Workshop on the Mathematical Modelling of Variant Replacement of Infectious Diseases Pathogens

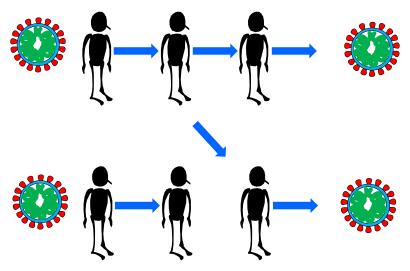
Instantaneous Reproduction Number

Kimihito Ito International Institute for Zoonosis Control Hokkaido University

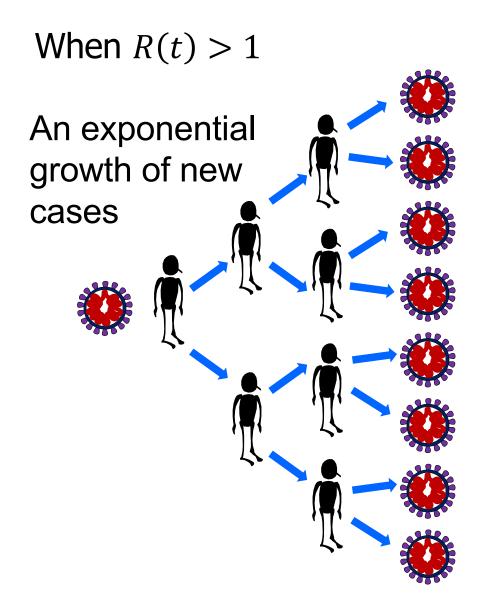
Effective Reproduction Number R_t The average number of secondary infections

When R(t) = 1

A constant number of new cases



The number of new cases declines when R(t) < 1



Estimation of Effective Reproduction Numbers

The average number of people an infected individual at time *t* could infect

Instantaneous Reproduction Number

$$R(t) = \frac{I(t)}{\sum_{j=1}^{l} g(j)I(t-j)}$$
(Fraser 2007)

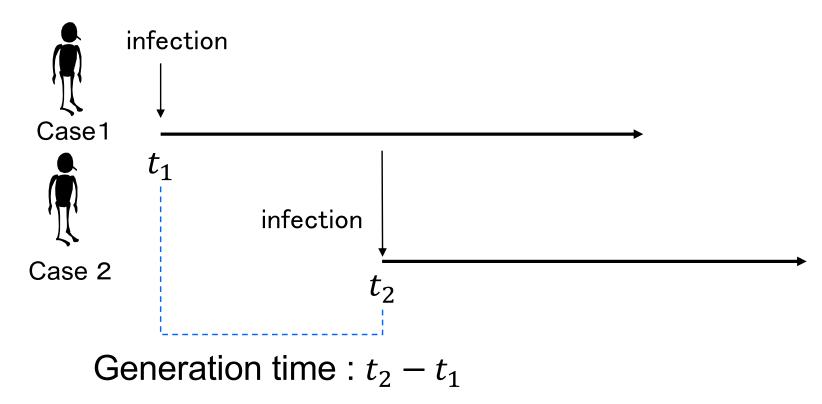
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I(*t*): The number of new cases at time *t* g(j): The probability that generation time is *j* days

 $R(t) = \frac{\text{(the number of new cases of the current generation)}}{\text{(the number of new cases of the previous generation)}}$

Generation time

The time between infection of a primary case and infection of secondary cases caused by the primary case





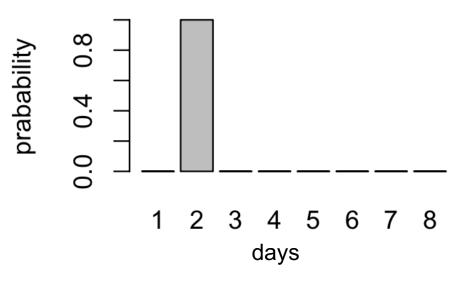
t	I(t)
•	:
2021-06-01	1
2021-06-02	2
2021-06-03	4
2021-06-04	5
2021-06-05	8
	•

What is R(t) at June 5?



t	I(t)
:	:
2021-06-01	1
2021-06-02	2
2021-06-03	4
2021-06-04	5
2021-06-05	8
•	•

Let's sssume the generation time is exactly two days.

