# Some notes on state-space LBM

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**Abstract**

In response to the global coronavirus pandemic, we study co-clustering of multivariate time-series data as a way to simultaneously cluster both geographical regions and time periods after the outbreak of the pandemic. The resulting blocks of clusters, identified with a latent block model component, are integrated with an extended SIR model that takes both geographical clusters as well as clusters of time periods into account. We consider US data (or global or both?) and show how the novel latent block SIR model produce better prediction accuracy of the epidemic, and gives further understanding of how the virus is spreading in different geographical regions during different periods of time.

## 1 The Extended SIR model

The latent block model (Gérard Govaert and Nadif, 2003) is a commonly used model for co-clustering of large data matrices. It is a model-based approach that assumes that the rows and columns of the data matrix can be arranged according to latent row and column clusters. It has been extended to cover the case of counting data (Gérard Govaert and Nadif, 2010), continuous data (Nadif and Gerard Govaert, 2010), categorical data (Keribin et al., 2015), ordinal data (Jacques and Biernacki, 2018; Corneli, Charles Bouveyron, and Latouche, 2020), functional data (C. Bouveyron et al., 2018) and tensor data (Boutalbi, Labiod, and Nadif, 2020). In this work, the latent block model is extended in two ways: first by covering time-series data of proportions, and secondly by being integrated with the SIR model (Kermack and McKendrick, 1927), commonly used in the analysis of disease spread.

To specify the suggested State-Space Latent Block Model (SS-LBM), we introduce the following notation: $\mathbf{y} = (\mathbf{y}_{it}, i = 1, \ldots, n; t = 1, \ldots T)$ denotes the data matrix which is a multivariate time series: $\mathbf{y}_{it} = (y_i^1(t), \ldots, y_i^S(t))$ where $t \in [0, T]$. In the context of analyzing the 2020 coronavirus pandemic, $\mathbf{y}_{it} = (y_i^I(t), y_i^R(t))^\top$ where $y_i^I(t)$ and $y_i^R(t)$ denote the proportion of infected and removed (recovered or dead) by the virus, respectively, at time point $t$. The index $i$ denotes a geographical region, like for example country or state. Further, let $\boldsymbol{\theta} = (\theta_t^S, \theta_t^I, \theta_t^R)^\top$, where $\theta_t^S$, $\theta_t^I$ and $\theta_t^R$ is the probability of a person being susceptible, infected and removed, respectively, at time point $t$. They thus satisfy $\theta_t^I + \theta_t^I + \theta_t^R = 1$ and $\theta_t^S, \theta_t^I, \theta_t^R > 0$ for all $t \in [0, T]$ (Osthus et al., 2017). We will take the same approach as in Osthus et al. (2017) and Song et al. (2020) and assume that $\boldsymbol{\theta}_{0:T} = (\boldsymbol{\theta}_0, \boldsymbol{\theta}_1, \ldots, \boldsymbol{\theta}_T)$ is a first-order Markov chain. This implies that $g(\boldsymbol{\theta}_t | \boldsymbol{\theta}_{0:(t-1)}) = g(\boldsymbol{\theta}_t | \boldsymbol{\theta}_{t-1})\, \forall t \in [0 : T]$. Specifically, the extended SIR model as suggested by Osthus et al. (2017) and extended by Song et al. (2020), assumes the following model for $\boldsymbol{\theta}$:

