

A PHYLOGENETIC ANALYSIS OF THE EARLY COVID-19 SPREAD IN THE NATIONAL CAPITAL REGION OF THE PHILIPPINES



230,418,451 confirmed cases worldwide

Nationwide Cases Data

Total Cases
2,470,175

+16,907 added on 09/25

Active Cases
165,092

Recovered
2,267,678

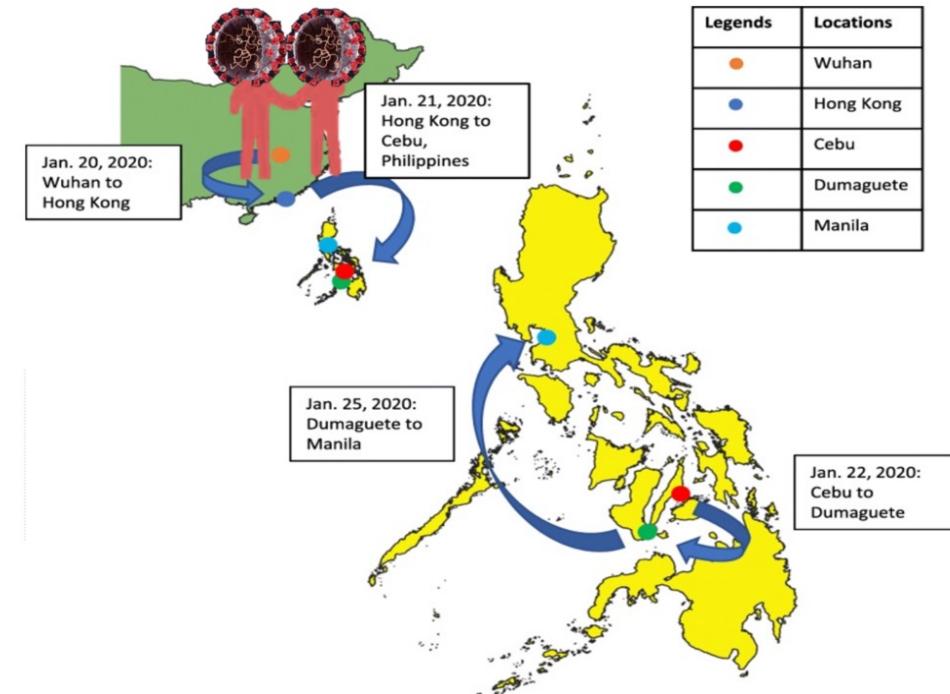
Died
37,405

32%

Confirmed cases are those that tested RT-PCR positive by a DOH-RITM

Lifted from the DOH COVID-19 Tracker as of 25 September 2021

NCR 788,119



Adapted from Edrada et al. (2020)

Application of Genomics In Covid-19 Disease

Phylogenetic and phylodynamic analyses of SARS-CoV-2

Qing Nie^{a,*},¹ Xingguang Li^{b,*},¹ Wei Chen^a, Dehui Liu^a, Yingying Chen^a, Haitao Li^a, Dongying Li^a, Mengmeng Tian^a, Wei Tan^c, Junjie Zai^d

³ Department of Microbiology, Weifang Center for Disease Control and Prevention, Weifang, 261061, China

^b Hubei Engineering Research Center of Viral Vector, Wuhan University of Bioengineering, Wuhan, 430415, China

^c Department of Respiratory Medicine, Weifang People's Hospital, Weifang, 261061, China

^d Immunology Innovation Team, School of Medicine, Ningbo University, Ningbo, 315211, China

^d Immunology Innovation Team, School of Medicine, Ningbo University, Ningbo, 315211, China.

Tracking the COVID-19 pandemic in Australia using genomics

Torsten Seemann^{1,2,6}, Courtney R. Lane^{1,6}, Norelle L. Sherry^{1,6}, Sebastian Duchene³, Anders Gonçalves da Silva¹, Leon Caly⁴, Michelle Sait¹, Susan A. Ballard¹, Kristy Horan¹, Mark B. Schultz^{1,2}, Tuyet Hoang¹, Marion Easton⁵, Sally Dougall⁵, Timothy P. Stinear^{1,2,3}, Julian Druce⁴, Mike Catton⁴, Brett Sutton⁵, Annaliese van Diemen⁵, Charles Alpren⁵, Deborah A. Williamson^{1,3,4,7 &} Benjamin P. Howden^{1,2,3,783}

Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV-2)

Ruiyun Li^{1*}, Sen Pei^{2*}, Bin Chen^{3*}, Yimeng Song⁴, Tao Zhang⁵, Wan Yang⁶, Jeffrey Shaman²

Early phylodynamics analysis of the COVID-19 epidemics in France using 194 genomes - April 10, 2020

samuel.alizon

Early phylogenetics analysis of the COVID-19 epidemics in France

21-Apr-2020

Gonché Danesh, Baptiste Elie and **Samuel Alizon**

ETE Modelling group , MIVEGEC, CNRS, IRD, Université de Montpellier

Apr '20

ARTICLE

<https://doi.org/10.1038/s41467-020-19248-0>

OPEN

Full genome viral sequences inform patterns of SARS-CoV-2 spread into and within Israel

Danielle Miller^{1,6}, Michael A. Martin^{2,3,16}, Noah Harel^{1,6}, Omer Tirosi^{1,6}, Talia Kustin^{1,6}, Moran Meir^{1,6}, Nadav Sorek⁴, Shiraz Gefen-Halevi⁵, Sharon Amit⁵, Olesya Vorontsova⁶, Avraham Shaagid^{1,6}, Diana Wolf⁶, Yonat Peretz^{7,8}, Yonat Sherman-Avram⁹, Diana Roif-Kaminsky¹⁰, Naama M. Kopelman¹¹, Amit Huppert^{12,13}, Katia Koelle^{2,14} & Adi Stern^{2,3,15*}

Molecular Phylogenetics and Spatiotemporal Spread of SARS-CoV-2 in Southeast Asia

Mingjian Zhu¹, Jian Shen¹, Qianli Zeng², Joanna Weihui Tan³, Jirapat Kleebua⁴, Ian Chew⁵, Jia Xian Law⁶, Sien Ping Chew⁷, Anita Tangathajinda⁴, Natthijija Latthitham⁴ and Lanjuwan Lai^{1*}

Phylogenetics reveals the role of human travel and contact tracing in controlling COVID-19 in four island nations

Jordan Douglas^{1,2,†,*}, Fábio K. Mendes^{1,2,3,†,*}, Remco Bouckaert^{1,2},
 Dong Xie^{1,2}, Cinthy L. Jiménez-Silva^{1,3}, Christiaan Swanepoel^{1,2},
 Joep de Ligt⁴, Xiaoyun Ren⁴, Matt Storey⁴, James Hadfield⁵, Colin R. Simpson⁶,
 Jemma L. Geoghegan^{4,7}, David Welch^{1,2} and Alexei J. Drummond^{1,2,3}



