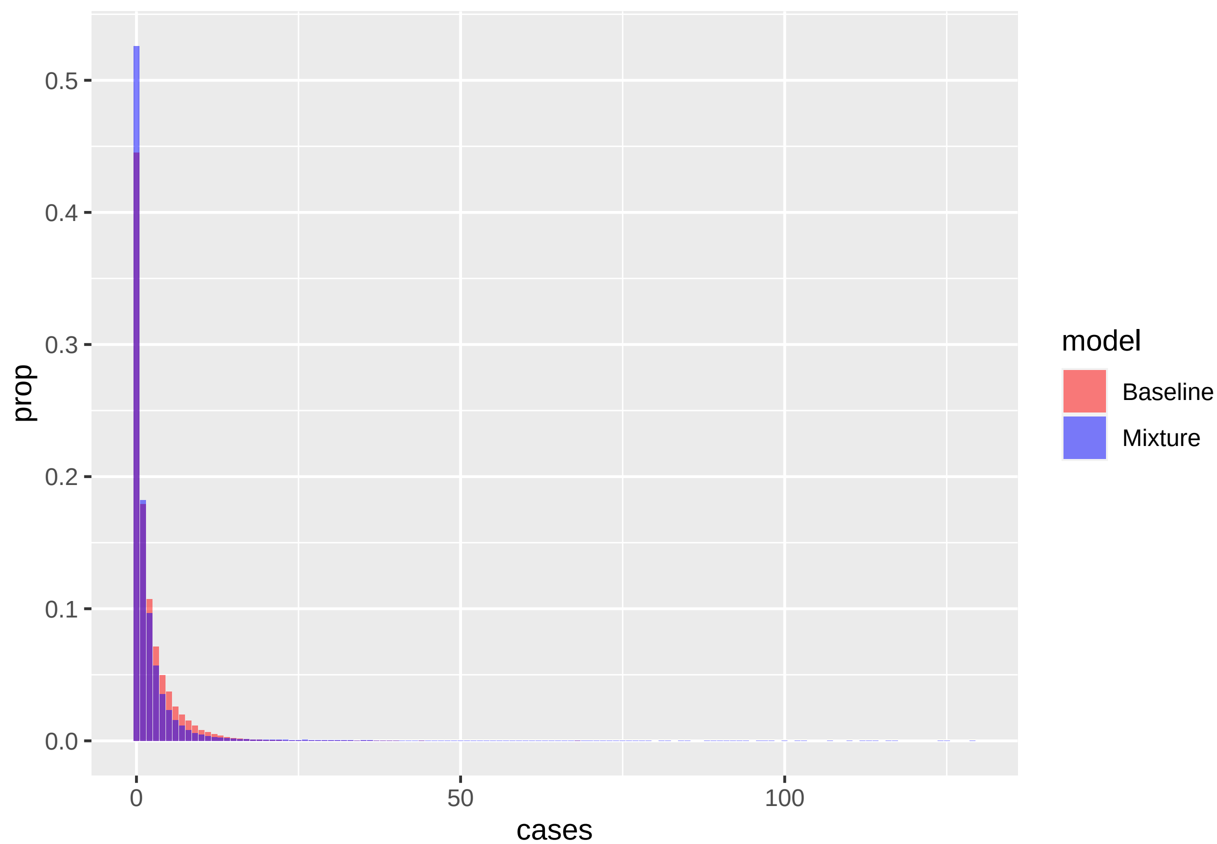
Superspreading negative binomial simulations




```
##      cases     n
## 1        0 52595
## 2        1 18207
## 3        2  9657
## 4        3  5680
## 5        4  3531
## 6        5  2317
## 7        6  1554
## 8        7  1139
## 9        8   800
## 10       9   599
## 11      10   457
## 12      11   376
## 13      12   301
## 14      13   246
## 15      14   211
## 16      15   170
```

```
## 17       16   143
## 18       17   142
## 19       18   112
## 20       19   112
## 21       20    96
## 22       21   112
## 23       22    88
## 24       23    82
## 25       24    71
## 26       25    65
## 27       26    84
## 28       27    69
## 29       28    63
## 30       29    52
## 31       30    47
## 32       31    54
## 33       32    46
## 34       33    44
## 35       34    34
## 36       35    38
## 37       36    40
## 38       37    29
## 39       38    34
## 40       39    30
## 41       40    34
## 42       41    19
## 43       42    27
## 44       43    26
## 45       44    22
## 46       45    18
## 47       46    15
## 48       47    23
## 49       48    13
## 50       49    20
## 51       50     7
## 52       51    16
## 53       52    11
## 54       53    14
## 55       54    10
## 56       55     9
## 57       56    10
## 58       57     8
## 59       58     9
## 60       59     9
## 61       60     9
## 62       61     7
## 63       62     3
## 64       63     6
## 65       64     6
## 66       65    11
## 67       66     6
## 68       67     2
## 69       68     3
## 70       69     4
```

```
## 71      70      5
## 72      71      6
## 73      72      5
## 74      73      6
## 75      74      9
## 76      75      2
## 77      76      5
## 78      77      6
## 79      78      4
## 80      79      3
## 81      81      4
## 82      82      4
## 83      84      4
## 84      85      2
## 85      88      1
## 86      89      2
## 87      90      1
## 88      91      1
## 89      92      2
## 90      93      1
## 91      94      1
## 92      96      2
## 93      97      2
## 94      98      1
## 95     100      1
## 96     102      1
## 97     103      1
## 98     107      2
## 99     110      2
## 100    112      1
## 101    113      2
## 102    114      1
## 103    116      1
## 104    117      1
## 105    124      2
## 106    125      1
## 107    129      1
```

If p is small but δ is large, then the range of cases is large.

Now we wish to plot typical chains.