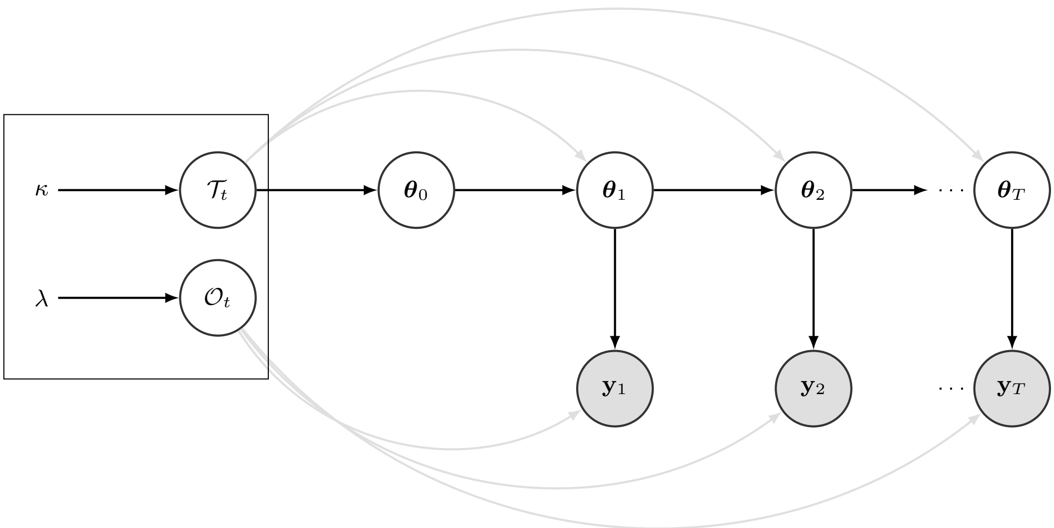
$$\boldsymbol{\theta}_t|\boldsymbol{\theta}_{t-1}, \boldsymbol{\Omega}_1 \sim \text{Dirichlet}(\kappa f(\boldsymbol{\theta}_{t-1})),$$

where $\boldsymbol{\Omega}_1$ denotes the set of model parameters, $\kappa$ scales the variance of the Dirichlet distribution, and the function $f(\cdot)$ is a 3-dimensional vector that sets the mean of the Dirichlet distribution. The form of the function $f(\cdot)$ will be presented in what follows. For the observed data $\mathbf{y}$, Song et al. (2020) make the following distributional assumptions,

$$\begin{aligned} y_i^I(t)|\boldsymbol{\theta}, \boldsymbol{\Omega}_1 &\sim \text{Beta}(\lambda^I \theta_t^I, \lambda^I(1-\theta_t^I)) \\ y_i^R(t)|\boldsymbol{\theta}, \boldsymbol{\Omega}_1 &\sim \text{Beta}(\lambda^R \theta_t^R, \lambda^R(1-\theta_t^R) \end{aligned} \tag{1}$$

for $i = 1, \dots, n$, $t = 1, \dots, T$, and $\boldsymbol{\Omega}_1 = (\rho, \gamma, \boldsymbol{\theta}, \lambda^I, \lambda^R, \kappa)^\top$, where $\lambda^I$ scales the variance in each respective distribution of $y_i^I(t)$ and $y_i^R(t)$.

The extended SIR model thus considers a bivariate stochastic process $\{\boldsymbol{\theta}_t, \mathbf{y}_t\}$ that is modeled using a state-space model: $\boldsymbol{\theta}_t$ is the underlying, latent process that guides the observed data $\boldsymbol{y}_t = (y_i^I(t), y_i^R(t))$. This can be graphically summarized as




Regarding the function $f(\cdot)$, it is the solution to the dynamic system

$$\frac{d\theta_t^S}{dt} = -\rho\pi(t)\theta_t^S\theta_t^I, \quad \frac{d\theta_t^I}{dt} = \rho\pi(t)\theta_t^S\theta_t^I - \gamma\theta_t^I, \quad \frac{d\theta_t^R}{dt} = \gamma\theta_t^I, \tag{2}$$

where $\rho > 0$ is the transmission rate of the disease, and $\gamma > 0$ is the rate of recovery. The term $\pi(t)$ is a transmission modifier equal to $\pi(t) = (1 - q^S(t))(1 - q^I(t))$, where $q^S(t)$ denotes the probability of a susceptible person being in-home isolation, and $q^I(t)$ the probability of an infected person being in-hospital quarantine. The term $\pi(t)$ therefore is a transmission modifier in the sense that it modifies the probability of a susceptible person getting in contact with an infected person. The chance of such a meeting to occur is to a great extent determined by which restrictions on social gatherings are in place. For example, if a geographical region does not impose a quarantine, $\pi(t) = 1$, and the dynamic system in (2) reduces to the clasic formulation of the SIR model. As the rules of social distancing gets stricter, the transmission modifier $\pi(t)$ decreases, making the overall transmission rate to decrease as well. In this work, the $\pi(t)$ term is allowed to differ from 1.