230,418,451 confirmed cases worldwide



Variant calling



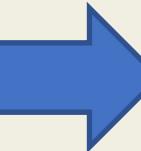
Phylogenetics



Phylogeography



Phyldynamics



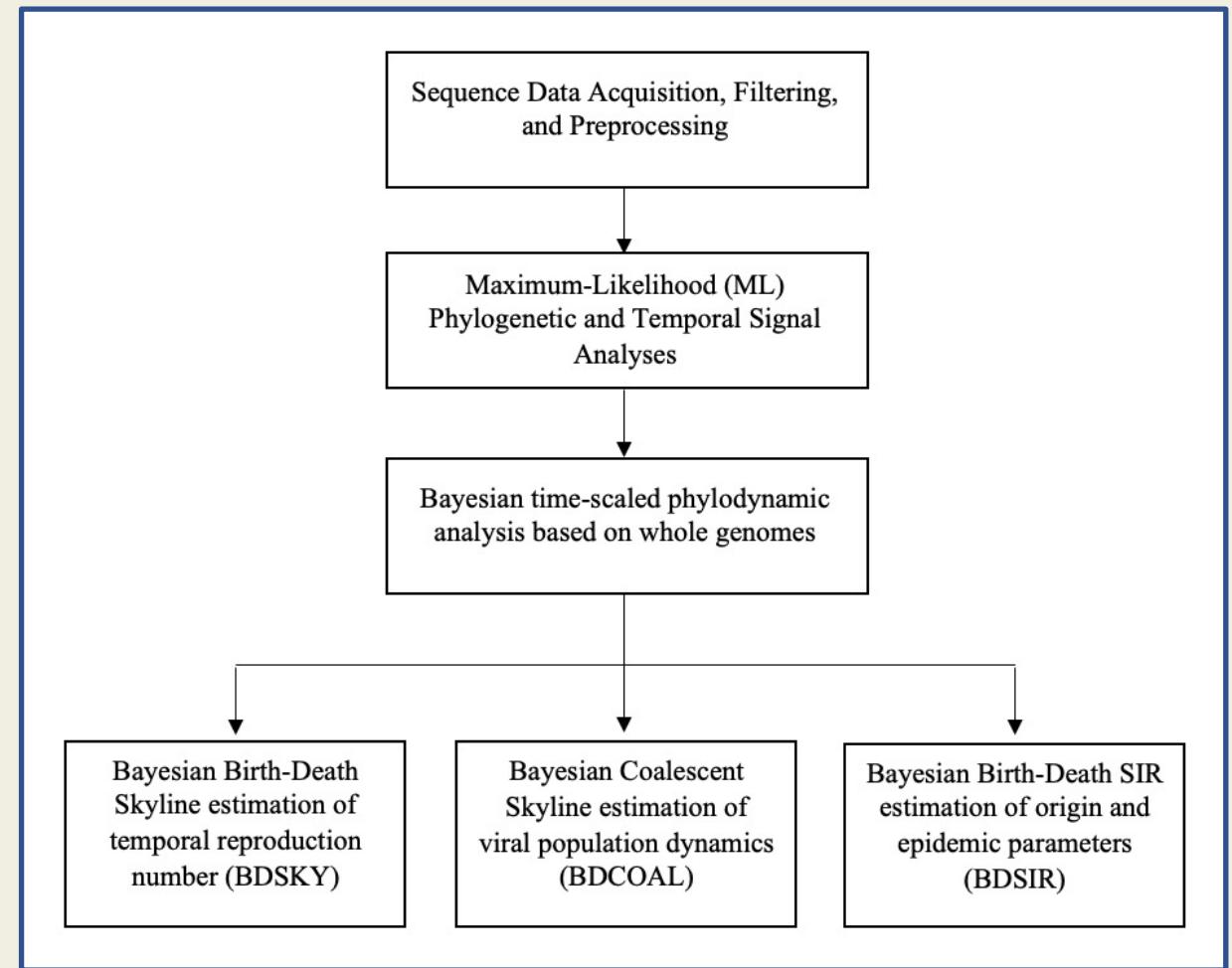
- To detect variant of concern (VOC)
- To determine if the increase in cases in a particular area are attributable to the VOC
- To give comprehensive picture of the circulating variants and identify clustered cases (Track and trace)
- To provide information on the incidence and prevalence of infections and its geographical source
- Detailed information on the interaction of host population dynamics and evolutionary history



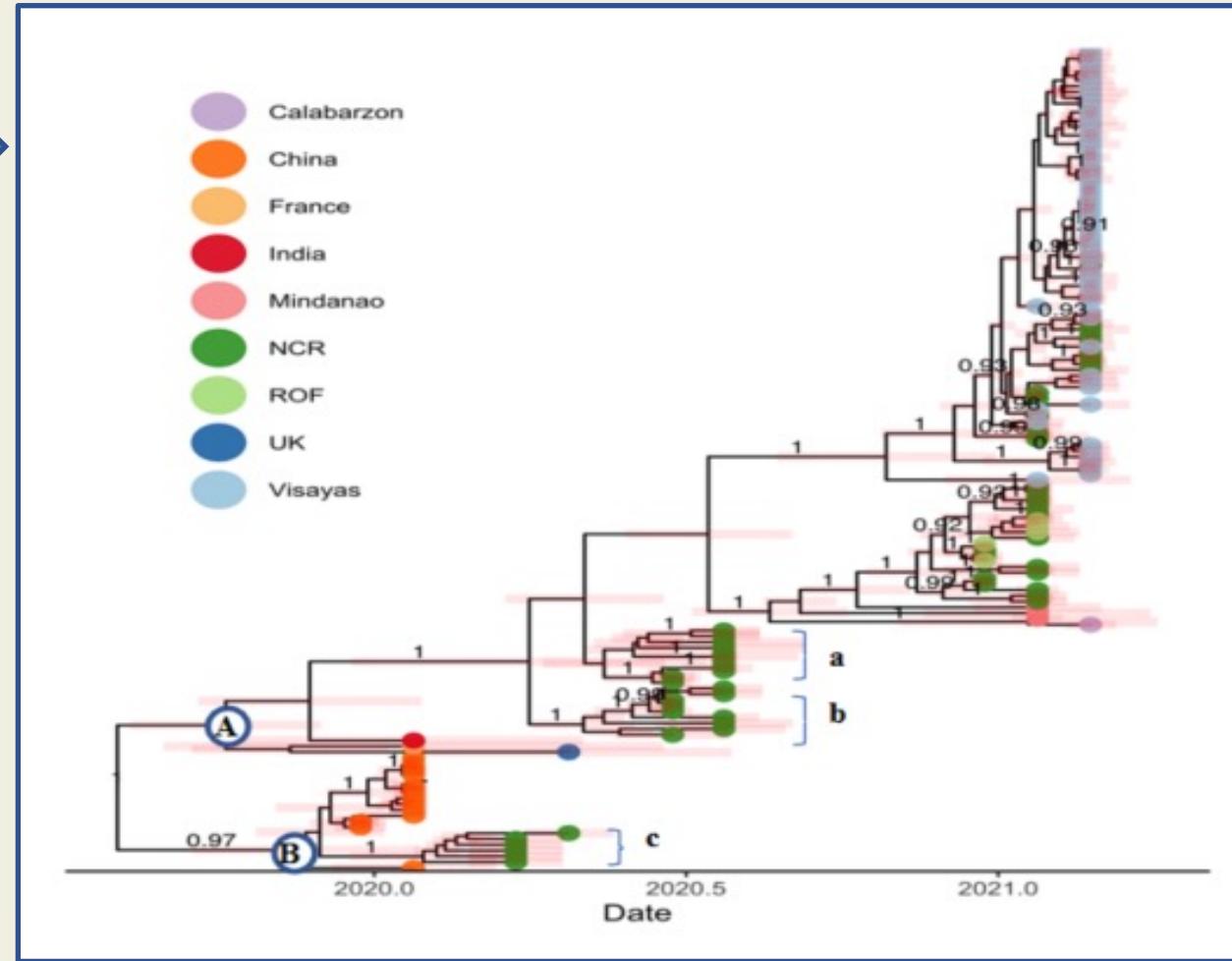
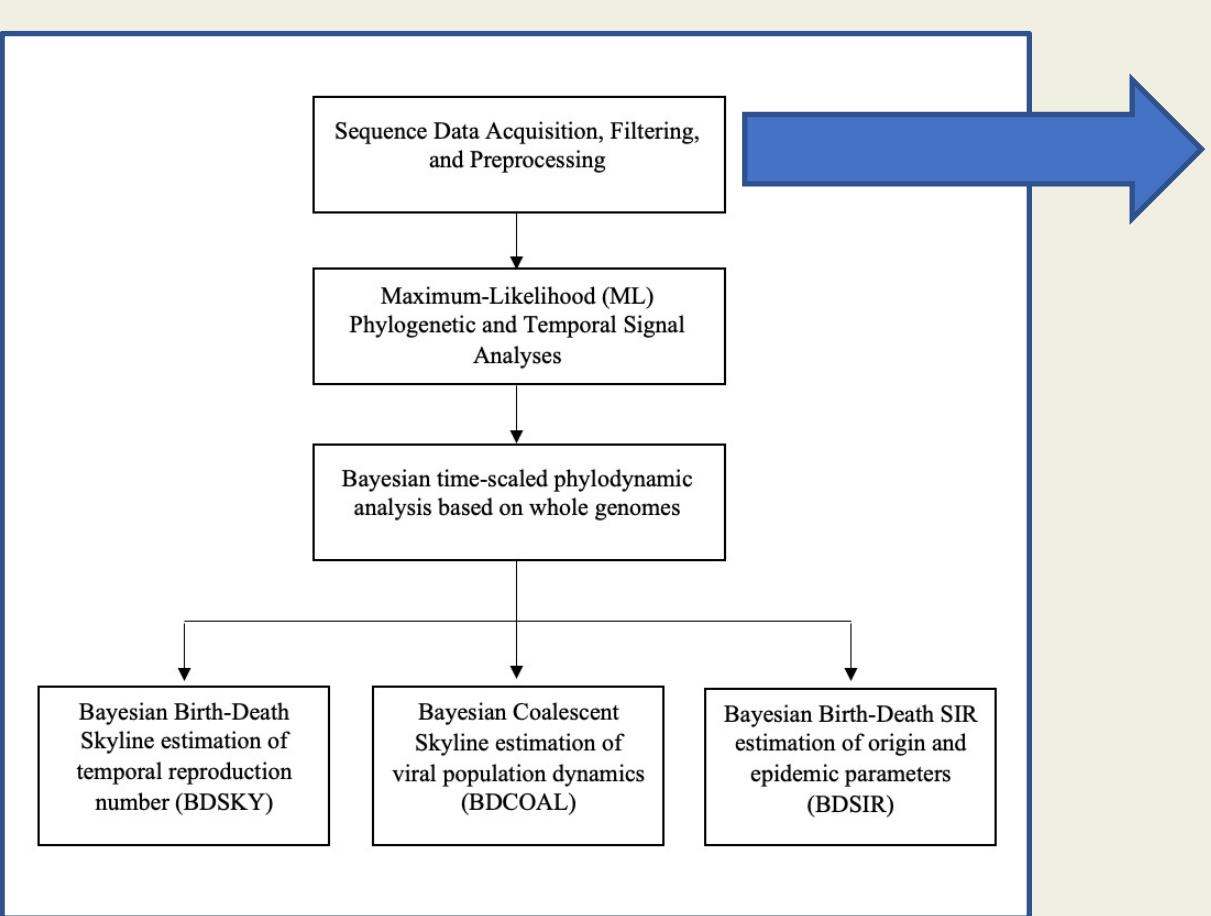
AMDABiDSS-Health