First lets look at the mean size of small (clusters < 10) and large clusters (>10). The median clusters are typically bigger in the standard model than the mixture model but the mean is smaller, and mean chain sizes conditioned on extinction are similar in both models. If chopping the chain should condition on extinction/non-extinction?

```
## [1]  7681.927    10.000 88920.000
```

```
## [1] 2773
```

```
## [1] 1.762483
```

```
## [1]  4725.168    10.000 29088.000
```

```
## [1] 3077.5
```

```
## [1] 1.641694
```

```
## [1] 47.10569
```

```
## [1] 22
```

```
## [1] 1.928164
```

```
## [1] 19.5098
```

```
## [1] 16
```

```
## [1] 1.565859
```

```
##       [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
##  [1,]    1    1    1    1    1    1    1    1    1     1
##  [2,]    9    0    0    0    0    0    1    0    3     2
##  [3,]    3    0    0    0    0    0    0    0    2     2
##  [4,]    4    0    0    0    0    0    0    0    0     0
##  [5,]    3    0    0    0    0    0    0    0    0     0
##  [6,]    0    0    0    0    0    0    0    0    0     0
##  [7,]    0    0    0    0    0    0    0    0    0     0
##  [8,]    0    0    0    0    0    0    0    0    0     0
##  [9,]    0    0    0    0    0    0    0    0    0     0
## [10,]    0    0    0    0    0    0    0    0    0     0
## [11,]    0    0    0    0    0    0    0    0    0     0
```

Probability of a major outbreak for mixture model is about 0.1.

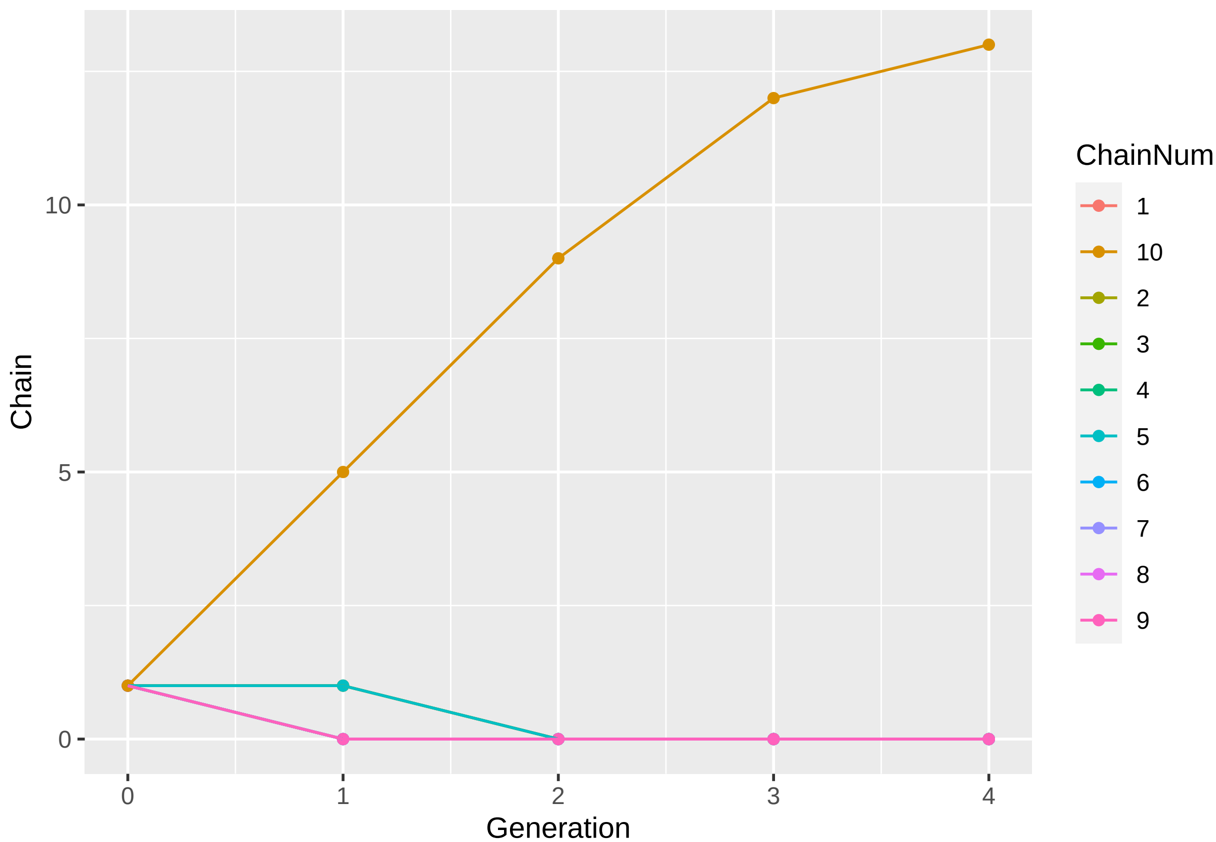
```
##       [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
##  [1,]    1    1    1    1    1    1    1    1    1     1
##  [2,]    1    1    0    0    1    0    0    0    0     5
##  [3,]    0    0    0    0    0    0    0    0    0     9
##  [4,]    0    0    0    0    0    0    0    0    0    12
##  [5,]    0    0    0    0    0    0    0    0    0    13
##  [6,]    0    0    0    0    0    0    0    0    0     6
##  [7,]    0    0    0    0    0    0    0    0    0     7
##  [8,]    0    0    0    0    0    0    0    0    0     2
##  [9,]    0    0    0    0    0    0    0    0    0     5
## [10,]    0    0    0    0    0    0    0    0    0     5
## [11,]    0    0    0    0    0    0    0    0    0     8
```

Probability of a major outbreak for standard model is about 0.4. Here four have taken off, but none are as large as the mixture that has taken off?

```
##       [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
##  [1,]    1    1    1    1    1    1    1    1    1     1
##  [2,]    0    1    0   10    3    2    2    5    0     5
##  [3,]    0    5    0   16    2    0    2    1    0    18
```

