



AMDABiDSS-Health

Phylodynamic Study of SARS-CoV-2: A case study in the National Capital Region of the Philippines

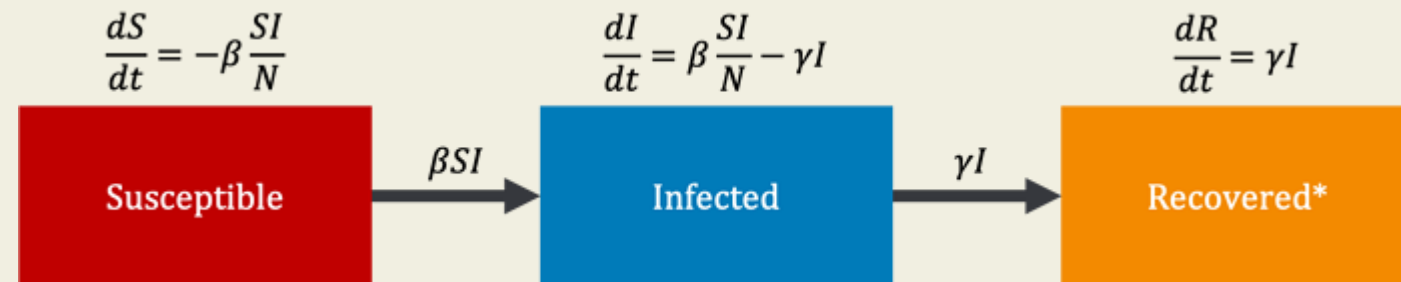
Sheryl Grace Buenaventura
Imari Joy C. Borda



Introduction: Phylodynamics in Epidemiology

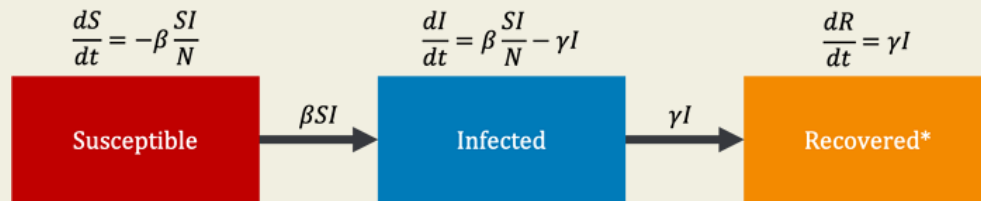
Phylodynamics

- First coined by Grenfell et. al. (2004) as defined as the study of how epidemiological, immunological, and evolutionary processes act and potentially interact to shape viral phylogenies.
- Phylodynamics = Phylogeny + Population Dynamics
= Genomic + Epidemiological Model



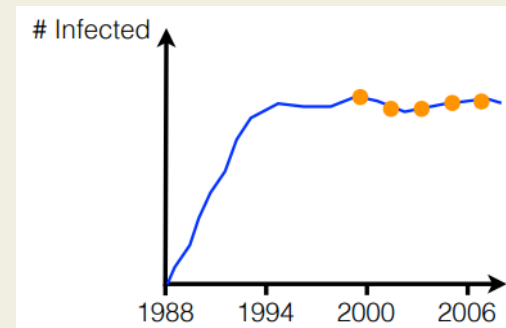
Motivation: Phylodynamics in Epidemiology

Data: Number of infected individuals through time.



Limitations:

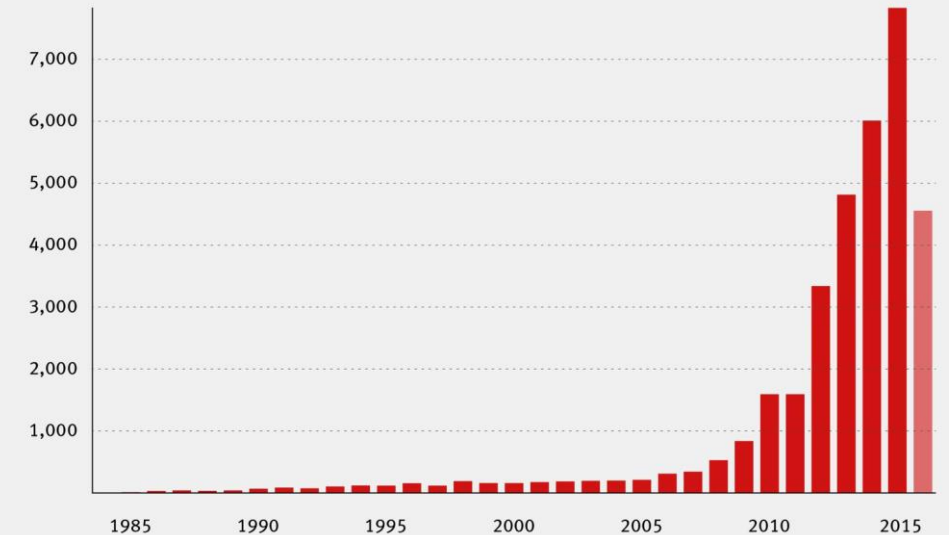
- Incomplete data
Origin date?
- Population Structure
Who infected whom?



