Model G – a SEIR filter

October 29, 2020

1 Model Definition

Assume an infinite population, each individual of which finds himself in one of the compartments $S_0, \ldots, S_k$. Let $I_t \in \mathbb{N}_0^k$, $t \in \mathbb{N}_0^+$, be an external inflow (import) of individuals into the compartments $(1, \ldots, k)$ and let $Z_t \in \mathbb{R}^n$, $t \in \mathbb{N}_0^+$, be an observed exogenous process.

For any $t \in \mathbb{N}_0$, let $X_t = (X_t^1, \ldots, X_t^k) \in \mathbb{N}_0^k, t \in \mathbb{N}_0$, be a possibly hidden stochastic process of the compartment sizes which we define later. Let

$$Y_t \in \mathbb{R}^n, \qquad Y_t = FX_t + \epsilon_t, \qquad t \in \mathbb{N}_0,$$

be a process of observations where F is a deterministic $n \times k$ matrix with rank n, and ϵ_t is a random vector. Denote $\mathcal{F}_t$ and $\mathcal{G}_t$ the filtrations induced by (X, Y, I, Z), by (Y, I, Z), respectively, $\mathcal{F}_t$ representing all the information, $\mathcal{G}_t$ the observable one. We assume that

$$\mathbb{E}(\epsilon_{t+1}|\mathcal{F}_t) = 0, \qquad \mathrm{var}(\epsilon_{t+1}|\mathcal{F}_t) = \mathrm{diag}(\Gamma_t X_t), \qquad t \in \mathbb{N}_0,$$

where $\Gamma_t \in \mathcal{G}_t$ is a random matrix.

We define X recursively. Namely, we let X_0 be possibly random and, for any $t \in \mathbb{N}$, we put

$$X_{t+1} = I_t + M_{t+1} + N_{t+1}.$$

Here, $N_{t+1} \in \mathbb{N}_0^k$ is the inflow (of the newly infected) from S_0 into the remaining compartments fulfilling $N_{t+1}|\mathcal{F}_t \sim \mathrm{Po}(G_t X_t)$ where $G_t = (\gamma_t^{ij})_{1 \le i,j \le k} \in \mathcal{G}_t$ is a random matrix and, for any vector x, $\mathrm{Po}(x)$ stands for a vector of independent Poisson variables with the intensities given by x. Further, $M_{t+1} \in \mathbb{N}_0$ is the vector such that, for each i, with $M_{t+1}^i$is the number of the individuals who found themselves in one of the compartments $(1, \ldots, k)$ at t and are in compartment i at $t+1$. Assuming the individuals to change their state according to a common transition matrix $P_t = (p_t^{ij})_{1 \le i,j \le k} \in \mathcal{G}_t$ with the changes being conditionally independent given $\mathcal{F}_t$, we get $M_{t+1}|\mathcal{F}_t \sim \bigcirc_{1 \le i \le k} \mathrm{Mult}(X_t^i, P_t^i)$, where $\bigcirc$ stands for convolution, Mult stands for the multinomial distribution and, for any matrix A, A^i is the i-th column of A.

Finally, we assume that N_{t+1}, M_{t+1} and ϵ_{t+1} are mutually conditionally independent given $\mathcal{F}_t$ (which roughly means that all the dependence between the inflows, the transitions and the observation can be explained by the state of the system at t).

1.1 Model Properties

By probability calculus, we get that

$$\mathbb{E}\left[\begin{array}{c} X_{t+1} \\ Y_{t+1} \end{array}\middle|\, \mathcal{F}_t\right] = \begin{bmatrix} E \\ F \end{bmatrix}(T_t X_t + I_t), \tag{1}$$

$$\mathrm{var}\left(\begin{array}{c} X_{t+1} \\ Y_{t+1} \end{array}\middle|\, \mathcal{F}_t\right) = \begin{bmatrix} E \\ F \end{bmatrix}\Lambda_t(X_t)\begin{bmatrix} E \\ F \end{bmatrix}^T + \mathrm{diag}\begin{pmatrix} 0_{\mathrm{k}} \\ \Gamma_{\mathrm{t}}\mathrm{X}_{\mathrm{t}} \end{pmatrix}, \qquad t \geq 0,$$

where E is the identity matrix and

$$T_t \stackrel{\mathrm{def}}{=} P_t + G_t, \qquad \Lambda_t(X_t) \stackrel{\mathrm{def}}{=} \sum_{i=1}^{k} [\mathrm{diag}(P_t^i) - P_t^i (P_t^i)^T] X_t^i + \mathrm{diag}(G_t X_t), \qquad t \geq 0.$$

