

# **Estimating the strength, speed, and final size of disease outbreaks: application to 2019-nCoV**

**Joshua S. Weitz**

School of Biological Sciences and School of Physics  
Center for Microbial Dynamics and Infection,  
Georgia Institute of Technology,  
Atlanta GA, USA

Technical References:

Sang Woo Park et al. (in review & available on medrxiv: 2020.01.30.20019877v3)  
Sang Woo Park et al., *Epidemics* 27:12 (2019)  
Taylor et al. *J. Theor. Biol.* 408: 145-154 (2016)  
Weitz & Dushoff, *Scientific Reports* 5: 8751 (2015)

Email: [jsweitz@gatech.edu](mailto:jsweitz@gatech.edu)  
Web: <http://ecothery.biology.gatech.edu>



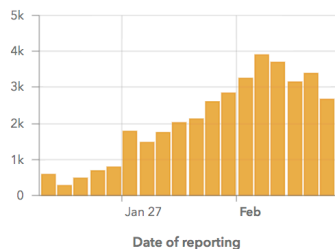
# Novel coronavirus (2019-nCoV) situation as of 09 February 2020, 16:00 (CET)

**37,499**  
confirmed cases

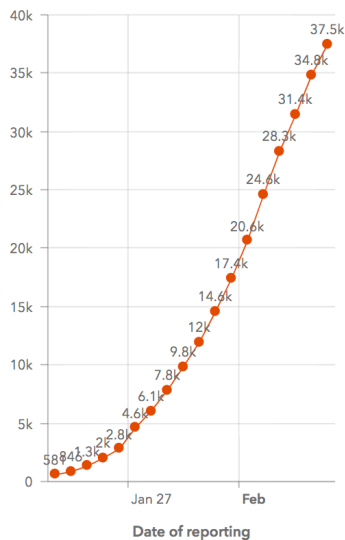
**813**  
deaths

Cases from  
**25**  
countries

## Cases by date of report

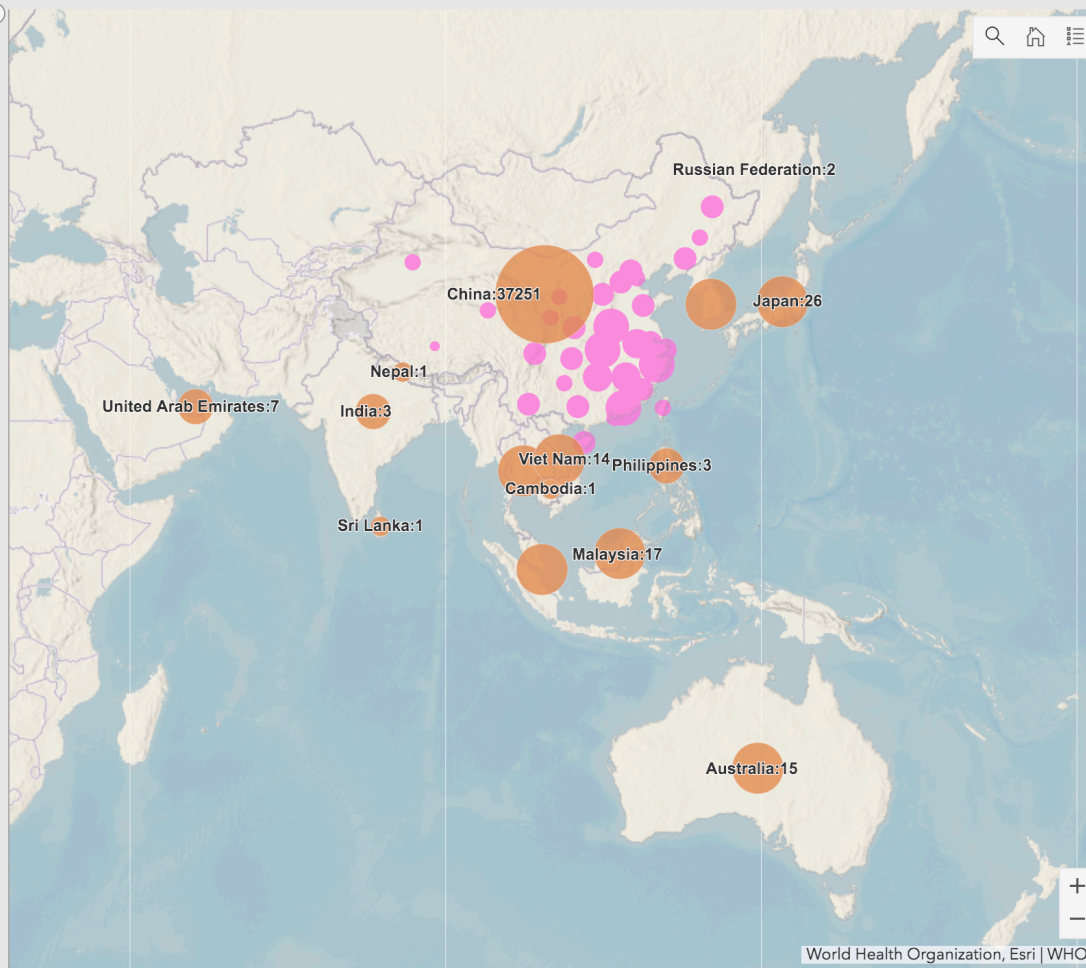


## Cumulative confirmed cases



## Countries with confirmed cases

<u>China</u> : 37251 Cases
<u>Singapore</u> : 43 Cases
<u>Thailand</u> : 32 Cases
<u>Republic of Korea</u> : 27 Cases
<u>Japan</u> : 26 Cases
<u>Malaysia</u> : 17 Cases
<u>Australia</u> : 15 Cases
<u>Germany</u> : 14 Cases
<u>Viet Nam</u> : 14 Cases
<u>United States of America</u> : 12 Cases
<u>France</u> : 11 Cases
<u>Canada</u> : 7 Cases
<u>United Arab Emirates</u> : 7 Cases
<u>United Kingdom</u> : 4 Cases
<u>India</u> : 3 Cases
<u>Italy</u> : 3 Cases
<u>Philippines</u> : 3 Cases
<u>Russian Federation</u> : 2 Cases
<u>Spain</u> : 2 Cases
<u>Cambodia</u> : 1 Cases
<u>Finland</u> : 1 Cases
<u>Nepal</u> : 1 Cases
<u>Sri Lanka</u> : 1 Cases
<u>Sweden</u> : 1 Cases
<u>Belgium</u> : 1 Cases