Adapted from Stadler (2021)

HIV Cases Reported in the Philippines

January 1984 to June 2016

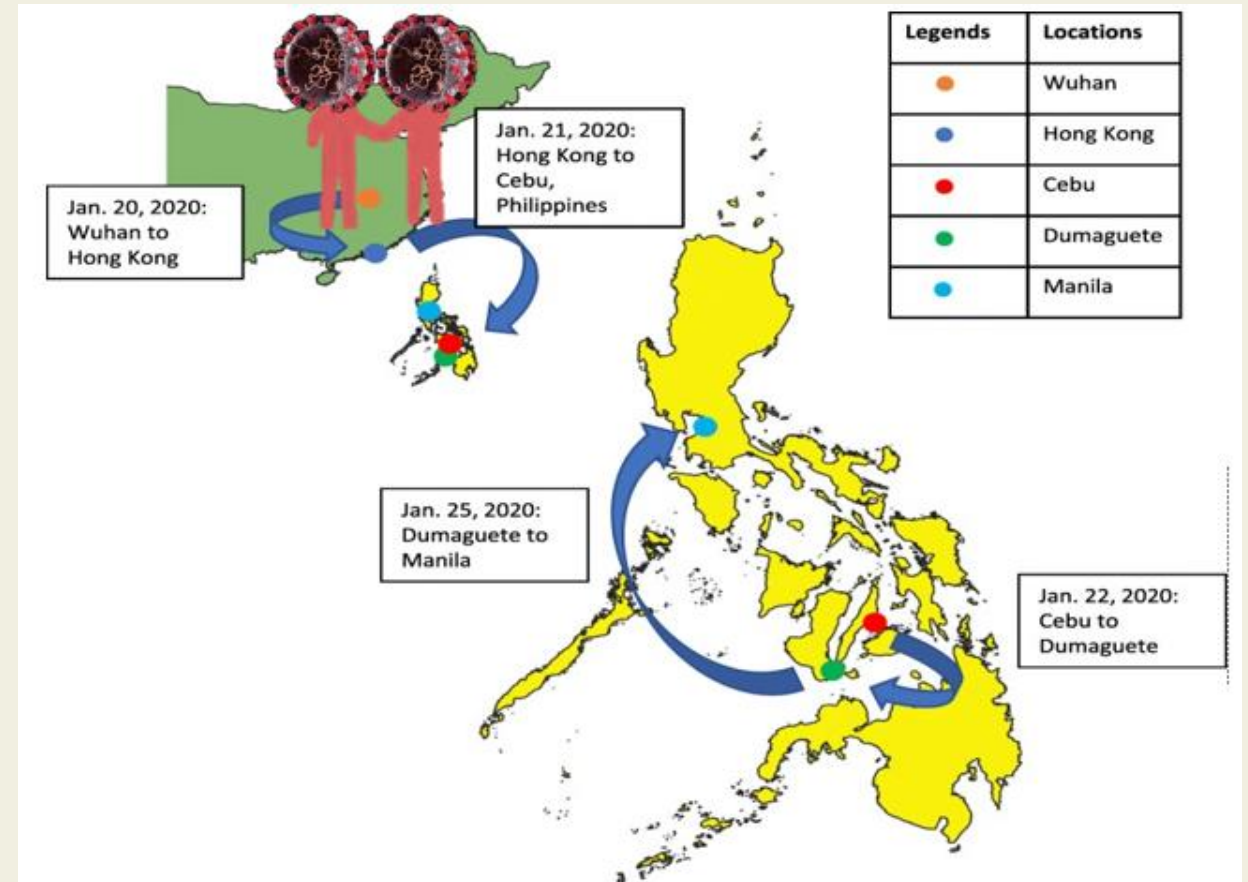


Retrieved from <https://www.hrw.org/news/2016/12/08/philippines-policy-failures-fuel-hiv-epidemic>