Note that

$$\Lambda_t(x) = \sum_{i=1}^{k} \Phi_{t,i} x^i, \qquad \Phi_{t,i} \stackrel{\mathrm{def}}{=} \mathrm{diag}(G_t^i + P_t^i) - P_t^i (P_t^i)^T, \qquad t \geq 0, x \in \mathbb{R}_+^k,$$

i.e. Λ_t is linear in x.

We call the subset of states $D = \{s_1, \ldots, s_m\}$ *self-sufficient* if, for any t and any $1 \leq i \leq m$, both the s_i-th row and the s_i-th column of G_t are identically zero and s_i is not accessible outside D in the matrix P_t. In words, this means that, for any $i \in D$, the i-th compartment does not increase through direct infection, the infection does not depend on the compartment size and it is impossible to get to the state i once being outside D.

Let, after a possible re-ordering, $m \in \mathbb{N}$ be such that $\{1, \ldots, m\}$ is self-sufficient (such m always exists because it can be always put to k). For any vector $x \in \mathbb{R}^k$, denote $\overline{x}$ its restriction to $(1, \ldots, m)$ and, for any matrix $A \in \mathbb{R}^{k \times k}$, denote $\overline{A}$ its restriction to $(1, \ldots, m) \times (1, \ldots, m)$

Observe that X follows its own version of our model, namely that

$$\xi_{t+1} | \, \mathcal{F}_t = \bigcirc_{1 \leq i \leq m} \mathrm{Mult}(\xi_t^i, Q_t^i) \circ \mathrm{Po}(K_t \xi_t) \circ \delta(H_t),$$

where Q_t and K_t are the restrictions of P_t, G_t, respectively, to $(1, \ldots, m) \times (1, \ldots, m)$ and H_t is the restriction of I_t to $(1, \ldots, m)$ and, for any $t, s \in \mathbb{N}_0, s > t$,

$$\mathbb{E}(\xi_t | \mathcal{G}_s) = \mathbb{E}(\mathbb{E}(\xi_t | \mathcal{F}_s) | \mathcal{G}_s) = \mathbb{E}(T_{s,t-1} X_s + \sum_{\theta=s}^{t-1} T_{\theta+1,t-1} H_\theta | \mathcal{G}_s) = \mathbb{E}(T_{s,t-1} | \mathcal{G}_s) X_s + \sum_{\theta=s}^{t-1} \mathbb{E}(T_{\theta+1,t-1} H_\theta | \mathcal{G}_s),$$

where,

$$T_t = Q_t + K_t +$$

for any matrix process A_t, $A_{t,s} \stackrel{\mathrm{def}}{=} \prod_{\theta=t}^{s} A_\theta$ with $A_{t,t-1} \stackrel{\mathrm{def}}{=} E$.

In the special case that

$$K_\tau \equiv K_{t-1}, \qquad Q_\tau \equiv Q_{t-1}, \qquad t-1 \leq \tau \leq s-1, \tag{2}$$

we have

For any t, we define the reproduction number r_t (of a self-sufficient set $\{1,\dots,m\}$) as

$$r_t \stackrel{\text{def}}{=} \sum_{\tau=t}^{\infty} \mathbf{1}^T \mathbb{E}(K_\tau Q_{t,\tau-1}\pi_t|\mathcal{F}_{t-1}), \qquad \pi_t = \mathbb{E}\left\{\nu\left(O_t + H_{t-1}\right)|\,\mathcal{F}_{t-1}\right\}$$

where ν stands for unit normalization, O_t is the restriction of N_t to $(1,\dots,m)$ and,. Observe that r_t complies with the usual definition of reproduction number as it equals to the conditional expectation (w.r.t. $\mathcal{F}_{t-1}$) of the infections caused by an individual having arrived at t. To see it, note that π_t is the conditional distribution of the state in which a randomly chosen newcomer (the one brought by the import or by the infection) finds himself at t, and observe that, for each newcomer at t, the expected number of those infected by him at $t+1$ is given by the sum of the components of $K_t\pi_t$, the expected number infected at $t+1$ is given by the sum of components of $K_{t+1}Q_t\pi_t$ etc.

