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

#### **General Discussions**

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#### Count Data

How can we obtain count data of variants?

- Metadata from sequence database, such as GISAID.
- Realtime PCR.
- Serological data
- Rapid test

### Lineage Designation

- In GISAID, a pangolin lineage name is assigned to each SARS-CoV-2 sequence.
- What are the criteria to define a new lineage of viruses?

#### **Automation of Prediction**

- Can we automate the prediction of frequencies of variants in the future?
- What are the problems to be solved?
  - Needs finantial support to obtain realtime sequence data

#### **Automation of Prediction**

- Delay from collection to submit data
  - Transport: 14 days
  - Sequencing: 5 days
  - Median delay: 63 days
- Political issue
  - Local institute dose not want to send samples to centers imediately.

#### **Automation of Prediction**

- Collaborate with IT
- Ministry of Health
- We can try

## Constant Assumption of R<sub>RI</sub>

- We assume that  $R_{RI}$  is constant over time, and prediction is accurate.
- What is the situation where R<sub>RI</sub> is not constant over time?

### Heterogeneity in Immun Status

How can we take immunity into account?

- No one has immunity to emerging infectious diseases.
- Adults have more chance to acquire immunity to infectious diseases than children.

#### How to stop the replacement

Is it possible to stop the replacement of variants?

#### My Favorite Words

# "All models are wrong", (but some are useful).

by George Edward Pelham Box



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