Since there are no explicit solutions available to (2), the so-called fourth-order Runge-Kutta approximation is implemented, meaning that

$$\begin{pmatrix} f(\theta^S_{t-1}) \\ f(\theta^I_{t-1}) \\ f(\theta^R_{t-1}) \end{pmatrix} = \begin{pmatrix} \theta^S_{t-1} + 1/6[k^{\theta^S_1}_{t-1} + 2k^{\theta^S_2}_{t-1} + 2k^{\theta^S_3}_{t-1} + k^{\theta^S_4}_{t-1}] \\ \theta^I_{t-1} + 1/6[k^{\theta^I_1}_{t-1} + 2k^{\theta^I_2}_{t-1} + 2k^{\theta^I_3}_{t-1} + k^{\theta^I_4}_{t-1}] \\ \theta^R_{t-1} + 1/6[k^{\theta^R_1}_{t-1} + 2k^{\theta^R_2}_{t-1} + 2k^{\theta^R_3}_{t-1} + k^{\theta^R_4}_{t-1}] \end{pmatrix}$$

where

$$\begin{aligned} k^{\theta^S_1}_{t-1} &= -\rho\pi(t-1)\theta^S_{t-1}\theta^I_{t-1}, \\ k^{\theta^S_2}_{t-1} &= -\rho\pi(t-1)[\theta^S_{t-1} + 0.5k^{\theta^S_1}_{t-1}][\theta^I_{t-1} + 0.5k^{\theta^I_1}_{t-1}], \\ k^{\theta^S_3}_{t-1} &= \rho\pi(t-1)[\theta^S_{t-1} + 0.5k^{\theta^S_2}_{t-1}][\theta^I_{t-1} + 0.5k^{\theta^I_2}_{t-1}], \\ k^{\theta^S_4}_{t-1} &= \rho\pi(t-1)[\theta^S_{t-1} + k^{\theta^S_3}_{t-1}][\theta^I_{t-1} + k^{\theta^I_3}_{t-1}], \end{aligned}$$

$$\begin{aligned} k^{\theta^I_1}_{t-1} &= \rho\pi(t-1)\theta^S_{t-1}\theta^I_{t-1} - \gamma\theta^I_{t-1}, \\ k^{\theta^I_2}_{t-1} &= \rho\pi(t-1)[\theta^S_{t-1} + 0.5k^{\theta^S_1}_{t-1}][\theta^I_{t-1} + 0.5k^{\theta^I_1}_{t-1}] - \gamma[\theta^I_{t-1} + 0.5k^{\theta^I_1}_{t-1}], \\ k^{\theta^I_3}_{t-1} &= \rho\pi(t-1)[\theta^S_{t-1} + 0.5k^{\theta^S_2}_{t-1}][\theta^I_{t-1} + 0.5k^{\theta^I_2}_{t-1}] - \gamma[\theta^I_{t-1} + 0.5k^{\theta^I_2}_{t-1}], \\ k^{\theta^I_4}_{t-1} &= \rho\pi(t-1)[\theta^S_{t-1} + k^{\theta^S_3}_{t-1}][\theta^I_{t-1} + k^{\theta^I_3}_{t-1}] - \gamma[\theta^I_{t-1} + k^{\theta^I_3}_{t-1}], \end{aligned}$$

and

$$\begin{aligned} k^{\theta^R_1}_{t-1} &= \gamma\theta^I_{t-1}, \\ k^{\theta^R_2}_{t-1} &= \gamma[\theta^I_{t-1} + 0.5k^{\theta^I_1}_{t-1}], \\ k^{\theta^R_3}_{t-1} &= \gamma[\theta^I_{t-1} + 0.5k^{\theta^I_2}_{t-1}], \\ k^{\theta^R_4}_{t-1} &= \gamma[\theta^I_{t-1} + k^{\theta^I_3}_{t-1}]. \end{aligned}$$

## 2 Latent Block Model

With $n$ countries measured on $T$ time points, the data matrix $\mathbf{y}$ that we wish to co-cluster equals

$$\mathbf{y} = \begin{bmatrix} (y^I_1(1), y^R_1(1)) & (y^I_1(2), y^R_1(2)) & \dots & (y^I_1(T), y^R_1(T)) \\ (y^I_2(1), y^R_2(1)) & (y^I_2(2), y^R_2(2)) & \dots & (y^I_2(T), y^R_2(T)) \\ \vdots & \vdots & \dots & \vdots \\ (y^I_n(1), y^R_n(1)) & (y^I_n(2), y^R_n(2)) & \dots & (y^I_n(T), y^R_n(T)) \end{bmatrix}$$

