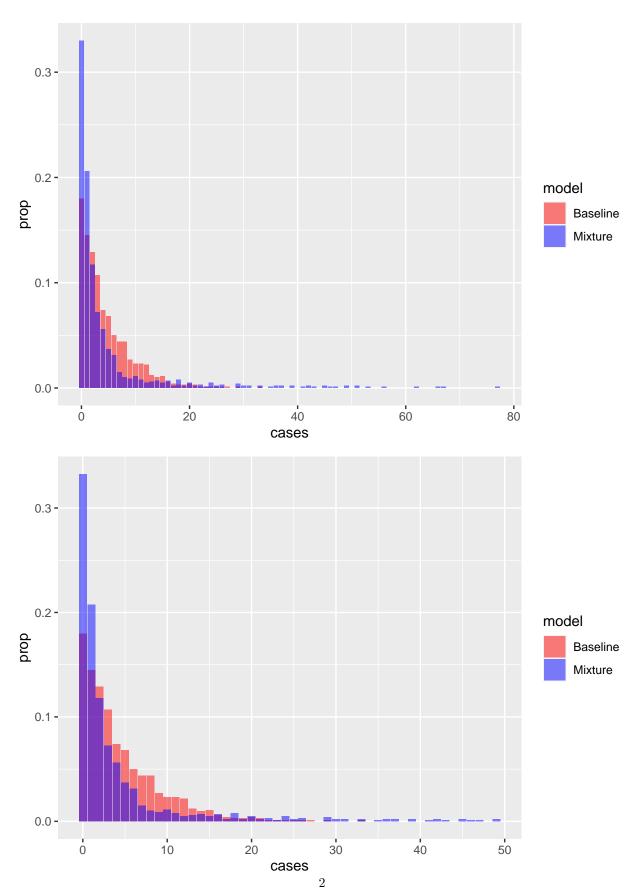
Superspreading geometric mixture branching process

Offspring Distribution



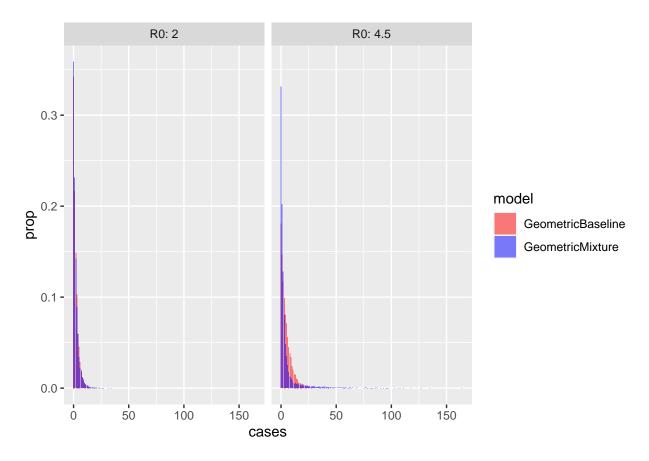


Figure. The case distribution generated by a geometric mixture compared with baseline geometric distributions with the same R_0 . The geometric mixture offspring distribution with p=0.8, $R_0^D=1.5$ and $R_0^A=4$ (mean $R_0=2$) and the geometric mixture offspring distribution with p=0.8, $R_0^D=1.5$ and $R_0^A=16.5$ (mean $R_0=4.5$) are both right skewed. The case distribution generated by the respective baseline geometric offspring distributions are right skewed but have shorter tails. To generate the barplots, we used 10,000 realizations of each offspring distribution. Purple indicates overlap of the baseline and mixture distributions.

Probability at least one becomes infected

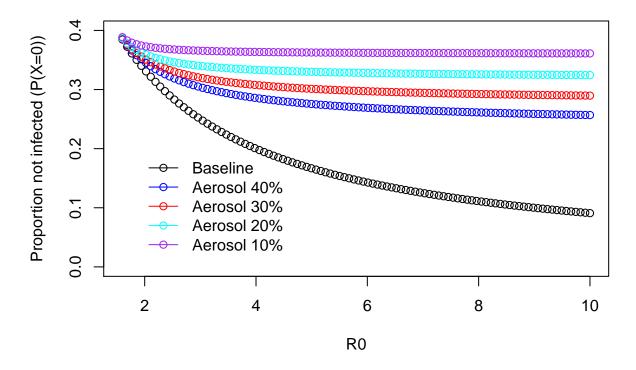


Figure. For each value of R_0 , the mixture models predict that a higher proportion of individuals remain uninfected than the baseline Poisson model, and the proportion decreases with increasing aerosol transmission. Geometric mixture models saturate more slowly than corresponding Poisson models.

Probability of major epidemic

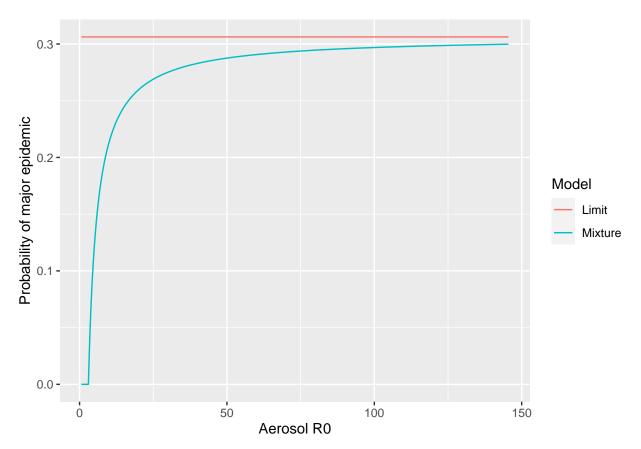
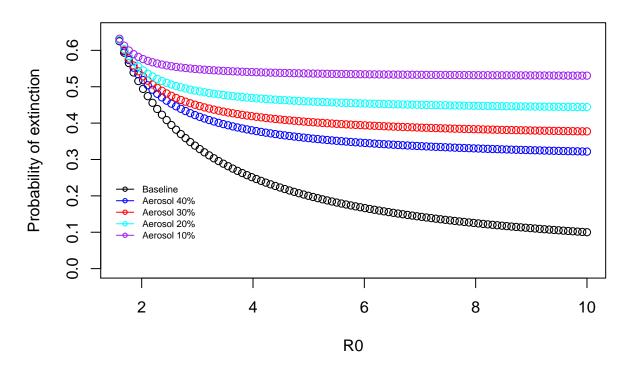


