

Calculating the probability that a previously susceptible individual is infected as a function of time following exposure to SARS-CoV-2

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Supplementary Tables and Methods

This supplementary document provides additional methodological detail and tabulated parameter values used in the Bayesian framework for estimating post-exposure SARS-CoV-2 infection state probabilities. The tables summarize the assumptions underlying the disease-progression model, test-performance characteristics, and probability calculations described in the main manuscript.

Specifically, the supplementary tables document the structure and parameterization of the latent–infectious–recovered disease model following a single, identified exposure event. S.Tables 1–3 present the Gamma-distributed time-in-state parameters and probability splitting assumptions used to model progression through asymptomatic, presymptomatic, mild, and severe disease states for both the original SARS-CoV-2 strain and Omicron variants. These values were derived from prior literature and chosen to reflect plausible ranges reported during different phases of the pandemic.

S.Table 4 specifies the diagnostic test model, giving the assumed probability that a PCR or antigen test is positive conditional on the individual’s true underlying disease state. These values represent literature-informed assumptions about test performance across infection phases and serve as inputs to the Bayesian framework.

S.Table 5 enumerates the possible progression paths through the disease states, including the probability of each path and the conditional probability of occupying each state at time x following exposure. Together, these tables define the complete probability structure used to compute unconditional and conditional infection state probabilities, as well as posterior probabilities of infection given symptoms and testing observations.

S.Table 6 summarizes the observation model, presenting the conditional probabilities of observable clinical and testing outcomes in the absence of symptoms, infection status, and negative test results, given each disease state. The test-related probabilities in S.Table 6 are derived directly from the test-performance parameters defined in S.Table 4 and are organized to support likelihood construction and Bayesian updating.

The supplementary materials are intended to enhance transparency and interpretability of the modeling framework by providing full numerical detail for all parameters used in the analyses. Researchers and policymakers may use these tables to understand the basis of the model implementation results presented in the main text or to adapt the framework to alternative assumptions, viral variants, or diagnostic tests.

S.Table 1: Gamma time-in-state distribution parameters and summary values for the original SARS-CoV-2 strain.

Parameter	Name	Shape	Rate	Mean	Variance	Lower	Upper
U	Sus	1.00	0.001	1000.00	1000000.00	25.32	3688.88
V	Lat	3.47	0.680	5.10	7.50	1.22	11.70
W	Asy	6.53	0.933	7.00	7.50	2.71	13.30
X	Pre	9.00	3.000	3.00	1.00	1.37	5.25

Y	Mld	0.55	0.110	5.00	45.50	0.01	24.06
Z	Svr	2.66	0.242	11.00	45.50	1.97	27.62

S.Table 2: Probability parameter values specifying the path through the course of infection for the original SARS-CoV-2 strain.

Parameter	Name	Value
q	Symptomatic	0.50
r	Severe	0.10

S.Table 3: Gamma time-in-state distribution parameters and summary values for more recent SARS-CoV-2 Omicron variants.

Parameter	Name	Shape	Rate	Mean	Variance	Lower	Upper
U	Sus	1.00	0.001	1000.00	1000000.00	25.32	3688.88
V	Lat	3.47	1.133	3.06	2.70	0.73	7.02
W	Asy	6.53	1.037	6.30	6.08	2.43	11.97
X	Pre	9.00	3.333	2.70	0.81	1.23	4.73
Y	Mld	0.55	0.122	4.50	36.86	0.01	21.66
Z	Svr	2.66	0.269	9.90	36.86	1.78	24.86

S.Table 4: Assumed probabilities of a positive test, given as percentages, by test type and underlying disease states.

State	Parameter	Antigen test	PCR test
Sus	s_S	0.5	0.5
Lat	s_L	0.5	0.5
Asy	s_A	50.0	95.0
Pre	s_P	50.0	95.0
Mld	s_M	70.0	95.0
Svr	s_V	80.0	95.0
RecS	s_{RS}	0.5	95.0
RecA	s_{RA}	0.5	95.0

S.Table 5: The probability, $P(H)$, of following each possible path H of progression through the infection, and the probability of being in each state at time x given the path, $P(S_x|H)$.

	Path H					
	1	2	3	4	5	6
	$P(H)$					
	pqr	$pq(1-r)$	$p(1-q)$	$(1-p)qr$	$(1-p)q(1-r)$	$(1-p)(1-q)$
	$P(S_x H)$					
Sus	0	0	0	$1 - F_U$	$1 - F_U$	$1 - F_U$
Lat	$1 - F_V$	$1 - F_V$	$1 - F_V$	$F_U - F_{UV}$	$F_U - F_{UV}$	$F_U - F_{UV}$
Asy	0	0	$F_V - F_{VW}$	0	0	$F_{UV} - F_{UVW}$
Pre	$F_V - F_{VX}$	$F_V - F_{VX}$	0	$F_{UV} - F_{UVX}$	$F_{UV} - F_{UVX}$	0
Mld	0	$F_{VX} - F_{VXY}$	0	0	$F_{UVX} - F_{UVXY}$	0
Svr	$F_{VX} - F_{VXZ}$	0	0	$F_{UVX} - F_{UVXZ}$	0	0
RecS	F_{VXZ}	F_{VXY}	0	F_{UVXZ}	F_{UVXY}	0
RecA	0	0	F_{VW}	0	0	F_{UVW}

S.Table 6: For each state we give $P(M_x = 0 | S_x)$, the probability of no symptoms up to time x given the state, $P(I_x = 1 | S_x)$, the probability of being infected given the state, $P(T_x = 0 | S_x, \text{Negative test})$, the probability of having a negative test given the state. The values in the final column will depend on the test, antigen or PCR.

S_x	$P(M_x = 0 S_x)$	$P(I_x = 1 S_x)$	$P(T_x = 0 S_x, \text{Negative test})$
Sus	1	0	$1 - s_S$
Lat	1	1	$1 - s_L$
Asy	1	1	$1 - s_A$
Pre	1	1	$1 - s_P$
Mld	0	1	$1 - s_M$
Svr	0	1	$1 - s_V$
RecS	0	0	$1 - s_{RS}$
RecA	1	0	$1 - s_{RA}$