If ξ is not observed, then the reproduction number has to be estimated, most naturally by its conditional expectation with respect to the known information:

$$\tilde{r}_t \stackrel{\text{def}}{=} \sum_{\tau=t}^{\infty} \mathbf{1}^T \mathbb{E}(K_\tau Q_{t,\tau-1}\pi_t|\mathcal{G}_{t-1}).$$

In the special case of TBD with $\rho(Q_{t-1}) < 1$ where ρ is the spectral radius, the formula simplifies to

$$\tilde{r}_t = \mathbf{1}^T K_{t-1}\left(\sum_{i=0}^{\infty} Q_{t-1}^i\right)\mathbb{E}(\pi_t|\mathcal{G}_{t-1}) = \mathbf{1}^T K_{t-1}(E - Q_{t-1})^{-1}\mathbb{E}(\pi_t|\mathcal{G}_{t-1})$$

Note and that there could be difficulties computing π_t – yet the estimate $\pi_t \doteq \nu(K_{t-1}\hat{X}_{t-1|t-1} + H_{t-1})$ seems straightforward, it is generally not unbiased due to the normalization. This problem, however, vanishes if the imports and new infections all fall into a single state (typically called exposed), in which case $\pi_t = (1,0,\dots,0)^T$.

1.2 Asymptotic behavior

The next Proposition states conditions, for vanishing, explosion and "stationary" behavior of the process.

Proposition 1. *(i) If $T_t \le S$ component-wise, where S is deterministic with $\sigma \stackrel{def}{=} \rho(S) < 1$, and if $\mathbb{E}H_t = o(t^{-\alpha})$ for some $\alpha > 0$ then $\xi_t \to 0$ almost sure. Here, ρ denotes the spectral radius of a matrix.*
(ii) If $T_t \ge R$ where R is deterministic irreducible with $\varrho \stackrel{def}{=} \rho(R) > 1$ and

either $\mathbb{E}\xi_0 \neq 0$ *or* $\mathbb{E}H_\tau \neq 0$ *for some* τ*, then* $\|\mathbb{E}\xi_t\| \to \infty$.
(iii) If $\mathbb{E}H_t \equiv \mu$ *for some* μ *and* $R \leq T_t \leq S$ *such that* $\sigma \overset{def}{=} \rho(S) < 1$*, then*

$$\liminf_t \mathbb{E}\xi_t \geq (E-R)^{-1}\mu, \qquad \limsup_t \mathbb{E}\xi_t \leq (E-S)^{-1}\mu$$

Proof. (i) We have

$$\mathbb{E}\xi_t = \mathbb{E}(\mathbb{E}(\xi_t|\mathcal{G}_0)) = \mathbb{E}(T_{0,\tau-1}X_0 + \sum_{\theta=0}^{t-1} T_{\theta+1,t-1}\mathbb{E}(H_\theta|\mathcal{G}_0)) =$$

$$= T_{0,t-1}\mathbb{E}\xi_0 + \sum_{\theta=0}^{t-1} T_{\theta+1,t-1}\mathbb{E}H_\theta \leq a_t + b_t, \qquad a_t = S^t\mathbb{E}\xi_0, \qquad b_t = \sum_{\theta=0}^{t-1} S^{t-\theta-1}\mathbb{E}H_\theta$$

Thanks to the sub-unit spectral radius of S, $a_t \to 0$. Further, by the non-negativity of H and the properties of convergence, there exists $c \in \mathbb{R}_+^m$ such that $\mathbb{E}H_t \leq c(t+1)^{-1}$. Thus, for any ς fulfilling $\sigma < \varsigma < 1$, we get, after re-indexing the sum,

$$b_t = \sum_{\tau=0}^{t-1} S^\tau \mathbb{E}H_{t-\tau-1} \leq \sum_{\tau=0}^{t-1} S^\tau c \frac{1}{(t-\tau)^\alpha} = \underbrace{\frac{1}{t^\alpha}}_{\to 0} \times \underbrace{\sum_{\tau=0}^{t-1} (\varsigma^{-1}S)^\tau c}_{\to (E-\varsigma^{-1}S)^{-1}c} \underbrace{\left(\frac{\varsigma^{\tau/\alpha}}{t-\tau}\right)^\alpha}_{\leq d} \to 0.$$

