# THE LANCET **Global Health**

# **Supplementary appendix**

This appendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

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## **Supplementary Appendix**

- **S1- List of countries in the WHO Africa Region by income classifications**
- **S2- Parameter description and initialization**
- **S3- Model development for the SEIRD Partially Observed Markov Process**
- **S4- Regional analysis Tables**



<b>High / Upper Middle Income</b>	<b>Lower-middle Income</b>	<b>Low Income</b>
Seychelles (High Income)	Angola	Benin
Algeria	Cameroon	<b>Burkina Faso</b>
<b>Botswana</b>	Cabo Verde	<b>Burundi</b>
<b>Equatorial Guinea</b>	Comoros	Central African Republic
Gabon	Congo, Rep.	Chad
Mauritius	Cote d'Ivoire	Congo, Dem. Rep.
Namibia	Eswatini	Eritrea
South Africa	Ghana	Ethiopia
	Kenya	Gambia, The
	Lesotho	Guinea
	Mauritania	Guinea-Bissau
	Nigeria	Liberia
	Sao Tome and Principe	Madagascar
	Senegal	Malawi
	Zambia	Mali
	Zimbabwe	Mozambique
	United Republic of Tanzania	Niger
		Rwanda
		Sierra Leone
		South Sudan
		Togo
		Uganda

**Table S1: Classification of the WHO AFRO countries according to income levels**

#### **SUPPLEMENTARY APPENDIX 2: Parameter description and initialization**

We utilized the parameters in the table below to fit into the model for the different states

#### **Table S2. Parameter description and initialization**



### **SUPPLEMENTARY APPENDIX 3: Model development for the SEIRD Partially Observed Markov Process**

The evolutionary process of Covid-19 cases data is modeled as a Partially Observed Markov Process (POMP) also called Hidden Markov Model.<sup>12</sup> A POMP is a statistical Markov Model in which the hidden states are assumed to have the Markov property and emit symbols or observations. For the compartment model (SEIRD), the hidden states are the number of individuals in the compartments.

From Figure 1 in the text, let  $S(t)$ ,  $E(t)$ ,  $I(t)$ ,  $R(t)$  and  $D(t)$  be the numbers of individuals within the respective compartment at time *t*. Let also  $n_{ij}$  be a stochastic counting process with the value at time *t* being the number of individuals transiting from compartment *i* to *j* during the interval  $[t_0, t)$ , where  $t_0$  is the starting point. Further, let  $n_i$  and  $n_i$  be the births and deaths, respectively, in compartment *i*. The infinitesimal increment probabilities specify the continuous-time Markov process. Writing  $\Delta n(t) = n(t+h) - n(t)$ , we therefore have:

$$
\Pr\left[\Delta n_{s_1}(t) = 1 | F_t\right] = \nu N(t) h + o(h) \tag{1}
$$

*For i = 1, 2 for the not – immunized and immunized sub-models,*

 $Pr\left[\Delta n_{S_1S_2}(t)=1|F_t\right] = \varphi(t)N(t)h + o(h)$ , transiting from the not-immunized to the immunized at time t (2) immunized at time t<br>Pr  $\left[\Delta n_{S_i}\left(t\right)=1\middle|F_t\right]=\mu S_i\left(t\right)h+o\left(h\right)$ , general population mortality among the susceptible at time  $t$  (3)

$$
\Pr\left[\Delta n_{S_{ij}E_{ij}}(t) = 1 | F_t\right] = \sigma_{ij} S_i(t) h + o(h), \text{ with } j \in \{1, 2, 3, 4\} \text{ for exposure to the variants}
$$
\n(4)

 $\Pr\left[\Delta n_{E_{ij}I_{ij}}(t) = 1 | F_{t}\right] = \lambda_{ij}(t) E_{ij}(t) h + o(h),$ , with  $j \in \{1, 2, 3, 4\}$  for different infection severity

levels (5)<br>  $Pr\left[\Delta n_{I_{ij}R_{ij}}(t)=1|F_t\right] = \gamma_{ij}I_{ij}(t)h + o(h)$ , with  $j \in \{1,2\}$  for recovery differentials between the , with  $j \in \{1, 2\}$  for recovery differentials between the immunized and not immunized (6)

 $\Pr\left[\Delta n_{I_{ij}D_{ij}}(t)=1|F_{t}\right]=\omega_{ij}I_{ij}(t)h+o(h)$ , with  $j \in \{1, 2\}$  for COVID-19 mortality differentials between the immunized and not immunized (7)