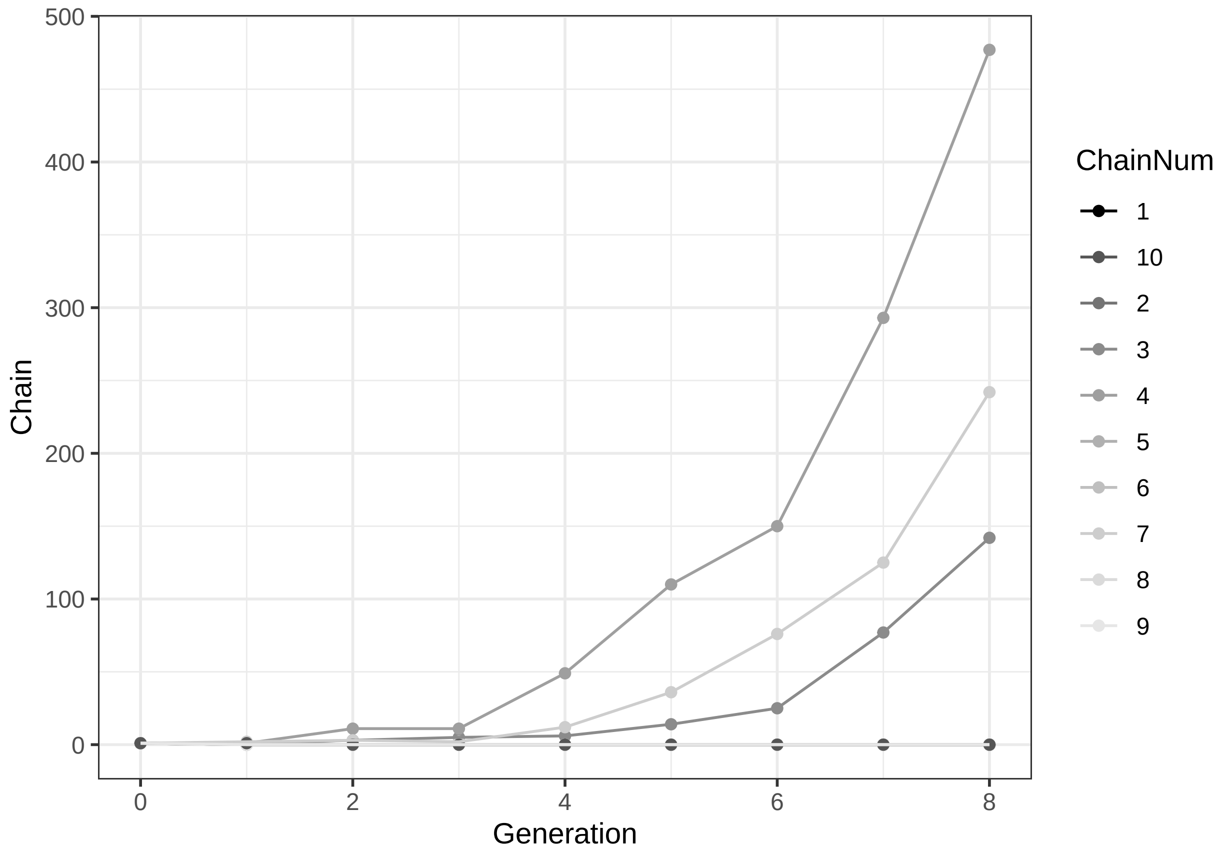
```
##  [4,]    0    5    0   21    6    0   13    1    0    47
##  [5,]    0   13    0   39    6    0   27   11    0   125
##  [6,]    0    5    0  102   13    0   41   20    0   233
##  [7,]    0   14    0  207   39    0   82   33    0   484
##  [8,]    0   14    0  349   64    0  153   90    0   895
##  [9,]    0   24    0  645   91    0  270  205    0  1652
## [10,]    0   48    0 1209  229    0  524  344    0  3369
## [11,]    0  135    0 2280  447    0 1061  666    0  7014
```

Plot the mixture chains assuming $k=1/2:

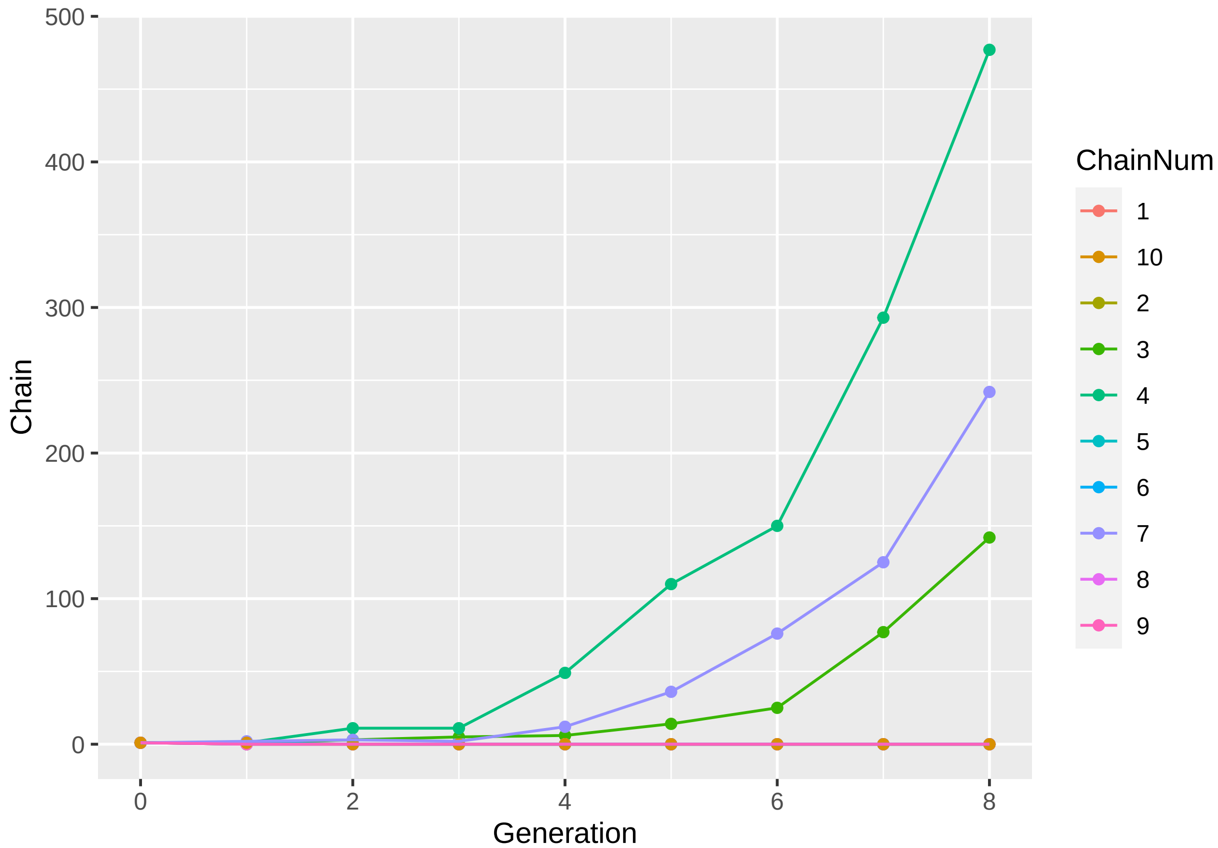



```
##       [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
##  [1,]    1    1    1    1    1    1    1    1    1     1
##  [2,]    0    0    1    1    1    0    2    0    0     1
##  [3,]    0    0    3   11    0    0    3    0    0     0
##  [4,]    0    0    5   11    0    0    2    0    0     0
##  [5,]    0    0    6   49    0    0   12    0    0     0
##  [6,]    0    0   14  110    0    0   36    0    0     0
##  [7,]    0    0   25  150    0    0   76    0    0     0
##  [8,]    0    0   77  293    0    0  125    0    0     0
##  [9,]    0    0  142  477    0    0  242    0    0     0
## [10,]    0    0  218 1015    0    0  457    0    0     0
## [11,]    0    0  494 2105    0    0  809    0    0     0
```

