Modelling, Detrending and Decorrelation of Network Time Series

Marina Knight, Matt Nunes and Guy Nason*

29th February 2016

Abstract

A network time series is a multivariate time series augmented by a graph that describes how variables (or nodes) are connected. We introduce the network autoregressive (integrated) moving average (NARIMA) processes: a set of flexible models for network time series. For fixed networks the NARIMA models are essentially equivalent to vector autoregressive moving average-type models. However, NARIMA models are especially useful when the structure of the graph, associated with the multivariate time series, changes over time. Such network topology changes are invisible to standard VARMA-like models. For integrated NARIMA models we introduce network differencing, based on the network lifting (wavelet) transform, which removes trend. We exhibit our techniques on a network time series describing the evolution of mumps throughout counties of England and Wales weekly during 2005. We further demonstrate the action of network lifting on a simple bivariate VAR(1) model with associated two-node graph. We show theoretically that decorrelation occurs only in certain circumstances and maybe less than expected. This suggests that the time-decorrelation properties of spatial network lifting are due more to the trend removal properties of lifting rather than any kind of stochastic decorrelation.

1 Background

Recently, the analysis of data on graphs through time (network time series) has become of increasing importance. We are now able to collect not only large multivariate time series but also strong and useful information on how individuals (variables) in those multivariate time series are related to each other via a graph (network) description. Such hard network information is typically more powerful than just relying on measures of association (correlation) between variables to gauge their real relationship. We are primarily interested in stochastic processes observed at nodes of a graph over time and so we use ‘variable’ and ‘node’ interchangeably as context demands.

Suitable models for multivariate (or vector) time series have existed for a long time. For example, vector autoregression (VAR) models, see Hamilton [1994], Chapter 11 or Wei [2006], Chapter 16. This article proposes a new class of models for network time series: the network autoregressive (integrated) moving average (NARIMA) processes.

*Corresponding author: Guy P. Nason, School of Mathematics, University of Bristol, Bristol UK; g.p.nason@bristol.ac.uk
NARIMA models borrow heavily from existing multivariate time series models and, for fixed networks in their simplest form, they are statistically equivalent to a VAR. However, the NARIMA structure forces analysts to undertake a different approach to data modelling as the network structure influences the type of NARIMA (or VAR) model fitted. VAR model fitting requires various approaches to be undertaken to reduce the model dimension to a manageable size. In NARIMA models such modelling is considerably aided by the network structure.

A major advantage of NARIMA models is how they easily cope with the “moving node” effect in dynamic networks. Many networks are not static. In particular, nodes can change their position within the network structure or they can disappear or reappear. A good example of this effect often arises in epidemiological studies. For example, in the evolution of a foot and mouth disease outbreak infected individuals (cows) can die (or be born) but crucially they can move around the network as they get bought, or sold or taken to market or quarantined. A standard multivariate time series model (like VAR) only looks at the number of cases in a herd (for example) and has no explicit mechanism for incorporating the “moving node” effect. However, NARIMA models can explicitly track this important and valuable information and use it for modelling and forecasting purposes.

Another interesting, and hard to deal with, feature of network time series is that of trend. Trend is well-handled in regular time series by the important techniques such as differencing or fitting curves and, as such, trend removal is a vital component of time series, see Chatfield (2003). Unremoved trend can severely distort estimation of remaining stochastic structure. We propose using the network lifting method from Jansen et al. (2001) and Jansen et al. (2009) to estimate and remove trend from networks as a preprocessing step that can be used prior to modelling using NARIMA models. Finally, we consider a simple prototype NARIMA model and show theoretically, for the first time, the conditions under which (spatial) network lifting can achieve decorrelation in time.

