Detecting changes in dispersion in COVID-19 case counts using a negative binomial model

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Why study variability?

- Highly variable case count time series suggest transmission heterogeneity(bc), demographic/environmental heterogeneity, or changes in R

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- Adam et al. [**adam˙time-varying˙2022**] found that COVID-19 transmission heterogeneity decreased over time and was associated with interventions to slow spread

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- Metrics of variability are often an overlooked way to understand systems (How is variability related to different phases of an epidemic? [**graham˙measles˙2019**]
- Adam et al. [**adam˙time-varying˙2022**] found that COVID-19 transmission heterogeneity decreased over time and was associated with interventions to slow spread
- Information about what phase/dynamic regime an epidemic is in, as well as potentially indicating the level of heterogeneity at finer spatial and temporal scales (in)

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- Dispersion around a rolling mean (moving window) of a case count time series may be a useful metric because it forms part of a framework that models variance more flexibly than a Poisson model
- A 'mean crowding' parameter [**lloyd˙mean˙1967**] was proposed, which is the mean number per individual of other individuals in the same quadrat
- Useful way to think about dispersion in case count time series, degree of dispersion is degree of clustering/crowding of cases (rel to crowdin parm) (from the perspective)

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Introduction to the method

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- Adjusted for population size using an offset in the model (directly model)
- Dispersion allowed to vary more slowly than the process mean
- Linear predictor includes a natural spline in time to account for autocorrelation in case counts (ns are)

$$log(E[Y_i]/n_i) = \beta_1 h_1(t_i) + \beta_2 h_2(t_i) + \beta_3 h_3(t_i) \quad (1)$$

$$log(E[Y_i]) - log(n_i) = \beta_1 h_1(t_i) + \beta_2 h_2(t_i) + \beta_3 h_3(t_i) \quad (2)$$

$$log(E[Y_i]) = \beta_1 (h_1(t_i) + \beta_2 h_2(t_i) + \beta_3 h_3(t_i) + log(n_i) \quad (3)$$

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Negative binomial model

- $$f_t(I) = \binom{I+\theta-1}{I} \frac{\mu}{\mu+\theta}^{I} \frac{\theta}{\mu+\theta}^{\theta} \quad (4)$$

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- $$E(I) = \mu \quad (5)$$

$$Var(I) = \mu + \frac{\mu^2}{\theta} \quad (6)$$

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Application to simulated data

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Application to simulated data

- For validity/power simulations, we used both Gaussian and uniform epidemic curves with an attack rate of 0.1
- Epidemic curves over 60 timesteps each were produced, and a likelihood-ratio test (LRT) procedure was applied to each
- Varying the effect size, location of the breakpoint, population size, and curve shape allowed us to test the validity and power of our approach

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- We estimated μ_t and θ_t using an iterative reweighted least-squares (procedure implemented via the NBPSeq package[**NBPSeq**] and from Di et al.[**yanming˙nbp˙2011**] with a moving window approach (for each window)

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Application to empirical data

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- We estimated μ_t and θ_t using an iterative reweighted least-squares (procedure implemented via the NBPSeq package[**NBPSeq**] and from Di et al.[**yanming˙nbp˙2011**] with a moving window approach (for each window)
- We investigated large counties (largest three counties in each state), due to power constraints

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Correspondence simulated and empirical

- We found that the negative binomial/LRT method is robust to differences in population size (for population sizes examined) (the criteria)