Plot the mixture chains assuming $k=2:

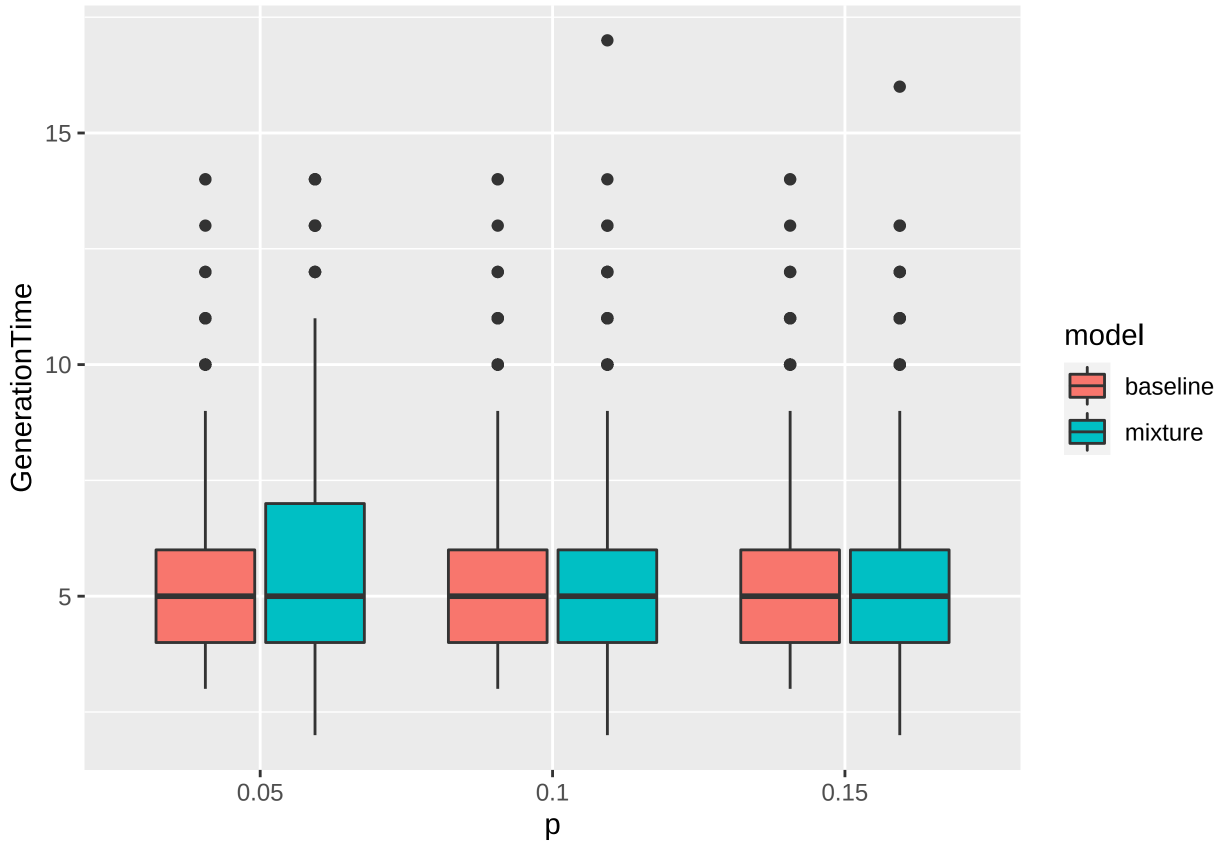


500
400
300
200
100
0
Chain
0
2
4
6
8
Generation
ChainNum
1
10
2
3
4
5
6
7
8
9



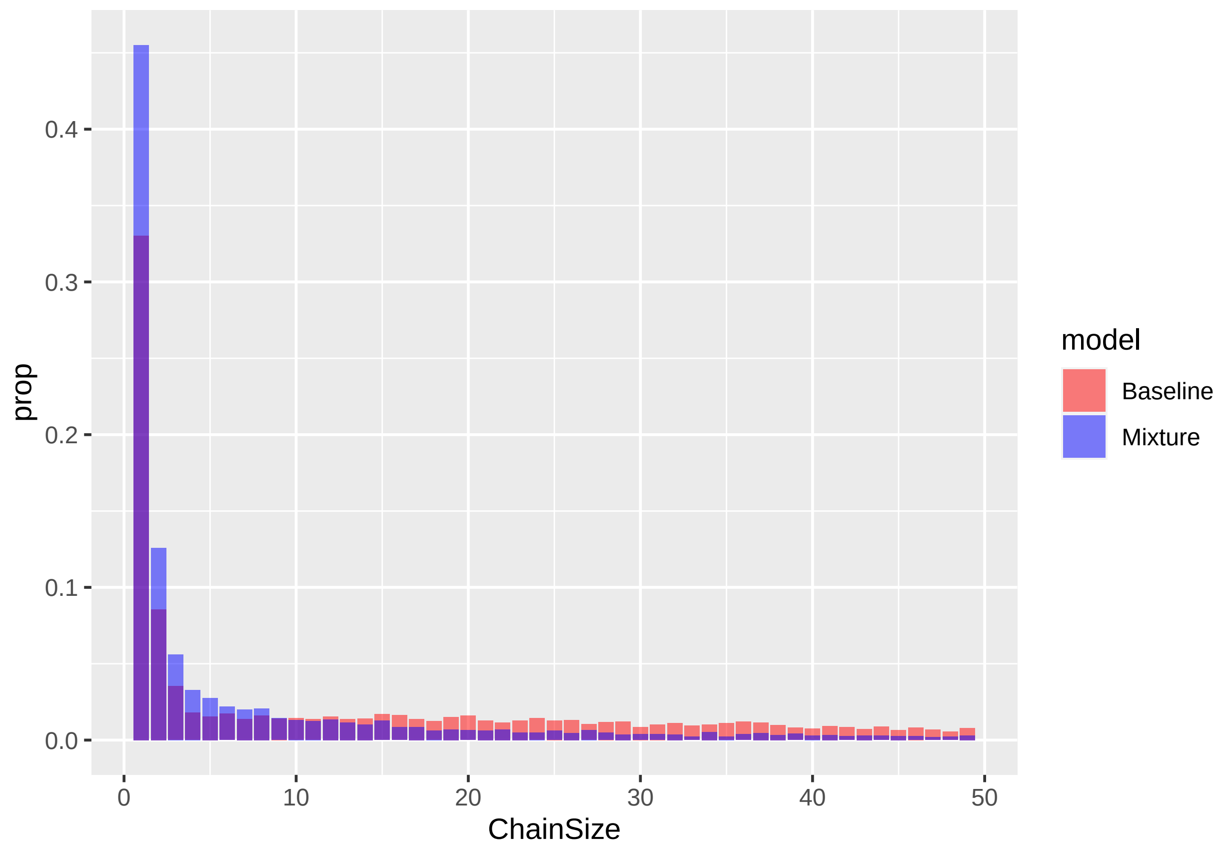

```
##        [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
##   [1,]    1    1    1    1    1    1    1    1    1     1
##   [2,]    1    1    1    2    6    1    3    5    1     2
##   [3,]    1    6    4    4   17    1    4    7    1     2
##   [4,]    0   12    7    5   44    1    3   14   11     1
##   [5,]    0   37   22   14  100    0    1   33   20     1
##   [6,]    0   56   42   28  211    0    2   86   41     4
##   [7,]    0   95   97   48  420    0    0  180   89    12
##   [8,]    0  203  210   92  842    0    0  348  183    24
##   [9,]    0  436  421  208 1616    0    0  677  388    47
##  [10,]    0  843  898  444 3197    0    0 1390  846    81
##  [11,]    0 1765 1884  902 6299    0    0 2730 1856   177
```