2 Setup and Notation

This article is concerned with data collected on graphs (networks). Our graph, \( \mathcal{G} = (\mathcal{K}, \mathcal{E}) \), consists of a set of nodes, \( \mathcal{K} \), some of which are joined together by edges from some set of edges \( \mathcal{E} \). We define the set of \( \mathcal{K} \) nodes \( \mathcal{K} = \{1, \ldots, K\} \). Two nodes, \( i, j \in \mathcal{K} \), connected by an (undirected) edge are denoted by \( i \leftrightarrow j \). The set of edges in the graph are defined by \( \mathcal{E} = \{(i, j) : i \leftrightarrow j; i, j \in \mathcal{K}\} \). Sometimes, the set of edges is supplemented by another set, the edge distances \( \mathcal{D} \) which merely contains the distance \( d(i, j) \) between nodes \( i, j \) when \( i \leftrightarrow j \).

Suppose \( A \subset \mathcal{K} \) is a subset of nodes. The neighbourhood set of \( A \) is defined by \( \mathcal{N}(A) = \{j \in \mathcal{K}/A : j \leftrightarrow i, i \in A\} \). We define the set of \( r \)-th-stage neighbours of a node \( i \in \mathcal{K} \) by

\[
\mathcal{N}^{(r)}(i) = \mathcal{N}(\mathcal{N}^{(r-1)}(i)) \cup \bigcup_{q=1}^{(r-1)} \mathcal{N}^{(q)}(i),
\]

for \( r = 2, 3, \ldots \) and \( \mathcal{N}^{(1)}(i) = \mathcal{N}(\{i\}) \). In other words, \( \mathcal{N}^{(r)}(i) \) is the set of any points connected to any element of \( \mathcal{N}^{(r-1)}(i) \) by an edge that has not appeared in any earlier neighbourhood set.
Initially, we will consider functions that are evaluated at the nodes, and further interested in these values as functions of time. So, we consider time points, \( t_1, \ldots, t_T \), initially focusing on \( t_m = m \in \mathbb{N} \). A key part of a network time series is its component multivariate time series \( X_{i,t} \) for the value of the time series at node \( i \in \mathcal{K}(G) \) at time \( t \in 1, \ldots, T \), where \( \mathcal{K}(G) \) is the set of nodes associated with graph \( G \). Then

\[
\text{A network time series is } \mathcal{X} = \{X_{i,t}\}_{i \in \mathcal{K}(G), t=1}^T, \quad G.
\]

**Mumps example:** We study the number of cases of mumps in each of 47 counties of England and Wales taken weekly during 2005 from week one to week 52. This period of time was particularly interesting for this disease as it was shortly after the MMR scare which resulted in an abnormally large proportion of the relevant population not receiving the MMR vaccine. Figure 1 shows the situation for the first and last week of 2005 with number of cases colour-coded with deep red indicating few cases and yellow through to white indicating a large number of cases. For example, during week one Wales (which is treated as a single county here) and Devon have very high counts and in week 52 Wales is still high, as is Essex, but Devon’s cases have subsided. In this example, \( X_{i,t} \) is the multivariate time series of the number of cases of mumps in county \( i = 1, \ldots, 47 \) for weeks \( t = 1, \ldots, 52 \).

Figure 2 shows the graph, \( G \), associated with our network time series. This particular graph was constructed by identifying a “county town” for each county (and Rhayader for Wales) and the constructing a graph that connects all towns less than radius of a predefined fixed number of kilometres which reflects the strength of communication links between different parts of the UK. Of course, depending on the disease epidemiology, different graphs could be constructed. For example, in animal diseases such as foot and mouth routes between farms and between farms and markets, as well as geographical proximity to allow for spread of the disease vector by wind would be instrumental in the development of a suitable graph.

We will now introduce some models for network time series.

### 3 Network Autoregressive Moving Average Model (NARMA)

Suppose that \( \mathcal{X} \) is a network time series. A network autoregressive process of order \( p \) and neighbourhood order vector \( s \) of length \( p \), denoted \( \text{NAR}(p, s) \), is given by:

\[
X_{i,t} = \sum_{j=1}^{p} (\alpha_j X_{i,t-j} + \sum_{t=1}^{s_j} \sum_{q \in \mathcal{N}(r_q(i))} \beta_{j,r,q} X_{q,t-j}) + \epsilon_{i,t}, \tag{2}
\]

where, for this article at least, we assume \( \epsilon_{i,t} \) are a set of mutually uncorrelated random variables with mean zero and variance of \( \sigma^2 \).