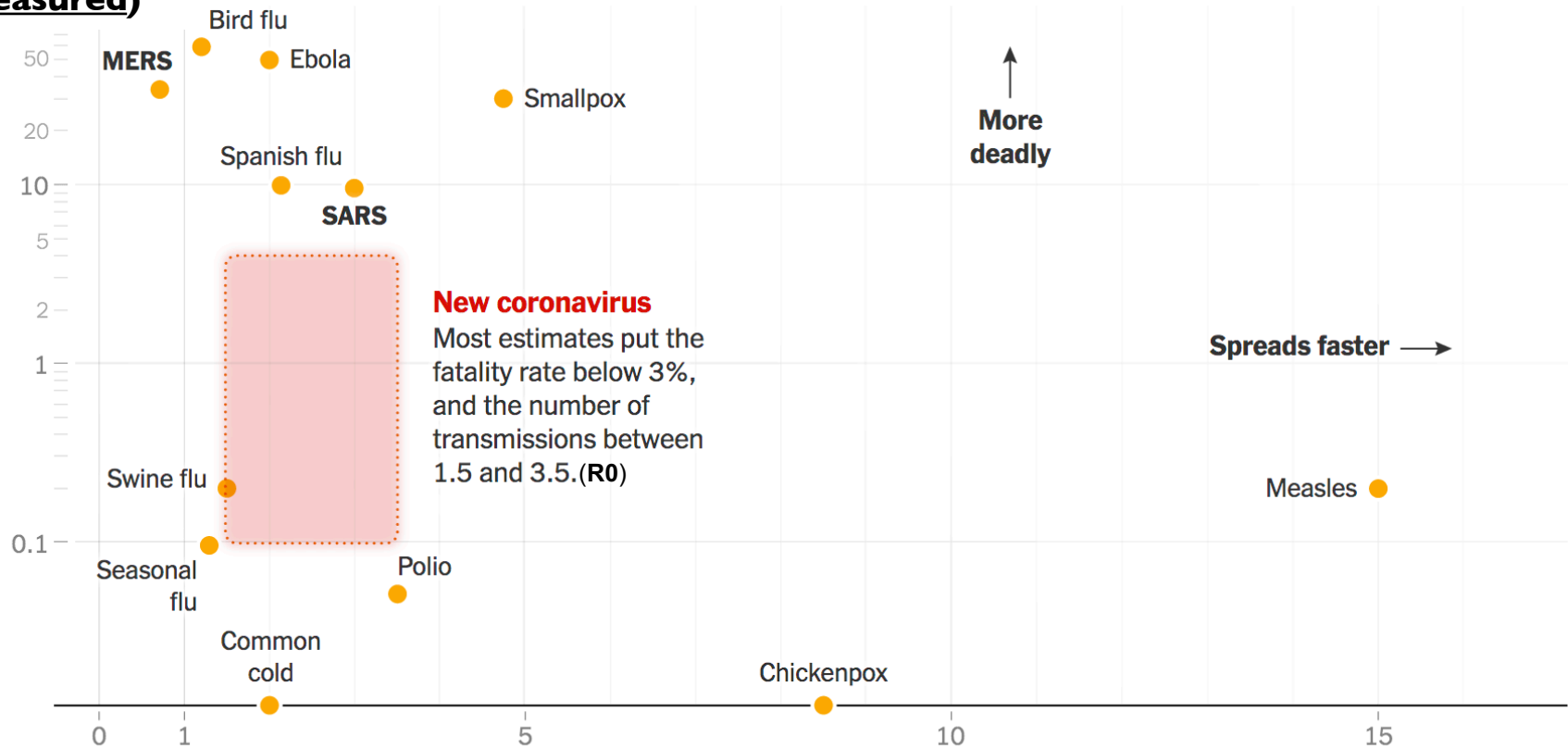


The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data source: [WHO](#), National Health Commission of the People's Republic of China  
Map production: WHO Health Emergencies Programme  
© World Health Organization 2020. All rights reserved.

**Source:** WHO, Feb 9, 2020

**Fatality rate  
(directly  
measured)**

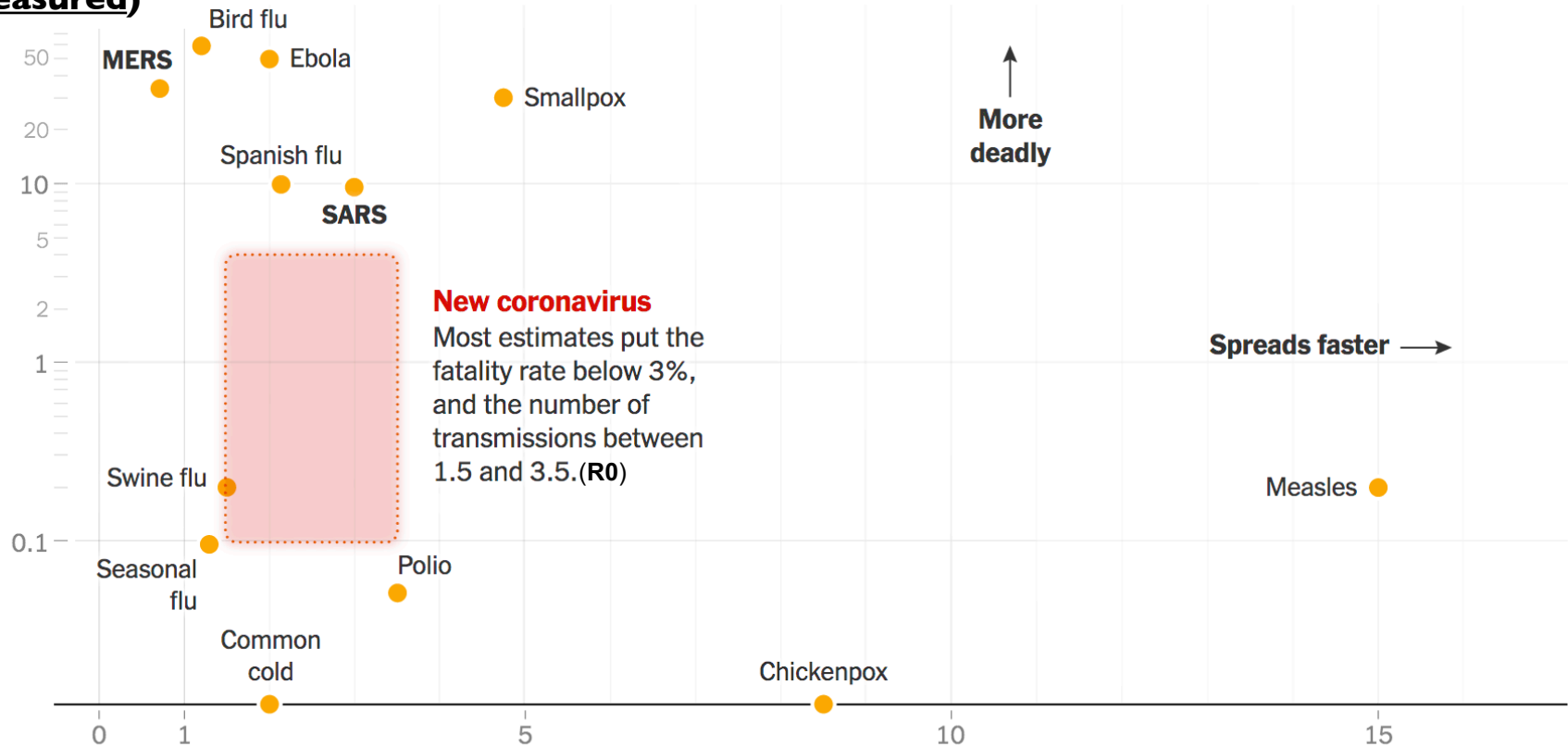


**Basic reproductive number, " $R_0$ "**  
**Equal to the average number of new infections per sick person**  
**Indirectly measured**

# Question Motivating Today's Talk:

How certain should we be about estimates of the strength –  $R_0$  – of a disease at the outset of an outbreak?