COVID-19 in Philippines

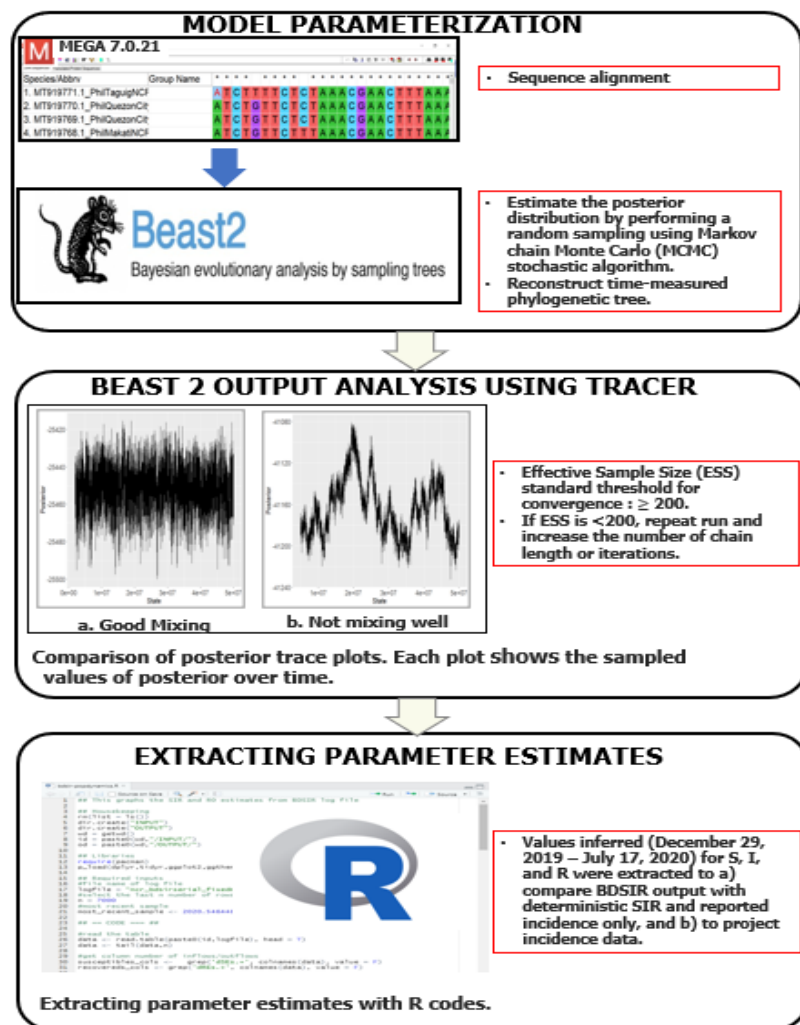
Travel history of Philippine's first recorded COVID-19 cases



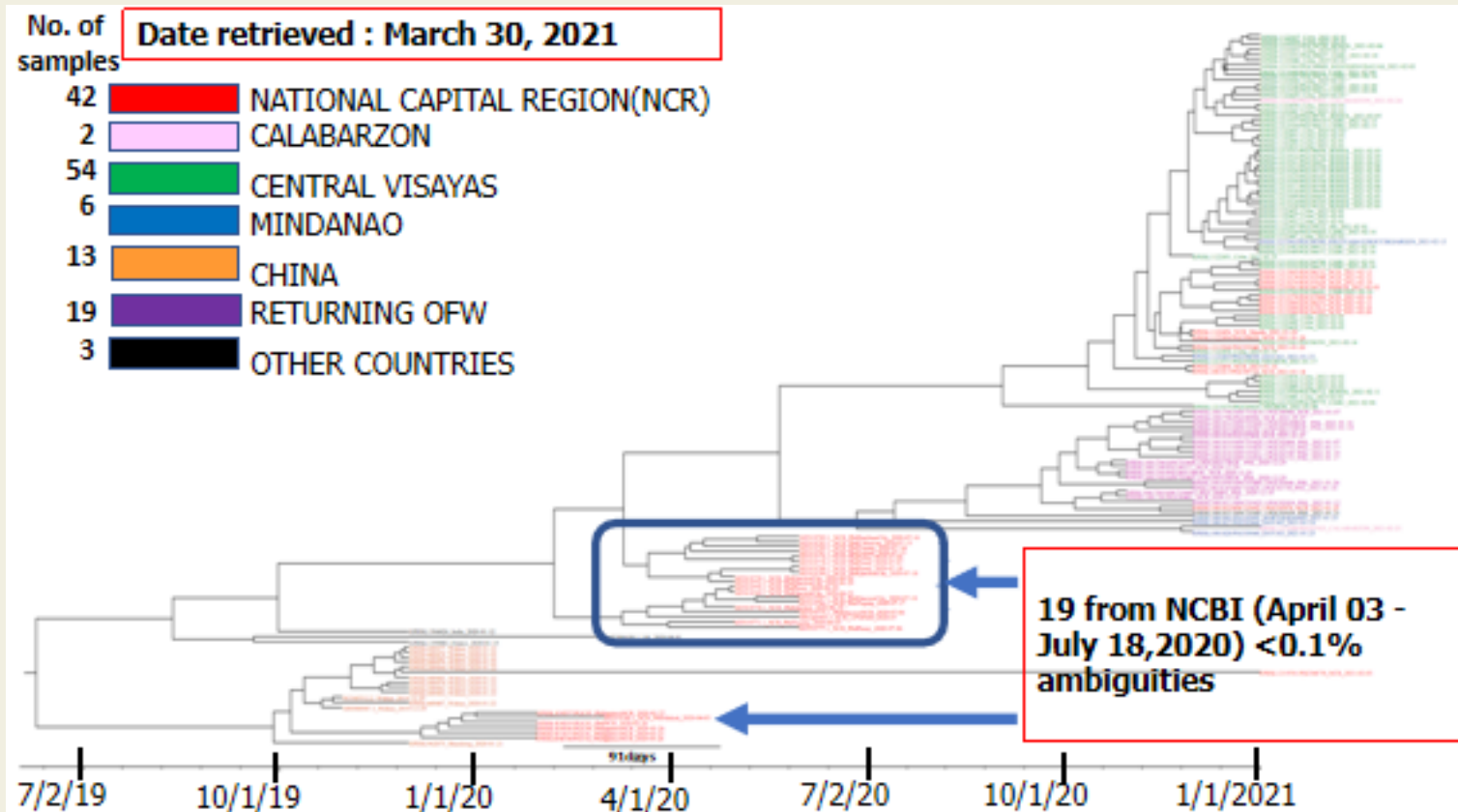
Source: Edrada, E. M., Lopez, E. B., Villarama, J. B., Villarama, E. P. S., Dagoc, B. F., Smith, C., ... & Solante, R. M. (2020). First COVID-19 infections in the Philippines: a case report. *Tropical medicine and health*, 48(1), 1-7.