Writing the vector \( X_t = (X_{1,t}, \ldots, X_{K,t})^T \) and letting \( \{Z_t\} \) be a standard vector moving average model of order \( q \), with first term \( (\epsilon_{1,t}, \ldots, \epsilon_{K,t}) \), a network autoregressive moving average process of order \( (p, s; q) \) is given by \( Y_t = X_t + Z_t \). Clearly, such a model specification can get quite complicated, particularly for larger \( p, q \) and the majority of this article deals with NAR or NARI models.

An integrated model can be obtained after some differencing operator, \( \mathcal{D} \), is applied to some network \( X_t \) by \( W_t = \mathcal{D} X_t \) and \( W_t \) is then modelled as a NARMA
Figure 1: Number of cases of Mumps in each UK county during week 1 (left) and week 52 (right).
Figure 2: Graph showing connected edges between UK county towns.
process. This is analogous to the standard ARIMA mode of operations for univariate time series. We shall say more on ‘network differencing’ or detrending in Section 4.

Model (2) expresses how past values of the network time series influence the current values. In particular, \( X_{i,t} \) depends directly on its past values at that node via the \( \alpha_j \) term and also on past values of its neighbours (and neighbours of neighbours, etc) through the \( \beta_{j,r,q} \) term. Our NAR\((p, s)\) model assumes that the \( \{\alpha_j\} \) and \( \{\beta_{j,r,q}\} \) parameter sets do not depend on \( t \) (hence, stationarity is assumed), neither do they depend on the node \( i \) (spatial homogeneity). Naturally, both of these assumptions might be questioned in real examples and the model extended.

A NAR\((p, \mathbf{0}, \mathbf{0}, \ldots, \mathbf{0})\) means a model consisting of \( K \) separate regular AR\((p)\) time series models, one for each node. A general NAR\((p, s)\) model, as it is shown in (2) can be viewed as a vector autoregressive VAR model with a specific set of constraints on the VAR parameters. However, the modelling process is somewhat different with NARIMA models as past regressors depend on neighbours (and stage-\( r \) neighbours) of all nodes in the same way. More importantly, the way in which node neighbour contributions are constructed in NARIMA models is specialized and strongly relate to the structure and topology of the associated graph \( G \).

Later, though, we will define a gNARIMA process which is similar to NARIMA except that nodes can drop-out and reappear arbitrarily which is not covered by VAR. One might think that multivariate time series with missing observations can deal with this case, but nodes can disappear and reappear and change their geometry within the network in the meantime. So, in terms of the node and what it represents it refers to the same object, but its position in the graph might be quite different. gNARIMA models can handle this, whereas VAR can not.

### 3.1 NAR\((1, 1)\) example

To explain the key features of network autoregressive models we focus on the NAR\((p, s)\) model with \( p = 1 \) and \( s = 1 \) which can be written as

\[
X_{i,t} = \alpha X_{i,t-1} + \sum_{q \in \mathcal{N}(i)} \beta_q X_{q,t-1} + \epsilon_{i,t}, \tag{3}
\]

here we can drop the \( j \) and \( r \) subscripts for a simplified presentation. In this simpler example the value at node \( X_{i,t} \) depends directly on \( X_{i,t-1} \) in the usual autoregressive way, but also depends on the neighbours of node \( i \) at the previous time step \( t - 1 \).