Figure. Approaches the limit of the solution of $z = p/(1 + R_0^D(1-z))$ much more slowly relative to Poisson epidemic (the equation has two solutions; one lies between 0 and 1).

Probability of extinction of a minor outbreak



First generation to 50 cases

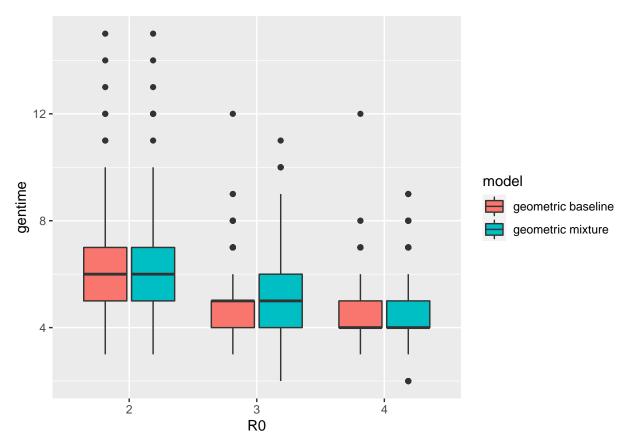


Figure. More variability in geometric epidemics than Poisson epidemics. When $R_0 = 4$ about 21% of epidemics have generation times between 2 and 3 (i.e. are explosive) and about 8% have generation times greater or equal than 7 (i.e are relatively slow).

```
##
##
                                    9
##
        92 160 131
                     57
                          33
                                    3
##
      Min. 1st Qu.
                     Median
                                 Mean 3rd Qu.
                                                  Max.
##
      2.00
               4.00
                        4.00
                                 4.63
                                         5.00
                                                  9.00
##
##
       2
              3
                     4
                           5
                                  6
                                        7
                                               8
## 0.016 0.184 0.320 0.262 0.114 0.066 0.032 0.006
## [1] NA
```

Cluster size distribution conditioned on extinction

Need to have cluster sizes greater than 10 to capture the theoretical prediction $1/(1-R_0^*)$ for the mean chain size:

[1] 2.116855

[1] 56212 1

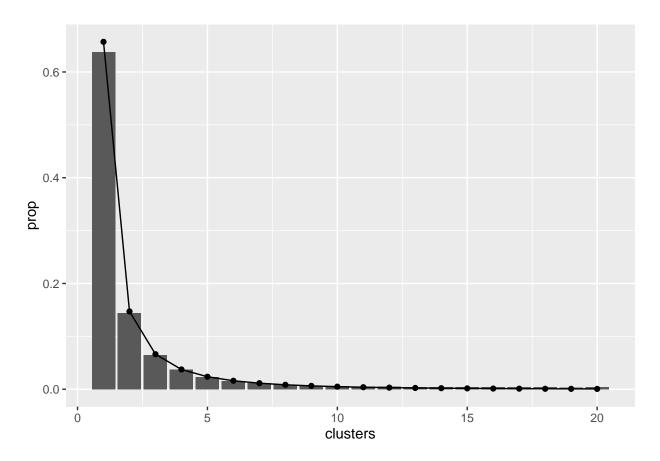


Figure. Geometric mixture cluster size distribution obtained from simulation (gray bars) compared to the theoretical prediction (points). We generated 100000 simulations of a geometric mixture branching process with p=0.8, $R_0^D=1.5$ and $R_0^A=4$, retaining those that went extinct within 6 generations (n=56150). Points are the theoretical predictions for the probability of observing a cluster of size $y=1,2,\ldots,10$ generated using equations (??) and (??) conditioned on the probability of extinction, $z_{\infty}=0.548$.

The theoretical cluster size distribution is given by:

```
##
       n
                    p
## 1
       1 0.6569835991 0.65698360
## 2
       2 0.1471643262 0.29432865
       3 0.0662659937 0.19879798
##
##
  4
       4 0.0373915120 0.14956605
##
       5 0.0236645027 0.11832251
##
       6 0.0160612820 0.09636769
##
       7 0.0114270357 0.07998925
##
  8
       8 0.0084107567 0.06728605
       9 0.0063514257 0.05716283
## 10 10 0.0048934259 0.04893426
## 11 11 0.0038313214 0.04214454
## 12 12 0.0030396670 0.03647600
## 13 13 0.0024383832 0.03169898
```

```
## 14 14 0.0019744582 0.02764242
## 15 15 0.0016117202 0.02417580
## 16 16 0.0013248488 0.02119758
## 17 17 0.0010957276 0.01862737
## 18 18 0.0009111476 0.01640066
## 19 19 0.0007613181 0.01446504
## 20 20 0.0006388760 0.01277752
```

Use the theoretical distribution to calculate the mean chain size, the sum of the n*p column (mean = $\sum_i y_i P(Y = y_i)$). Note that the sum of the probabilities is close to 1, but less than one, so the calculation yields an underestimate of the mean:

```
## n p n * p
## 210.000000 0.9962413 2.0133448
```