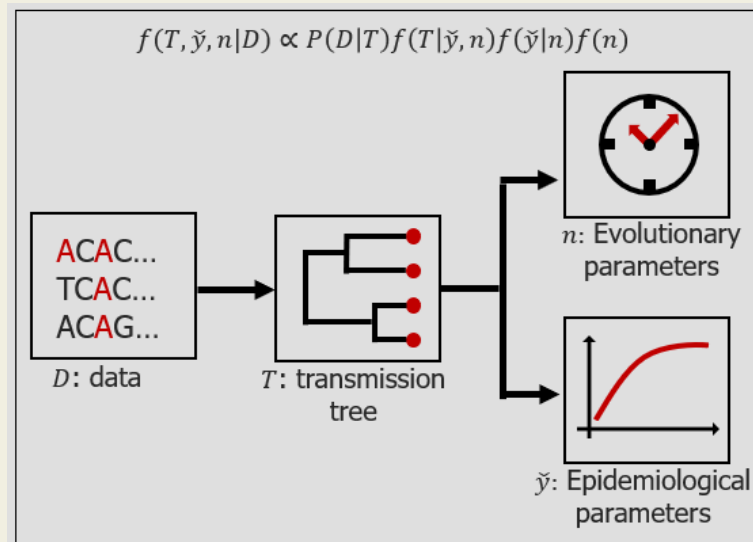
Flow of Analysis



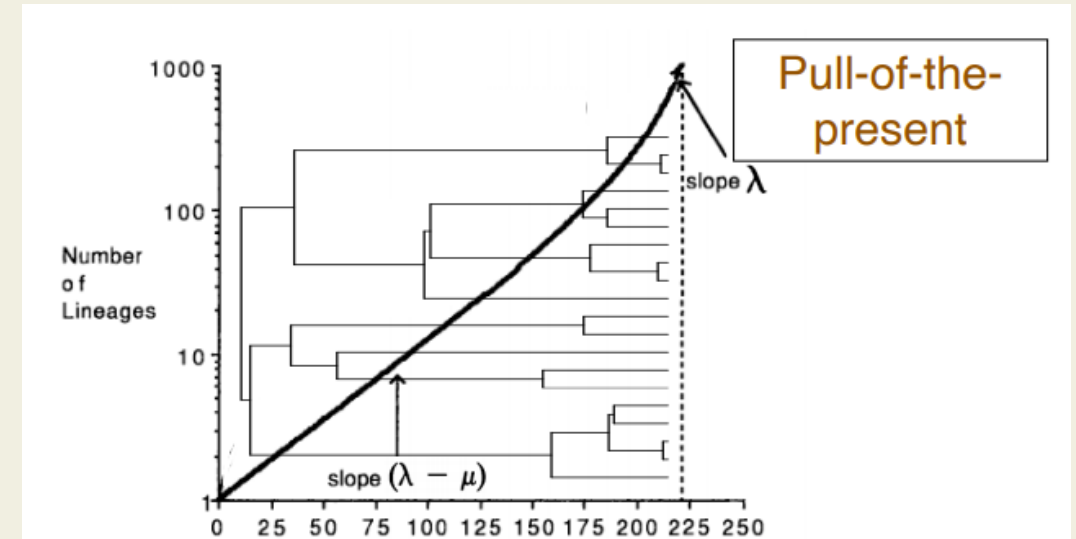
Intuition: Phylodynamics in Epidemiology

Input: Pathogen genetic data from different hosts.

Output: Transmission chain (who infected whom)



Schematic overview of phylodynamic model inference.



Harvey et. al. (1994); Stadler et. al. (2021).

λ : Speciation rate

μ : Death rate

Speciation: Transmission Event

Extinction: Death or Recovery Event



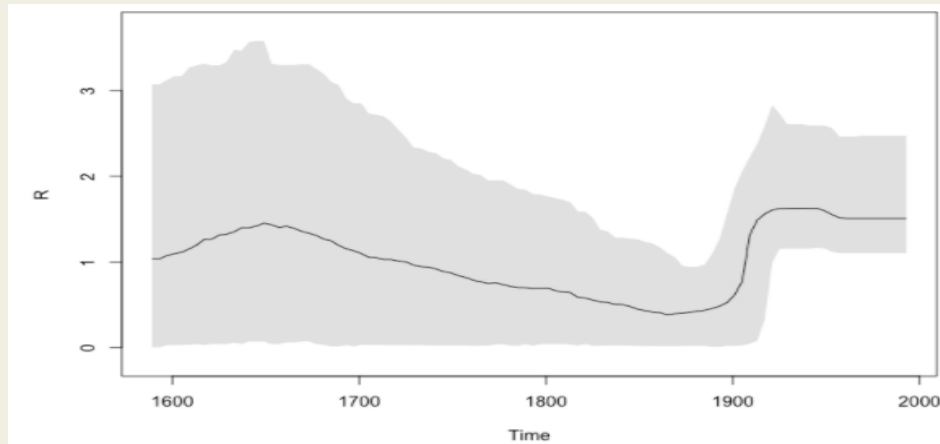
Two Classes of Framework

Birth-Death Model

Tree generation is **forward in time**.