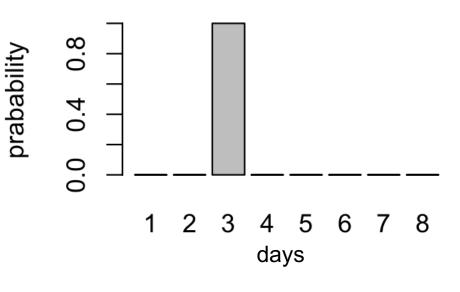


 $R(t) = \frac{8}{4} = 2.0$



t	I(t)
:	:
2021-06-01	1
2021-06-02	2
2021-06-03	4
2021-06-04	5
2021-06-05	8
	:
	: 2021-06-01 2021-06-02 2021-06-03 2021-06-04

Let's assume the generation time is exactly three days.

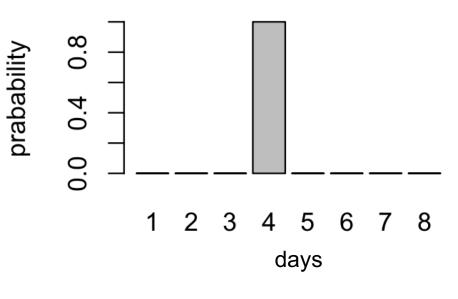


 $R(t) = \frac{8}{2} = 4.0$



t	I(t)
:	:
2021-06-01	1
2021-06-02	2
2021-06-03	4
2021-06-04	5
2021-06-05	8
	•

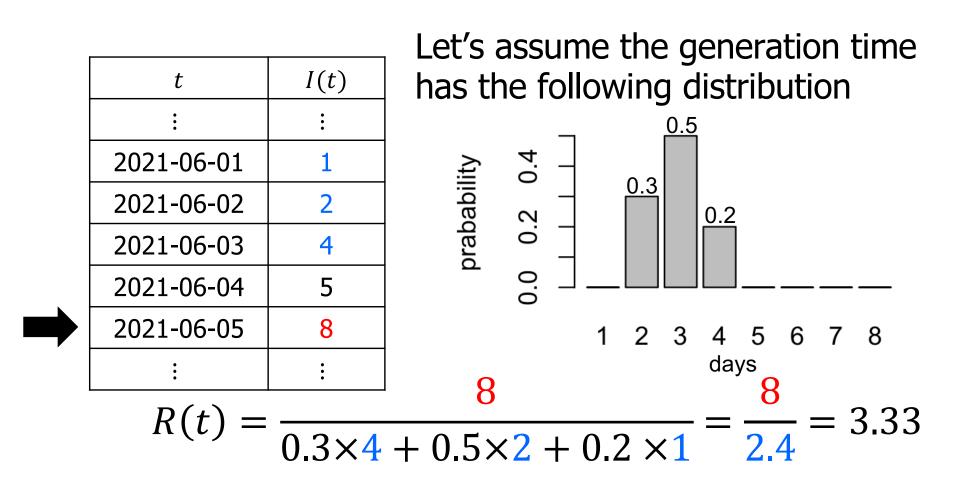
Let's assume the generation time is exactly four days.



 $R(t) = \frac{8}{1} = 8.0$

Example

Suppose that the observed numbers of new cases were as follows.



Estimation of Effective Reproduction Numbers

The average number of people an infected individual at time *t* could infect

Instantaneous Reproduction Number

$$R(t) = \frac{I(t)}{\sum_{j=1}^{l} g(j)I(t-j)}$$
(Fraser 2007)