Indeed, $\rho(\varsigma^{-1}S) = \frac{\sigma}{\varsigma_t} < 1$, and the upper bound d exists as $f(\tau) \overset{\text{def}}{=} \frac{t\varsigma^{\tau/\alpha}}{t-\tau}$ increases in $\tau = t-1$ and its derivative has only a single root, so we have $f(\tau) \leq \max(f(0), f(t-1)) = \max(1, \varsigma^{\frac{t-1}{\alpha}}t) \leq d \overset{\text{def}}{=} \max(1, \frac{1}{e\varsigma^{1/\alpha}|\alpha^{-1}\ln\varsigma|})$ on $[0, t-1]$. Finally, thanks to the non-negativity of ξ, convergence of $\mathbb{E}\xi_t$ suffices for a.s. convergence of ξ_t.

(ii) Let $\mathbb{E}\xi_0 \neq 0$ and $\varrho > 1$. As R is irreducible non-negative ϱ is its eigenvalue and the corresponding eigenvector x is positive by the Perron-Frobenius Theorem. Further, by the irreducibility of T, there exists n such that $y \overset{\text{def}}{=} R^n\mathbb{E}\xi_0 > 0$ component-wise, so there exist $e > 0$ such that $y \geq ex$. Thus

$$\mathbb{E}\xi_t \geq R^t\mathbb{E}\xi_0 \geq R^{t-n}y \geq eR^{t-n}x$$

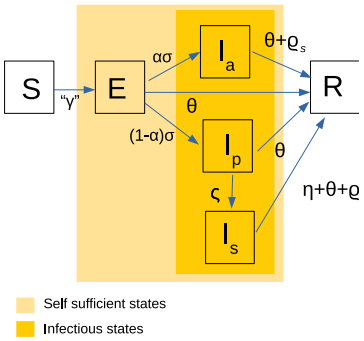
norm of which converges to infinity. The proof for $\mathbb{E}H_\tau \neq 0$ is analogous.

(iii)

$\mathbb{E}\xi_t = \sum_{\tau=0}^{t-1} T_{\tau,t-2}\mu + T_{0,t-1}\mathbb{E}\xi_0 \leq \sum_{\tau=0}^{t-1} S^\tau\mu + S^{t-1}\mathbb{E}\xi_0 \to (\sum_{\tau=0}^{\infty} S^\tau)\mu = (E-S)^{-1}\mu$ and similarly for R. □

Example 2. Say there are five states E – exposed, I_a – infectious asymptomatic, who will never exhibit symptoms, I_p – infectious pre-symptomatic, who will later exhibit symptoms, I_s – infectious symptomatic, and R – removed, including recovered, dead, and infectious isolated. All the $I_\bullet$ states are equally infectious, i.e. $\gamma_t^{Ex} = \gamma_t$, $x \in \{I_a, I_p, I_s\}$, where γ is a $\mathcal{G}_t$-adapted process. The

probability that the exposed transits to $\{I_a, I_p\}$ is σ, the probability of completely asymptomatic course is α, the probability of transition from I_p to I_s is ς. Further, the probability of ending I_a and I_s, by natural causes (recovery, end of infectiousness, death in case of I_s) is ϱ_a, ϱ_s, respectively. Finally, the probability that a symptomatic individual isolates herself is η and the probability that the individual is isolated regardless of his state is θ_t for some $\mathcal{G}_t$-adapted process θ. The situation is illustrated on the following Figure