- **Effective Reproductive Number**



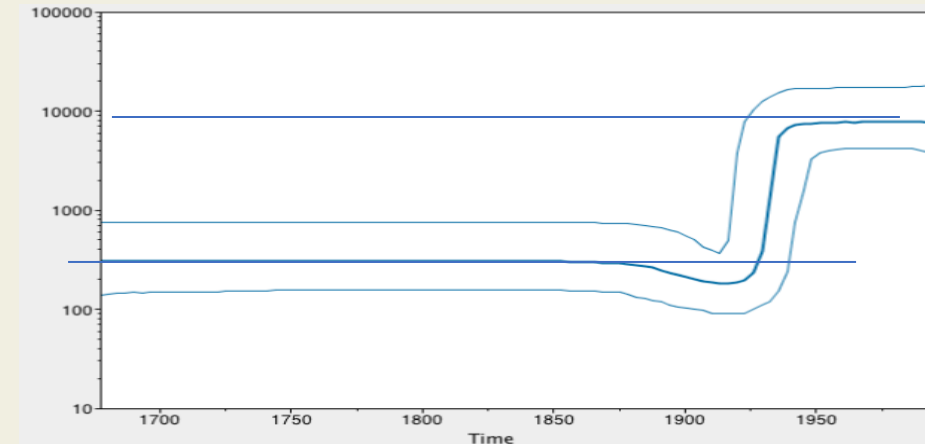
Adapted from <https://taming-the-beast.org/tutorials/Skyline-plots/>

Coalescent Model

Tree generation is **backward in time**.



- **Effective Population Size**



Adapted from <https://taming-the-beast.org/tutorials/Skyline-plots/>





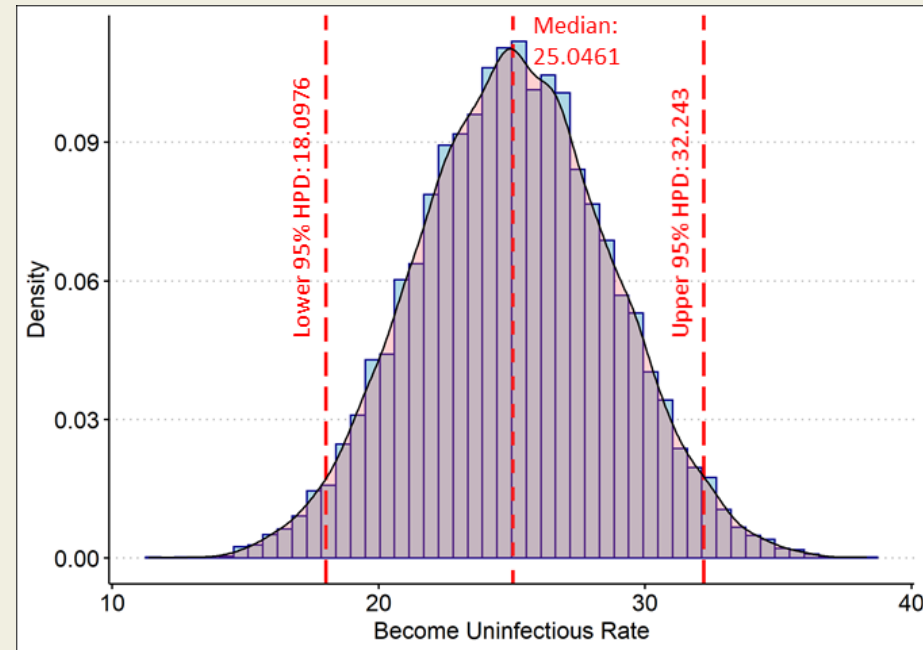
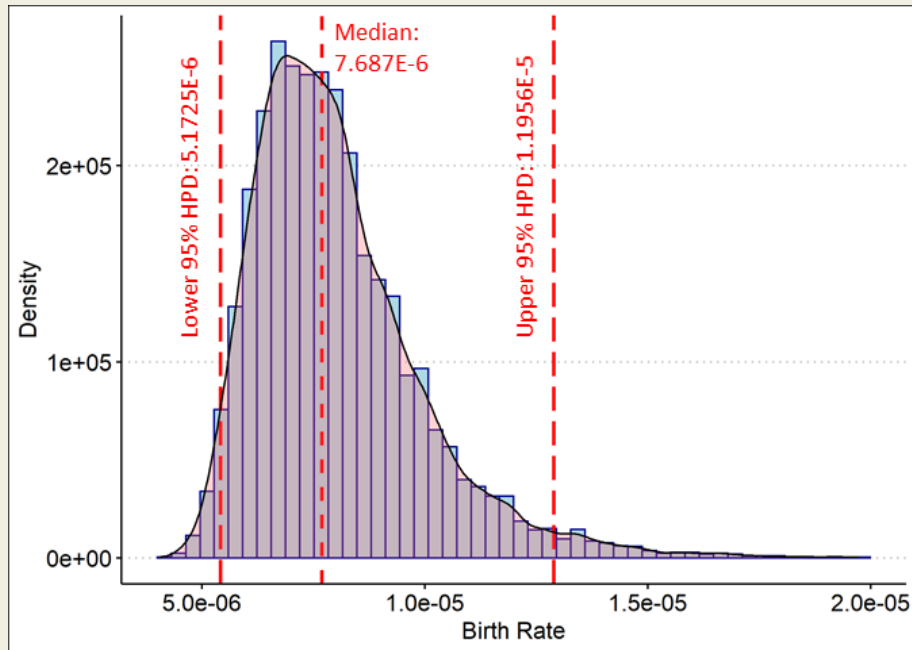
19 SARS-CoV-2 whole-genome sequences from NCR sampled from April 3 to July 18 2020