Median generation time same for all mixtures. Generation time has most variability for p=0.05, with 25% taking 11 generations or more to take off. 25% take 3 generations or less (most explosive for p =0.05, 0.1). 75% take 9 generations or less if p=0.1 (most explosive?)

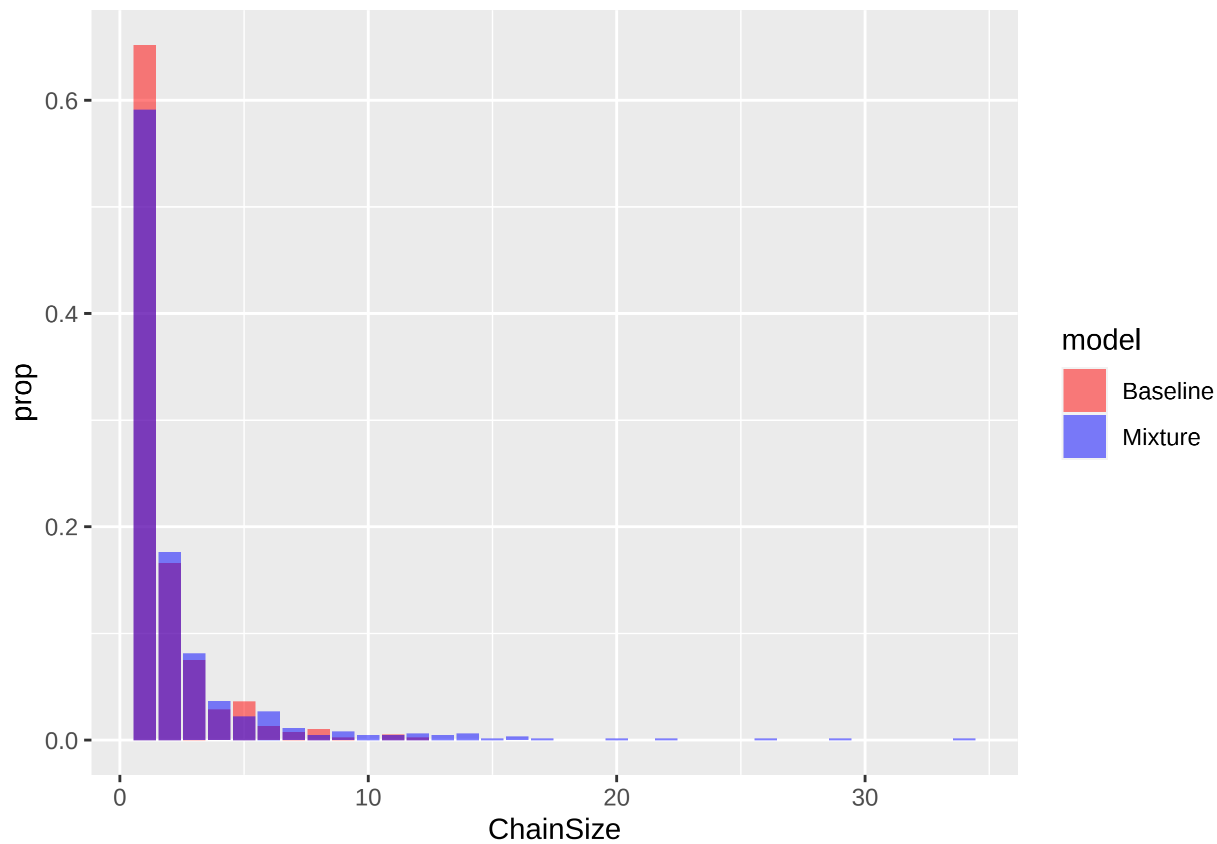


Corresponding chain size distributions

$k = 2$, 4 generations (snapshot in time), plot only chains with size < 50:



Include only chains that have gone extinct after 10 generations:




```
## [1] 0.629
```

```
## [1] 0.385
```