**Fatality rate  
(directly  
measured)**

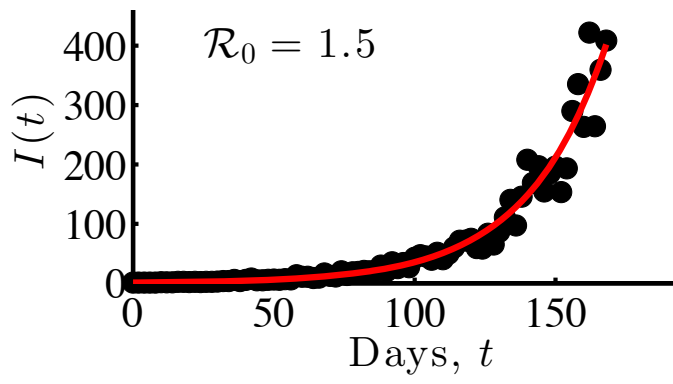


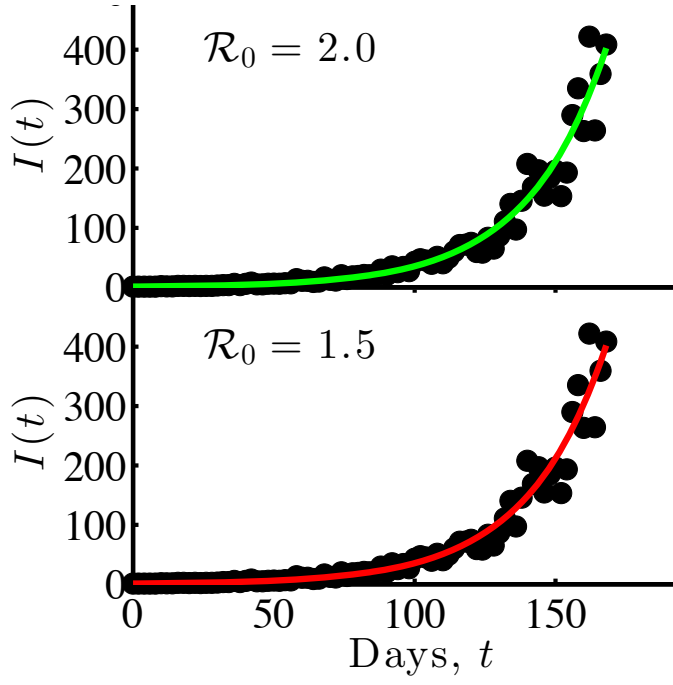
**Basic reproductive number, " $R_0$ "**

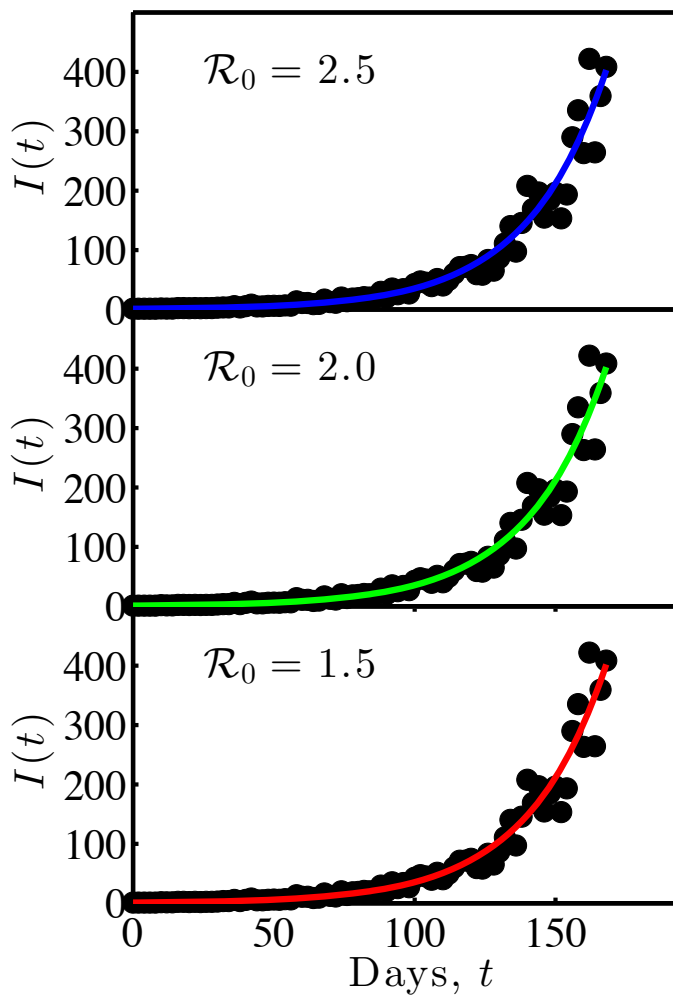
**Equal to the average number of new infections per sick person**

