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Multiscale Spatio-temporal Modeling of Covid-19 case incidence and mortality

Introduction

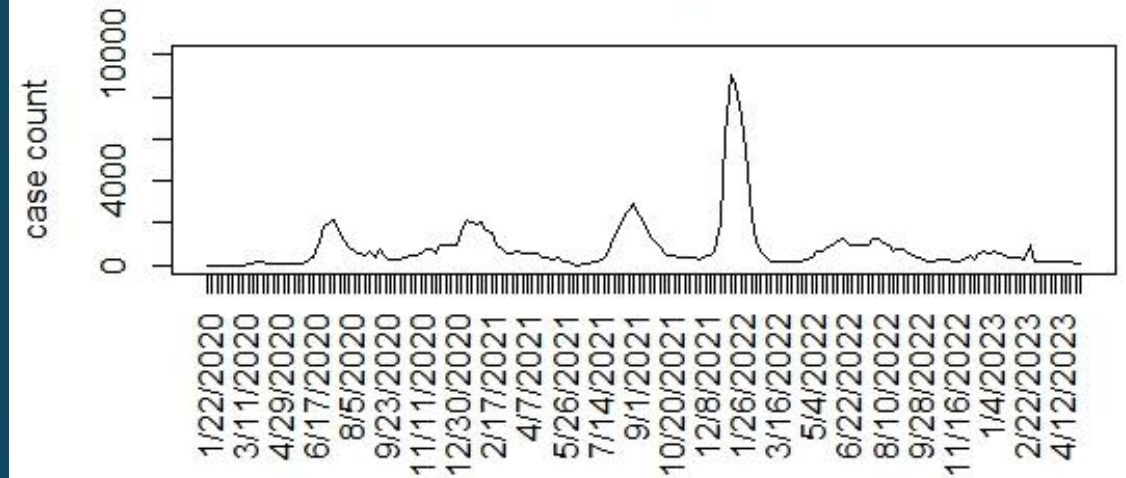
- During the Covid-19 pandemic many attempts were made to model state or national level time series of case counts or mortality
- To a much lesser extent, some effort was focused on spatial aspects of the pandemic and there are a few example of spatio-temporal modeling at finer spatial scales.
- It is clear that spatial aspects are important in pandemic spread at a variety of scales (both spatial and temporal)
- The idea that super scale modeling could be carried out at same time as fine scale has not been explored and yet multiple scales are a major focus of public health pandemic management.

Multiscale background

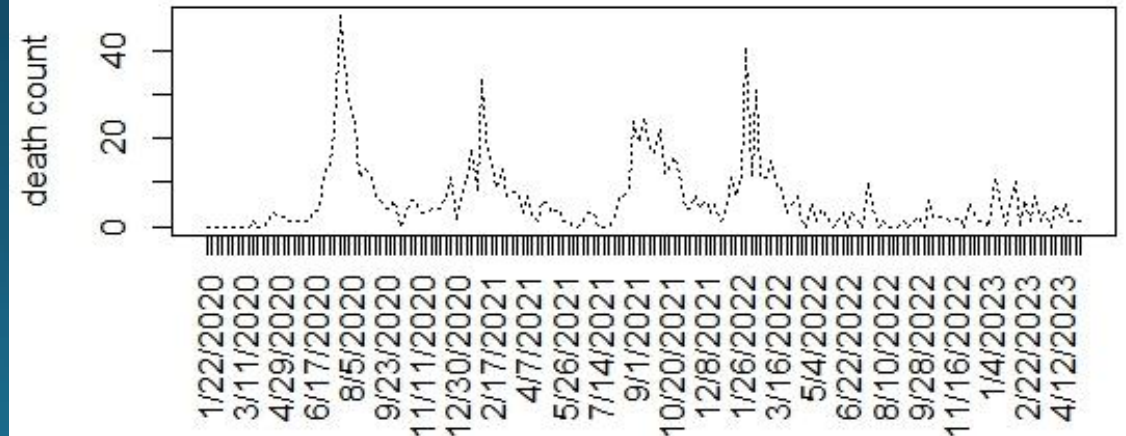
- Multiscale modeling: the Covid-19 pandemic has yielded a considerable amount of (since) validated data ...
- This includes data at different spatial scales
- In the US the CDC now provides weekly summary counts for case incidence and mortality at county level for 173 weeks from January 2020 to May 2023.
- These data also include state level case numbers and mortality
 - Both incident and cumulative numbers are available.

