Negative binomial mixture branching process model of transmission with R0<1

Key question

- Does the mechanistic addition of population structure induce qualitatively different outbreak patterns from a standard superspreading model when $R_0 < 1$?

Model Assumptions

We assume that infected individuals can be divided into two disjoint groups - a fraction p that contribute to transmission via superspreading, and the remaining fraction of the population $1-p$ that that do not contribute to superspreading transmission. In the superspreading cohort, the mean cumulative number of contacts leading to transmission of infection per infected individual per unit time is high at $\beta_1 = \beta_D + \delta$, whereas in the non-superspreading group, it is low $\beta_2 = \beta_D < \beta_1$. In both groups the contact process follows a Poisson distribution with mean β_i $i, = 1, 2$. Then the contact process for the entire population is a finite Poisson mixture with random variates,

$$\text{number of cumulative contacts per infectious individual per unit time} \sim p\text{Poisson}(\beta_1) + (1-p)\text{Poisson}(\beta_2). \tag{1}$$

In both groups,we assume the infectious period is gamma distributed with mean $1/\gamma$ and coefficient of variation $1/\sqrt{k}$ with probability density function

$$f(x) = \frac{(\gamma k)^k}{\Gamma(k)} x^{k-1} e^{-k\gamma x}$$

The gamma distribution is flexible in that allows for right-skewed distributions (i.e., $k < 1$) and distributions with a central tendency ($k > 1$), with $k = 1$ leading to the exponential distribution. The probability generating function for the mixture follows

$$\begin{aligned} h(s) &= \int_0^\infty \left(p e^{\beta_1 x(s-1)} + (1-p) e^{\beta_2 x(s-1)} \right) \frac{(\gamma k)^k}{\Gamma(k)} x^{k-1} e^{-k\gamma x} dx \\ &= p \frac{(\gamma k)^k}{(\gamma k + \beta_1(1-s))^k} + (1-p) \frac{(\gamma k)^k}{(\gamma k + \beta_2(1-s))^k} \\ &= p \left(\frac{1}{(1 + \frac{\beta_1}{\gamma k}(1-s))} \right)^k + (1-p) \left(\frac{1}{(1 + \frac{\beta_2}{\gamma k}(1-s))} \right)^k \\ &= \frac{p}{(1 + \frac{R_0^A}{k}(1-s))^k} + \frac{(1-p)}{(1 + \frac{R_0^D}{k}(1-s))^k}, \end{aligned} \tag{2}$$

where $R_0^D = \beta_2/\gamma = \beta_D/\gamma$ and $R_0^A = \beta_1/\gamma = (\beta_D + \delta)/\gamma$. Therefore equation (2) shows that a finite mixture of negative binomial distributions models a combination of close contact transmission and superspreading. The number of secondary infections per generation is obtained from

$$\text{number of secondary infections} \sim p\text{Negative Binomial}(R_0^A, k) + (1-p)\text{Negative Binomial}(R_0^D, k). \tag{3}$$

The mean number of secondary infections is $R_0 = pR_0^A + (1-p)R_0^D = R_0^D + p\delta$.