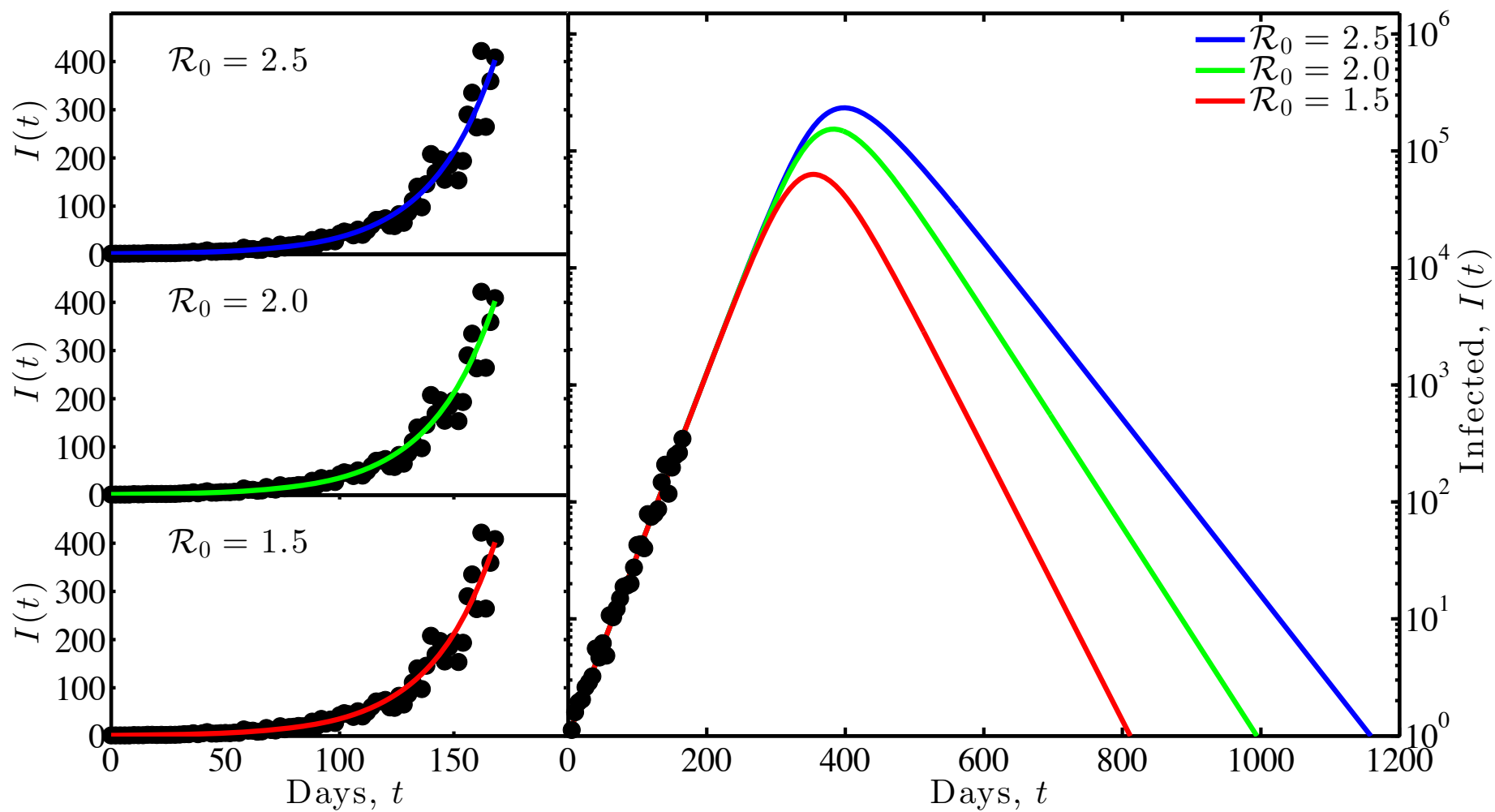
**Indirectly measured**

**Source:** NY Times, Feb 7, 2020

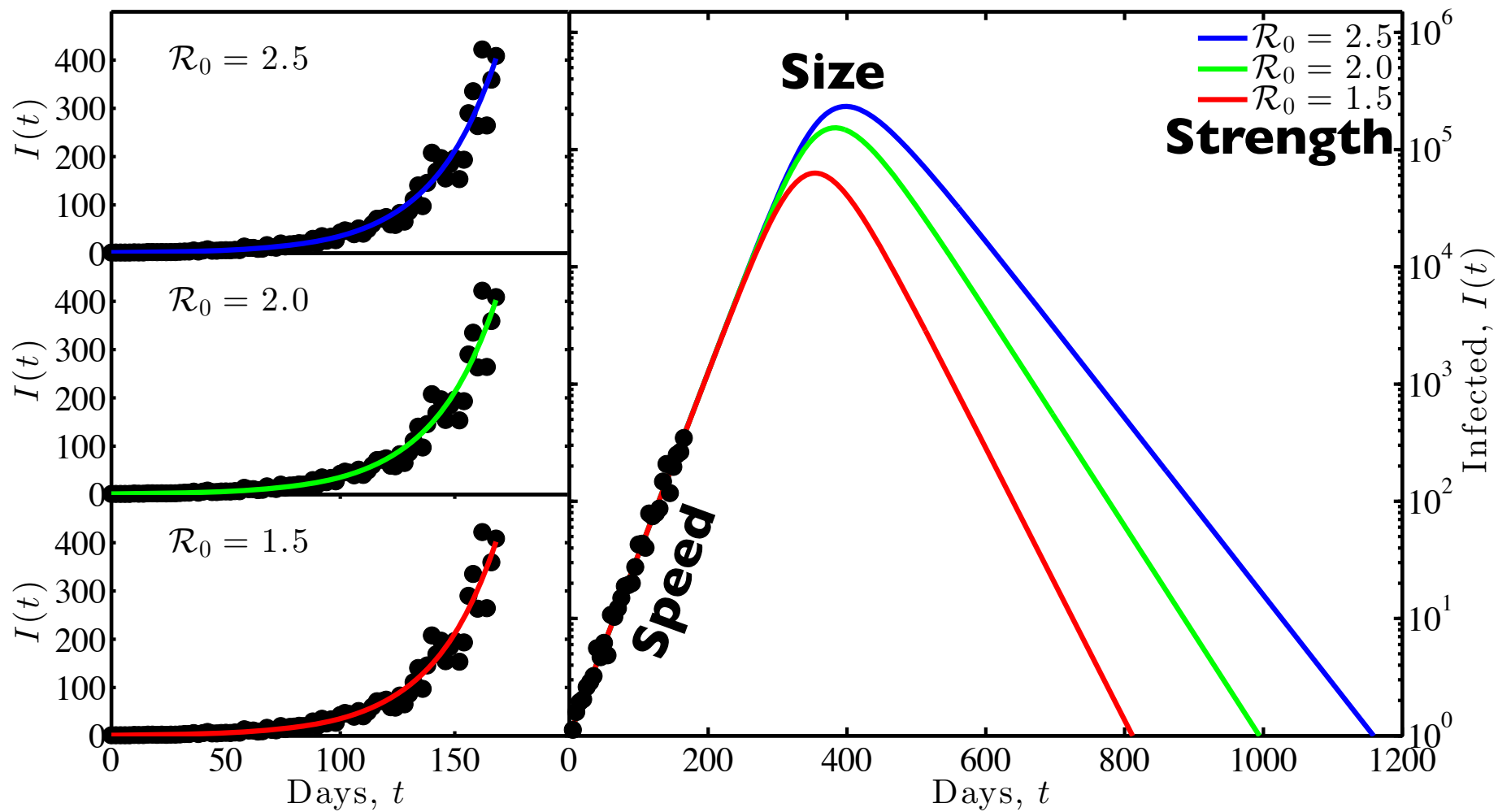


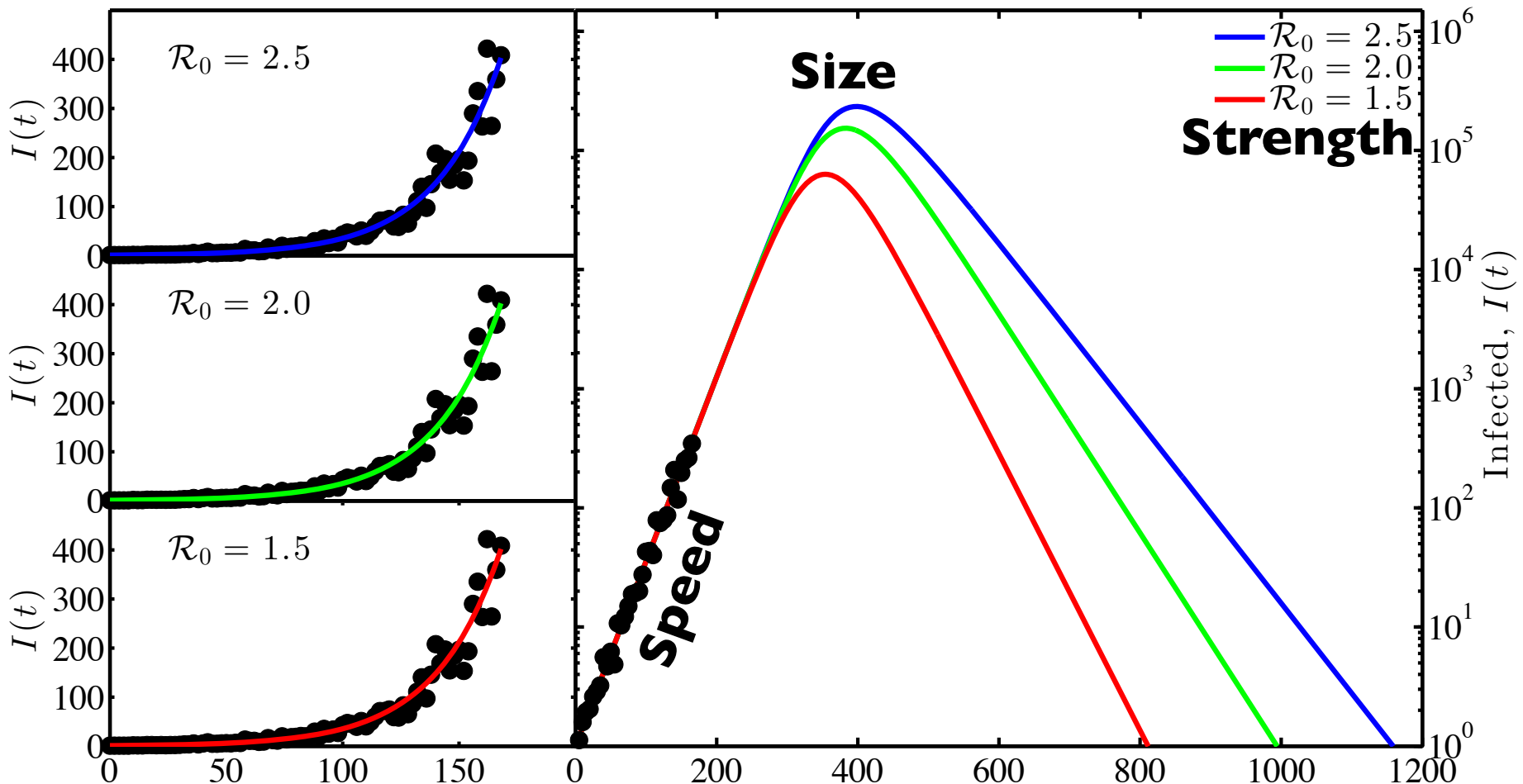






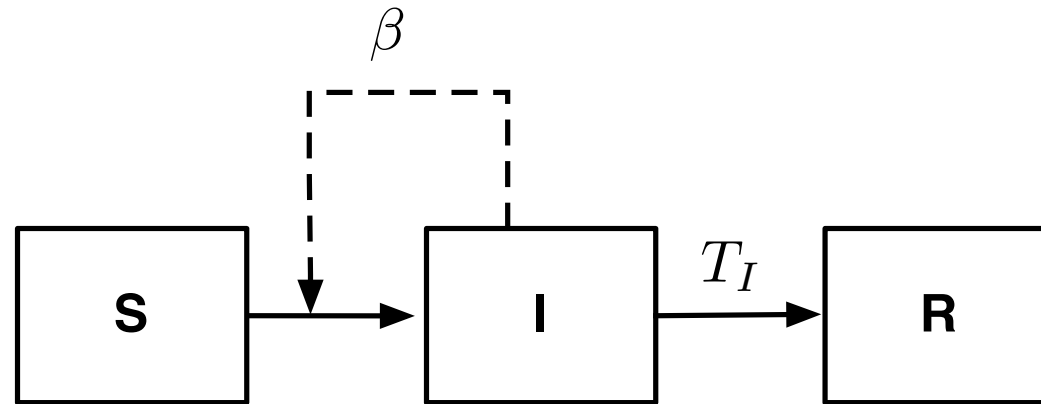






**Tentative conclusion: Many values of  $R_0$  can be compatible with the same observed rate of increase in cases – even if projected outbreak sizes are different.**

# SIR Model - Basics



## Population “Classes”

**S** – The number of susceptible individuals

**I** – The number of infectious individuals

**R** – The number of “removed” individuals (through recovery or, possibly, death)

## Mechanisms

**Infection:** Requiring contact between a **S** and a **I** individual at rate  $\beta$ .

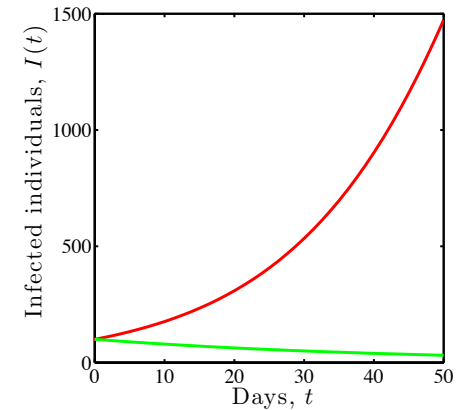