Proof of concept for phylodynamic models demonstrated to be applicable to NCR

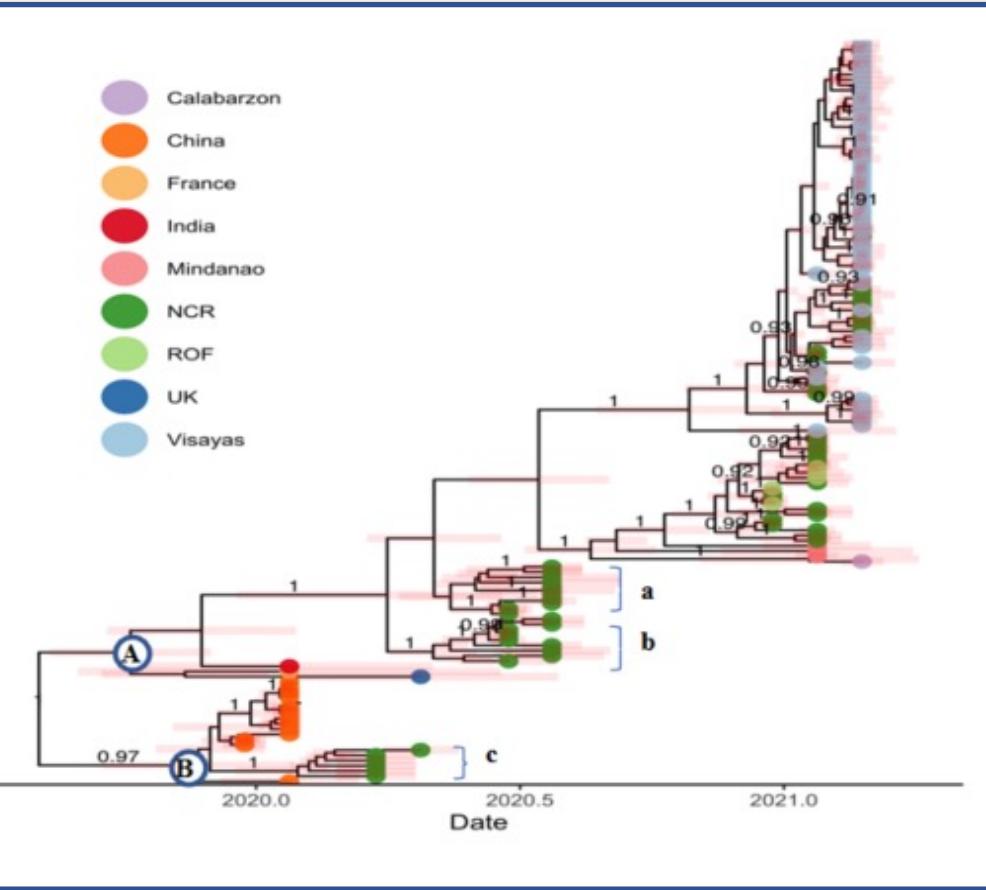
Describe the early COVID-19 epidemic in the National Capital Region