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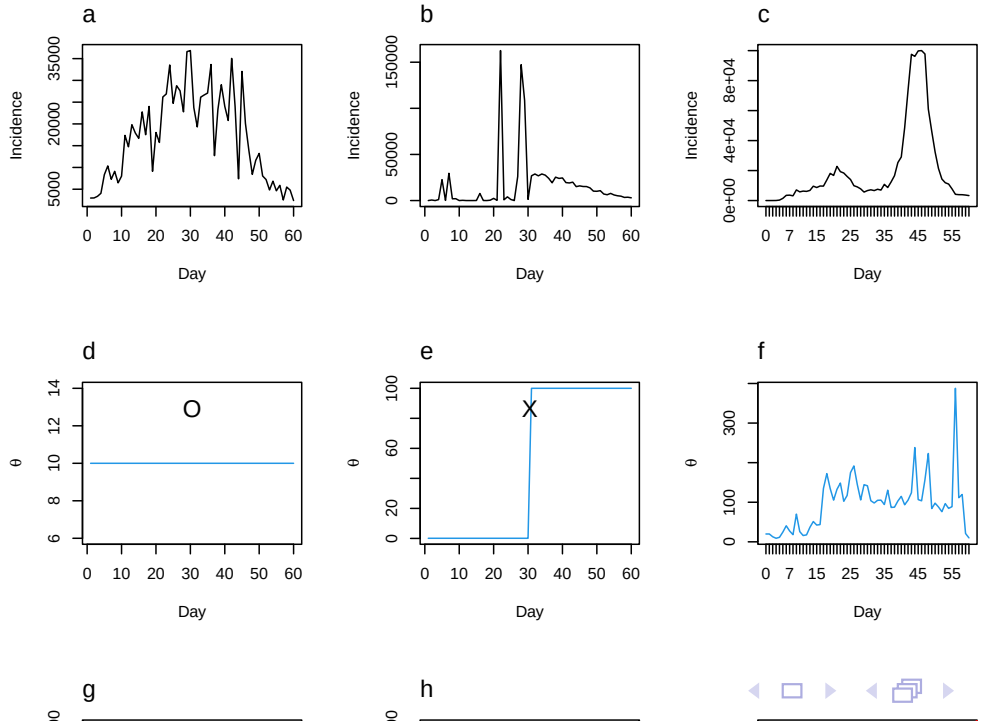
- We found that the negative binomial/LRT method is robust to differences in population size (for population sizes examined) (the criteria)
- In row one and two of Fig. 1, we illustrated that an increase in θ is associated with decreased variability in simulated incidence time series (same relationship is observable in the empirical time series), with an increase in θ corresponding to a decrease in variability around the trend in incidence



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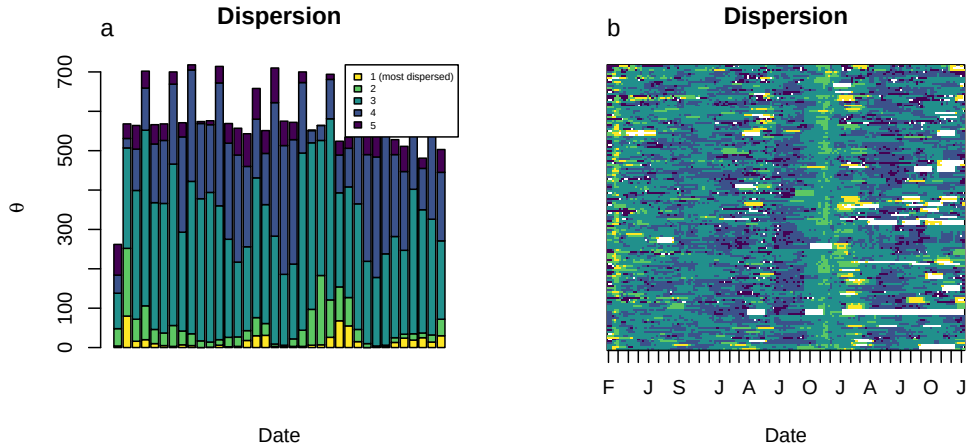
- The evidence for a change in θ was observed across many counties (evidenced by concentration of low p-values around peak incidence) (Fig. 3 (d))



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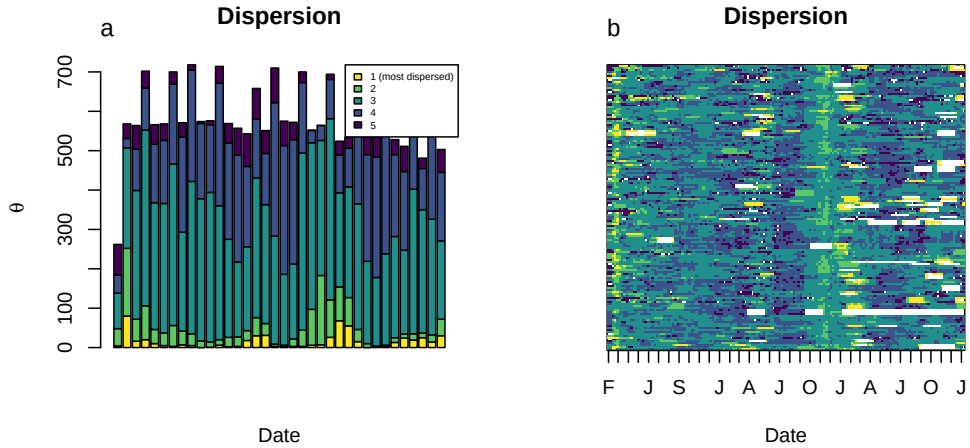