There are several modelling choices to be made for network autoregressive models. We might choose to incorporate distance information into our specification of \( \beta_q \) such as weighting neighbours of \( i \) more if they are closer to \( i \). For example, we might compute inverse distance weights \( w_j(i) = d(i, j)/\sum_{k \in \mathcal{N}(i)} d(i, k) \) for \( j \in \mathcal{N}(i) \). Then we might parametrise \( \beta_q \) in (3) by

\[
\beta_q = \beta \ w_q(i), \tag{4}
\]

for \( q \in \mathcal{N}(i) \). This model specifies the overall first-stage neighbour autoregression strength by \( \beta \) but modulated by the inverse distance weights. With a gNARIMA model we permit the weights to change as a node changes its position (or existence) within the network topology. Such changes can be easily incorporated into the least-squares estimation process as the overall model description does not change.
3.2 NAR(1, 1) modelling for mumps data

We can use the `nar()` function in R to model mumps using the NAR(1, 1) model as an example and examine the fit. We first apply the modelling to the disease incidence, that is we divide the raw mumps counts by an estimate of the population size for each county. This information is stored in the network time series `mumpsPcor`.

We modelled the `mumpsPcor` series using the NAR(1, 1) model with the inverse distance weights specification for $\beta_q$ given in (4) using the command:

```r
model1 <- nar(vts=mumpsPcor, net=townnet2)
```

The model is fitted using least squares although it is easy to see that maximum likelihood or Bayesian inference might well be preferable in some circumstances, particularly when it comes to formulating uncertainty measures. From this model fit we estimated $\hat{\alpha} \approx 0.683$ and $\hat{\beta} \approx 0.263$. We also compute the residual matrix:

$$r_{i,t} = \hat{\epsilon}_{i,t} = X_{i,t} - \hat{\alpha}X_{i,t-1} - \sum_{q \in N^{(1)}(i)} \hat{\beta}_q X_{q,t-1},$$

for $t = 2, \ldots, 52$. The residuals are, as usual, vital for assessment of model fit. Figure 3 shows the residuals plotted against time for four counties and one can see that the residuals indicate that the model is not a good fit as the variance appears not to be constant over time. In time-honoured tradition we apply a variance stabilizing logarithmic transform. More precisely, we model $Y_{i,t} = \log(1 + X_{i,t})$ and this new multivariate time series is stored in the object `LmumpsPcor`. We refit the new model by

```r
model2 <- nar(vts=LmumpsPcor, net=townnet2)
```

which results in new estimates of $\hat{\alpha} \approx 0.647$ and $\hat{\beta} \approx 0.330$. Similar residual plots to those produced in Figure 3 are shown in Figure 4, although not perfect, show a much more reasonable adherence to constancy of variance.

We can further investigate the correlation structure of the residual series by using a cross-covariance analysis. Figure 5 shows the cross-covariance analysis for the $Y_{i,t}$ series (log population corrected mumps). The autocorrelation plots for Avon and Somerset show significant autocorrelations which decay slowly, not inconsistent with an autoregressive structure or possibly due to trend. (we will say more on which it might be in Section 5).

At this point we should mention that we have only showed autocorrelation plots for two counties. Similar plots occur for most of the other pairs and these two counties are fairly representative behaviour for all that comes below.

A further partial autocorrelation analysis (not shown) suggests and AR(2) structure for Avon and an AR(1) structure for Somerset. This means that we should investigate maybe a NAR{2, $(s_1, s_2)$} model, for some $s_1, s_2$ neighbour extent for each of the autoregressive components. Figure 5 also shows significant cross-correlations between the two series. Investigation of cross-plots for other pairs of cities (even those further apart) show similar information.