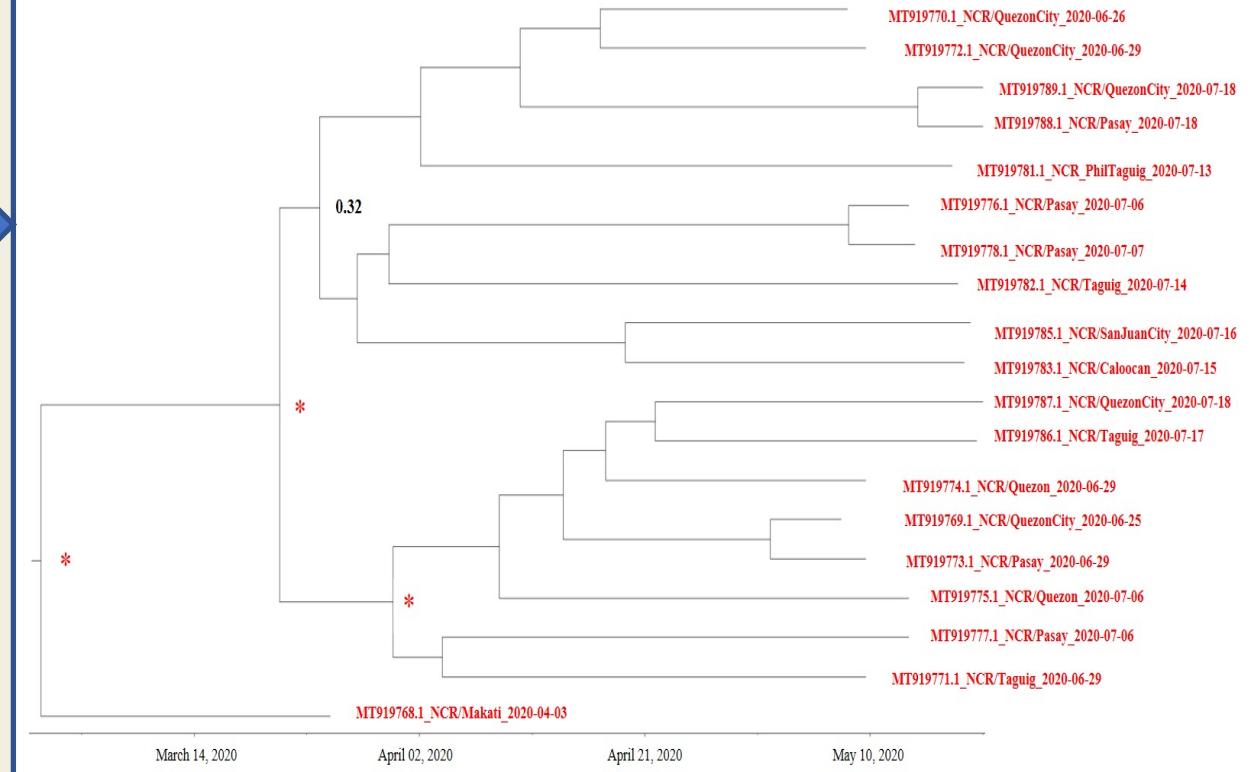
Data Acquisition and Filtering



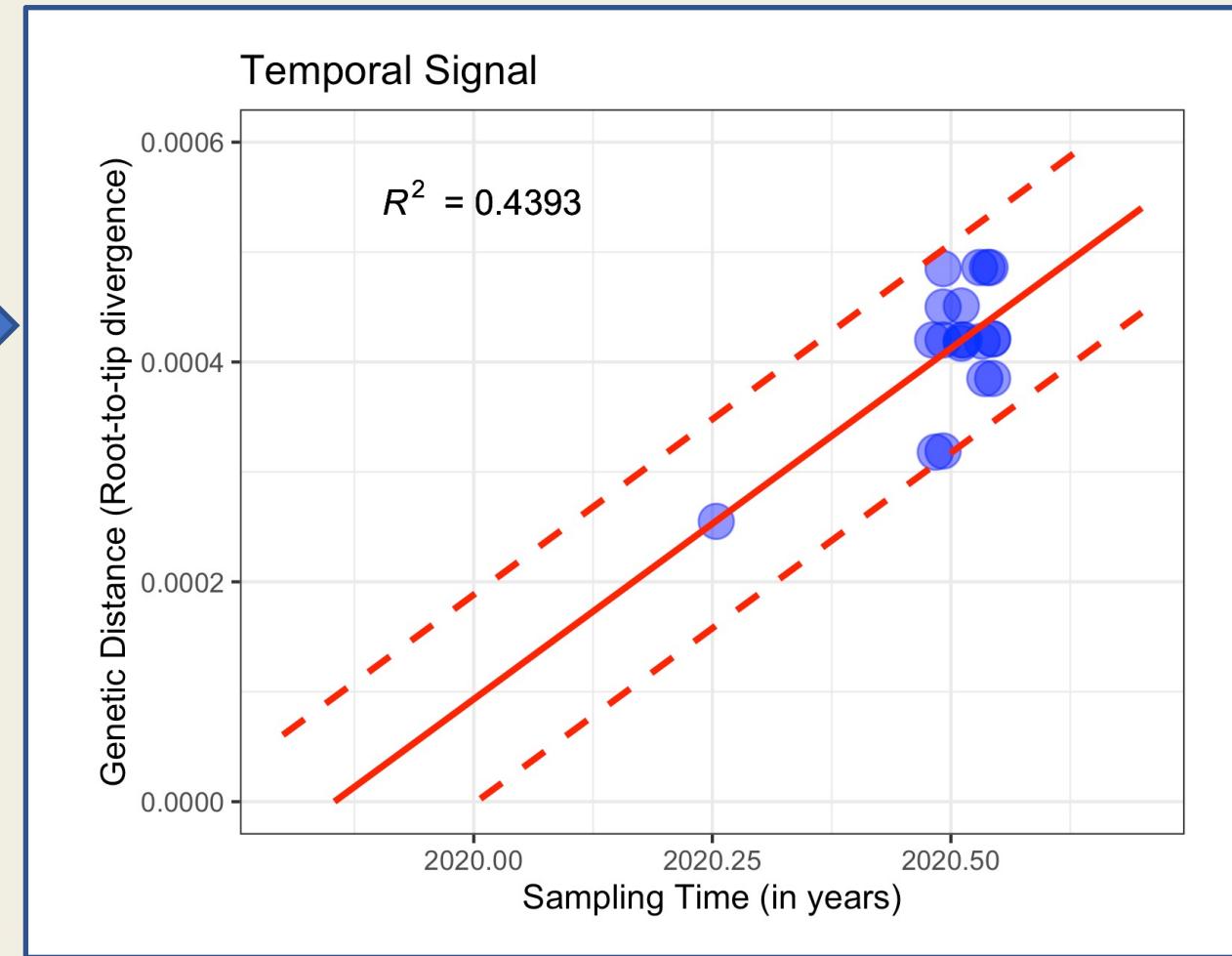
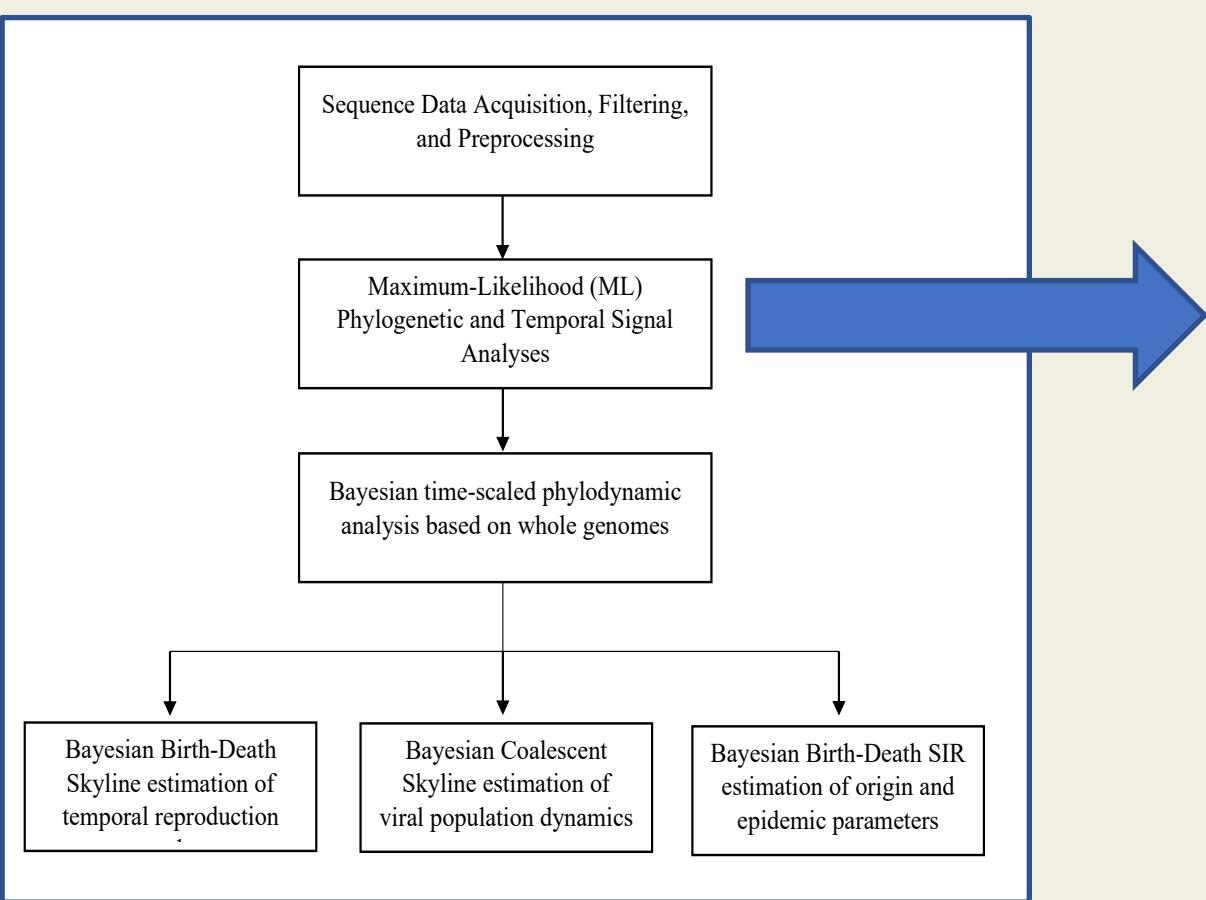
Data Acquisition and Filtering