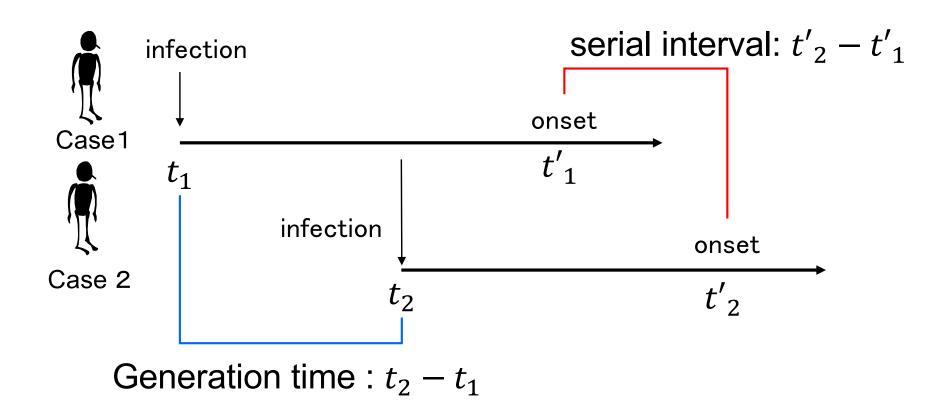
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I(*t*): The number of new cases at time *t* g(j): The probability that generation time is *j* days

R(t) depends on the generation time distribution.

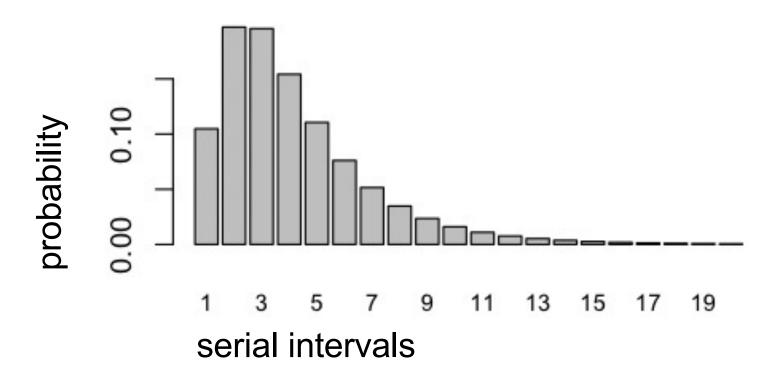
Serial Interval

The time from symptom onset in a primary case to symptom onset in secondary cases



Serial Intervals of the Wuhan strain

Probability distribution of serial intervals



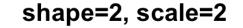
Log-normal distribution with a mean of 4.7 days and a standard deviation of 2.9 days (Nishiura H et al. Int J Infect Dis. 2020)

The Generation Times Differ Depending on Viruses

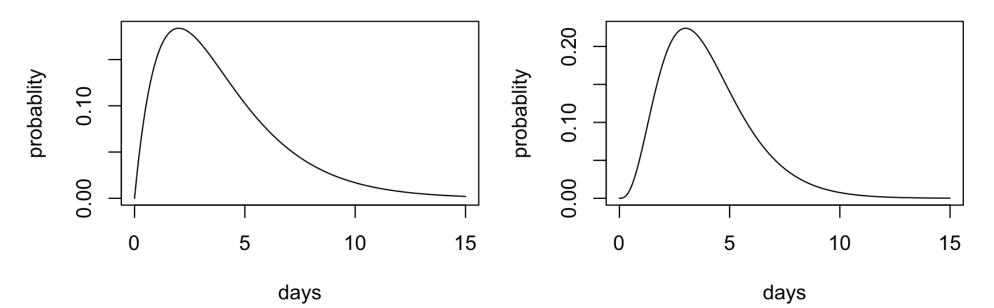
Virus	Mean	S.D.	Remarks
SARS-CoV-2 (Delta)	4.7	3.3	Hart et al. Lancet Infect Dis. 2022
SARS-CoV-2 (Omicron)	2.97	1.48	Park et al. PNAS, 2023
Influenza Virus (H1N1)	2.95	1.43	Roll et al. BMC Infect Dis . 2011
Measles Virus	11.7	3.0	Akhmetzhanov, et al. PLoS Currents, 2018

Modeling generation time with Gamma Distribution

A gamma distribution has two parameters of shape (α) and scale (θ).



shape=4, scale=1



Mean and variance of Gamma Distribution

A gamma distribution with shape α and scale θ has a mean $\mu = \alpha \theta$ and variance $\sigma^2 = \alpha \theta^2$.