Charleston county, SC: 173 week profiles

Charleston county new cases

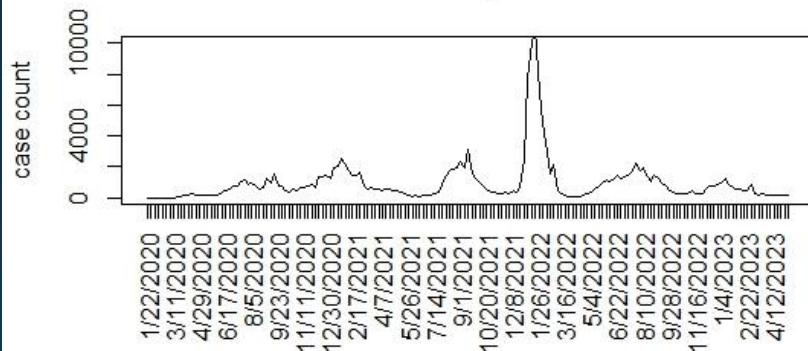


Charleston county new deaths

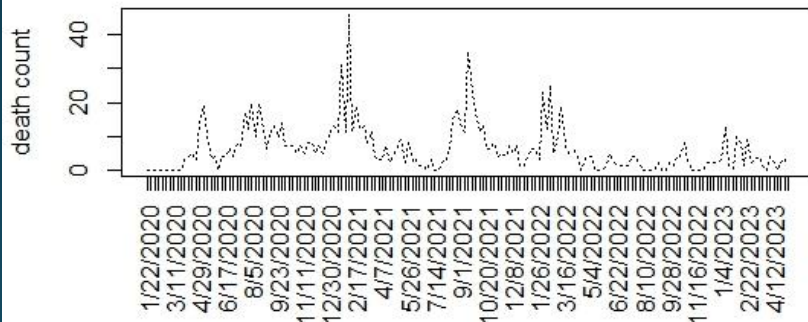


Greenville and Richland counties

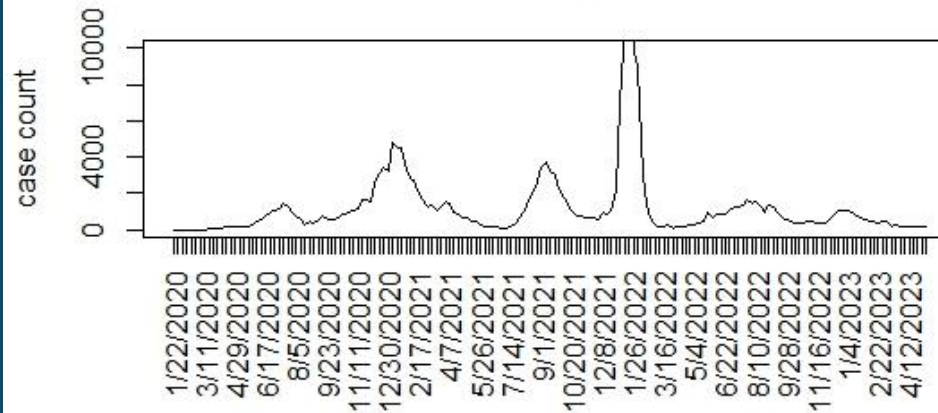
Richland county new cases



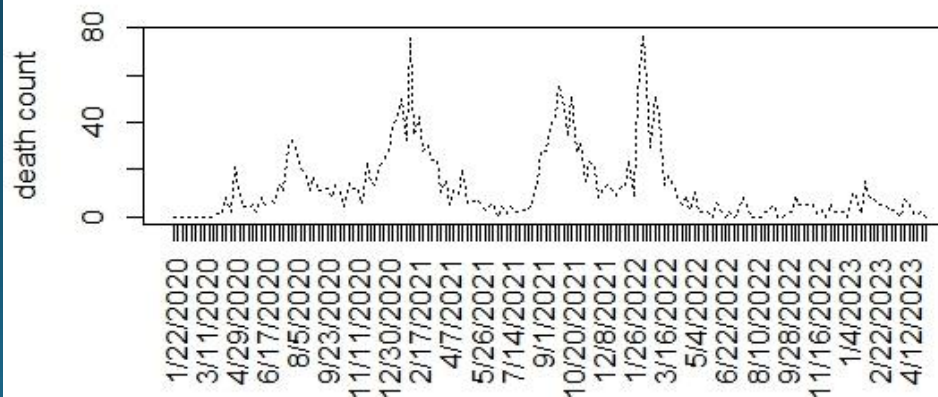
Richland county new deaths



Greenville county new cases

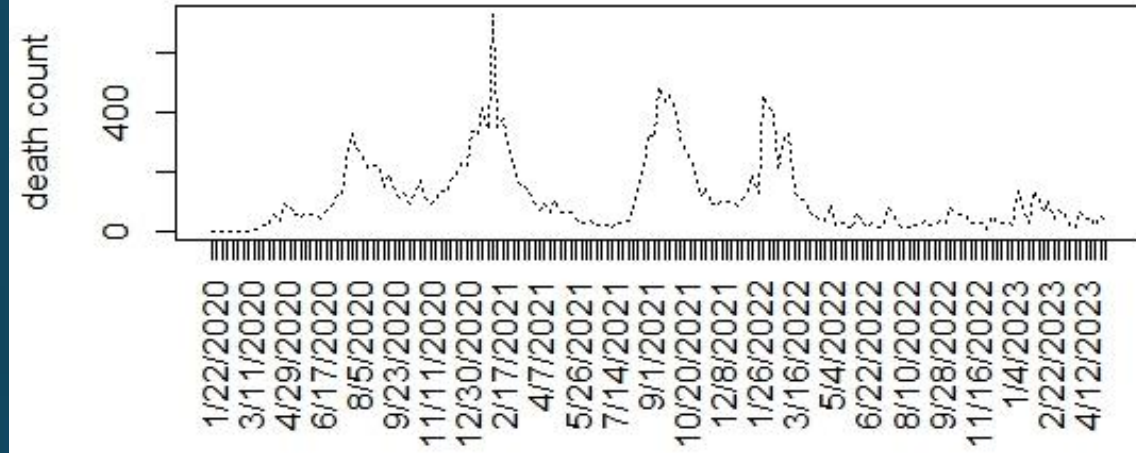


Greenville county new deaths

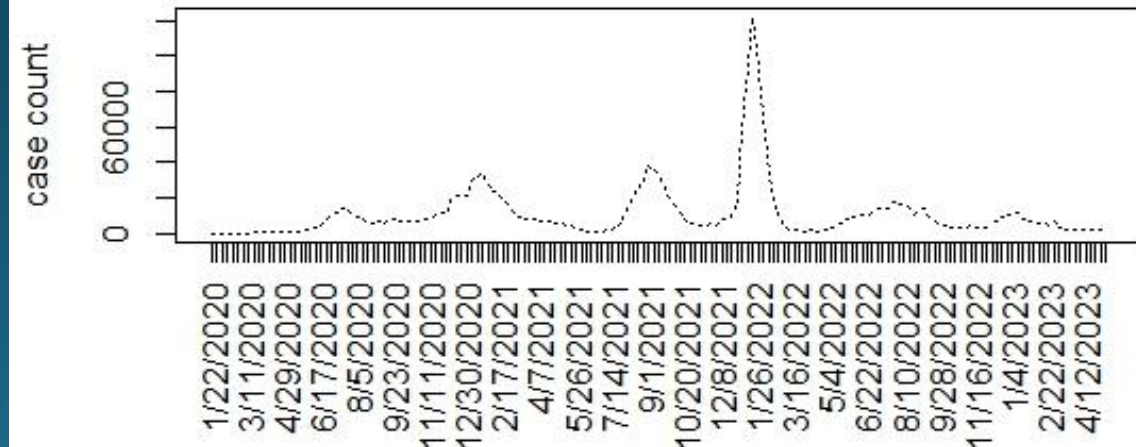


SC state level

SC mortality profile



SC case count profile



Multivariate multiscale ST modeling

- Potentially it is possible to consider joint models at different scales and for different disease outcomes in space-time.
- In essence this is an example MsMVST Bayesian modeling
- In our case we consider the state level and county level as our multiple scales and initially we considered mortality modelling only
- The results reported here are for weekly mortality at the county level in SC (low level) and at the state level (high level)
- There are 46 counties and 1 state in the initial results

