Abstract. Spatio-temporal models for infection counts generally follow themes of the broader disease mapping literature, but may need to address specific features of spatio-temporal infection data including considerable time fluctuations (with epidemic phases) and spatial diffusion. Low order autoregression is a feature of several recent spatio-temporal studies of infection data, possibly with lags on both within area infections and on infections in adjacent areas. Many epidemic time series show a period of relatively stable infection levels (possibly characterized as endemicity), followed by a sudden sharp phase of increasing infection levels. After the epidemic peak there is a period of descending rates and return to stability. Hence one may seek to adapt the autoregressive scheme to these pronounced fluctuations, with temporary departures from stationarity, but returning to stationarity as rates descend and infections resume endemic levels. We consider a mixture link model for infection counts that allows adaptivity to both explosive phases and static endemicity. Two case study applications involve COVID area-time data, one for 32 London boroughs since the start of the COVID epidemic, the other focusing on the epidemic phase in 144 area of South East England associated with the Delta variant.

Keywords Autoregressive. COVID. Endemic. Epidemic. Link mixture. Spatio-temporal

Introduction

There have been a considerable number of spatio-temporal studies of disease patterns, often adopting a Bayesian perspective (e.g. Lagazio et al, 2021). Spatio-temporal models for infection counts (e.g. Lowe et al, 2021; Coly et al, 2021; Jalilian and Mateu, 2021; Lawson and Song, 2010) are a particular sub-theme. These may incorporate the themes of the broader disease mapping literature, such as the gains through borrowing strength, and the need to reflect spatial correlation in disease; for example, see Andrews et al (2021) on spatial clustering in COVID rates.

However, spatio-temporal infection data raises particular new issues. These include considerable time fluctuations (with epidemic phases) in many infectious diseases; spatial diffusion or spillover (e.g. Dalvi and Braga, 2019) related to behaviours such as commuting (Mitze and Kosfeld, 2021), and the occurrence of hotspots for disease propagation early in infectious outbreaks (Dowdy et al, 2012). It is also especially useful in policy terms to be able to extrapolate the infectious disease evolution beyond the observation span, as illustrated in some studies of the COVID epidemic (Vahedi et al, 2021; Rui et al, 2021; Watson et al, 2017; Giuliani et al, 2020).
Low order autoregression is a feature of several recent spatio-temporal studies of infection data. For example, Paul and Held (2011) and Shand et al (2018) adopt first order autoregression (AR1) models, where the autoregressive coefficients on counts or rates in the previous period are spatially correlated. The model of Paul and Held (2011) includes a spatial lag on infection counts in adjacent areas that allows for the spatial spillover effect; related approaches are considered by Martines et al (2021) and Griffith and Li (2021). In infections spread by human contact it is implausible that higher counts or rates in one period generate smaller infection levels in the next period, and so a positive constraint on the AR1 coefficient may be adopted. Stationarity may also be assumed (e.g. Shand et al, 2018), but flexibility to epidemic fluctuations may be gained by allowing non-stationarity.

A particular feature of epidemic time series is that a period of relatively stable infection levels (possibly seen as an endemic phase) is followed by a sudden sharp phase of increasing infection levels. After the epidemic peak there is a period of descending rates and return to stability. Hence one may seek to allow the autoregressive scheme to adapt to these pronounced fluctuations, with temporary departures from stationarity, but returning to stationarity as rates descend and infections resume endemic levels. For example, assuming an identity link in count regression, AR1 coefficients exceeding 1 may better represent and reproduce sharply increasing infection levels during an explosive phase. In this paper we consider a mixture link model for infection counts that allows such adaptivity to both explosive phases and static endemicity.

Two case study applications involve area-time data for COVID-19 infection counts. The first case study considers the 32 London boroughs which exemplify the sudden growth in COVID infections due to the Omicron variant at the end of 2021. The link mixture approach is applied to data from the start of the epidemic in March 2020 through to early 2022 for the London boroughs, and shows better fit than simpler options and improved short term forecasts. The second case study considers data for the South East of England (144 areas), and considers especially the weeks up to and including the peak of infections due to the Delta variant at the end of 2020.