If we neglect (small) joint probabilities of natural exits from the infectious states and the isolations, we get,

$$P_t = \begin{bmatrix} 1-\sigma-\theta_t & 0 & 0 & 0 & 0 \\ \alpha\sigma & 1-\varrho_a-\theta_t & 0 & 0 & 0 \\ (1-\alpha)\sigma & 0 & 1-\varsigma-\theta_t & 0 & 0 \\ 0 & 0 & \varsigma & 1-\varrho_s-\eta-\theta_t & 0 \\ \theta_t & \theta_t+\varrho_a & \theta_t & \theta_t+\eta+\varrho_s & 1 \end{bmatrix}, \qquad G_t = \begin{bmatrix} 0 & \gamma_t & \gamma_t & \gamma_t & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Clearly, we can put $m = 4$ (the first four states are self-sufficient), getting

$$U_t = B(\gamma_t) - \theta_t E, \qquad B(\gamma) = \begin{bmatrix} 1-\sigma & \gamma & \gamma & \gamma \\ \alpha\sigma & 1-\varrho_a & 0 & 0 \\ (1-\alpha)\sigma & 0 & 1-\varsigma & 0 \\ 0 & 0 & \varsigma & 1-\varrho_s-\eta \end{bmatrix}.$$

By the well known rule, we have $\rho(U_t) = \rho(B(\gamma_t)) - \theta_t$, $g(\gamma) = \rho(B(\gamma))$. So, given that $\rho(U_t) \geq 1$, there are two ways of decreasing the spectral radius: to decrease the infection rate γ_t (typically by some counter-epidemic measures) or to increase the isolation rate θ_t (e.g. by strengthening the tracing capacity). Further, once there is a "target" spectral radius ρ_0, all the combinations of γ and θ yielding $\rho(U_t) = \rho_0$ fulfill $\rho_0 + \theta - g(\gamma) = 0$ giving a "marginal rate of substitiution" $\theta(\gamma)' = -g'(\gamma)$ of the measures by the quarantine, i.e. how much we have to increase the isolation speed when releasing the restrictions.

$\mathbf{1}^T$

Example 3. Assume the fraction ν of the population is non-compliant, which means that, once a restriction on social contacts is imposed, the non-compliant part applies it only partially. In particular, we assume that, without restrictions,

the population is mixed, which means that each individual, compliant or not, has, up to a constant, $(1-\nu)$ contacts with the compliant individuals and ν contacts with the non-compliant ones. Given a restriction, the compliant individuals restrict their opportunities to contacts by ϕ while the non-compliant ones only to $f(\phi) > \phi$. As a result, the compliant ones will have, up to a constant, $\phi^2(1-\nu)$ contacts with the compliant ones, $\phi f(\phi)\nu$ contacts with the non-compliant ones, while the non-compliant will have $\phi f(\phi)(1-\nu)$ and $f(\phi)^2\nu$ contacts with the compliant, non-compliant, respectively.

Assuming a simple model with compartments I_c - infected compliant, I_n - infected non-compliant, and R - removed, where the course of infection is the same for both the comparments, this gives

$$P_t = \begin{bmatrix} 1-\varrho & 0 & 0 \\ 0 & 1-\varrho & 0 \\ \varrho & \varrho & 1 \end{bmatrix}, \qquad G_t = \begin{bmatrix} \beta\phi^2(1-\nu) & \beta\phi f(\phi)\nu & 0 \\ \beta\phi f(\phi)(1-\nu) & \beta f(\phi)^2\nu & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

where ϱ is a removal rate (perhaps consisting of an artificial and a natural part) and β is a constant. This gives

$$U_t = \beta C + (1-\varrho)E, \qquad C = \begin{bmatrix} \phi^2(1-\nu) & \phi f(\phi)\nu \\ \phi f(\phi)(1-\nu) & f(\phi)^2\nu \end{bmatrix}$$

with

$$\varrho(U_t) = \beta\rho(C) + (1-\varrho).$$

The characteristic polynomial of C is

$$\lambda^2 - \lambda g, \qquad g = g(\phi,\nu) = \phi^2(1-\nu) + f(\phi)^2\nu$$

so $\rho(C) = g$.

