|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Names\*** | **Description** | **Fixed** | **Values** | **Priors** | **Lower**  **bound** | **Upper**  **bound** |
| tshift | Time from infection to initial viral growth | yes | 0 | - | 0 | 3 |
| viral\_peak | Modal Ct Value at peak viral load | no | 19.7359875 | Normal(19.7, 2.00) | 0 | 40 |
| obs\_sd | Initial scale parameter for the Gumbel Distribution until a = t\_eclipse + t\_peak + t\_switch | no | 5 | Normal(5.00, 0.50) | 0 | 25 |
| sd\_mod | Multiplicative factor applied to scale parameter for the Gumbel distribution starting at a = teclipse+tpeak+tswitch+tscale | yes | 0.78 | - | 0 | 1 |
| sd\_mod\_wane | Time from secondary waning phase until Gumbel distribution reaches its minimum scale parameter | yes | 14 | - | 0 | 14 |
| true\_0 | Ct value at time of infection | yes | 40 | - | 40 | 100 |
| intercept | Limit of detection of Ct value | yes | 40 | - | 35 | 100 |
| LOD | Limit of detection of viral load (log10 RNA copies / mL) | yes | 3 | - | 0 | 10 |
| incu | Time from initial viral growth to peak viral load | yes | 5 | - | 0 | 10 |
| t\_switch | Time from peak viral load to secondary waning phase | no | 13.3 | Normal(13.3, 3.00) | 0 | 30 |
| level\_switch | Modal Ct Value at a = t\_eclipse + t\_peak + t\_switch | yes | 38 | - | 0 | 40 |
| wane\_rate2 | Time from infection until modal Ct value is equal to the limit of detection | yes | 1000 | - | 0 | 10000 |
| prob\_detect | Daily probability of detectability loss | no | 0.1032993 | Beta(10.5, 91.2) | 0 | 1 |
| R0 | Basic Reproductive Number | no | 2 | Log-normal(log(2.00), 0.60), and is bounded between Uniform(1.00, 10.0) | 1 | 10 |
| infectious\* | Infectious period | yes | 3 | - | 0 | 25 |
| incubation\* | Incubation period | yes | 4 | - | 0 | 25 |
| t0\* | Effective seed time | yes | 1 | - | 0 | 100 |
| I0\* | Proportion infected at seed time | no | 0.0001 | Normal (0.0001,0.01) | 0 | 0.01 |

\*These parameters were modified compared to previously-published work (3) for the current study to account for Omicron variant kinetics as described in the Methods.

SEIR: susceptible-exposed-infected-recovered