Notation

$y_{k,j}^{DH}$ death count at the higher level (state)

$y_{k,j}^{CH}$ case count at higher level

$y_{i,j}^{DL}$ death count at lower level

$y_{i,j}^{CL}$ case count at lower level

$i = 1, \dots, m$ areas (in this case counties)

$j = 1, \dots, T$ time periods (in this case weeks)

Assumptions 1

- We assume that the counts of cases or deaths can be regraded as conditionally independent Poisson distributed

$$y_{k,j}^{DH} \sim \text{Pois}(\mu_{k,j}^{DH})$$

$$y_{i,j}^{DL} \sim \text{Pois}(\mu_{i,j}^{DL})$$

$$\log(\mu_{k,j}^{DH}) = \alpha_0^{DH} + \dots$$

$$\log(\mu_{k,j}^{DL}) = \alpha_0^{DL} + \dots$$

Assumptions 2

- Each level has a model and a potential linkage with the other level
- In the simplest model we assume that the high level (H) mean is simply a sum of the low level (L).
- In this case H: state and L: county
- Poisson aggregation assumption initially :

$$\log(\mu_{k,j}^H) = \log(\sum_{i \in k} \mu_{i,j}^L)$$

- More sophisticated models also developed.

Assumptions 3

- General prior distributions
- Zero mean Gaussian prior distributions of regression parameters
- Weakly informative Gamma prior distributions for precisions
- ICAR prior distributions for spatial effects
- ST random effects assumed to have uncorrelated prior distributions

Basic model (mo)

- Sum at H level and dependence on case count at L Level , with Res in space and time at L level

$$\log(\mu_{k,j}^H) = \log\left(\sum_{i \in k} \mu_{i,j}^L\right)$$

$$\log(\mu_{i,j}^{DL}) = \alpha_0 + \alpha_1 \log(y_{i,j}^{CL}) + v_i + \lambda_j$$

$$\alpha_* \sim N(0, \tau_*^{-1})$$

$$v_i \sim N(0, \tau_v^{-1})$$

$$\lambda_j \sim N(0, \tau_\lambda^{-1})$$

GOF: Joint models

Combined high and low level models

Model	DIC	Total DIC3	Total PWAIC	Total WAIC	Total
m0	23670	23741	221.1	23764	
m1	23822	23868	296.9	23918	
m2	23275	23292	283.3	23340	
m3	23828	23872	301.2	23922	
m4	23831	23873	301.2	23924	
m5	23299	23319	283.2	23367	
m6	23988	21828	1041.4	22234	
m7	23273	23303	273.0	23350	
m8	23286	23278	277.0	23325	
m9	23953	21810	1040.1	22218	
m10	23316	23311	286.4	23361	

GOF: separate models

Combined high and low level models

Model	DIC	DIC3	PWAIC	WAIC
m0	23670	23741	221.1	23764
m1	23824	23870	298.1	23919
m2	23567	23490	389.2	23593
m3	24132	24085	421.4	24191
m4	24118	24074	417.5	24179
m5	23580	23504	383.7	23604
m6	24489	21977	1130.8	22449
m7	23292	23309	279.1	23357
m8	23258	23278	278.3	23327
m9	25370	22462	1631.6	23276
m10	23593	23481	388.0	23583

Model choice

- DIC₃ and WAIC seem to detect similar models and appear to be reliable
- DIC uses the variance(Dev) penalty and is conservative and also leads to different choice compared to DIC₃ and WAIC
- M6 is favored for separate models
- M9 is favored for joint models

Mg (joint model)