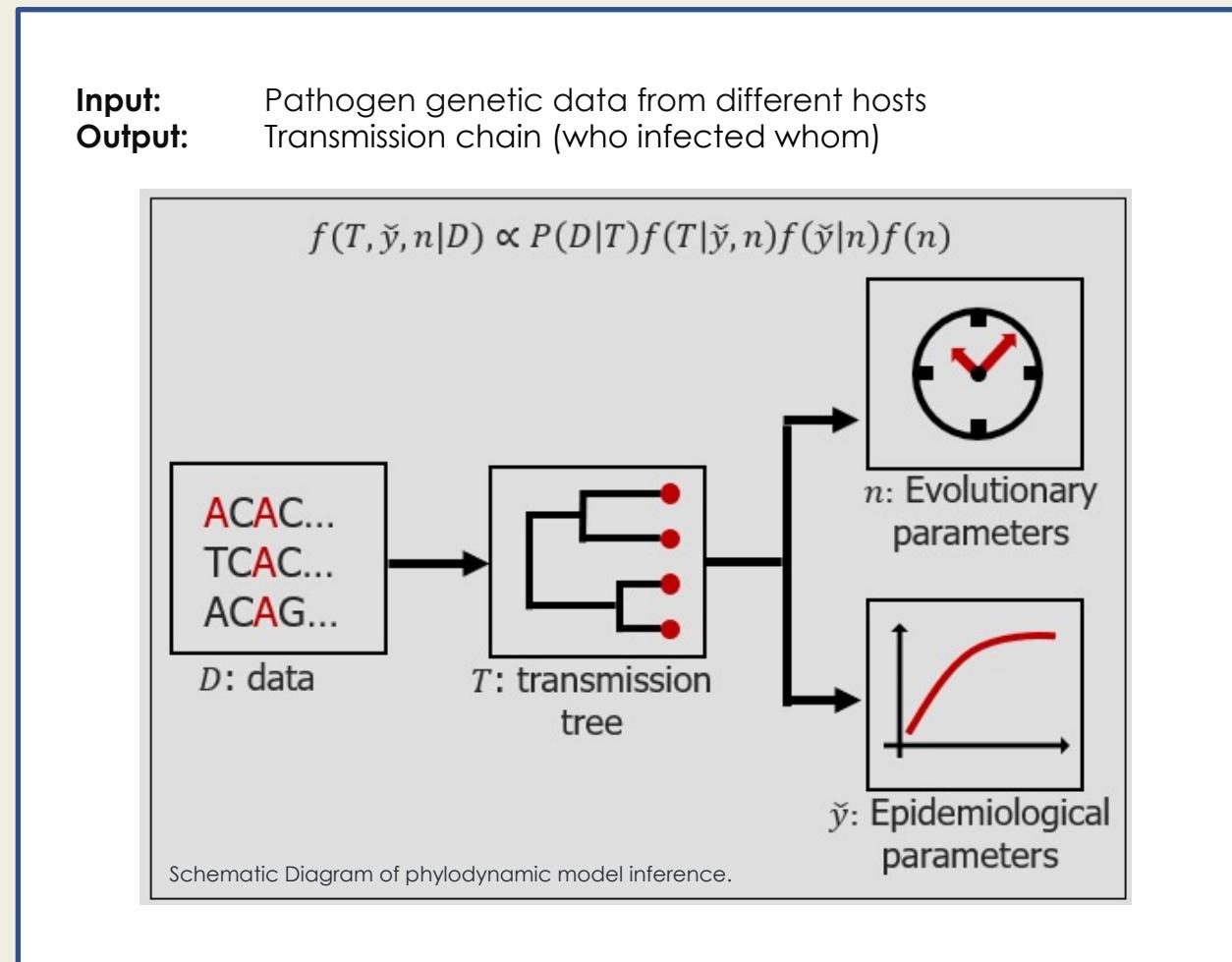
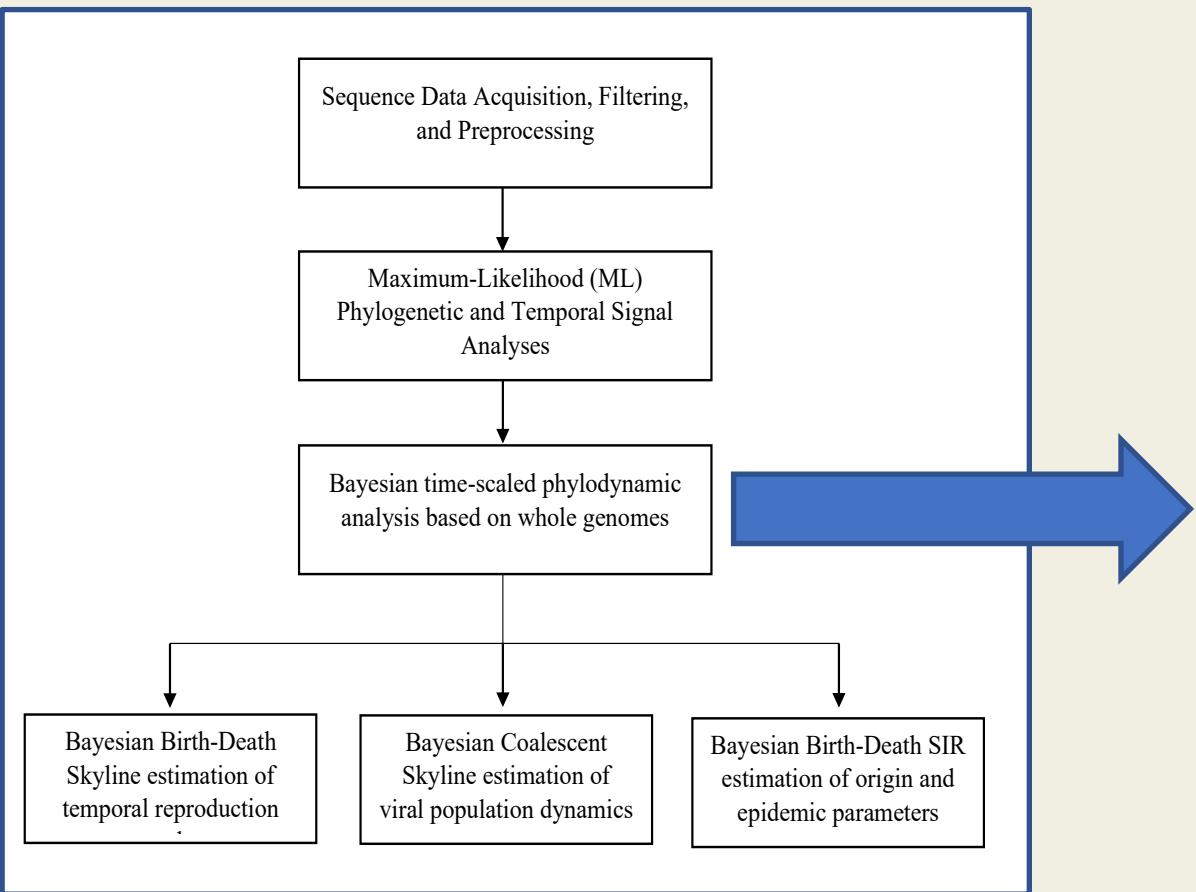
- 19 sequences used for Phylodynamic Analysis