 $\Pr\left[\Delta n_{R_{ij}S_2}\left(t\right)=1|F_t\right]=\varepsilon_{ij}R_{ij}\left(t\right)h+o\left(h\right)$ , with  $j \in \{1, 2\}$  for the different rates of moving from the recovered to susceptible among the immunized and not immunized groups (8)

Allowing for non-zero probability general population mortality in the compartments, we have: Allowing for non-zero probability generally provide  $\Pr\left[\Delta n_{E_{ij}}(t) = 1 | F_t\right] = \mu E_{ij}(t) h + o(h)$ 

$$
\Pr\left[\Delta n_{E_{ij.}}(t) = 1 | F_t \right] = \mu E_{ij}(t) h + o(h)
$$
\n
$$
\Pr\left[\Delta n_{I_{ij.}}(t) = 1 | F_t \right] = \mu I_{ij}(t) h + o(h)
$$
\n(10)

$$
\Pr\left[\Delta n_{I_{ij.}}(t) = 1 | F_t \right] = \mu I_{ij}(t) h + o(h)
$$
\n
$$
\Pr\left[\Delta n_{R_{ij.}}(t) = 1 | F_t \right] = \mu R_{ij}(t) h + o(h)
$$
\n(11)

 $\Pr[\Delta n_{R_{ij}}(t) = 1 | F_t] = \mu R_{ij}(t) h + o(h)$  (11)<br>With the filtration  $F_t = \{ S_i(u), E_{ij}(u), I_{ij}(u), R_{ij}(u),$  for all  $0 \le u \le t \}$  represents the history of the process up to time *t*. The counting processes governing Figure 1 are represented by the following identities:

$$
\Delta S_{1}(t) = \Delta n_{S_{1}} - \Delta n_{S_{1}S_{2}} - \Delta n_{S_{1}E_{1j}} - \Delta n_{S_{1}}\n\Delta S_{2}(t) = \Delta n_{S_{1}S_{2}} + \Delta n_{R_{1j}S_{2}} + \Delta n_{R_{2j}S_{2}} - \Delta n_{S_{2}E_{2j}} - \Delta n_{S_{2}}\n\Delta E_{1j}(t) = \Delta n_{S_{1}E_{1j}} - \Delta n_{E_{1j}I_{1j}} - \Delta n_{E_{1j}}\n\Delta E_{2j}(t) = \Delta n_{S_{2}E_{2j}} - \Delta n_{E_{2j}I_{2j}} - \Delta n_{E_{2j}}\n\Delta I_{1j}(t) = \Delta n_{E_{1j}I_{1j}} - \Delta n_{I_{1j}D_{1j}} - \Delta n_{I_{1j}} - \Delta n_{I_{1j}R_{1j}}\n\Delta I_{2j}(t) = \Delta n_{E_{2j}I_{2j}} - \Delta n_{I_{2j}D_{2j}} - \Delta n_{I_{2j}} - \Delta n_{I_{2j}R_{2j}}\n\Delta R_{1j}(t) = \Delta n_{I_{1j}R_{1j}} - \Delta n_{R_{1j}} - \Delta n_{R_{1j}S_{2}}\n\Delta R_{2j}(t) = \Delta n_{I_{1j}R_{1j}} - \Delta n_{R_{1j}} - \Delta n_{R_{1j}S_{2}}\n\Delta D_{1j}(t) = \Delta n_{I_{1j}D_{1j}} - \Delta n_{R_{2j}} - \Delta n_{R_{2j}S_{2}}
$$
\n
$$
\Delta D_{2j}(t) = \Delta n_{I_{1j}D_{1j}}
$$
\n
$$
\Delta D_{2j}(t) = \Delta n_{I_{2j}D_{2j}}
$$

By taking expectations on both sides of the set of equations, dividing through by *h*, and taking the limit as  $h \to 0^+$ , substituting the values in the set of probability equations we obtain:

$$
\frac{dS_1(t)}{dt} = (\nu - \varphi) N(t) - \sigma_{1j} S_1(t) - \mu S_1(t)
$$
\n
$$
\frac{dS_2(t)}{dt} = \varphi N(t) + \varepsilon_{1j} R_{1j}(t) + \varepsilon_{2j} R_{2j}(t) - \sigma_{2j} S_2(t) - \mu S_2(t)
$$
\n
$$
\frac{dE_1(t)}{dt} = \sigma_{1j} S_1(t) - \lambda_{1j}(t) E_{1j}(t) - \mu E_{1j}(t)
$$
\n
$$
\frac{dE_2(t)}{dt} = \sigma_{2j} S_2(t) - \lambda_{2j}(t) E_{2j}(t) - \mu E_{2j}(t)
$$
\n
$$
\frac{dI_1(t)}{dt} = \lambda_{1j}(t) E_{1j}(t) - \omega_{1j} I_{1j}(t) - \mu I_{1j}(t) - \gamma_{1j} I_{1j}(t)
$$
\n
$$
\frac{dI_2(t)}{dt} = \lambda_{2j}(t) E_{2j}(t) - \omega_{2j} I_{2j}(t) - \mu I_{2j}(t) - \gamma_{2j} I_{2j}(t)
$$
\n(13)

