

BOX. Model parameters and assumptions for branching process model of Ebola disease outbreak caused by Bundibugyo virus, 2026

Parameter	Prior assumptions	Notes
Mean of negative binomial offspring distribution	Log-normal distribution with median 2.87 and interquartile range 2.60–3.16.	The negative binomial offspring distribution generates the number of secondary infections per infection. However, in this model, transmission events scheduled to occur after recovery do not happen. Consequently, the basic reproduction number R_0 depends not only on the offspring distribution but also on values for the case fatality rate, the recovery delay, and the generation interval distribution. For the mean prior values of these parameters (see below), R_0 is approximately 87% of the value of the mean of the negative binomial offspring distribution (i.e., 2.87 corresponds to R_0 of 2.5). Published estimates of R_0 for Ebola vary widely. Publications that inform this prior include Van Kerkhove et al. 2015 and Rosello et al. 2015.*, [†]
Concentration, k	Uniform from 0.02 to 2.20	Parameter that defines variability in the number of secondary infections per infection, i.e., a measure of “superspreading”. This range is from Nash et al. 2024 [§] , who note that it corresponds to “30–90% of transmission being attributed to the most infectious 20% of persons”; it is not specific to BVD.
Generation interval offset	Uniform from 5.7 days to 11.3 days	Time from infection to start of any infection potential (i.e., the latent period, which is assumed to also be the incubation period); this value is constant within each simulated outbreak but varies across simulations. Distribution is based on the range of central estimates for the incubation period of BVD as reviewed by Nash et al. 2024. [§]
Generation interval shape	2	Fixed value that controls the shape of the Weibull-distributed generation intervals.

Generation interval scale	Uniform from 5.40 to 10.07	Values of scale parameter for Weibull distribution. Meta-analysis of Nash et al. 2024 [§] reports a 95% CI for the mean serial interval for Ebola disease (not BVD specifically) of 13.29 to 17.42 days. The bounds of this distribution yield offset Weibull distributions with means that correspond to that range, assuming an 8.5 day offset / latent period.
Recovery delay	Uniform from 9.9 days to 10 days	Time between symptom onset and recovery; this value is constant within each simulated outbreak but varies across simulations. This distribution is based on the range of central estimates for the time from symptom onset to recovery/non-infectiousness of BVD as reviewed by Nash et al. 2024. [§]
Mortality delay	Uniform from 9 days to 11.4 days	Time between symptom onset and death; this value is constant within each simulated outbreak but varies across simulations. The distribution is based on the range of central estimates for the time from symptom onset to death of BVD as reviewed by Nash et al. 2024. [§]
Case fatality ratio	Beta distribution with alpha = 13.2 and beta = 26.8	Probability that an infected person dies. This parameterization corresponds to the observed CFRs for the 2007 and 2012 BVD outbreaks (32% and 34%, respectively). ^{¶**} This distribution corresponds to 95% certainty that the CFR is between 19.5% and 48.1%.
Isolation probability	20%, 50%, 70%, 95%	Probability that an infection is identified once symptomatic.
Isolation lag	2 days	Mean of exponentially distributed time lag between symptom onset and entering isolation.
Isolation effectiveness	100%	Reduction in infectiousness once an infectious person is in isolation.

Abbreviations: BVD = Bundibugyo virus disease; CFR = case fatality rate; R_0 = basic reproduction number, a measure of the contagiousness of an infectious disease, representing the number of persons to whom a single infected person will transmit the disease, assuming a nonimmune population.

* Van Kerkhove MD, Bento AI, Mills HL, Ferguson NM, Donnelly CA. A review of epidemiological parameters from Ebola outbreaks to inform early public health decision-making. *Sci Data* 2015;2:150019. doi: 10.1038/sdata.2015.19. PMID: 26029377.

† Rosello A, Mossoko M, Flasche S, et al. Ebola virus disease in the Democratic Republic of the Congo, 1976-2014. *Elife* 201;4:e09015. doi: 10.7554/eLife.09015. PMID: 26525597

§ Nash RK, Bhatia S, Morgenstern C, et al.; Pathogen Epidemiology Review Group; Imai-Eaton N, Cori A, Unwin HJT. Ebola virus disease mathematical models and epidemiological parameters: a systematic review. *Lancet Infect Dis* 2024;24:e762–73. doi: 10.1016/S1473-3099(24)00374-8. Epub 2024 Aug 7. PMID: 39127058; PMCID: PMC7616620.

¶ Albariño CG, Shoemaker T, Khristova ML, et al. Genomic analysis of filoviruses associated with four viral hemorrhagic fever outbreaks in Uganda and the Democratic Republic of the Congo in 2012. *Virology* 201;442:97–100. doi: 10.1016/j.virol.2013.04.014. PMID: 23711383.

** MacNeil A, Farnon EC, Wamala J, et al. Proportion of deaths and clinical features in Bundibugyo Ebola virus. infection, Uganda. *Emerg Infect Dis* 2010;16:1969–72. doi: 10.3201/eid1612.100627. PMID: 21122234.