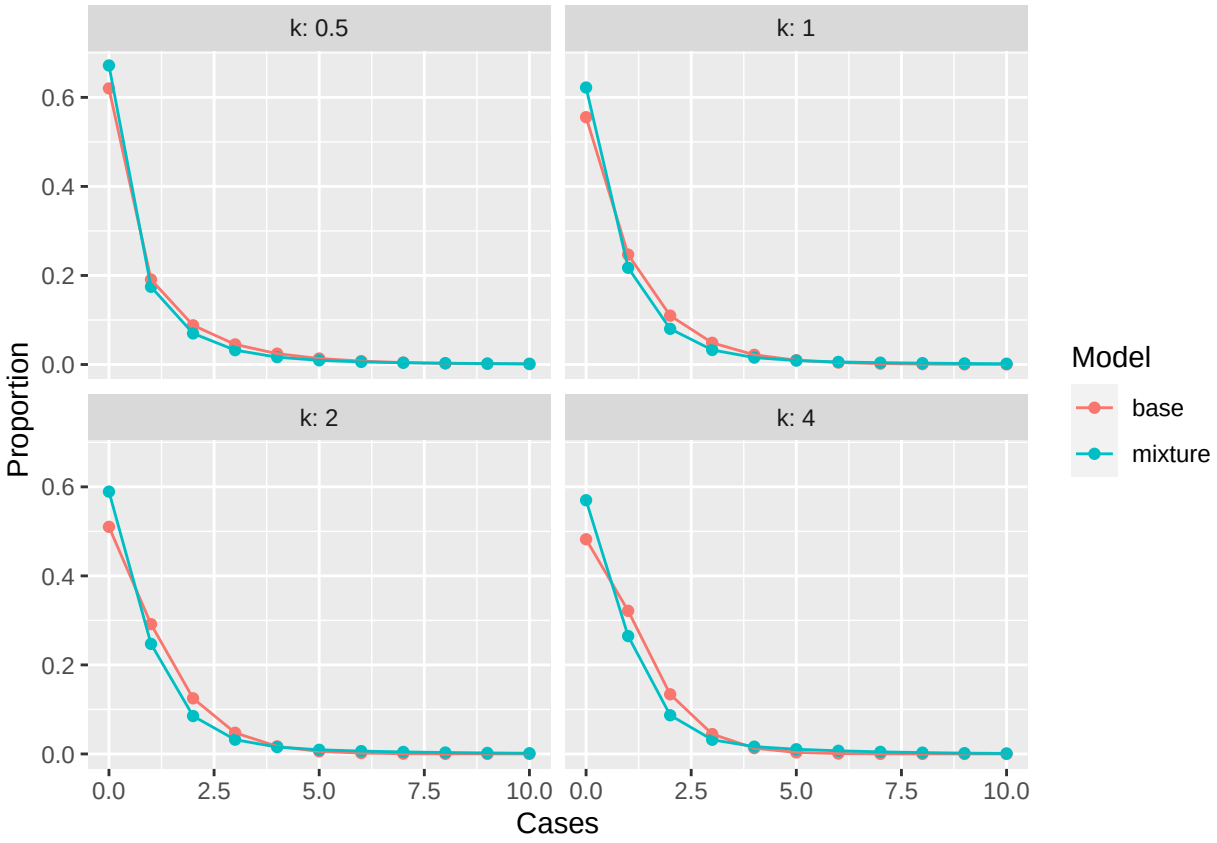
We compare the mixture model with a baseline negative binomial model with the same R_0 and dispersion parameter k.

Numerical studies (assuming $R_0 < 1$)

- How statistics vary with p, δ and k, keeping R_0 fixed, for the baseline and mixture models (compare the degree of heterogeneity in outbreak patterns)

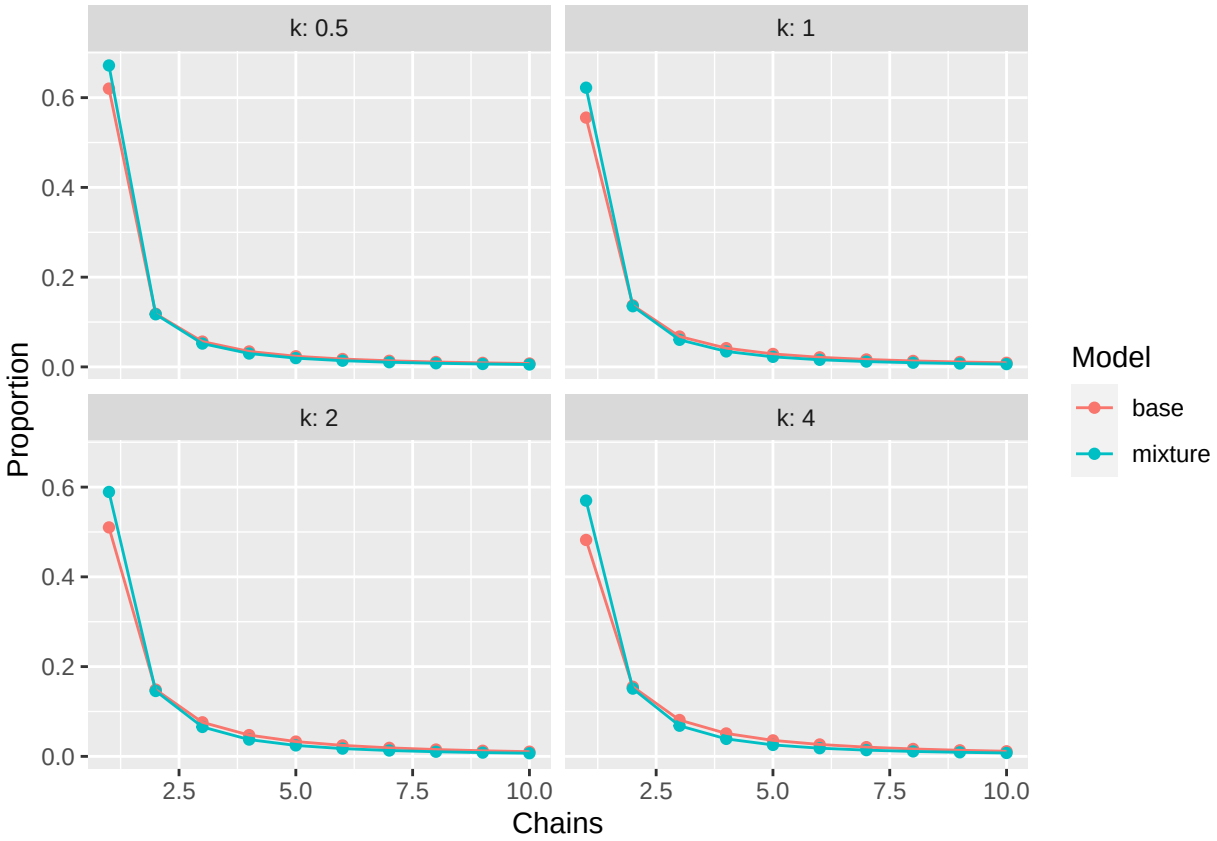
Probability mass functions for baseline and mixture models