Figure 6 shows a cross-covariance analysis applied to the residuals of the NAR(1, 1) fit. Very little cross-correlation exists and much of the correlation in the series themselves is much reduced with maybe some slight further autoregressive structure remaining to be modelled. Since we believe there is further autoregressive structure to
Figure 3: Residual plots for Bedfordshire, Buckinghamshire, Cambridgeshire and Cheshire after fitting NAR(1, 1) model with inverse distance weight $\beta$ specification on population-corrected mumps counts.
Figure 4: Residual plots for Bedfordshire, Buckinghamshire, Cambridgeshire and Cheshire after fitting NAR(1, 1) model with inverse distance weight $\beta$ specification on logarithmic population-corrected mumps counts.
Figure 5: Cross covariance of log population corrected mumps series for Somerset and Avon (neighbouring counties).
Figure 6: Cross covariance of the residual following the NAR(1, 1) fit for Somerset and Avon (neighbouring counties).
be modelled we then fitted a NAR\((2, [1, 0])\) model (so, up to lag two standard AR structure, plus contributions from immediate neighbours of lag-one nodes). The associated cross-covariance of residuals plot is shown in Figure 7. Pleasingly, the autocorrelation plots look more consistent with white noise. The parameters of the NAR\((2, [1, 0])\) model were \(\hat{\alpha}_1 \approx 0.394\), \(\hat{\alpha}_2 \approx 0.380\) and \(\hat{\beta} \approx 0.204\).

We can also carry out a simple ANOVA analysis shown in Table 1. The table shows the benefits of moving from a NAR\((1, 0)\) model to a NAR\((2, [1, 0])\) model, but little benefit in going further and using a NAR\((2, [1, 1])\) model.

### 4 Trend Removal and Network Differencing

For a network time series there are a large number of possibilities to remove trend. We propose using the network lifting transform as described in [Jansen et al. (2001)] and [Jansen et al. (2009)]. Effectively, this transform performs a wavelet transform on
Table 1: ANOVA of selected NARIMA models on log-transformed data.

| Model          | Residual Sum of Squares |
|----------------|-------------------------|
| NAR(1, 0)      | 1212.2                  |
| NAR(1, 1)      | 1029.8                  |
| NAR(2, [1, 0]) | 862.2                   |
| NAR(2, [1, 1]) | 862.1                   |

Figure 8: Left: state of mumps network time series shown at time $t = 6$ weeks. Right: spatially detrended network at time $t = 6$ weeks. Four counties are shown for reference.

After trend removal we fitted several NARIMA models. Table 2 shows the ANOVA associated with some of these. Here, we have used a new model the NAR$(1, [2, 0])$ which only uses one-step temporal dependence, but with neighbours and neighbours of neighbours which corresponds to

$$X_{i,t} = \alpha X_{i,t-1} + \sum_{q \in N^1(i)} \beta_{q(1)}^{(1)} X_{q,t-1} + \sum_{r \in N^2(i)} \beta_{r(2)}^{(2)} X_{r,t-1} + \epsilon_{i,t}. \quad (6)$$
Figure 9: Density of values of mumps cases (solid) and detrended cases (dashed). 

Table 2: ANOVA of selected NARIMA models on detrended data.

| Model       | Residual Sum of Squares |
|-------------|-------------------------|
| NAR(1, 0)   | 1190.309                |
| NAR(1, 1)   | 1190.306                |
| NAR(1, [2, 0]) | 1182.4           |
| NAR[2, [1, 0]] | 961.1                 |
| NAR[2, [1, 1]] | 959.5                 |
Here, the parametrisation of $\beta^{(1)}_q$ is the same as above whereas $\beta^{(2)}_r$ is similar but the inverse distance weights are computed from new distances obtained by adding the distance of ‘neighbour of neighbour’ $r$ to neighbour $q$ and then the distance of $q$ to the original node $i$. This new total distance represents our best informed guess about the overall distance from ‘neighbour of neighbour’ $r$ to $i$.

The Table ANOVA shows that neighbours and neighbours of neighbours seem to have little explanatory power and, at this stage, without further investigation, we might be better off modelling the series purely as a set of separate univariate autoregressive processes as proposed and studied in this after-lifting context by Nunes et al. (2015).

5 Time-decorrelation achieved by spatial differencing

An intriguing empirical observation of the study exploited in Nunes et al. (2015) was that network differencing (across space) seemed to result in substantial decorrelation across time and the great practical advantage of being able to model a network series as a set of separate ARMA processes (i.e. not requiring VAR at all).