**Recovery:** After a period of infectiousness of average duration  $T_I$ .

# SIR Model – Initial Dynamics

## Depend on Basic Reproductive Number, $R_0$

The expected number of cases, initially changes like:

$$\dot{I} = \frac{I}{T_I} (\mathcal{R}_0 - 1)$$



# SIR Model – Initial Dynamics

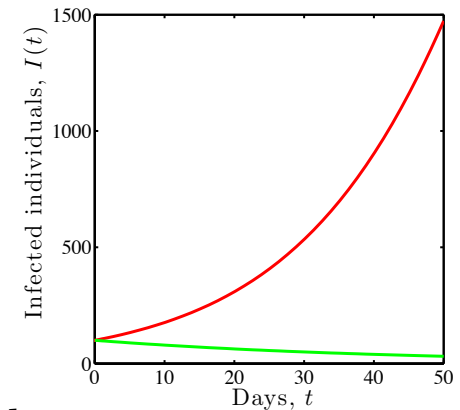
Depend on Basic Reproductive Number,  $R_0$

The expected number of cases, initially changes like:

$$\dot{I} = \frac{I}{T_I} (\mathcal{R}_0 - 1)$$

where

$$\mathcal{R}_0 \equiv \underbrace{\text{infections per time}}_{\beta} \times \underbrace{\text{infectious period}}_{T_I}$$



# SIR Model – Initial Dynamics

## Depend on Basic Reproductive Number, $R_0$

The expected number of cases, initially changes like:

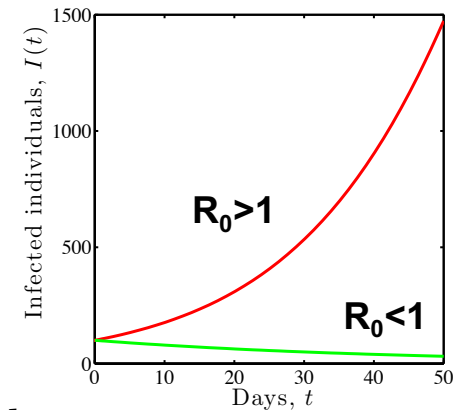
$$\dot{I} = \frac{I}{T_I} (\mathcal{R}_0 - 1)$$

where

$$\mathcal{R}_0 \equiv \underbrace{\text{infections per time}}_{\beta} \times \underbrace{\text{infectious period}}_{T_I}$$

such that

- Disease spreads whenever the average number of new cases exceeds unity, i.e:  $\mathcal{R}_0 > 1$
- The increase is exponential



# Estimating, $R_0$ , for 2019-nCoV

	Basic reproductive number $\mathcal{R}_0$
Study 1	1.5–3.5
Study 2	2.5 (1.5–3.5)*
Study 3	2.92 (95% CI: 2.28–3.67)
Study 4	3.8 (95% CI: 3.6–4.0)
Study 5	2.2 (90% CI: 1.4–3.8)
Study 6	5.47 (95% CI: 4.16–7.10) <sup>‡</sup>
Study 7	2.0–3.1

Bedford <i>et al.</i> [4]
Imai <i>et al.</i> [5]
Liu <i>et al.</i> [6]
Read <i>et al.</i> [8]
Riou and Althaus [10]
Zhao <i>et al.</i> [9]
Majumder and Mandl [7]

## Many model choices:

Branching process

SEIR model (like SIR but with an asymptomatic class)

Exponential growth...

# Estimating, $R_0$ , for 2019-nCoV

	Basic reproductive number $\mathcal{R}_0$	Mean generation interval $\bar{G}$ (days)	Generation-interval dispersion $\kappa$	
Study 1	1.5–3.5	10	1	Bedford <i>et al.</i> [4]
Study 2	2.5 (1.5–3.5)*	8.4	unspecified <sup>†</sup>	Imai <i>et al.</i> [5]
Study 3	2.92 (95% CI: 2.28–3.67)	8.4	0.2	Liu <i>et al.</i> [6]
Study 4	3.8 (95% CI: 3.6–4.0)	7.6	0.5	Read <i>et al.</i> [8]
Study 5	2.2 (90% CI: 1.4–3.8)	7–14	0.5	Riou and Althaus [10]
Study 6	5.47 (95% CI: 4.16–7.10) <sup>‡</sup>	7.6–8.4	0.2	Zhao <i>et al.</i> [9]
Study 7	2.0–3.1	6–10	0	Majumder and Mandl [7]

## Many model choices & latent assumptions:

Branching process

SEIR model (like SIR but with an asymptomatic class)

Exponential growth...

**How to reconcile and weight different models to get a pooled estimate and uncertainty in  $R_0$ ?**



# Pooled estimates via a speed-strength relationship (technically using generation intervals)

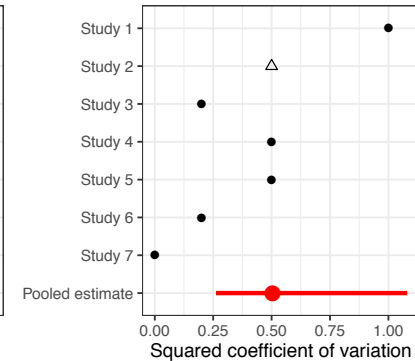
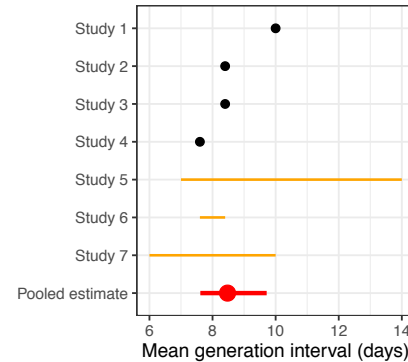
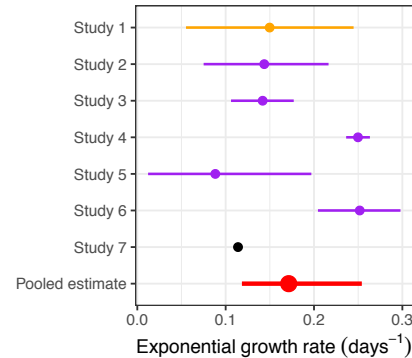
Sang Woo Park