Temporal Signal Analysis



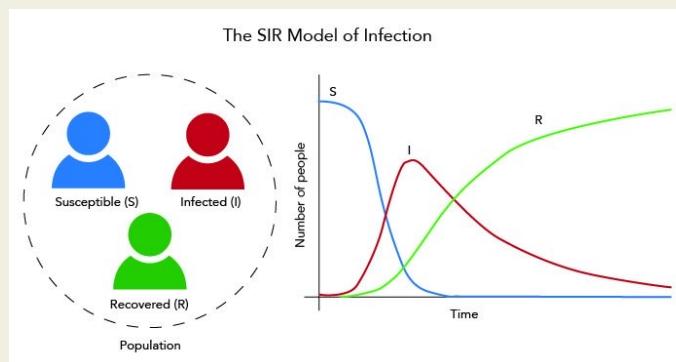
Phylogenetic Analysis



Phyldynamic Models

1. Birth Death SIR Mode (**BDSIR**) by Kühnert et al., 2013

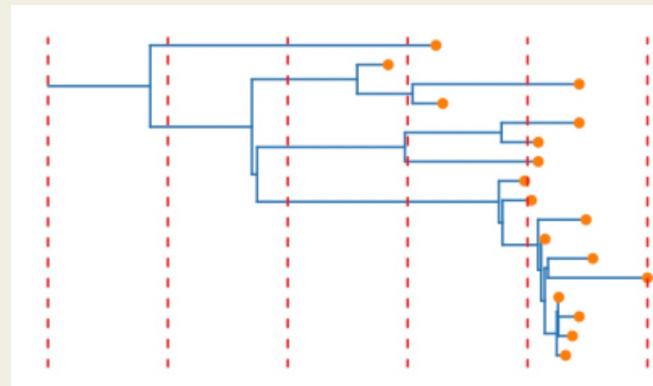
- Parametric (i.e., has underlying population structure)
- Infers the origin and the basic reproductive number



Adapted from IndiaBioscience website

2. Birth Death Skyline Model (**BDSKY**) by Stadler et al., 2013

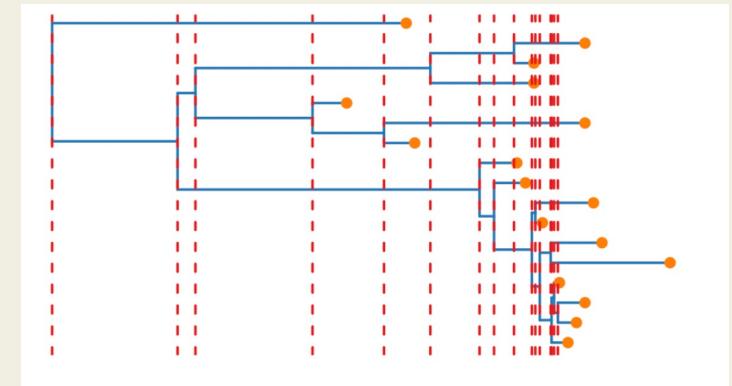
- Non-parametric
- Infers the effective reproductive number in a piecewise manner (equally spaced intervals)
- Relies on the estimate of origin



Adapted from Taming the BEAST website

3. Coalescent Skyline Model (**BDCOAL**) by Drummond et al., 2005

- Non-parametric
- Infers the effective population size in a piecewise manner (per coalescent events)
- Relies on the coalescent events



Adapted from Taming the BEAST website

Origin and R_0 estimates

Origin Estimate

Median: Feb. 4, 2020

95% Credible Interval: Nov. 18, 2019 to Mar. 25, 2020

First known report: January 30, 2020 (Edrada al. 2020)

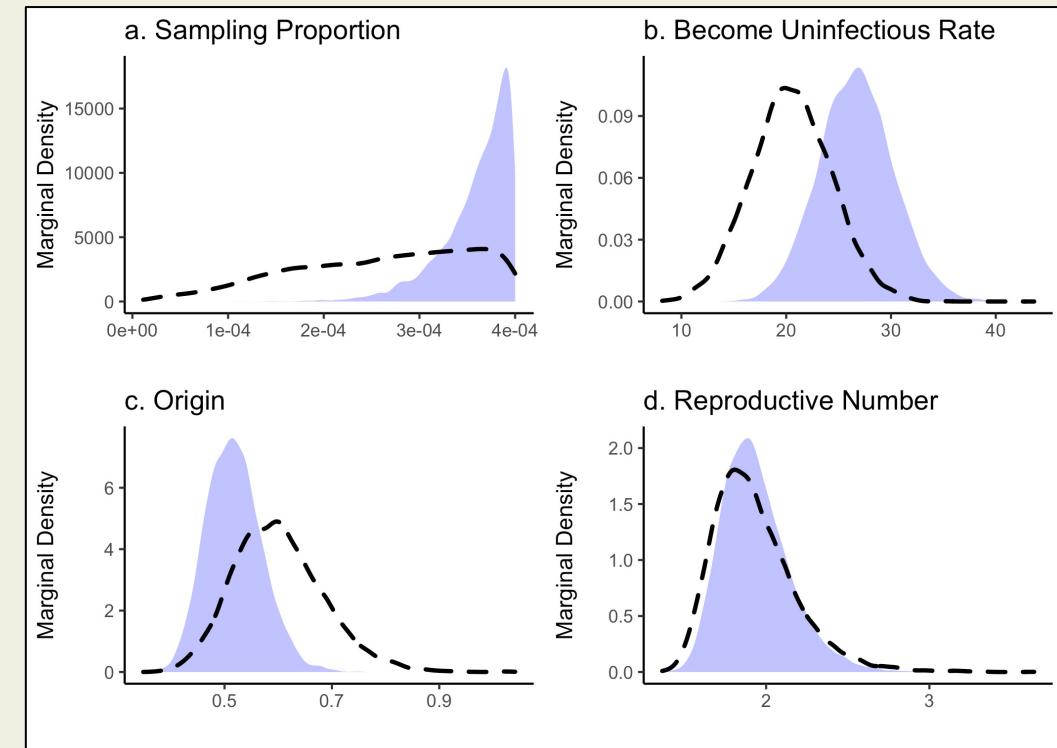
Basic Reproductive Number (R_0) Estimate