However, there is an important question. Is the excellent low-autocorrelation nature of the lifted multivariate series due to trend removal or decorrelation?

To study this phenomenon theoretically we begin with the simplest two-node network and endow it with a zero mean two-dimensional VAR(1) time series model. We label the nodes $i$ and $q$. The VAR(1) model we use parallels the one in (3) given as follows. Let $X_t = (X_{i,t}, X_{q,t})^T$. Then

$$X_t = \Pi_1 X_{t-1} + \epsilon_t,$$

where

$$\Pi_1 = \begin{pmatrix} \alpha & \beta \\ \beta & \alpha \end{pmatrix},$$

and $\epsilon_t$ is a bivariate white noise process with zero mean and variance $\sigma^2 I$. The eigenvalues of $\Pi_1$ are $\alpha + \beta$, $\alpha - \beta$ and standard texts show that conditions for stationarity are $|\alpha + \beta| < 1$ and $|\alpha - \beta| < 1$. The region of stationarity can be graphically depicted by the square of side length $\sqrt{2}$, centered on the origin rotated by $\pi/4$. The stationary covariance matrix of $X_t$ is given by $\Sigma_X = \sigma^2 \sum_{k=0}^{\infty} \Pi_1^{2k} = (I - \Pi_1^2)^{-1}$. Let $\sigma^2_i = \text{var}(X_{i,t})$ and $\sigma^2_{i,q} = \text{cov}(X_{i,t}, X_{q,t})$. Due to the symmetry in the model $\sigma^2_q = \sigma^2_i$ for this system. Moreover, it can be shown that the cross-correlation $\rho_{i,q} = \sigma_{i,q}/\sigma^2_i = 2\alpha\beta/(1 - \alpha^2 - \beta^2)$.

We desire to study the network lifted version of this VAR(1) process. The lifted coefficients in this case are particularly simple and just differences:

$$d_{i,t} = X_{i,t} - X_{q,t} \quad \text{and} \quad d_{q,t} = X_{q,t} - X_{i,t} = -d_{i,t},$$

for all $t$.

Hence, now we have a lifted VAR(1) process what is its autocorrelation? First, we compute the autocovariance of the process $X_{i,t}$ at lag one

$$c_X = \text{cov}(X_{i,t}, X_{i,t-1}) = \text{cov}(\alpha X_{i,t-1} + \beta X_{q,t-1}, X_{i,t-1}) = \alpha \sigma^2_i + \beta \sigma_{i,q},$$

for all $t$. The Table ANOVA shows that neighbours and neighbours of neighbours seem to have little explanatory power and, at this stage, without further investigation, we might be better off modelling the series purely as a set of separate univariate autoregressive processes as proposed and studied in this after-lifting context by Nunes et al. (2015).
Figure 10: Left: regions where $\text{ad}(\alpha, \beta) < 0$ (red) and $\text{ad}(\alpha, \beta) > 0$ (blue). Right: contour plot of $\rho_{i,q}(\alpha, \beta)$ where deep reds/blues correspond to large positive/negative correlations. Both plots have $\alpha - \beta$ on the horizontal axis and $\alpha + \beta$ on the vertical axis which correspond to rotating and shrinking the actual stationary region to the unit square centred at the origin.

Our empirical results on real data suggested that $|c_d|$ is often less than $|c_X|$ in the general multivariate lifting situation. Is this true for our cut-down model?

