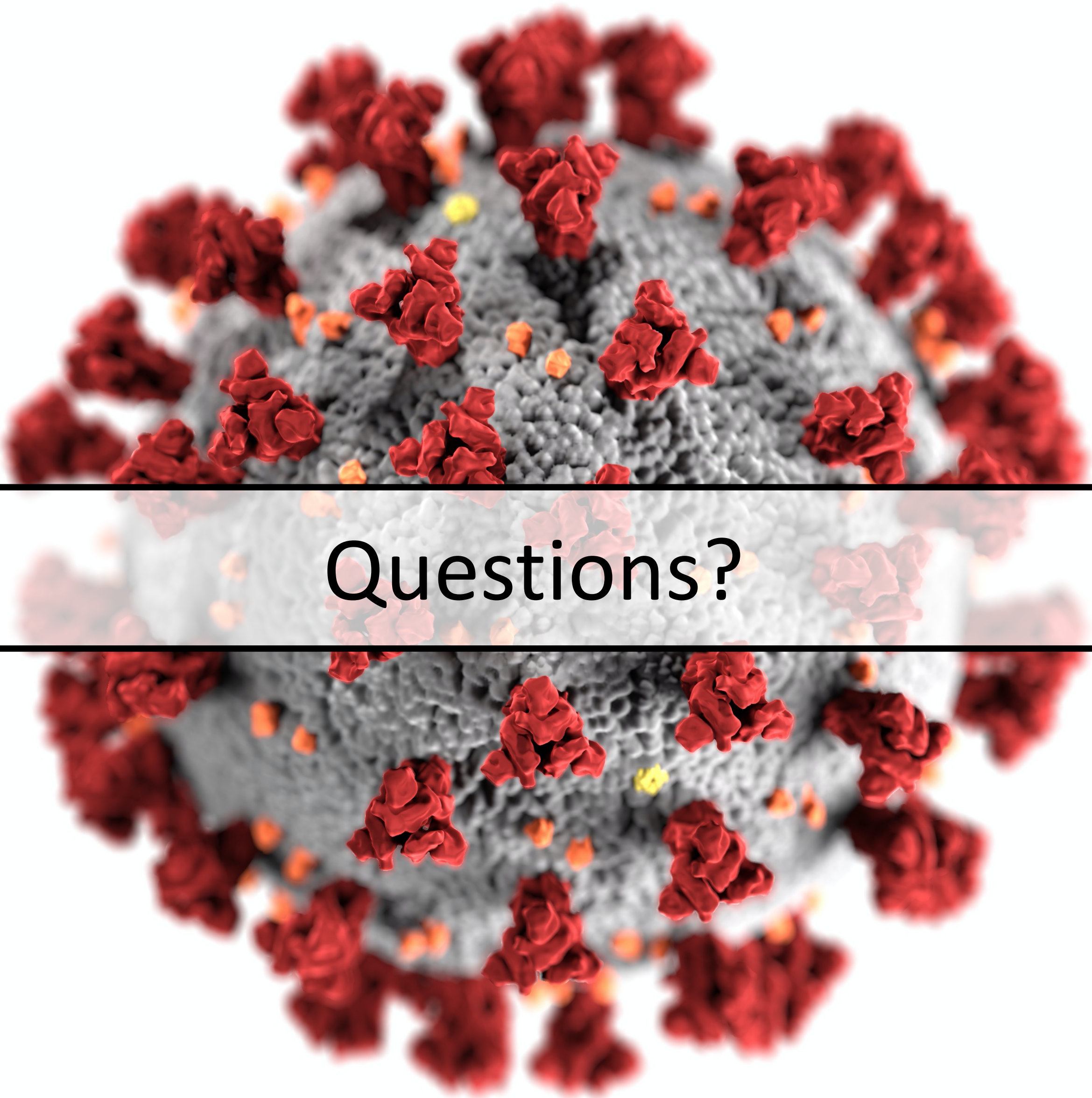
Recent publications on 2019-nCoV using compartmental epidemiological models

- **Wu et al. (2020)**: Susceptible-exposed-infectious-recovered (SEIR) model based on data from 31/12/2019 to 28/01/2020, estimation of basic reproductive number using MCMC methods with Gibbs sampling and flat prior
  - Basic reproductive number: **2.68** (95% CI: 2.47-2.86)
  - Suspected exponentially growing epidemics in multiple cities in China based on assumption of stable domestic transmissibility (1-2 weeks lag time)
- **Kucharski et al. (2020)**: Susceptible-exposed-infectious-recovered (SEIR) model based on data from multiple sources from 01/12/2019 to 11/02/2020, estimation of transmission rate using sequential MC simulation
  - Basic reproductive number: **2.35** (95% CI: 1.15-4.77) down to **1.05** (95% CI: 0.41-2.39) in Wuhan
  - Highlighted importance of early detection of cases and subsequent isolation

Kucharski et al. (2020). Early dynamics of transmission and control of COVID-19: a mathematical modelling study. *The Lancet Infectious Diseases*, Published online: March 11, 2020.

Wu et al. (2020). Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *The Lancet*, 395(10225):689-697.

Questions?



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