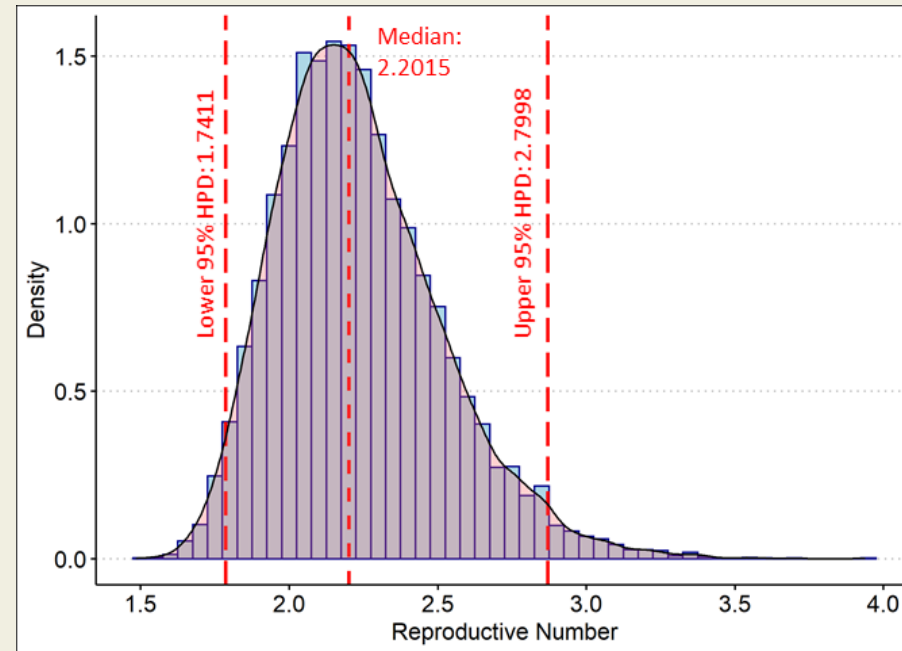
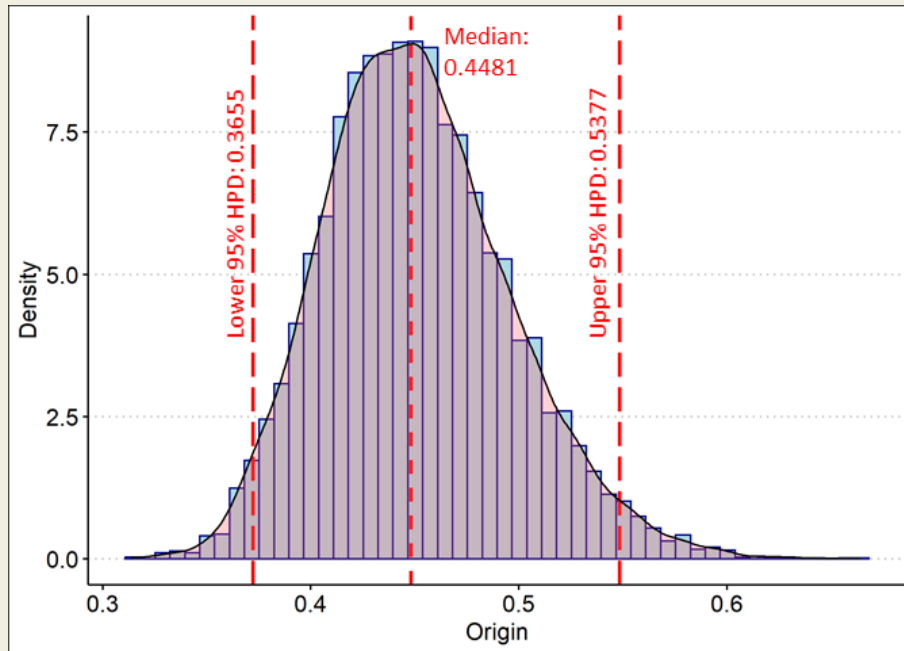
Velasco, John Mark, et al. "Coding-complete genome sequences of 23 SARS-CoV-2 samples from the Philippines." *Microbiology Resource Announcements* 9.43 (2020): e01031-20.