Methods

Autoregression for Infection Counts

Consider area-time infection count data $y_{it}$ for areas $i = 1, ..., N$ and times $t = 1, ..., T$, and assume these are negative binomial (NB), $y_{it} \sim NB(\mu_{it}, \Psi)$. The NB parameterisation is

$$p(y|\mu, \Psi) = \frac{(y+\Psi-1)!}{y!(\Psi-1)!} \left( \frac{\mu}{\mu+\Psi} \right)^y \left( \frac{\Psi}{\mu+\Psi} \right)^\Psi.$$

Assume an AR1 model on previous infection counts in the same area. Additionally stable effects of predictors $X_i$, and constant unobserved area effects $u_i$ (random or fixed), may
be represented by a term $\eta_i = X_i \beta + u_i$. Then for a basic model, and conditioning on the first period's data, one may adopt an identity link
\[ \mu_{it} = \rho_i y_{i,t-1} + \exp(\eta_i), \] (1)
providing positivity in $\rho_i$ is ensured. The $\rho_i$ may well be spatially correlated, and typically taken as random effects.

One may add lags to infection counts in spatially close areas to reflect infection spillover from neighbouring areas - due, for example, to social interactions between residents in different areas, or to cross boundary commuting (Mitze and Kosfeld, 2021). Let $h_{ij}$ measure spatial interactions between areas $i$ and $j$, and $w_{ij} = h_{ij} / \sum_j h_{ij}$ be row standardised spatial weights, with $\sum_j w_{ij} = 1$. Then spatial spillover, also with lag 1, can be represented (e.g. Paul and Held, 2011) by adding a spatially averaged term $\lambda_i \sum_j w_{ij} y_{j,t-1}$ to the above basic model. Then one has
\[ \mu_{it} = \rho_i y_{i,t-1} + \lambda_i \sum_j w_{ij} y_{j,t-1} + \exp(\eta_i), \] (2)
providing positivity in $\rho_i$ and $\lambda_i$ is ensured.

Assuming that $\rho_i$ and $\lambda_i$ are positive is justified in epidemiological terms, since - for infections spread by human contact or interaction - higher current totals of infectees, $y_{i,t-1}$, and $\sum_j w_{ij} y_{j,t-1}$, are expected to cause higher future infections. A negative effect of existing infection levels on future infections is implausible.

One then requires an appropriate link function relating $\rho_i$ and $\lambda_i$ to relevant parameters. For example, assume spatially correlated conditional autoregressive random effects $f_{1i}$ and $f_{2i}$ (Besag et al, 1991) involved in predicting $\rho_i$ and $\lambda_i$, and assume these are zero-centred. Paul and Held (2011, p. 1121) adopt a log link by default, so that with intercept terms $\alpha_1$ and $\alpha_2$, one has
\[ \log(\rho_i) = \alpha_1 + f_{1i}, \] (3)
\[ \log(\lambda_i) = \alpha_2 + f_{2i}. \]
A log link allows for explosive effects ($\rho_i$ and/or $\lambda_i$ exceeding 1), but does not necessarily select explosive behaviour. Whether it does will depend on the estimated values of the intercepts and spatial effects. If most of the epidemic series consists of stable infection levels (endemicity) then the estimated constants may tend to favour $\rho_i$ and $\lambda_i$ below 1.

For some infectious diseases, with endemic recurrence now predominant, such as HIV in developed countries, a stationary autoregressive effect may be appropriate as a default. See, for example, the analysis of Shand et al (2018) who consider time variations in HIV in US counties. For an AR1 model on lagged infections, this implies a logit link so that $\rho_i$ and $\lambda_i$ are constrained between 0 and 1. Thus, with the same overall model (2) for counts, and spatial effects $f_{3i}$ and $f_{4i}$, one has
\[ \logit(\rho_i) = \kappa_1 + f_{3i}, \] (4)
\[ \logit(\lambda_i) = \kappa_2 + f_{4i}, \]
with expit equivalents
\[ \rho_i = \frac{1}{1 + \exp(-\kappa_1 - f_{3i})} \]
\[ \lambda_i = \frac{1}{1 + \exp(-\kappa_2 - f_{4i})} \]

In fact, if positivity of \( \rho_i \) and \( \lambda_i \) cannot be assumed on substantive grounds (e.g. for infections such as malaria not spread by human interaction), then a mapping to the interval \([-1, 1]\) for \( \rho_i \) and \( \lambda_i \) can be obtained. If \( h \) is the argument of the expit transform, then the mapping \( 2\expit(h) - 1 \) is to the interval \([-1, 1]\).