$$
\frac{dR_1(t)}{dt} = \gamma_{1j}I_{1j}(t) - \mu R_{1j}(t) - \varepsilon_{1j}R_{1j}(t) \n\frac{dR_2(t)}{dt} = \gamma_{2j}I_{2j}(t) - \mu R_{2j}(t) - \varepsilon_{2j}R_{2j}(t) \n\frac{dD_1(t)}{dt} = \omega_{1j}I_{1j}(t) \n\frac{dD_2(t)}{dt} = \omega_{2j}I_{1j}(t)
$$

(c)<br>  $\frac{f(t)}{t} = y_1, l_1, (t) = \mu R_2, (t) - \varepsilon_1 R_1, (t)$ <br>  $\left(\frac{t}{t}\right) = \omega_2, l_2, (t) - \mu R_2, (t) - \varepsilon_2, R_2, (t)$ <br>  $\left(\frac{t}{t}\right) = \omega_2, l_1, (t)$ <br>  $\left(\frac{t}{t}\right) = \omega_2, l_1, (t)$ <br>
Fastivity in the system was accounted for by factoring in Stochasticity in the system was accounted for by factoring in gamma noise. The main challenge while monitoring the compartments *S, E, I, R* and *D,* is that the process is evaluated based on the number of cases recorded/observed. The observed cases represent the "top layer" of the Partially Observed Markov Processes and it is modelled using a count process. Aaron A. King Dao Nguyen, and Edward L. Ionides (2016) model the number of cases, *C(t1, t2)*, recorded within a given reporting interval  $[t_1; t_2)$  using a negative binomial process, <sup>12</sup>

That is

$$
C(t_1, t_2) \sim NegBin\big(\rho \Delta n_{SI}(t_1, t_2), \theta\big) \tag{14}
$$

where  $\Delta n_{\rm SI}(t_1,t_2)$  is the true incidence (the accumulated number of new infections that have *occurred over the [t<sub>1</sub>; t<sub>2</sub>) interval),*  $\rho$  *is the reporting rate, (the probability that an infection is observed and recorded*), *θ* is the negative binomial "size" parameter.

The historical data were applied in the Exposed to the Infected  $(E \rightarrow I)$  and the most appropriate count process for the data will be fitted. Similarly, the methodology was also applied to the number of deaths observed, given that some of the COVID-19 deaths may have been missed out in the records. This implies that we have two levels of output, the observed incidence "top layer" and the "Hidden layer".



**Figure S1:** Reporting rates for the COVID-19 cases and deaths across the countries giving the proportions of the "top layer" to the "Hidden layer" (Source: Model output)

The model's measurement component "top layer" was estimated in relation to the observed data using gradient search methods, deriving a quantity *contact rate* for each of the country. The optimization involved minimizing the difference between the observed data and the top layer of the model estimates that is directly linked to the hidden layer. Country specific contact rates were later explored and found to be dependent on, but not limited to: Population ages 0-14 (% of total), Population ages 15-64 (% of total), Population ages 65 and above (% of total), Total proportion of the population in formal employment, in services, Population living in slums (% of urban population), Proportion of population living in urban areas, Connectivity per sq km, Population density, People using at least basic sanitation services (% of population) all of which accounted for 30.7% ( $R^2 = 0.307$ ) of the variations across the countries.



**Figure S2:** Contact rates across the 47 WHO AFRO countries

The model was sensitive to the number of COVID-19 specific deaths reported as a function of the population according to a power function

$$
y = ax^b \tag{15}
$$

where  $a = 48,064.9$  and  $b = -0.992$ , with y being the weight and x, the population size. Vulnerability index $31$  for each of the countries were also used to modulate the death rates according to the country specific experience. Immunized population was determined by factoring in the vaccinated among the true burden, which was obtained from the community infections. This was done using the following formula:

*Immunized population proportion = vaccinated proportion \*(1 – True burden proportion) + True burden proportion* (16)



#### **SUPPLEMENTARY APPENDIX 4**

**Figure S3:** Proportions of fully vaccination vs immunized population as at Dec 31, 2021

## Regional analysis Tables



Table S4: Estimated burden and deaths per 100,000 populations across the different income groups





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