Parameter Estimates



Parameter Estimates



November 18, 2019 to March 25, 2020

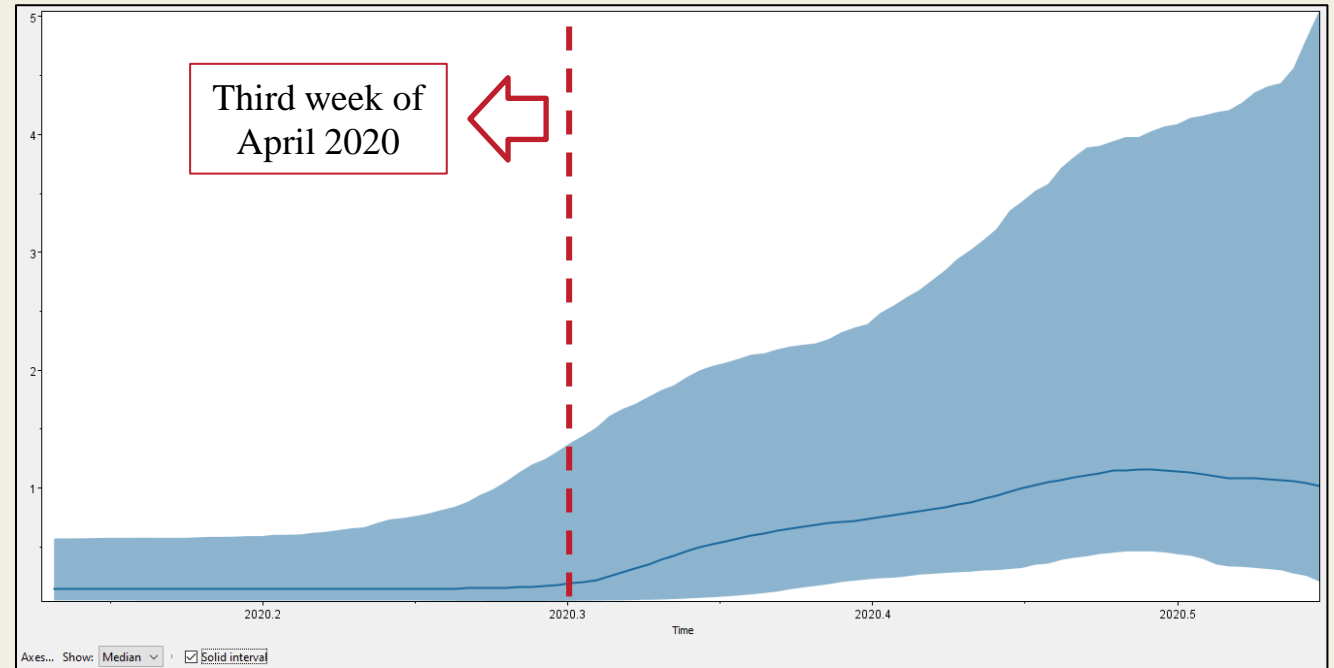


Effective Population Size

- The number of infection appears to triple from 2020.3 (third week of April 2020) to 2020.4 (fourth week of May 2020).