**A Link Mixture Mechanism**

For infections such as COVID, both mechanisms may be relevant. A logit link may be relevant when infections are at a low and/or stable level, whereas a log link, allowing \( \rho_i > 1 \) and \( \lambda_i > 1 \), may be more flexible in periods with explosive growth in infections (e.g. due to a new virus or new variants of that virus). An example is the rapid increase in COVID infections linked to the emergence of the Omicron variant, as considered in the first case study.

Here we consider a mixture model facilitating time-variation in which link is predominant, so reflecting the current infection phase. Other forms of mixing between links have been considered, or extra parameters introduced into modelling links. For example, Lang (1999) considers a mixture of the canonical symmetric logistic link and one or more asymmetric forms in modelling ordinal and binary outcomes, while Czado and Raftery (2006) consider right and/or left tail modifications to standard links.

Here we consider a situation not researched before (as far as the authors know), namely choosing between log and logit links. Thus, for weights \( \omega_t \) between 0 and 1, it is proposed that

\[ \rho_{it} = \omega_t \exp(\alpha_1 + g_{1i}) + (1 - \omega_t) \frac{\exp(\kappa_1 + g_{1i})}{1 + \exp(\kappa_1 + g_{1i})}, \]
\[ \lambda_{it} = \omega_t \exp(\alpha_2 + g_{2i}) + (1 - \omega_t) \frac{\exp(\kappa_2 + g_{2i})}{1 + \exp(\kappa_2 + g_{2i})}, \]

where \( \rho_{it} \) and \( \lambda_{it} \) now vary by area and time, and \( g_{1i} \) and \( g_{2i} \) are spatially correlated conditional autoregressive random effects. The \( \omega_t \) are in effect measuring stability or instability in infection rates, and so are taken as common to both own area and the neighbouring area lags, \( \rho_{it} \) and \( \lambda_{it} \) respectively. For \( \omega_t \) high and approaching 1, infections are typically rapidly increasing, whereas for low \( \omega_t \), stable endemicity is indicated. Low \( \omega_t \) may also be better for characterizing the descent phase after epidemic peaks.

If the stationary alternative to explosive growth involves the constraints \( \rho_{it} \in [-1, 1] \), and \( \lambda_{it} \in [-1, 1] \), rather than \( \rho_{it} \in [0, 1] \), and \( \lambda_{it} \in [0, 1] \), this can be achieved by the mapping

\[ \rho_{it} = \omega_t \exp(\alpha_1 + g_{1i}) + (1 - \omega_t) \left( \frac{2\exp(\kappa_1 + g_{1i})}{1 + \exp(\kappa_1 + g_{1i})} - 1 \right), \]
\[ \lambda_{it} = \omega_t \exp(\alpha_2 + g_{2i}) + (1 - \omega_t) \left( \frac{2\exp(\kappa_2 + g_{2i})}{1 + \exp(\kappa_2 + g_{2i})} - 1 \right). \]
There is no reason why spatial patterning in autocorrelation should be the same in epidemic or endemic phases, so a possible variation on the preceding model allows for differing spatial effects between phases, namely

$$
\rho_{it} = \omega_t \exp(\alpha_1 + g_{1i}) + (1 - \omega_t) \frac{\exp(\kappa_1 + g_{3i})}{1 + \exp(\kappa_1 + g_{3i})},
$$

$$
\lambda_{it} = \omega_t \exp(\alpha_2 + g_{2i}) + (1 - \omega_t) \frac{\exp(\kappa_2 + g_{4i})}{1 + \exp(\kappa_2 + g_{4i})}.
$$

(6)

Under both (5) and (6), focusing on area variations in $\rho_{it}$ and $\lambda_{it}$ during periods with explosive growth will indicate which areas have been more subject to such growth. The summary coefficients $\bar{\rho}_t$ and $\bar{\lambda}_t$, obtained by averaging $\rho_{it}$ and $\lambda_{it}$ over areas, give an overall impression of infection growth or endemic phases.

The $\rho_{it}$ and $\lambda_{it}$ can also be compared to the threshold of 1 to give a probability indication of explosive growth in different areas. Thus define indicators

$$
\bar{r}_{it}^x = I(\rho_{it} > 1),
$$

$$
\bar{l}_{it}^x = I(\lambda_{it} > 1),
$$

from which area-time exceedance probabilities can be estimated. Also the sums $R_{it}^x = \sum_i \bar{r}_{it}^x$ and $L_{it}^x = \sum_i \bar{l}_{it}^x$ show total areas with explosive infection growth in each period.