Following the latent block model, we assume that there is a partition $(Z, W)$ of the data matrix $\mathbf{y}$, where $Z = (z_{ik}; , i = 1, \ldots, n,\ k = 1, \ldots, K)$ represents the partitioning into $K$ clusters on the $n$ rows and $W = (w_{tl}; t = 1, \ldots, T,\ l = 1, \ldots, L)$ represents the partitioning into $L$ clusters on the $T$ columns. In other words, $Z_{ik},\ k = 1, ..., K$ and $W_{tl},\ l = 1, ..., L$ are binary matrices for which $Z_{ik} = 1$ if case $i$ belongs to row cluster $k$ and 0 otherwise, and $W_{jl} = 1$ if time point $t$ belongs to column cluster $l$ and 0 otherwise. The random matrices $Z$ and $W$ therefore are of dimension $n \times K$ and $T \times L$, respectively.

Co-clustering will yield subgroups, called blocks, such that $Z_{ik}W_{tl} = 1$. Each element $\mathbf{y}_{it}$ in $\mathbf{y}$ belongs to a block which is generated by a probability distribution. In this study it is assumed that $y_i^I(t)$ and $y_i^R(t)$ follow Beta distributions, meaning that these block distributions are given by the distributions specified by Equation 1. Specifically, we assume that

$$\begin{aligned} y_i^I(t)|Z_{ik}W_{jl} = 1, \mathbf{\Omega}_1 &\sim \text{Beta}(\lambda^I \theta_{kl}^I(t), \lambda^I(1 - \theta_{kl}^I(t)) \\ y_i^R(t)|Z_{ik}W_{jl} = 1, \mathbf{\Omega}_1 &\sim \text{Beta}(\lambda^R \theta_{kl}^R(t), \lambda^R(1 - \theta_{kl}^R(t)) \end{aligned} \tag{3}$$

and

$$\boldsymbol{\theta}_t|\boldsymbol{\theta}_{t-1}, \mathbf{\Omega}_1 \sim \text{Dirichlet}(\kappa f(\boldsymbol{\theta}_{kl}(t-1))) \tag{4}$$

where $\theta_{kl}^S(t)$, $\theta_{kl}^I(t)$ and $\theta_{kl}^R(t)$ denote the probabilities of a case in row cluster $k$ and column cluster $l$ being suscepted, infected and removed, respectively, at time point $t$. We thus assume that the latent process $\boldsymbol{\theta}(t)$ guides the observed data in each block cluster.

It is assumed that $Z$ and $W$ are independent from each other and that the random variables $\mathbf{y}$ are independent conditional on $Z$ and $W$. With this formulation of the model we further assume that there is a geographical partition of geographical regions that are homogeneous in terms of proportion infected $y^I(t)$ and removed $y^R(t)$, and that there is a partitioning of the time points $t$ that form homogeneous blocks.

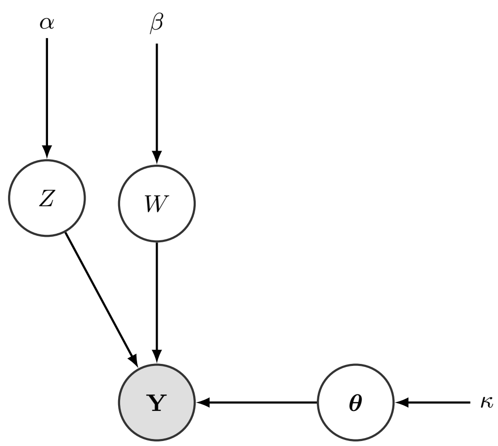
Now let $\alpha_k = P(Z_{ik} = 1)$ and $\beta_l = P(W_{jl} = 1)$ denote the respective row and column mixing proportions such that they both sum to 1 and $p(z; \theta) = \prod_{ik} \alpha_k^{z_{ik}}$ and $p(w; \theta) = \prod_{ik} \beta_l^{w_{jl}}$. Under the assumption of $Z$ and $W$ being independent, and by letting $\mathcal{Z}$ and $\mathcal{W}$ denote the sets of all possible partitions of $Z$ and $W$, the likelihood of the LBM equals

$$L(\mathbf{\Omega}_2) = \sum_{(z,w) \in \mathcal{Z}, \mathcal{W}} \prod_{i,g} \alpha^{z_{ig}} \prod_{j,l} \beta^{w_{jl}} \prod_{i,j,k,l} \varphi(\mathbf{y}_{ij}; \omega_{kl})^{z_{ig} w_{jl}},$$

where $\omega_{kl}$ represents the parameter of $\varphi$ for the $kl$ block. The log-likelihood equals

$$\log L(\mathbf{\Omega}_2) = \sum_{i,k} z_{ik} \log \alpha_k \sum_{j,l} w_{jl} \log \beta_l \sum_{i,j,k,l} z_{ik} w_{jl} \log \varphi(\mathbf{y}_{ij}; \omega_{kl}),$$