- State level:

$$\log(\mu_{k,j}^{DH}) = \log\left(\sum_{i \in k} \mu_{i,j}^{DL}\right) + \lambda_j$$

$$\lambda_j \sim N(0, \tau_\lambda^{-1})$$

- County level:

$$\log(\mu_{i,j}^{DL}) = \alpha_0 + \alpha_1 \log(y_{i,j}^{CL}) + \alpha_2 \log(y_{i,j-1}^{DL}) + \alpha_3 \log\left(\sum_{l \leq j} y_{i,l}^{CL}\right) + \psi_{i,j} + u_i + v_i + \lambda_j$$

$$\psi_{i,j} \sim N(0, \tau_\psi^{-1})$$

$$u_i \sim ICAR(\tau_u^{-1})$$

$$\alpha_* \sim N(0, \tau_*^{-1}); v_i \sim N(0, \tau_v^{-1}); \lambda_j \sim N(0, \tau_\lambda^{-1})$$

M6 (separate model)

- State level:

$$\log(\mu_{k,j}^{DH}) = \alpha_0 + \alpha_1 \log(y_j^{CH}) + \alpha_2 \log(y_{j-1}^{DH})$$

- County level:

$$\log(\mu_{i,j}^{DL}) = \alpha_0 + \alpha_1 \log(y_{i,j}^{CL}) + \alpha_2 \log(y_{i,j-1}^{DL}) + \alpha_3 \log\left(\sum_{l \leq j} y_{i,l}^{CL}\right) + \psi_{i,j} + u_i + v_i + \lambda_j$$

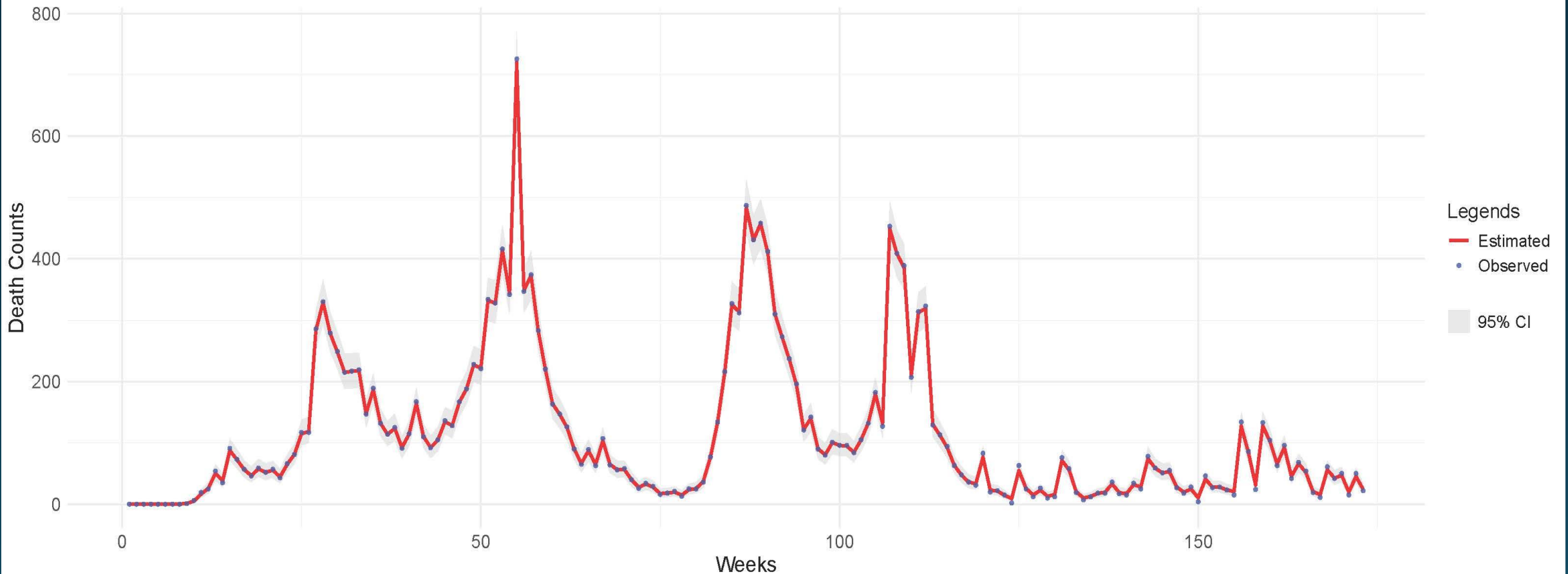
$$\psi_{i,j} \sim N(0, \tau_{\psi}^{-1})$$