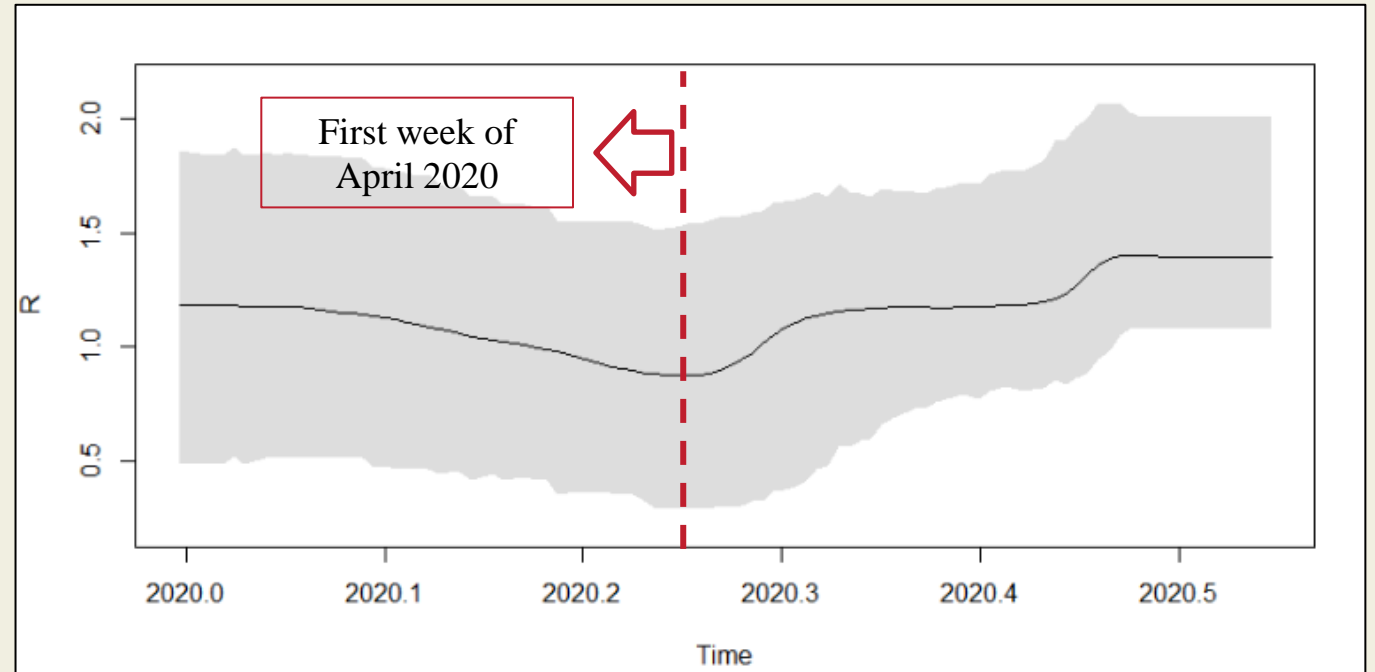
2020.3 -> 0.264288

2020.4 -> 0.769995



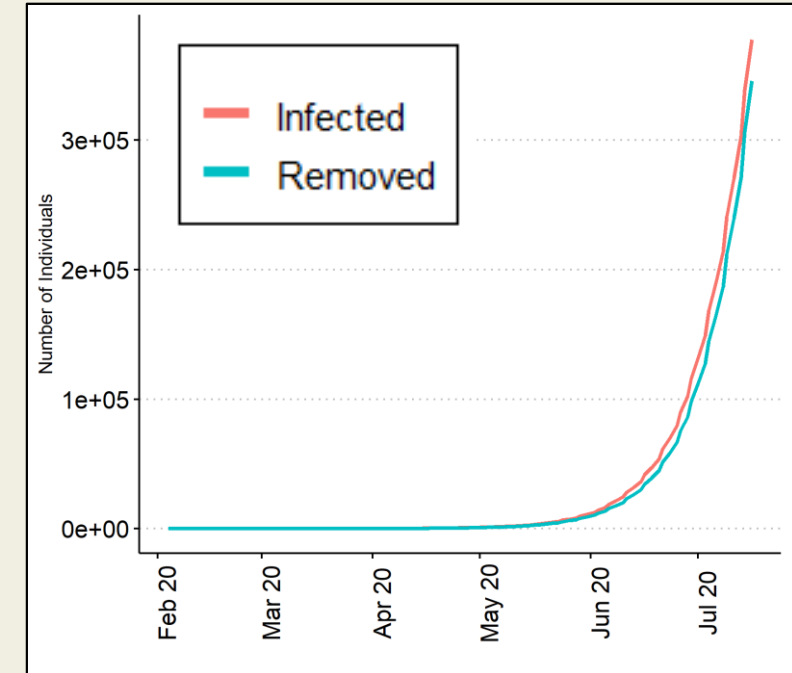
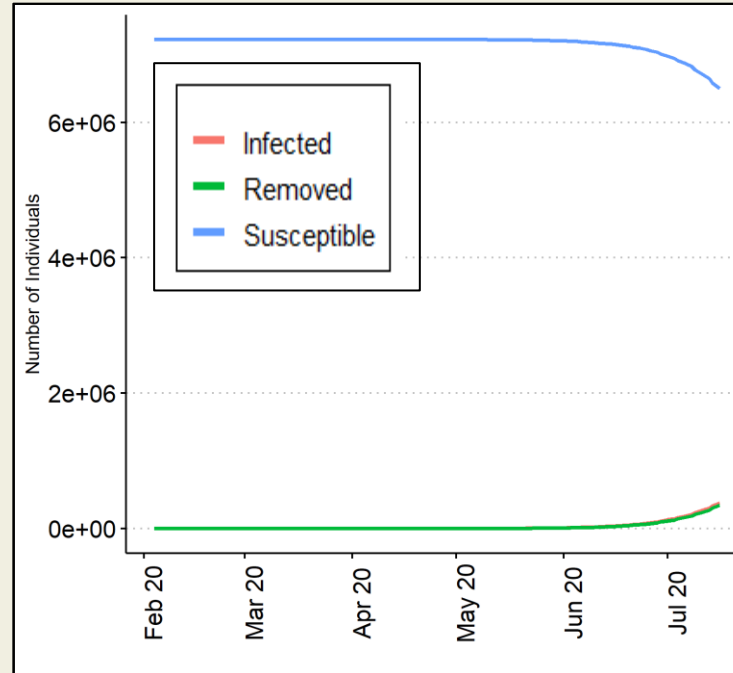
Effective Reproductive Number

- There is an increase in transmission around first week of April 2020.



Birth Death SIR

- The number of infection also appears to be increasing.
- As of the latest sampling date (July 18, 2020), the local epidemic is still on its early stage, approaching the peak.



Is 19 samples enough?

- The Prior and the Posterior are reasonably different.
- The data has effect on shaping the posterior distribution, although it is small in size.



DAGHANG SALAMAT



AMDABiDSS-Health
CSM Building, UP Mindanao , Mintal, Davao City
nicer.upmin@up.edu.ph