From mean μ and s.d. σ of generation time, we can obtain the shape parameter α and scale parameter θ of the gamma distribution

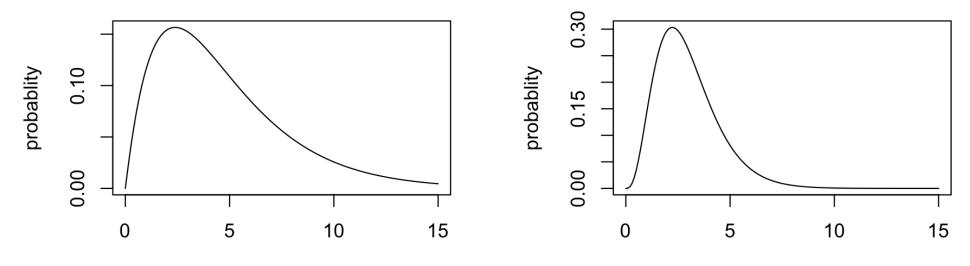
$$\begin{array}{lll} \alpha & = & \mu^2 / \sigma^2 \\ \theta & = & \sigma^2 / \mu \end{array}$$

Parameters for Gamma-distributed Generation Times

Virus	Mean	S.D.	α	θ	Remarks
SARS-CoV-2 (Delta)	4.7	3.3	2.03		Hart et al. Lancet Infect Dis. 2022
SARS-CoV-2 (Omicron)	2.97	1.48	4.03	0.735	Park et al. PNAS, 2023

SARS-CoV-2 (Delta)

SARS-CoV-2 (Omicron)



days

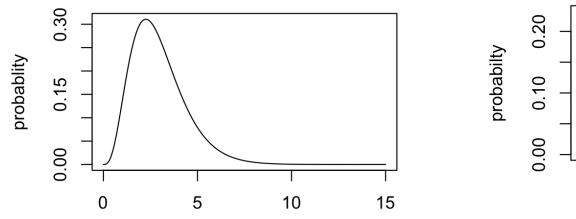
days

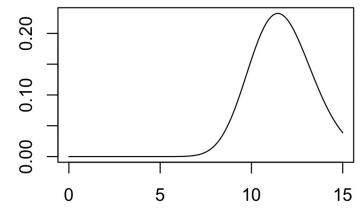
Parameters for Gamma-distributed Generation Times

Virus	Mean	S.D.	α	θ	Remarks
Influenza Virus (H1N1)	2.95	1.43	4.25	0.694	Roll et al. BMC Infect Dis . 2011
Measles Virus	11.7	3.0	45.6	0.26	Akhmetzhanov, et al. PLoS Currents, 2018

Influenza virus (H1N1)

Measles virus





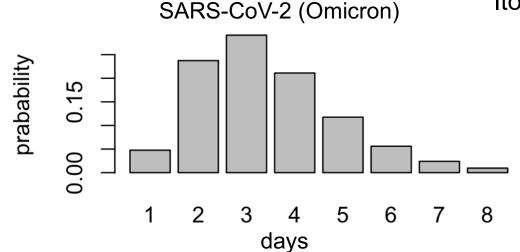
days

days

Discretization of Gamma-distributed Generation Time

The continuous generation time distribution of each variant $f_{\chi}(\tau)$ can be discretized using bins with a width of 1 day and truncated at $\tau = 1$ and $\tau = l$.

$$g_{\chi}(j) = \begin{cases} 0, & \text{if } j = 0\\ \int_{(j-1)}^{j} f_{\chi}(\tau) d\tau / \int_{0}^{l} f_{\chi}(\tau) d\tau, & \text{if } 1 \le j \le l\\ 0, & \text{if } j > l \end{cases}$$



Ito, K., et al. MBE (2022).



- Find the mean and s.d. (or variance) of the generation time (or serial intervals) of other viruses.
- Calculate shape and scale scale parameters from the mean and s.d. (or variance).

Summary

- R(t) is defined as the average number of people an infected individual at time t could be expected to infect given that conditions remain unchanged.
- R(t) depends on the generation time distribution.
- Generation times differ depending on viruses.
- Serial intervals are easier to estimate compared to generation times