$$u_i \sim ICAR(\tau_u^{-1})$$

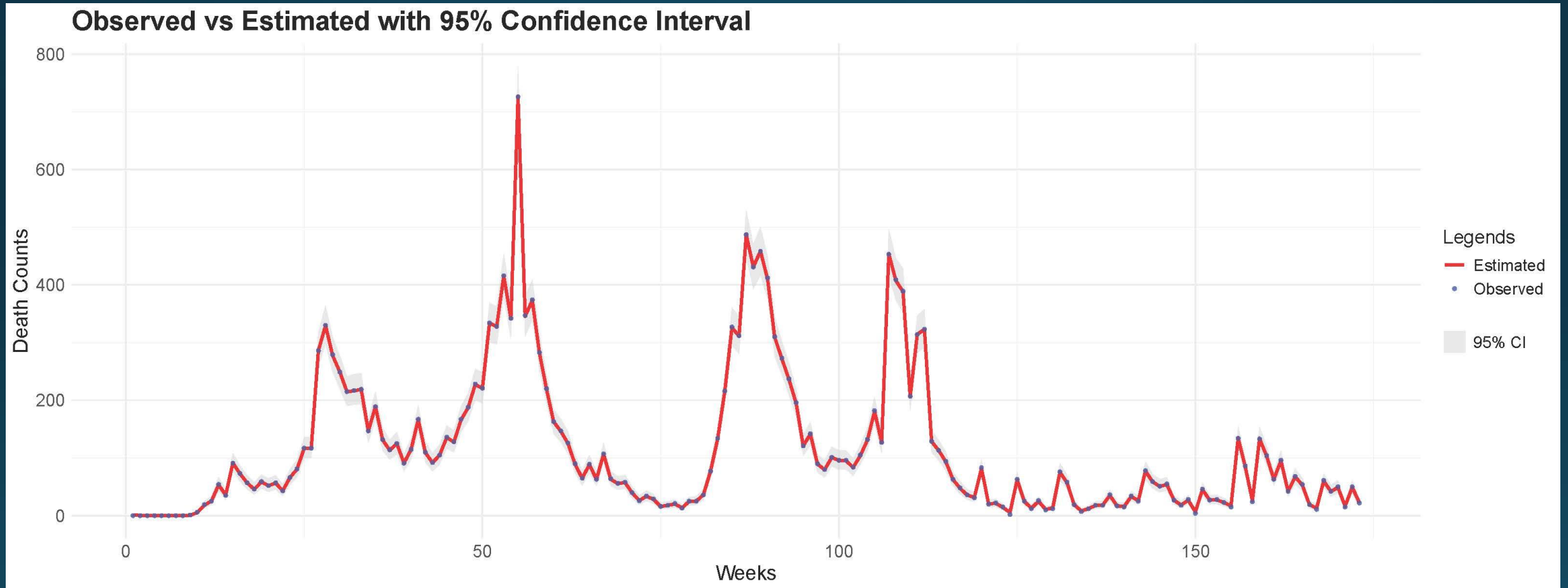
$$\alpha_* \sim N(0, \tau_*^{-1}); v_i \sim N(0, \tau_v^{-1}); \lambda_j \sim N(0, \tau_{\lambda}^{-1})$$

