# Detailed Parameters of the Branching Process Model

## k values

The k-value in the negative binomial offspring distribution represents the variation in infectiousness from individual to individual.[1] Generally, epidemiological information about a particular outbreak or epidemic, including the detailed transmission chain, is required to accurately estimate k. This information is not always available, and unfortunately, estimates of k using limited information typically lead to overestimations of k, making some published estimates unreliable.[2]

Computing k for influenza presents a particular challenge because outbreaks spread rapidly, and some persons may be contagious prior to symptoms, which results in an uncertain transmission chain and prevents epidemiological estimation in most circumstances. For this work, subject matter expert advice led to a consensus estimate range of k of 0.5-2.0, which we used in the branching process model simulations for influenza. This estimate was supported by one published source that used detailed historical records to compute an estimate of k for 1918 flu of 0.93 (95% CI 0.59-1.72).[3]

For coronaviruses, however, the lower transmissibility and longer generation time makes detailed transmission chains more frequently available, which lead to easier estimation. One study computed a range of k values of 0.006-0.17, with a minimum 90% CI limit of .002 and a maximum of 0.80 across all estimates, for the series of SARS outbreaks in 2005.[4] For MERS, one source performed a meta-analysis of several outbreaks and arrived at estimates of 0.26-2.94.[5] In support of these data, we created negative binomial offspring distributions based on two other reports of MERS outbreaks and the transmission chains therein, to arrive at estimates of k 0.66 (90% CI 0-1.35)[6] and 0.08 (90% CI 0.052-0.11).[7] Most estimates of k for each coronavirus were within the range 0.1-0.5 and this was used as the range in the model simulations. This range was also verified as reasonable by subject matter experts.

Finally, because the form of an outbreak is more sensitive to k when k has a low value (i.e. variation between individuals is high), more detailed sampling of the low k values representing coronaviruses was done compared to the higher ones used for influenza.

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[1] Lloyd-Smith JO *et al* (2005) Superspreading and the effect of individual variation on disease emergence. *Nature* 438**:** 355-359

[2] Lloyd-Smith JO (2007) Maximum likelihood estimation of the negative binomial dispersion parameter for highly overdispersed data, with applications to infectious diseases. *PloS one* 2**:** e180

[3] Fraser C *et al* (2011) Influenza transmission in households during the 1918 pandemic. *American journal of epidemiology* 174**:** 505-514

[4] Lloyd-Smith JO *et al* (2005) Superspreading and the effect of individual variation on disease emergence. *Nature* 438**:** 355-359

[5] Kucharski AJ, Althaus CL (2015) The role of superspreading in Middle East respiratory syndrome coronavirus (MERS-CoV) transmission. *Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin* 20**:** 14-18

[6] Al-Tawfiq JA *et al* (2013) Middle East respiratory syndrome novel corona MERS-CoV infection. Epidemiology and outcome update. *Saudi medical journal* 34**:** 991-994

[7] Lee SS, Wong NS (2015) Probable transmission chains of Middle East respiratory syndrome coronavirus and the multiple generations of secondary infection in South Korea. *International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases* 38**:** 65-67

## Control Measure Parameters

As mentioned in the main report, no data are available to quantify the strength of control measures in the wake of an outbreak, both in the extent to which people may reduce their contacts, and in the extent to which a public health campaign may be able to quarantine suspected or infected individuals. In addition, conversations with public health officials revealed deep uncertainties as to the timing of community control measures in the wake of an outbreak. These officials stated the rapidity of the response would depend highly on the rapidity with which the outbreak were identified as novel. However, identification of a novel outbreak may be affected by chance events, such as the degree to which a clinician is curious and orders a non-standard level of diagnostic tested on an individual, or whether infected individuals first a university-associated medical center, which typically have extensive diagnostic capacity, or a local clinic, which often have more limited capacity.

Because no data existed to either quantify the strength of control or the timing of the activation of control, these features were explored parametrically in the branching process model, using ranges believed to cover the full range of reasonable real-world scenarios.

A summary of all parameters used in the model are below. Every combination of possible parameters was simulated exhaustively.

**Table S1. Summary of All Parameter Values Used in Branching Process Model Simulations**

| **Parameter Name** | **Range of Values Used** |
|---|---|
| $R_0$ values | Influenza & MERS-CoV: [0.1:0.1:2.5]*<br>SARS: [0.1:0.1:2.5 3.0 3.5 4.0]* |
| k values | [0.05:0.1:0.5 1 1.5 2] |
| Infection Generations That Control Measures Became Active | [0:3 5 10] |
| Control Strengths | [0 0.1 0.25 0.5] |
| Number of Simulations per Parameter Set | 500 |

* Ranges are given in MATLAB notation, where x:y:z indicates all values from x to z in increments of y, inclusive of x and z. For example, [1:0.5:3 3.5] would expand to the set [1 1.5 2 2.5 3 3.5]