Jonathan Dushoff



**Step 1:** estimate latent uncertainty in 'parameters'.



# Pooled estimates via a speed-strength relationship (technically using generation intervals)

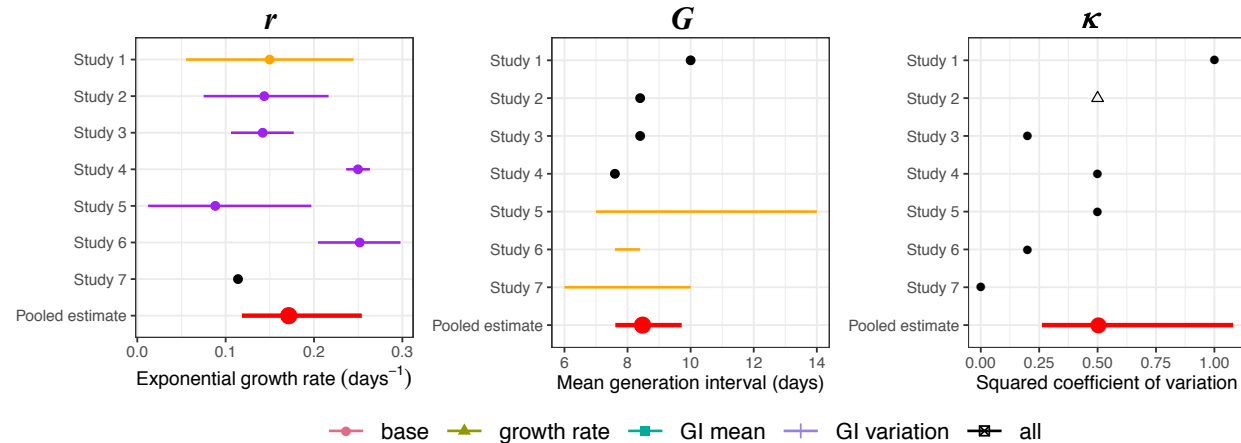
Sang Woo Park



Jonathan Dushoff

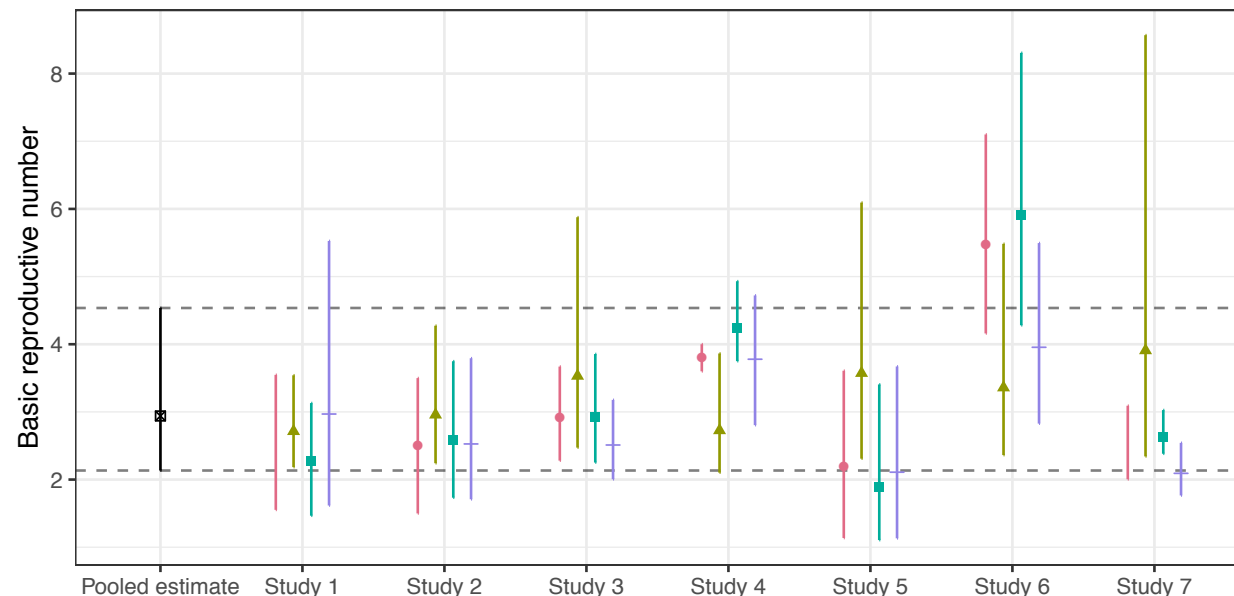


**Step 1:** estimate latent uncertainty in ‘parameters’.



**Step 2:** incorporate different types of uncertainty into  $R_0$  estimates by study or as part of a ‘pooled’ estimate (using a Bayesian multi-level model)

$$\mathcal{R}_0 = (1 + \kappa T \bar{G})^{1/\kappa}$$



# Pooled estimates via a speed-strength relationship (technically using generation intervals)

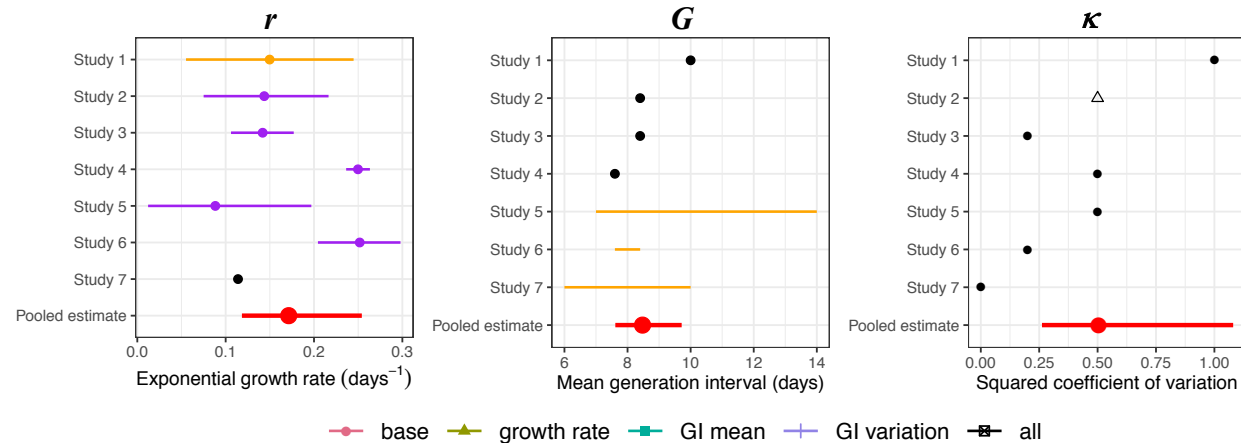
Sang Woo Park



Jonathan Dushoff

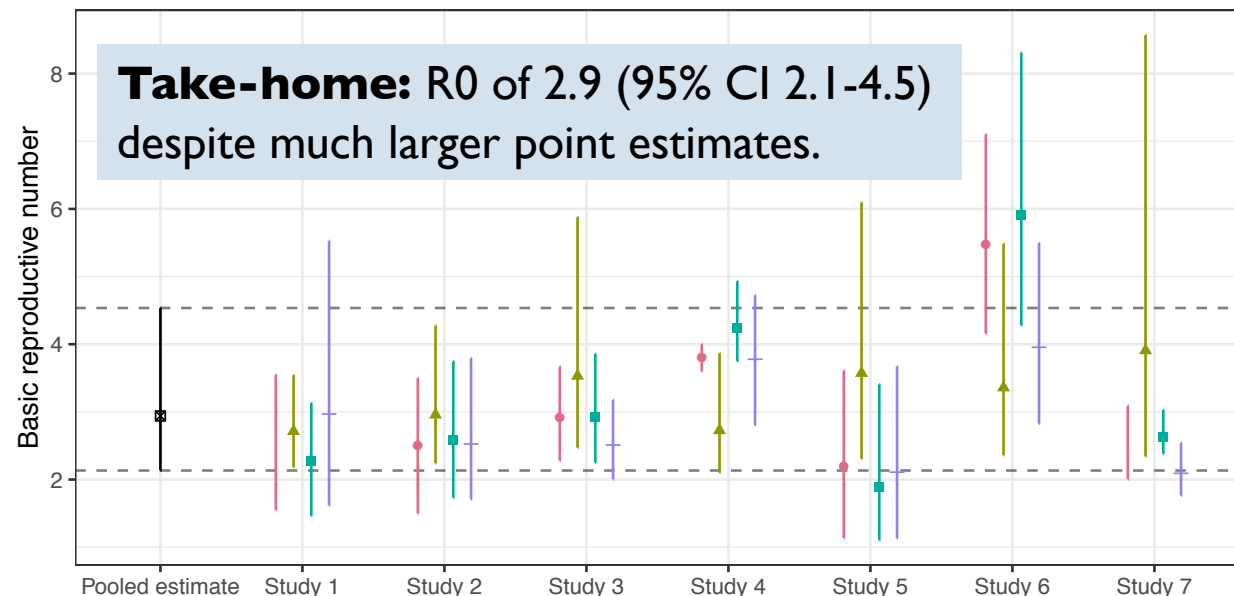


**Step 1:** estimate latent uncertainty in ‘parameters’.



**Step 2:** incorporate different types of uncertainty into  $R_0$  estimates by study or as part of a ‘pooled’ estimate (using a Bayesian multi-level model)

$$\mathcal{R}_0 = (1 + \kappa T \bar{G})^{1/\kappa}$$



# Conditions for epidemic growth

$$\mathcal{R}_0 \equiv \overbrace{\beta}^{\text{infections per time}} \times \overbrace{T_I}^{\text{infectious period}}$$