Median: 2.20

95% Credible Interval: 1.74 to 2.80

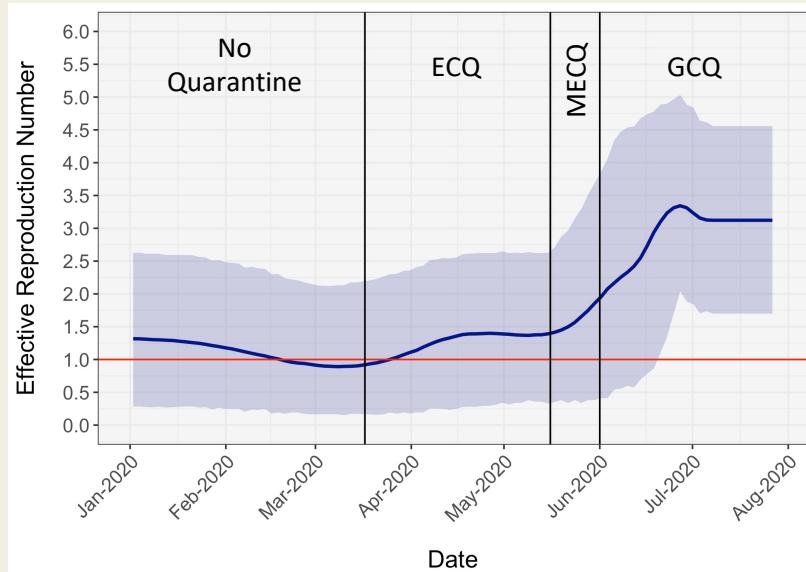
DOH Report: 1.19 as of July 2020 (From WHO Philippine Sitrep #52)

Modeling Result: Max of 2.41 (Haw al. 2020)



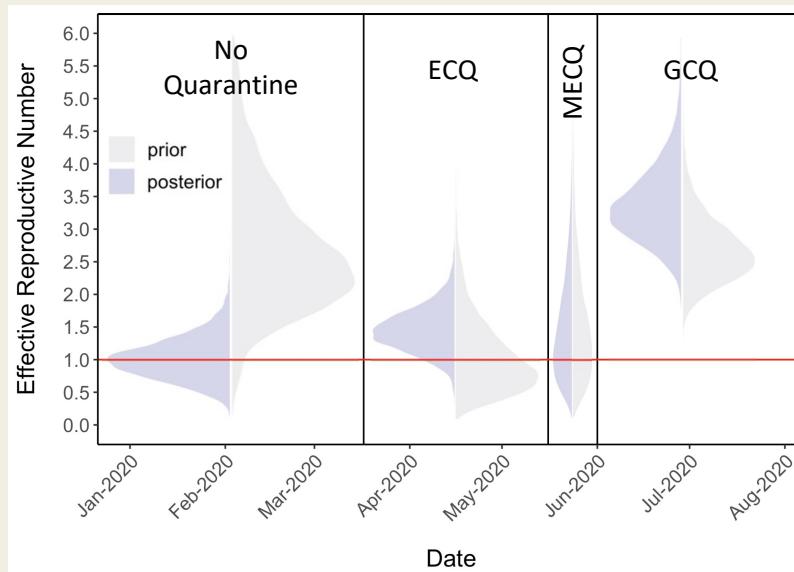
Prior (dashed black line) vs. Posterior (shaded in blue)
When data is not used vs. When data is used

Effective Reproductive (R_e) Number Estimates



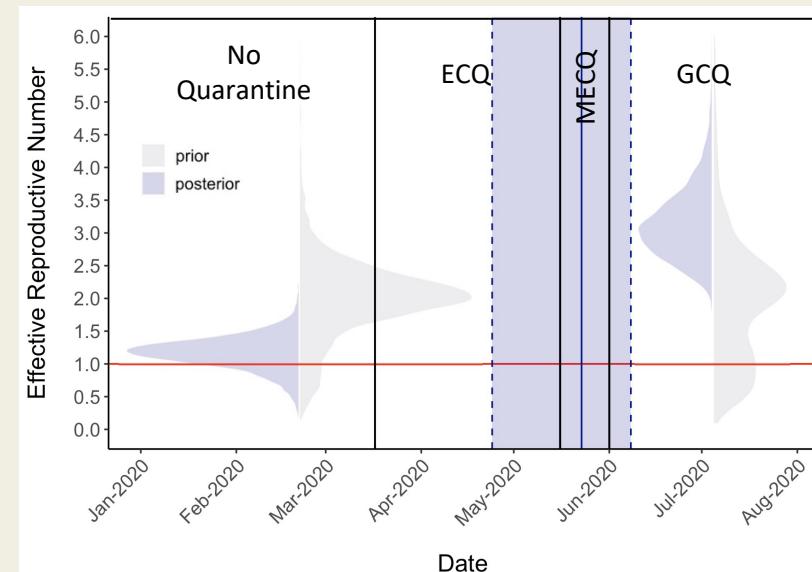
Timeseries of R_e

- Supports an overall progressive growth of virus spread



R_e per community quarantine (QC)