We can further simplify $c_X, c_d$ by dividing through by $\sigma_i^2$ to obtain $r_X = \alpha + \beta \rho_{i,q}$ and $r_d = 2(\alpha - \beta)(1 - \rho_{i,q})$ where we have an explicit expression for $\rho_{i,q}$ in terms of $(\alpha, \beta)$ from above. We examine:

$$\text{ad}(\alpha, \beta) = |c_X| - |c_d|, \quad (17)$$

as the difference of the absolute values of the unlifted and lifted lag-one covariance. We are interested in knowing when there is a reduction in absolute covariance and, hence, ask when is $\text{ad}(\alpha, \beta) > 0$? Figure 10 (left) shows that $\text{ad}(\alpha, \beta)$ is more often negative than positive, corresponding to an increase in the absolute value of the lag-one autocorrelation, the opposite of what we might have hoped from Nunes et al. (2015). It is also helpful to refer to Figure 10 (right) which shows the contours of $\rho_{i,q}(\alpha, \beta)$ in the same coordinate system as the left plot. It can be seen that $|\rho_{i,q}|$ is large near the boundaries of the region and from the left plot it can be seen the negative spatial correlations are associated with an increase in absolute autocorrelation, but
Figure 11: Autocorrelation plots of the $X_{i,t}$ series (top row) and $d_{i,t}$ series (bottom row) for the situation $\alpha = \beta = 0.4$ (left column) and $\alpha = 0.4, \beta = -0.4$ (right column).
with positive spatial correlations are associated with a decrease. Figure 11 shows the above result in action. For $\alpha = \beta = 0.4$ the quantity $\rho_{i,q} = 8/17$ is positive and, according to the theory, should result in a decrease in the absolute autocorrelation. Indeed, comparing the bottom with top plot in the left column of Figure 11 shows that the autocorrelations at lag one (and the rest) are all much smaller. However, for $\alpha = 0.4, \beta = -0.4$ we have $\rho_{i,q} = -8/17$ the theory says that the autocorrelation should increase in absolute value and, indeed, looking at the right column from top to bottom in Figure 11 this is indeed the case.

Overall, the message is that there is not a uniform reduction in the absolute value of autocorrelation, nor is it possible to say that it mostly happens. Whether it happens or not depends specifically on the choice of the parameters in this model.

At this point it should be stressed that this is a very simple case. The theory above only examines a simple bivariate VAR model on a network with two nodes. Our mumps network has 47 nodes and many real networks are much larger. For the two node network the lifting step is particularly simple (differencing of neighbouring values). For larger networks, nodes with a larger number of neighbours are not merely subject to differencing but subtract off some linear combination of its neighbour values. We conjecture when these are positively correlated then there will be a reduction in correlation, but for those situations where negative correlations are involved, the result will be unpredictable. Further study is required in this area.

In practical terms, it seems likely that our network differencing, $\mathcal{D}$, is responsible for removing trend which is causing slow autocorrelation decay akin to integrated processes in classical time series analysis.

Acknowledgements

We would like to thank Douglas Harding and Daniela DeAngelis of the Health Protection Agency for supplying the Mumps data.

References

Chatfield, C. (2003) *The Analysis of Time Series: An Introduction*, Chapman and Hall/CRC, London, sixth edition.

Hamilton, J. D. (1994) *Time Series Analysis*, Princeton University Press, Princeton, New Jersey.

Jansen, M., Nason, G. P., and Silverman, B. W. (2001) Scattered data smoothing by empirical Bayesian shrinkage of second generation wavelet coefficients, in M. Unser and A. Aldroubi, eds., *Wavelet applications in signal and image processing. Proceedings of SPIE*, volume 4478, pp. 87–97.

Jansen, M., Nason, G. P., and Silverman, B. W. (2009) Multiscale methods for data on graphs and irregular multidimensional situations, *J. R. Statist. Soc. B*, 71, 97–126.

Nunes, M., Knight, M., and Nason, G. (2015) Modelling and prediction of time series arising on a graph., in A. Antoniadis, J.-M. Poggi, and X. Brossat, eds., *Modeling*
and Stochastic Learning for Forecasting in High Dimensions, volume 217 of Lecture Notes in Statistics, pp. 183–192, Springer.

Wei, W. W. S. (2006) Time Series Analysis: Univariat and Multivariate Methods, Addison-Wesley, Boston.