M6s: high level profile

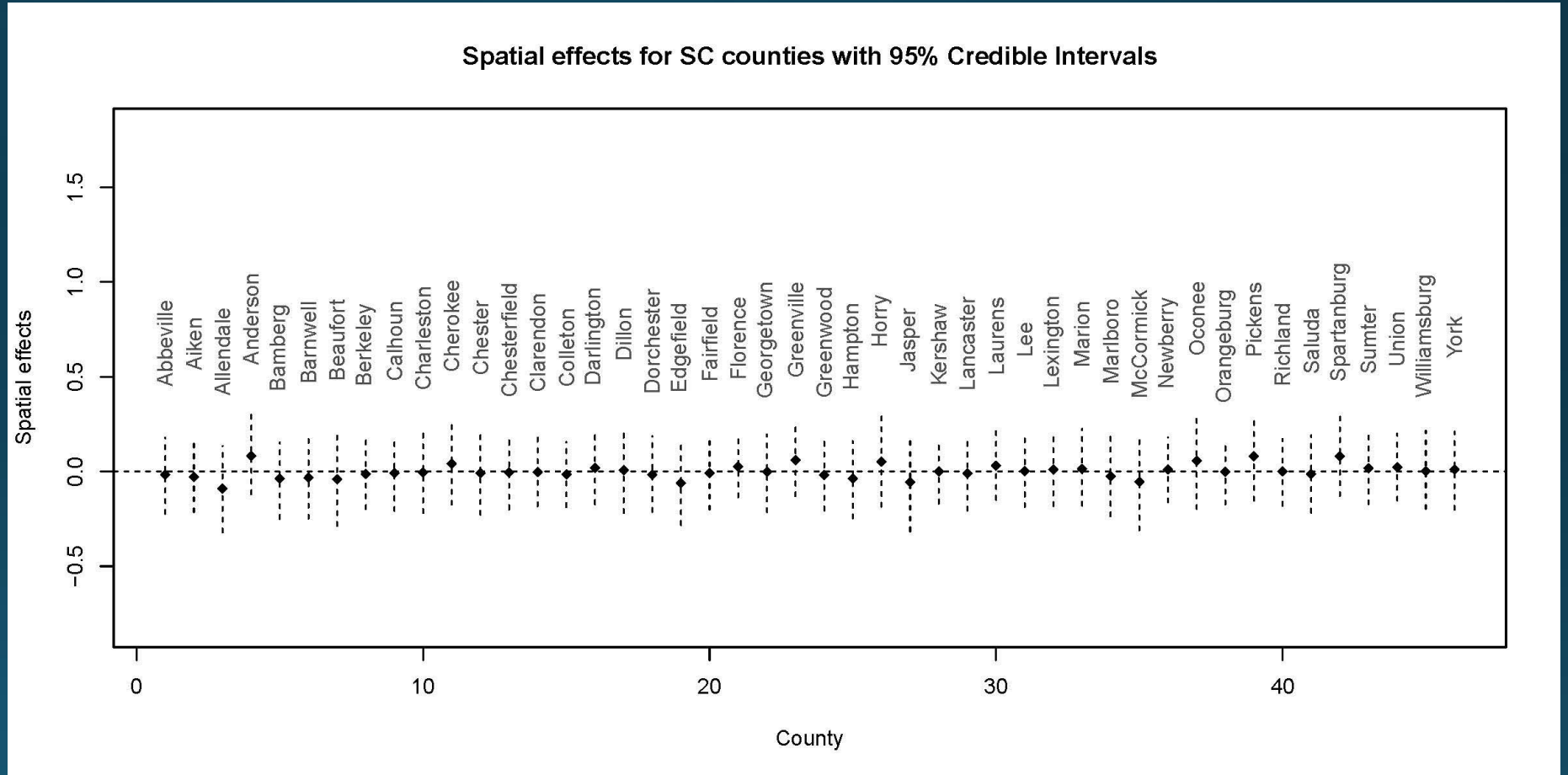
Observed vs Estimated with 95% Confidence Interval



Mg: high level profile



Spatial effects: mg



Conclusions

- We have attempted to model the multiple levels of risk which must arise during an infectious disease outbreak.
- Our example is Covid-19 in a single US state.
- However, we can easily extend the analysis to other states and multiple states to allow spatial modeling of the state level responses.
- The computational burden increases considerably and we are considering now strategies where approximate inference can be achieved in reasonable time scales for decision making.

Additional Conclusions

- The models display relative good fit to the time series at the high level, at least.
- Our ability to model the duration of the pandemic could be enhanced if time varying covariates were available.
- Viral load variation and vaccination coverage could be very important in both case event and mortality modeling.
- Extensions to joint modeling of deaths and case events across scales (both space and time) would be a clear possibility
- This can lead to MsMVST modeling

Thank you !