Here we compare the probability mass functions of the mixture model ($R_0^D = 0.5$, $p = 0.1$, additional contacts $\delta = 3$) with the base model for various values of k. The mean number of secondary infections for both models is $R_0 = 0.8$. For the mixture models, the probability of no secondary infections is always greater than the negative binomial model with the same R_0 and k. As k increases the central tendency in the number of secondary infections in the base model is not observed if $R_0 < 1$.



Corresponding chain size distributions

Here we compare the chain size distributions of the mixture model ($R_0^D = 0.5$, $p = 0.1$, additional contacts $\delta = 3$) with the base model for various values of k. The mean number of secondary infections for both models is $R_0 = 0.8$. When $R_0 < 1$ the chain size distribution is not fatter tailed for the mixture models compared to the corresponding base models. The base model is fatter tailed.



Statistics that show hallmarks of transmission heterogeneity

Hallmarks of heterogeneous transmission include:

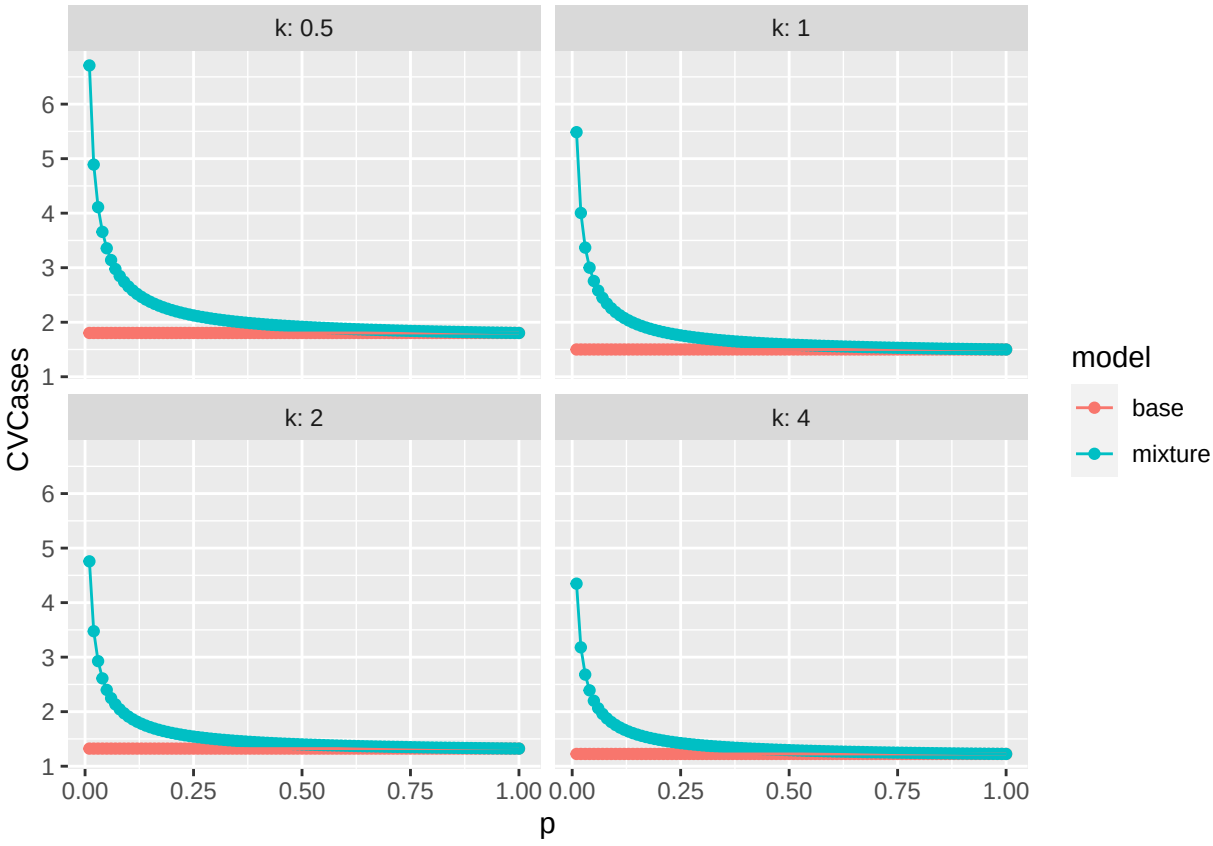
- Greater variability in the number of secondary infections (fat tailed)
- Smaller probability of major epidemics
- Greater variability in chain sizes
- Larger probability of observing no secondary infections and of observing small chains that go extinct