The $\omega_t$ in (5) and (6) are modelled as time-specific beta variables

$$
\omega_t \sim \text{Beta}(q_{1t}, q_{2t}),
$$

where $q_{1t}$ and $q_{2t}$ are positive parameters. Relevant covariates if available (e.g. the proportions of infections due to a new variant) may be used in predicting the $\omega_t$ via beta regression. Intervention variables may also be included in this regression.

The models in (2) may be extended to include time and area-time varying effects, such as seasonal effects, or unobserved area-time random effects $\delta_{it}$. These represent local trends not fully captured by autoregressive effects on lagged infection levels. Thus for representations (3) and (4), one has

$$
\mu_{it} = \rho_{it}y_{i,t-1} + \lambda_{it} \sum_j w_{ij}y_{j,t-1} + \exp(\eta_i + \delta_{it}),
$$

while for representations (5) and (6), one has

$$
\mu_{it} = \rho_{it}y_{i,t-1} + \lambda_{it} \sum_j w_{ij}y_{j,t-1} + \exp(\eta_i + \delta_{it}).
$$

(9)

Model Specification

The forms (8) and (9) are adopted in the case studies below. The spatial effects ($f_{1i}, f_{2i}, f_{3i}, f_{4i}$) and ($g_{1i}, g_{2i}, g_{3i}, g_{4i}$) involved in defining the autoregression coefficients are taken to follow the conditional autoregressive (CAR) scheme of Besag et al (1991). It is assumed that

$$
\eta_i = X_i \beta + u_i,
$$

where $u_i$ are also mean centred CAR spatial effects. It is assumed that the area-time effects $\delta_{it}$ follow a first order random walk $\delta_{it} \sim N(\delta_{i,t-1}, \sigma^2_{\delta})$, with initial conditions $\delta_{i1}$ taken as fixed effects, $\delta_{i1} \sim N(0, 1)$. For identification an intercept is omitted from $X_i \beta$, and covariates are centred. A single covariate is used in both case studies, the mid-2020 population estimates, divided by 100 thousand.
Gamma priors with shape one, and rate 0.01, are adopted on inverse variance parameters, the parameters \( \{q_{1t}, q_{2t}\} \), and on the negative binomial overdispersion parameter \( \Omega \). Normal \( \mathcal{N}(0,100) \) priors are assumed on fixed effects \( \{\alpha_1, \alpha_2, \kappa_1, \kappa_2, \beta_1\} \).

We consider one step ahead predictions. The predictive means are taken as
\[
\mu_{i,T+1} = \rho_{iT} y_{i,T} + \lambda_{iT} \sum_j w_{ij} y_{j,T} + \exp(\eta_i + \delta_{i,T+1}),
\]
and include the updated value \( \delta_{i,T+1} \sim N(\delta_{iT}, \sigma_\delta^2) \).

Analysis and Estimation

We apply the link mixture models specified in equations (5) and (6), and mean as in (9), these constituting models 3 and 4 respectively. Two simpler options are the log link as in (3), constituting model 1, and the other (as model 2) is the logit link, as in (4). Models 1 to 4 are denoted M1, M2, M3 and M4 respectively. Bayesian estimation is adopted, and implemented via the BUGS program (Lunn et al, 2009). Two chains of 20,000 iterations are taken, with inferences from the last 10,000, and convergence checks as in Brooks and Gelman (1998).

Fit is measured by the widely applicable information criterion (WAIC) (Watanabe, 2013). Performance of predictions \( P(y_{\text{rep},it}|y_{it}) = \int P(y_{\text{rep},it}|\theta) P(y_{it}|\theta) d\theta \) (where \( \theta \) denotes all parameters) is measured by the Dawid-Sebastiani score (DSS) and by the ranked probability score (RPS) (Czado et al, 2009). Let \( Y_t \) denote region wide totals at period \( t \) (i.e. total infections for all areas combined). Assume the models are fitted to \( T \) time periods, with period \( T+1 \) as hold out. One step ahead predictions to \( T+1 \) are assessed by whether these predictions include actual infection counts at \( T+1 \), and by the RPS for one step ahead predictions.