- Data is informative during MECQ

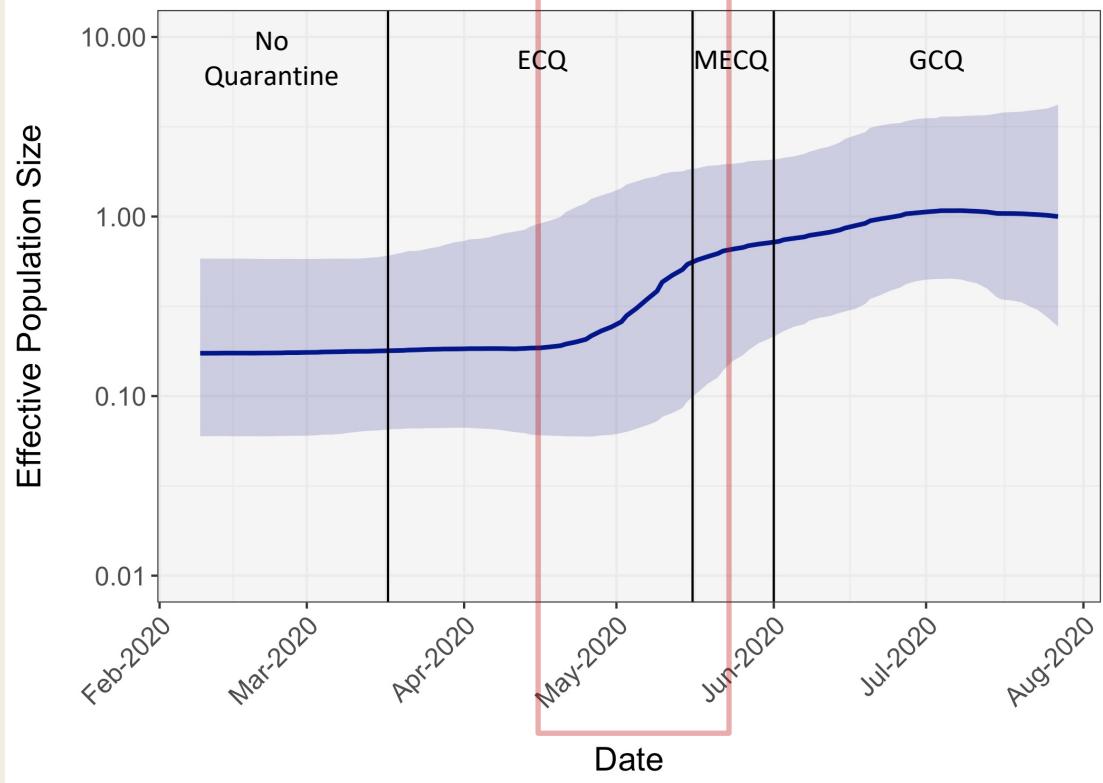


Co-estimated the date of major change in R_e

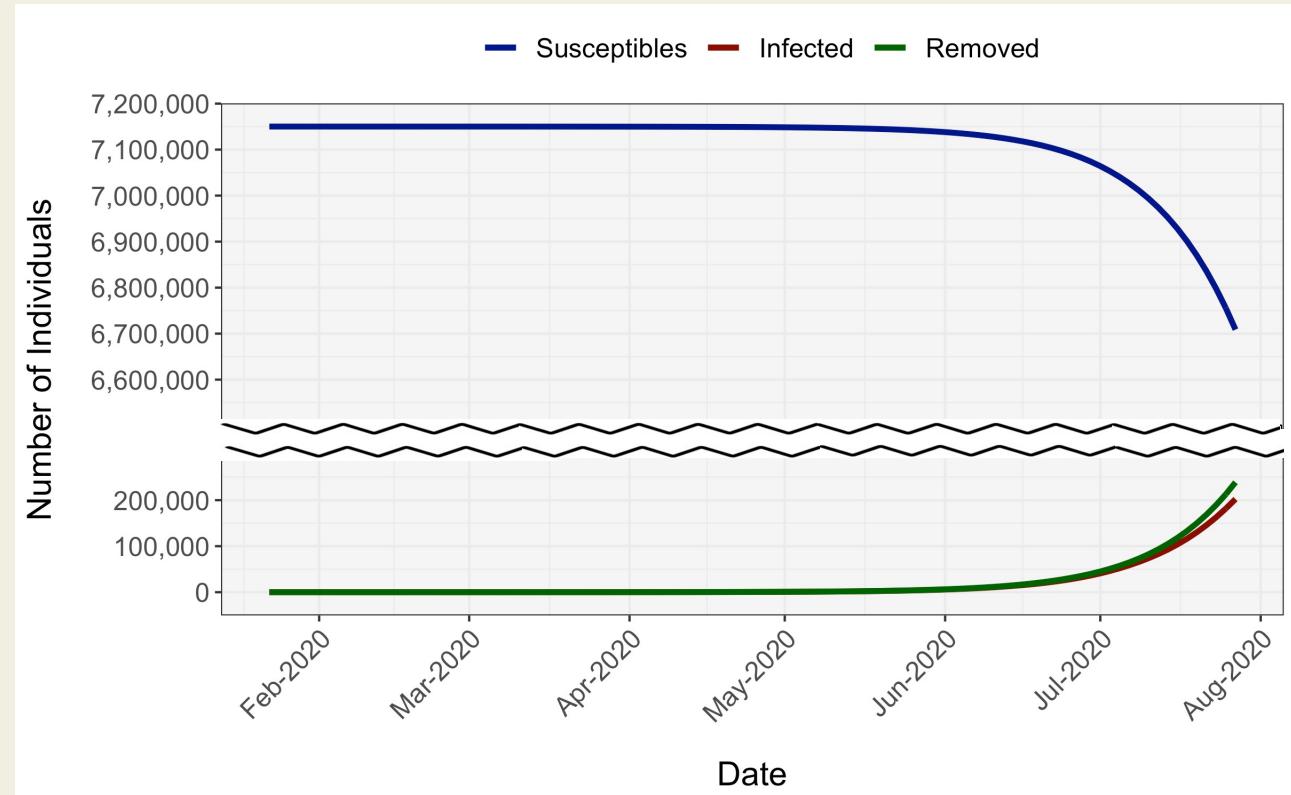
- Median: 20 May 2020
- 95% HPD: 06 Apr to 08 June 2020

Case Estimates

Major Population Expansion



Effective Population Size estimate
(y-axis is on log scale)



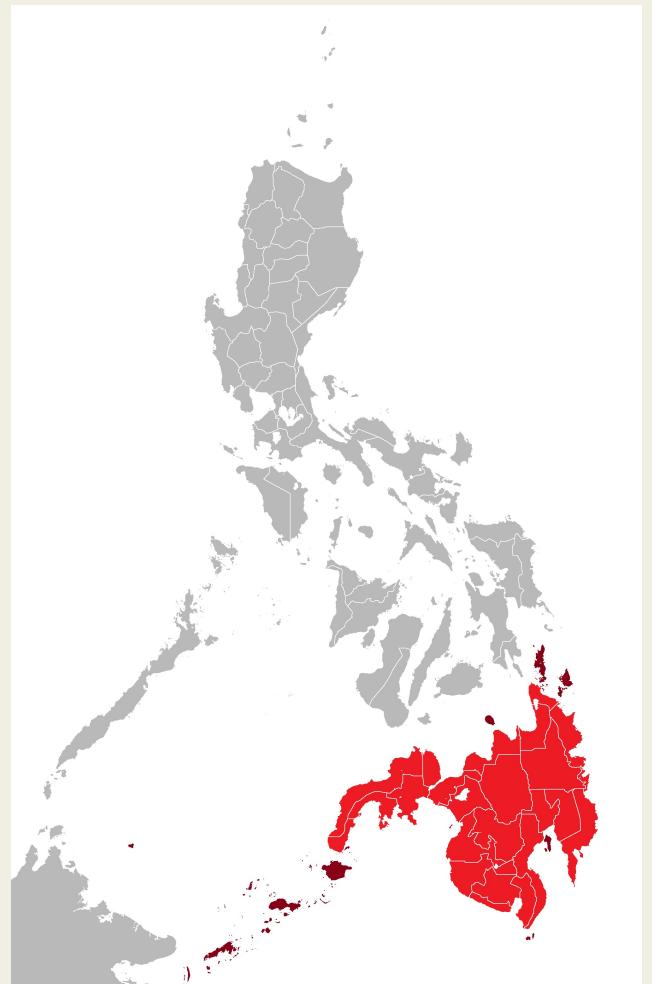
SIR estimate from the
BDSIR model

Conclusion

- The model was successful in reconstructing the origin and basic reproduction number of SARS-CoV-2 in NCR, during its early stage.
- There is an increasing number of cases and spread, with the peak still not reached by the end of July 2020.
- There is a pronounced increase in the spread of the virus during the transition from ECQ to MECQ on May 2020.
- Despite the small sample size of the genomic sequences used, the resulting estimates from the phylodynamic models were still informative.

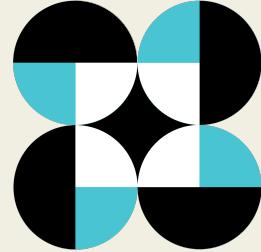
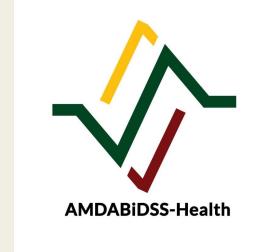
Current Work

- We are currently applying the phylogenetics, phylodynamics, and phylogeographic methodologies to describe the spread and transmission dynamics within and among different regions in Mindanao.



Acknowledgement

- Imari Joy Borda
- Sherly Grace Buenaventura
- Zython Paul Lachica
- Ricardo del Rosario
- Ivy Grace Panogalinog
- Ian Quibod
- May Anne E. Mata
- Lyre Anni E. Murao



Malayan Colleges Mindanao
A MAPÚA SCHOOL



AMDABiDSS-Health

DAGHANG SALAMAT



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