Where infections per time,  $\beta$ , is a product of:

- Contacts by infectious individuals per unit time
- Probability of contact with a susceptible ( $S_0/N$ )
- Probability that the contact transmits the disease

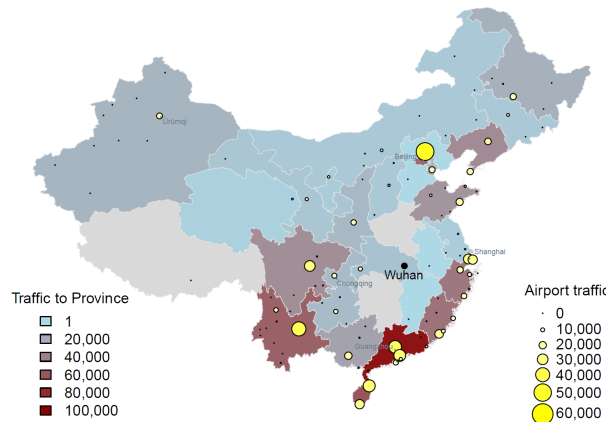
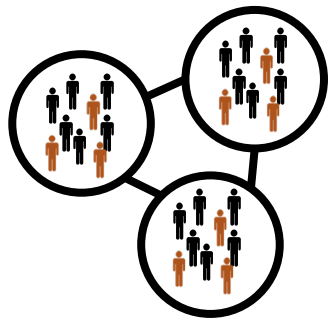
# Conditions for epidemic growth also suggest opportunities for **control**

$$\mathcal{R}_0 \equiv \overbrace{\beta}^{\text{infections per time}} \times \overbrace{T_I}^{\text{infectious period}} \quad \textbf{Hospitalization \& treatment}$$

Where infections per time,  $\beta$ , is a product of:

- Contacts by infectious individuals per unit time **Contact tracing & targeted isolation**
- Probability of contact with a susceptible ( $S_0/N$ ) **Vaccination (herd or ring)**
- Probability that the contact transmits the disease **Process engineering & PPE (masks)**

# Next-stage models (and efforts to control)



## SEIR Metapopulation Model

As per Read et al., medRxiv  
2020.01.23.20018549v2

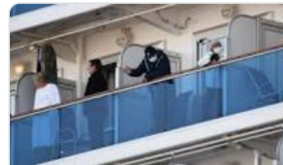
### Control (and consequences):

Limiting travel (but also has negative consequences for limiting medical supplies, increasing anxiety, and co-localizing infected patients).



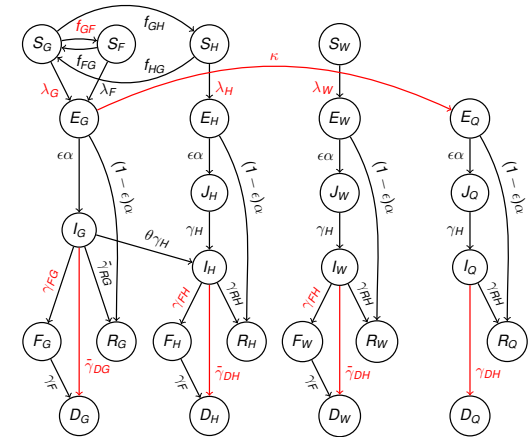
Cruise Ship's  
Coronavirus Outbreak  
Leaves Crew Nowhere  
to Hide

The New York Times  
4 hours ago



Diamond Princess  
Cruise Ship Has 65  
More Coronavirus  
Cases : Goats and...

NPR  
4 hours ago



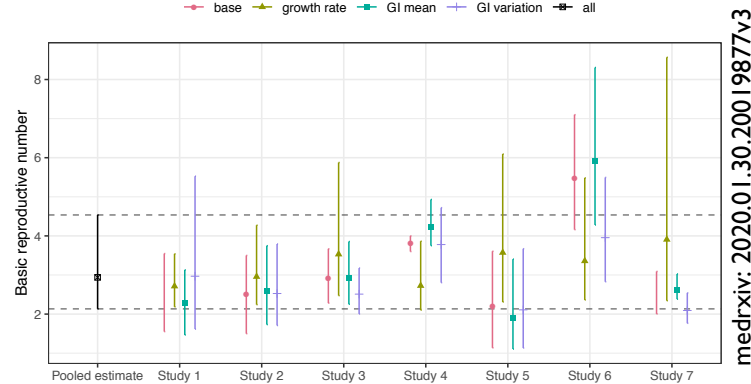
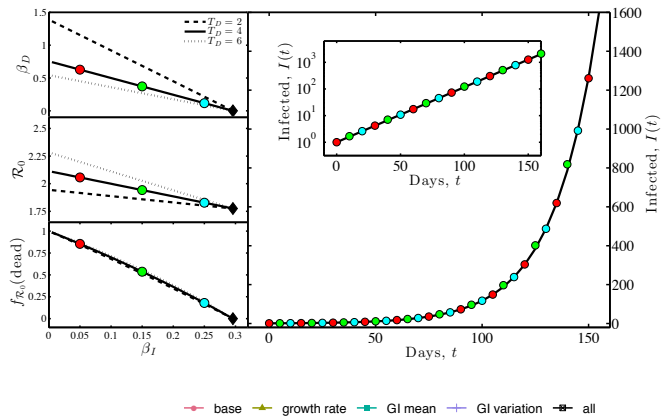
## Category based SEIR model

As per Pandey et al. Science (2014)

### Control (and consequences):

Focuses on risk groups, challenging to differentially target accurately given complexity of model.

# Estimating the strength, speed, and final size of disease outbreaks: application to 2019-nCoV



## Questions?

### Acknowledgements

Sang Woo Park, Princeton  
Jonathan Dushoff, McMaster  
Bradford Taylor, GT (now MSKCC)

### Technical References

Park, S.W., Bolker, B. M., Champredon, D. Earn, D.J., Li, M., Weitz, J.S., Grenfell, B.T., and Dushoff, J.D. Reconciling early-outbreak preliminary estimates of the basic reproductive number and its uncertainty: framework and applications to the novel coronavirus (2019-nCoV) outbreak. *Eurosurveillance* in review & medrxiv.

Park, S.W., Champredon, D., Weitz, J.S., and Dushoff, J. (2019) Exploring how generation intervals link strength and speed of epidemics. *Epidemics*. 27: 12-18.

Taylor, B.P., Dushoff, J. and Weitz, J.S. (2016) Stochasticity and the limits to confidence when estimating  $R_0$  of Ebola and other emerging infectious diseases. *J. Theor. Biol.* 408: 145-154.

J.S. Weitz and J. Dushoff (2015). Modeling post-death transmission of Ebola: challenges for inference and opportunities for control. *Scientific Reports* 5: 8751

Email: [jsweitz@gatech.edu](mailto:jsweitz@gatech.edu)

Web: <http://ecothery.biology.gatech.edu>