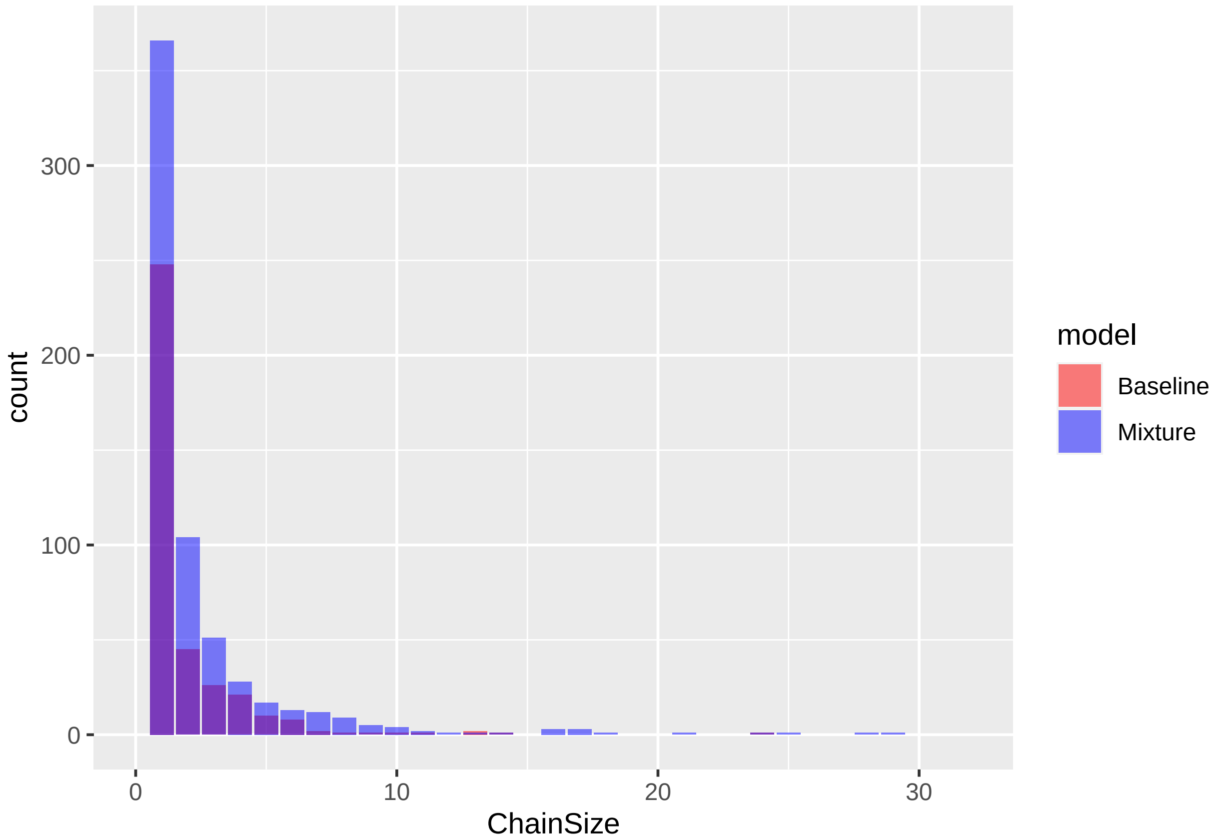
```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   1.000   2.432   2.000  34.000
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   1.000   1.000   1.000   1.834   2.000  12.000
```

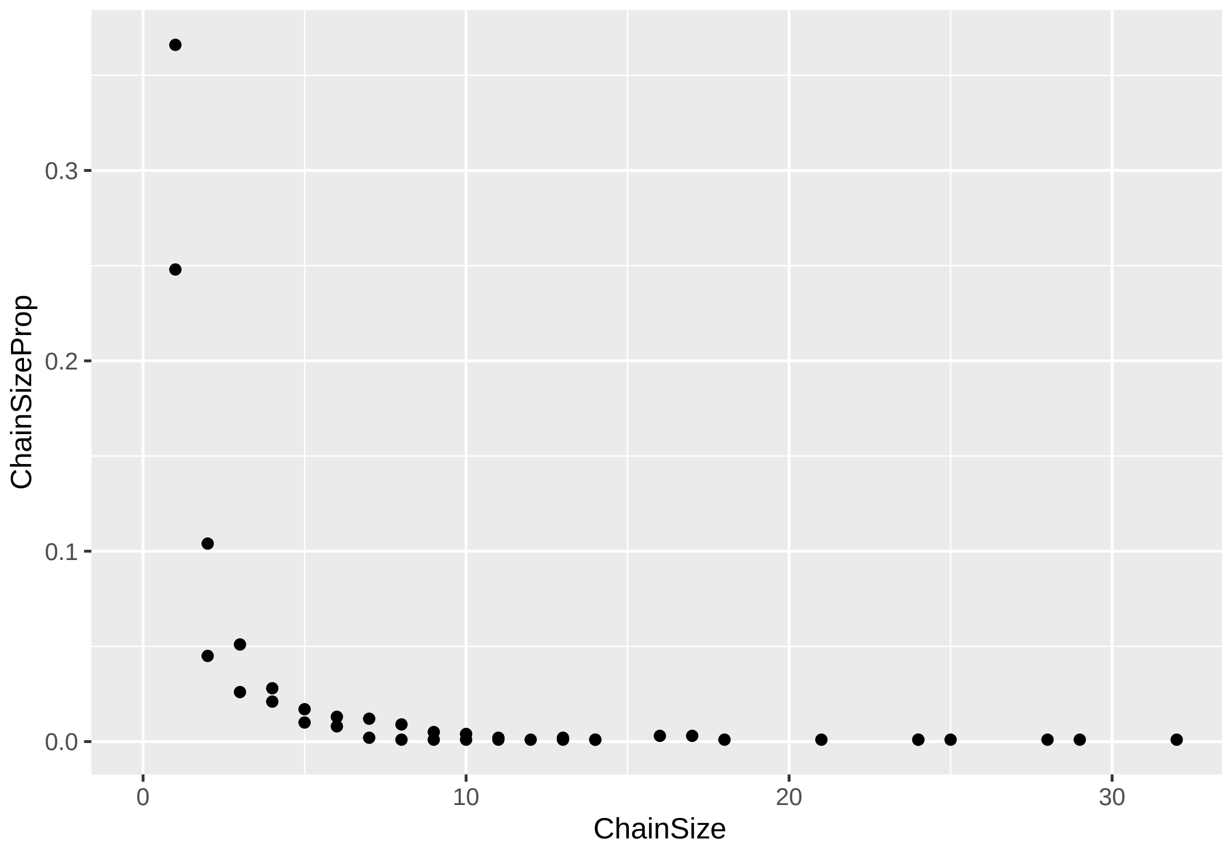
The mixture chain size distribution is longer tailed than the baseline. The mixture chain size distribution contains many more chains that go extinct (minor outbreaks) than the baseline. The plot above conditions upon the probability of extinction, i.e. we see $P(Z = 1)/z_\infty$, not $P(Z = 1)$, e.g. for the standard model this is

```
## [1] 0.6545041
```