Here we study the coefficient of variation of the number of secondary infections, the probability of observing a small transmission chain of less than or equal to 10 cases, and the coefficient of variation of small chain sizes (conditioned on extinction). Since $R_0 < 1$, the probability of extinction is unity and the mean chain size $1/(1 - R_0)$ is the same for all values of p.

In each of the following, p and δ are varied but $R_0 = R_0^D + p\delta$ is fixed at $R_0 = 0.8$. The following figures show that smaller values of p (and larger values of δ) lead to more heterogeneous epidemics, even if the dispersion parameter $k > 1$.

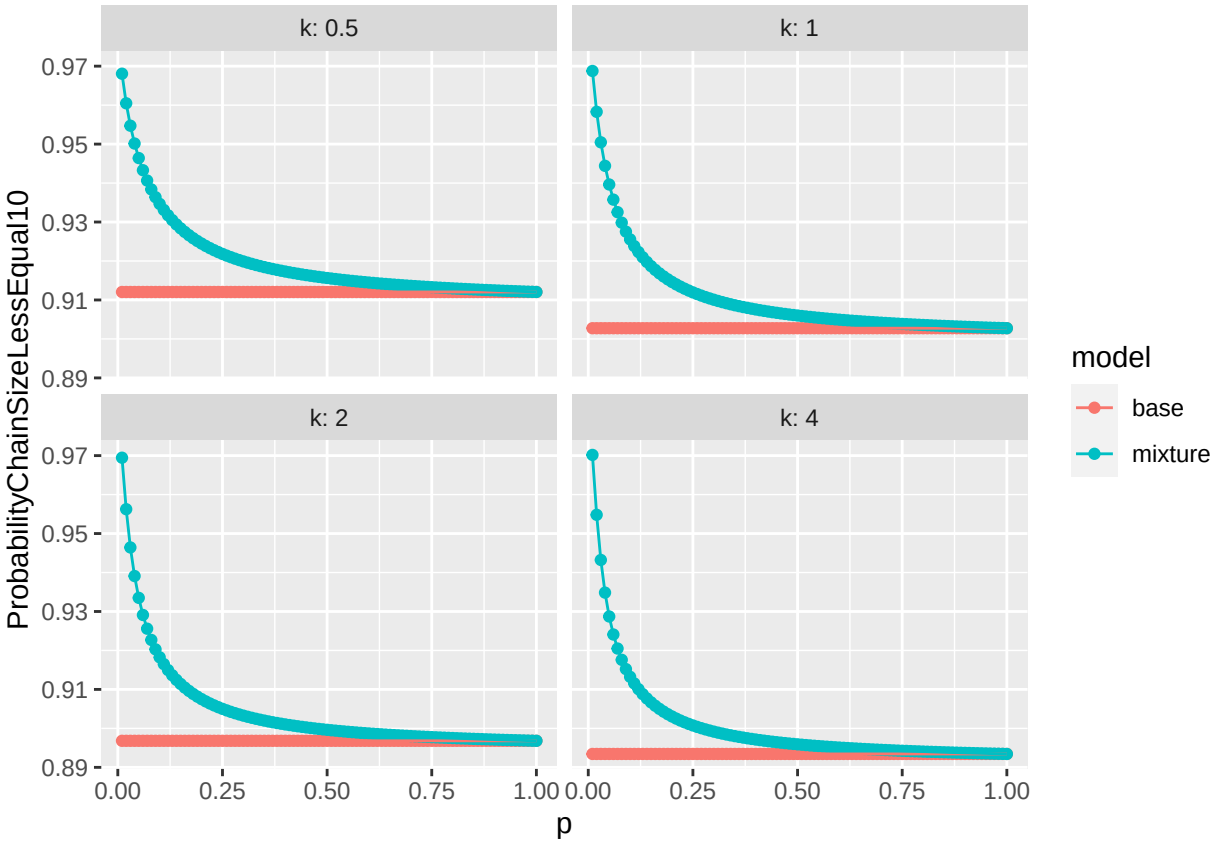
CV offspring distribution

There is greater variability in the number of secondary infections in the mixture model compared to the base model, even if $k > 1$, with the highest variability for small dispersion parameter k, small p and large number of additional contacts.