The state-space LBM can now graphically be represented as




# 3 Estimation

Since there are two model components of the eSIR LBM, we repeat the total set of parameters that needs to be estimated. The unknown parameters from the eSIR model component of the likelihood thus equals $\mathbf{\Omega}_1 = (\rho, \gamma, \boldsymbol{\theta}, \lambda, \kappa)$ and the LBM model component of the likelihood equals $\mathbf{\Omega}_2 = (\alpha, \beta, \omega)$. The total set of parameters to be estimated thus equals $\mathbf{\Omega} = \mathbf{\Omega}_1 + \mathbf{\Omega}_2 = (\rho, \gamma, \boldsymbol{\theta}, \lambda, \kappa, \alpha, \beta, \omega)$.

For the estimation of the eSIR LBM model, we will assume that $\varphi(\mathbf{y}_{ij}; \omega_{kl})$ follows a Dirichlet distribution:

$$\varphi(\mathbf{y}_{ij}; \omega_{kl}) = D(\omega_{kl})^{-1} \prod_{j=1}^{d+1} y_{ij}^{\omega_{kl}-1}$$

So should we model $\varphi(\cdot)$ as a bivariate beta distribution (meaning Dirichlet distribution)? Regarding this, see the paper "Time Series of Continuous Proportions", by Grunwald, Raftery and Guttorp (1993), where they model the time series of proportions using the Dirichlet distribution.

There is a paper ("Estimation and selection for the latent block model on categorical data" by Keribin et al.) that implements the LBM for multinomial data that in the estimation of the model sets prior distributions for the mixing proportions as well as the parameter that governs the $Y$ distribution. This would in a sense be similar to our case, since the eSIR model imposes a Dirichlet prior on the $\boldsymbol{\theta}$ parameter. If we would further impose Dirichlet priors on the mixing proportions, would we be able to do something similar as in Keribin et al.?

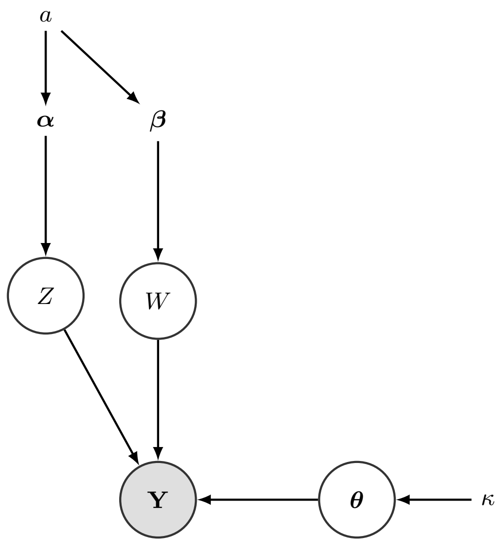
So specifically, following (Keribin et al., 2015) we can consider proper and non-informative priors for $\alpha$ and $\beta$ as

$$\begin{aligned} \boldsymbol{\alpha} &\sim \text{Dirichlet}(a, \dots, a) \\ \boldsymbol{\beta} &\sim \text{Dirichlet}(a, \dots, a) \end{aligned} \tag{5}$$

In (Keribin et al., 2015) they consider a very similar general modeling structure and estimate the model parameters $\boldsymbol{\tau}$ by maximizing the posterior density $p(\boldsymbol{\tau}|\boldsymbol{y})$, which leads to the Maximum A Posteriori (MAP) estimator:

$$\hat{\boldsymbol{\tau}}_{MAP} = \underset{\boldsymbol{\tau}}{\operatorname{argmax}}\, p(\boldsymbol{\tau}|\boldsymbol{y}) \tag{6}$$

We would thus be able to graphically represent the model as

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