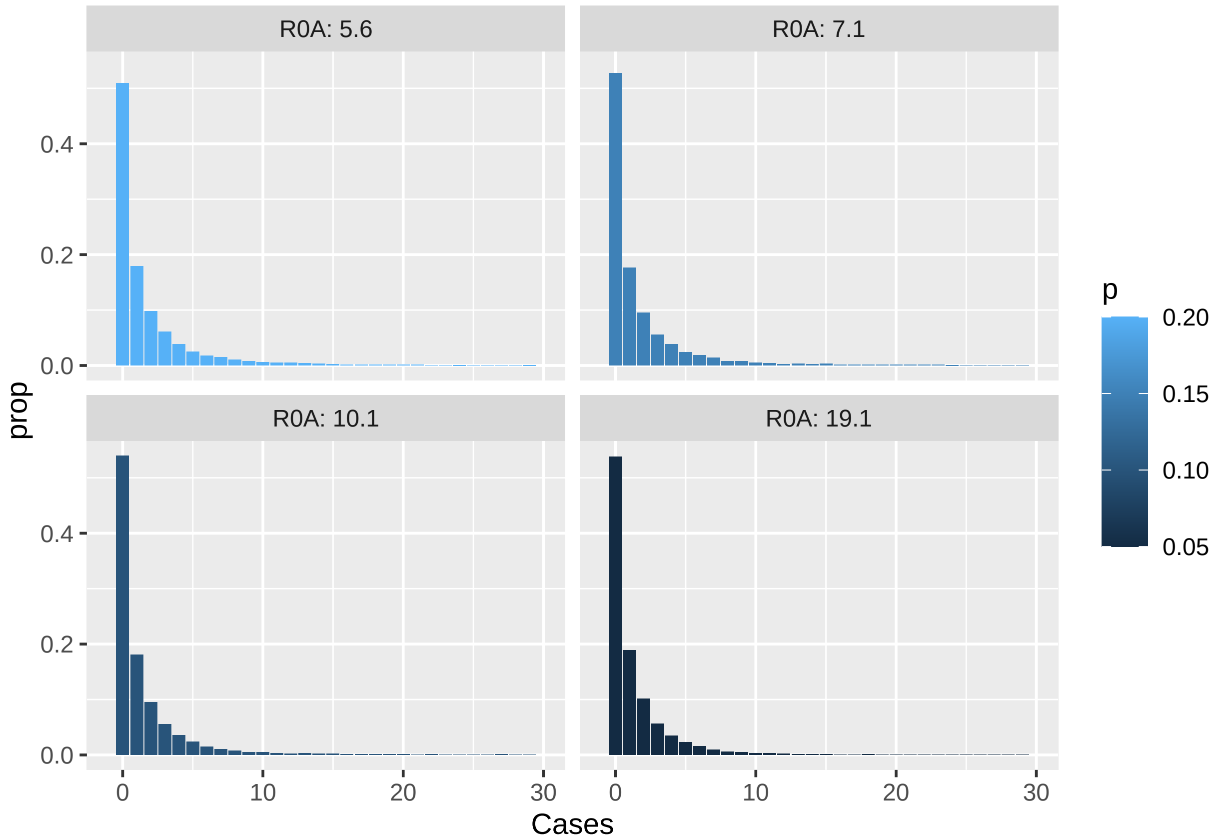
Plot that is not conditional upon extinction with largest chain size equal to the max of the chains that go ex-


300
200
100
0
count
0
10
20
30
ChainSize
model
Baseline
Mixture

tinct:



ChainSizeProp
0.3
0.2
0.1
0.0
0
10
20
30
ChainSize

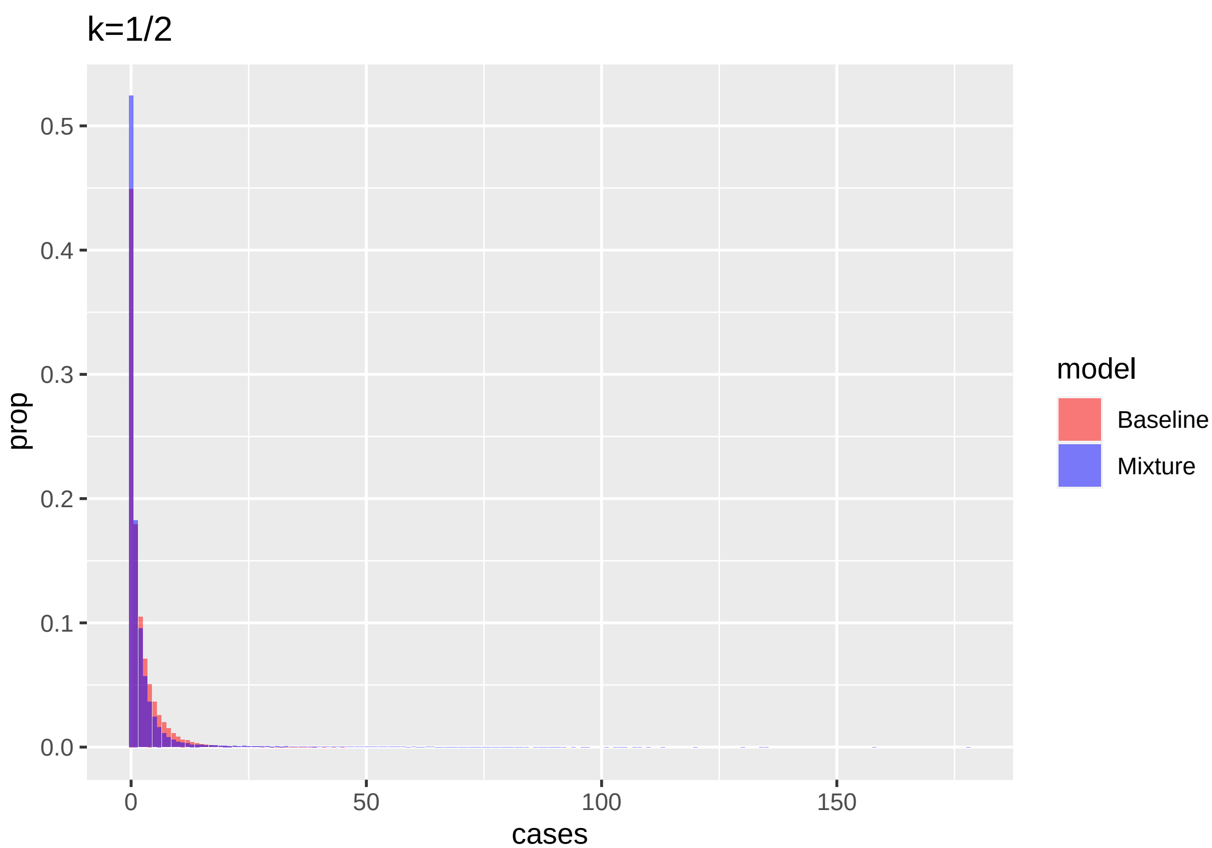



```
##    Cases    n
## 1      0 5316
## 2      1 1867
## 3      2 1000
## 4      3  561
## 5      4  342
## 6      5  227
## 7      6  152
## 8      7   98
## 9      8   61
## 10     9   49
## 11    10   35
## 12    11   28
## 13    12   18
## 14    13   16
## 15    14   14
## 16    15   11
## 17    16    4
## 18    17    8
## 19    18    9
## 20    19    7
## 21    20    3
## 22    21    4
## 23    22    8
## 24    23    4
## 25    24    5
```