Case Study 1: London Boroughs, 32 areas, 96 weeks
The data for the first study consist of weekly totals of new COVID cases in the 32 boroughs of London. The time span considered starts at the week ending Sunday, 8 March 2020 (constituting week 1). The final observation (week 96) is that ending Sunday 2nd January 2022. Figures 1A and 1B show the trajectory of total cases, in two successive sub-periods. The upturn due to Omicron is apparent in the last few weeks of the series. The peak infections were at week 94 (with 169322 cases, compared to 65771 in the previous week), after which a downturn started. At the peak of the London Omicron wave, the UK Office of National Statistics estimated that around 8.8% of Londoners had COVID-19 (ONS, 2022, Table 1e). An earlier upturn due to the Delta variant produced a peak infection count of 93798 for the week ending 03/01/2021 (week 44 of the series), with a lesser upturn peaking at week 72. The peak in infections early on in the epidemic (peaking at week 5) is dwarfed by later upturns.

We take weeks 1-95 as the observed data, with week 96 as hold out. There were 155181
cases in that week, as infection levels due to Omicron started to tail off from the peak at week 94. Table 1 compares the four models in terms of fit to the data and prediction accuracy within the observed span. Table 1 also compares their out of sample predictions to week 96.

Regarding fit to the observed data, the WAIC, RPS and DSS criteria are all lower for the link mixture models than for the log and logit models (equations 3 and 4 respectively). Figure 2 shows the posterior mean RPS values for models M1-M4 disaggregated by week, with worse predictions under models 1 and 2 showing especially in epidemic phases (M1 and M2 are the red and blue lines in Figure 2).

Models 3 and 4 also have greater accuracy in one step ahead prediction, in terms of the coverage of the 95% credible interval (crI) for \( Y_{rep,T+1} \) of the actual value, and the RPS for week \( T + 1 \). The 95% crI under model 4 is (154018, 175048) including the true value, and the one-step ahead RPS is 42923. The 95% crI under model 3 also includes the true value. By contrast, the one step ahead RPS posterior means for M1 and M2 are 96920 and 95520. These models over-predict \( Y_{T+1} \), and the 95% credible intervals for \( Y_{rep,T+1} \) under M1 and M2 do not include the actual value.

The posterior mean \( \rho_t \) under M1 (which are time constant) vary from 0.13 to 0.25, while the mean \( \lambda_t \) vary from 0.19 to 0.72. The higher values show which boroughs tended to have higher growth in cases over one or more epidemic upturns. By contrast, under models 3 and 4, \( \rho_{it} \) and \( \lambda_{it} \) parameters often exceed 1 in weeks with high growth in cases, and one may identify the upturn weeks where particular areas have higher growth. Table 2 accordingly shows the 20 weeks with the highest values of \( R^2_t \) under M4. In a few weeks (such as weeks 2 and 94), all 32 boroughs have nonstationary growth, but Table 2 shows that such growth is concentrated in a relatively few weeks in the observation span.

Figures 3A, 3B, and 3C plot out the posterior mean \( \omega_t \) under M4 for weeks 50-95, the observed relative growth ratios \( Y_t/Y_{t-1} \) and the averages \( \bar{\rho}_t \) of the \( \rho_{it} \). Plots including the full observation span are unduly dominated by the extremely high relative growth rate \( Y_2/Y_1 \), namely 8.3, as weekly infections in London rose sharply when the COVID epidemic started in March 2020. In fact for weeks 50-95, the \( \omega_t \) and \( \bar{\rho}_t \) correlate highly (over 0.99) with the ratios \( Y_t/Y_{t-1} \). For 6 of these 45 weeks, the London wide \( \bar{\rho}_t \) under M4 have posterior mean exceeding 1, with the highest \( \bar{\rho}_t \) being 1.81 for week 94. These results confirm the utility of the link mixture mechanism in reproducing actual infection count fluctuations.

**Case Study 2: South East England, 144 areas, 20 weeks.**
The data for this study relate to the broader South East of England, encompassing 144 local authority areas in three standard regions (London, East, and South East). The time span consists of 21 weeks from the week ending the 9th August 2020 through to the week ending 27th December 2020. This period includes a peak in cases related especially to the
Delta variant, namely week 21 with 210099 cases. Figure 4 shows a lesser peak at week 14. Relative increases in weeks 7 and 8 are also high (over 60%), but case numbers remained low as compared to later weeks. We consider observations for the first 20 weeks, with week 21 held out from estimation. We compare the four models in terms of their fit to the observed data (weeks 1-20), and one step ahead predictions to week 21 when cases peaked.