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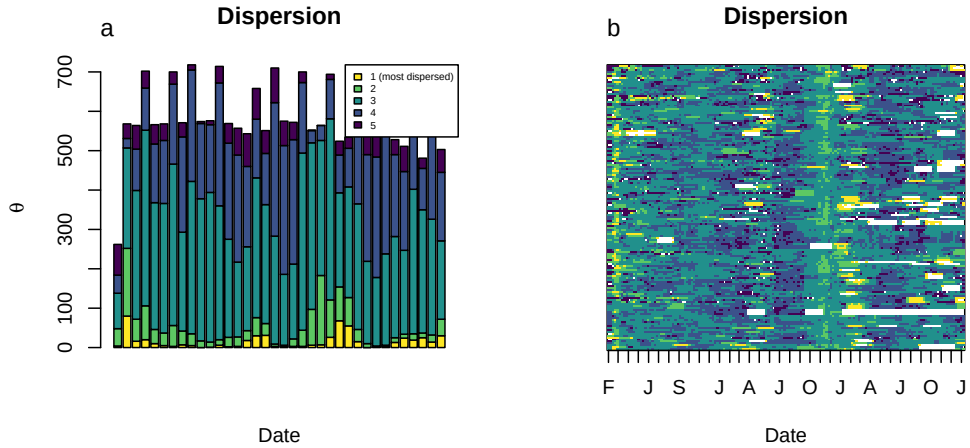

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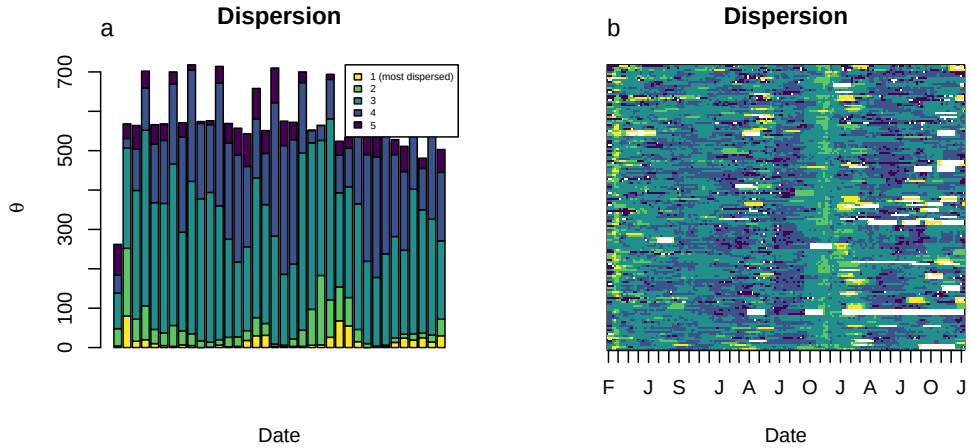

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- Methods that use incidence time series are a crucial part of this research area due to the ease of obtaining incidence data, so the timing/geographical allocation of public health resources can be achieved with limited resources
- Population-wide disease control approaches are often less effective than those which are targeted to individuals in high-transmission contexts [**lloyd-smith˙superspreading˙2005**] (catalyze the development of more efficient control strategies)

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- Methods that use incidence time series are a crucial part of this research area due to the ease of obtaining incidence data, so the timing/geographical allocation of public health resources can be achieved with limited resources
- Population-wide disease control approaches are often less effective than those which are targeted to individuals in high-transmission contexts [**lloyd-smith˙superspreading˙2005**] (catalyze the development of more efficient control strategies)
- Our results imply that we can revise our understanding of case count dispersion: dispersion is high at unexpected times (near peak incidence)

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Thanks!