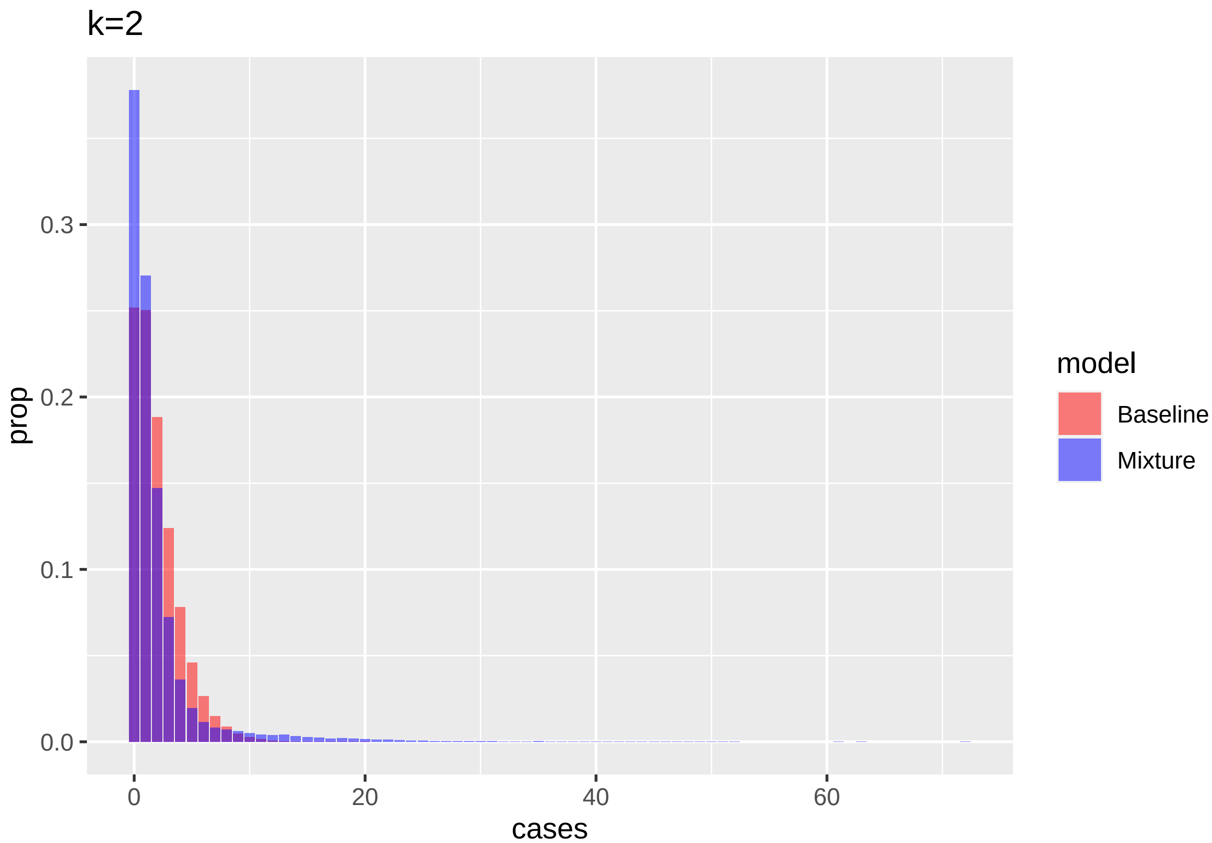
```
## 26     25     4
## 27     26     3
## 28     27     5
## 29     28     4
## 30     29     3
## 31     30     6
## 32     31     5
## 33     32     4
## 34     33     3
## 35     34     5
## 36     35     5
## 37     36     2
## 38     37     1
## 39     39     3
## 40     40     7
## 41     41     2
## 42     42     1
## 43     43     5
## 44     44     6
## 45     45     2
## 46     47     3
## 47     48     5
## 48     49     1
## 49     50     1
## 50     52     2
## 51     53     2
## 52     55     4
## 53     56     2
## 54     57     2
## 55     58     1
## 56     60     1
## 57     61     1
## 58     62     2
## 59     63     1
## 60     64     2
## 61     66     1
## 62     67     1
## 63     68     2
## 64     69     2
## 65     71     2
## 66     72     2
## 67     73     1
## 68     77     2
## 69     78     4
## 70     79     1
## 71     81     1
## 72     84     3
## 73     87     1
## 74     88     1
## 75     89     1
## 76     92     1
## 77     94     2
## 78     97     1
## 79     99     1
```

```
## 80    102     2
## 81    104     2
## 82    107     1
## 83    113     1
## 84    121     1
## 85    132     1
## 86    133     1
## 87    139     1
## 88    152     1
## 89    154     1
## 90    158     2
## 91    173     2
## 92    190     1
```

Compare negative binomial with $R_0 = 2$, $p = 0.1$, $k = 1/2$ with standard model, $R_0 = 2$, $k = 1/2$:



Compare negative binomial with $R_0 = 2$, $p = 0.1$, $k = 2$ with standard model, $R_0 = 2$, $k = 2$. Similar to probability mass function for $k = 2$ (below)


k=2
prop
0.0
0.1
0.2
0.3
0
20
40
60
cases
model
Baseline
Mixture