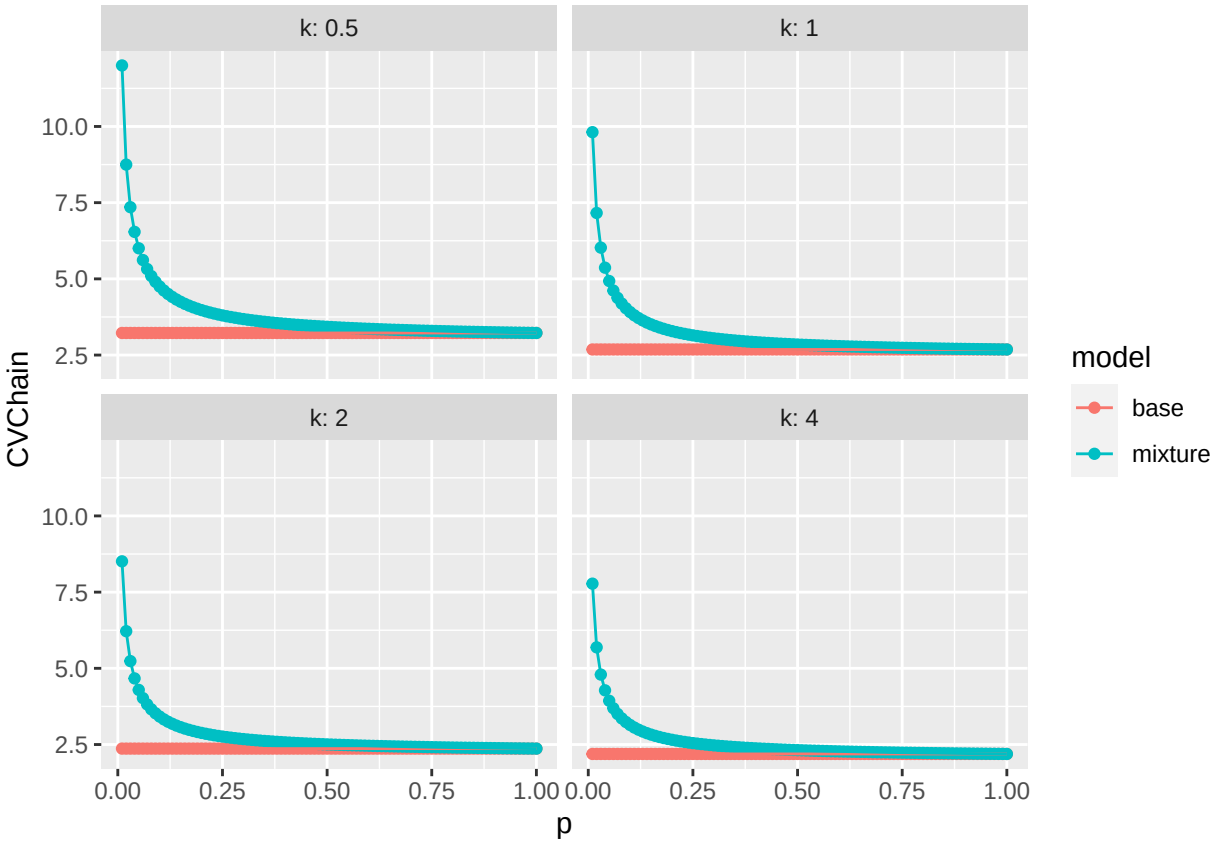
Probability of observing a transmission chain of size <= 10

There is larger probability of observing small chains that go extinct in the mixture model compared to the base model, with the highest probabilities for small dispersion parameter k, small p and large number of additional contacts.



CV chain size

There is greater variability in chain sizes in the mixture model compared to the base model, even if $k > 1$, with the highest coefficients of variation observed for small dispersion parameter k, small p and large number of additional contacts.


k: 0.5
k: 1
k: 2
k: 4
CVChain
10.0
7.5
5.0
2.5
0.00
0.25
0.50
0.75
1.00
p
model
base
mixture