Table 3 shows, as for the London study, that models 3 and 4 provide better fit and predictions to the observed data. Table 4 shows the RPS by week for the four models. Models M1 and M2 have worse predictive fit in weeks with rapid shifts in case numbers (large increases or falls, as in weeks 19 and 15). As to tracking extreme increases associated with the Delta variant, Figures 5A and 5B plot out the M4 posterior means by period of the statistics $R^e_t$ and $L^e_t$, the number of areas with slopes $\rho_{it}$ or $\lambda_{it}$ exceeding 1. These both peak in week 19, at 44.5 and 40.8 respectively (out of a total of 144 areas), implying that sharp growth in cases is from both local transmission and broader geographic diffusion. Comparison with Figure 5C shows how these statistics closely correlate with observed growth ratios $Y_t/Y_{t-1}$.

Models 3 and 4 also have better predictive out-of-sample performance for week 21 than M1 and M2. For example, the 95% crI for $Y_{Rep,T+1}$ under model 4 is (194169, 214482) comfortably including the actual value of 210099. By contrast models M1 and M2 tend to underpredict the future value, though the 97.5% point crI for M2 just includes the true value.

Discussion

Infection time series with explosive phases are of current concern due to repeated epidemic waves of the COVID outbreak. However, some infections may be characterized as endemic, and much recent commentary on COVID opines that it will eventually become an endemic disease. As noted by Katzorakis (2022), “an endemic infection is one in which overall rates are static — not rising, not falling”. Such infections may nevertheless have serious health impacts, examples being malaria and HIV.

Models suitable for relatively stable infectious diseases may not need to include any mechanism for sudden fluctuations, so justifying stationarity assumptions on autoregressive parameters. For an AR1 normal linear time series this would imply a constraint that the absolute autoregressive coefficient be under 1. Of course, formal definitions and properties of stationarity series have generally considered normal linear models, whereas the above analysis has considered modelling infection counts, albeit using identity links.

Stationarity in count time series (under a Poisson distribution), for an identity link, and with AR1 dependence on previous counts, is considered by Fokianos (2011), Fokianos and Tjostheim (2011) and Fokianos et al (2020). Thus with $y_t \sim Po(\mu_t)$, $\mu_t = d + by_{t-1}$, stationarity holds for $|b| < 1$. By contrast, as discussed by Fahrmeier and Tutz (2001, page 244), AR1 dependence on untransformed previous counts when a log-link is adopted leads
to explosive behaviour for any positive value of AR coefficient. If a log-link is adopted, one is instead led to models, called log-linear by Fokianos (2011), involving log-transformed previous counts, such as

$$\log(\mu_t) = d + b \log(y_{t-1} + 1).$$

In fact, the log-linear representation can be adapted to space-time infection data, but this has not been considered above. Another possible extension in both the linear and log-linear cases includes a lag on the intensity itself. Thus for the linear (identity link) case

$$\mu_t = d + by_{t-1} + c\mu_{t-1},$$

with again possible spatio-temporal modification possible.

For infection count time series with epidemic phases, stationarity is a restrictive assumption, and allowing non-stationary values is appropriate (e.g. Cazelles et al, 2018). The COVID epidemic has been characterised by extended periods of relatively stable infection levels followed by sudden sharp phases of increasing infection levels. Such epidemic peak are followed by a period of descending rates and subsequent return to stability. The above analysis has sought to allow an identity link autoregressive scheme to adapt to these pronounced fluctuations, with departures from stationarity during epidemic phases, but returning to stationarity as rates descend and infection rates resume broad stability. In particular, the mixture link model allows adaptivity to both explosive phases and static endemicity.

The above analysis of two sets of area-time COVID infection data has shown the mixture link approach, with a time varying weight that selects between explosive or stationary options, provides a better fit to the observed data. Both datasets include pronounced epidemic peaks as well as extended periods with relatively stable infection levels. The link mixture approach has also provided improved short term (one step ahead) predictions. Demand for such forecasts has been a central feature of the COVID pandemic (Rosenfeld and Tibshirani, 2021).

The methodology proposed here may have application beyond infectious disease counts, particularly to spatial and non-spatial panel data involving considerable time fluctuations, and especially when positive temporal autocorrelation or positive feedback from neighbouring locations is anticipated on substantive grounds (Glaser, 2017). Possible examples include urban crime (Liesenfeld et al, 2017), and spatial innovation diffusion (Bivand, 2015).

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