Now say that our goal is to decrease $\rho(U_t)$ to r by finding appropriate $\phi(\nu)$, i.e. we want

$$\beta g(\phi(\nu),\nu) + (1-\varrho) = r.$$

Given the absolute compliance ($\nu = 0$), clearly $\phi^2 = \frac{r-(1-\rho)}{\beta}$. For $\nu > 0$ we get, by the Implicit function theorem,

$$\frac{\partial}{\partial\nu}\phi = \frac{f(\phi(\nu))^2 - \phi(\nu)^2}{2\phi(\nu)(1-\nu) + 2f(\phi(\nu))f'(\phi(\nu))\nu}.$$

Note that the derivative depends neither on r nor on ϱ. By imposing $\nu = 0$, we get the rate of necessary adjustment of ϕ for small changes of ν :

$$\phi(\nu) \doteq \phi(0) + a\nu, \qquad a = \frac{f(\phi(0))^2 - \phi^2(0)}{2\phi(0)}.$$

2 Estimation

For any stochastic process A and integers $s > t$, denote $\hat{A}_{s|t} = \mathbb{E}(A_s|\mathcal{G}_t)$. When $T_\tau \in \mathcal{G}_t, t < \tau \leq s-1$ (which is trivially true if $s = t+1$), we get that

$$\begin{bmatrix} \hat{X}_{s|t} \\ \hat{Y}_{s|t} \end{bmatrix} = \mathbb{E}\left(\mathbb{E}\left(\begin{bmatrix} \hat{X}_s \\ \hat{Y}_s \end{bmatrix} \middle| \mathcal{F}_{s-1} \right) \middle| \mathcal{G}_t \right) = \begin{bmatrix} E \\ F \end{bmatrix} \left(T_{s-1}\hat{X}_{s-1|t} + \hat{I}_{s-1|t} \right)$$
$$= \begin{bmatrix} E \\ F \end{bmatrix} \left(T_{t,s-1}X_t + \sum_{\theta=t}^{s-1} T_{\theta+1,s-1}\hat{I}_{\theta|t} \right),$$

$$W_{s|t} \stackrel{\text{def}}{=} \operatorname{var}(X_s|\mathcal{G}_t) = \operatorname{var}(\mathbb{E}(X_s|\mathcal{F}_{s-1})|\mathcal{G}_t) + \mathbb{E}(\operatorname{var}(X_s|\mathcal{F}_{s-1})|\mathcal{G}_t)$$
$$= \operatorname{var}(T_{s-1}X_{s-1} + I_{s-1}|\mathcal{G}_t) + \mathbb{E}(\Lambda_{s-1}(X_{s-1})|\mathcal{G}_t)$$
$$= T_{s-1}W_{s-1|t}T_{s-1}^T + 2T_{s-1}\operatorname{cov}(X_{s-1}, I_{s-1}|\mathcal{G}_t) + \operatorname{var}(I_{s-1}|\mathcal{G}_t) + \Lambda_{s-1}(\hat{X}_{s-1|t})$$

and

$$V_{s|t} \stackrel{\text{def}}{=} \operatorname{var}\left(\begin{matrix} X_s \\ Y_s \end{matrix} \middle| \mathcal{G}_t \right) = \operatorname{var}\left(\begin{matrix} X_s \\ FX_s + \epsilon_s \end{matrix} \middle| \mathcal{G}_t \right) = \begin{bmatrix} E \\ F \end{bmatrix} W_{s|t} \begin{bmatrix} E \\ F \end{bmatrix}^T + \operatorname{diag}\left(\begin{matrix} 0_{\mathrm{k}} \\ \Gamma_{\mathrm{s-1}}\hat{\mathrm{X}}_{\mathrm{s-1|t}} \end{matrix} \right)$$

Unfortunately, due to the non-Gaussianity, we do have analytical formulas neither for $X_{t|t}$ nor for $\mathrm{W_{t|t}}$, so we can formulate neither the likelihood function nor a least square estimate. Two, from the computational point of view equivalent, ways to cope with this could either using estimates of the conditional expectation and variance, or normally approximating the residuals. We go the latter way: in the present Section, we assume that $\begin{bmatrix} X_{t+1} \\ Y_{t+1} \end{bmatrix} \middle| \mathcal{F}_t$ is normal with mean given by (1) and

$$\operatorname{var}\left(\begin{matrix} X_{t+1} \\ Y_{t+1} \end{matrix} \middle| \mathcal{F}_t \right) = \begin{bmatrix} E \\ F \end{bmatrix} \Lambda_t(X_t \vee 0) \begin{bmatrix} E \\ F \end{bmatrix}^T + \operatorname{diag}\left(\begin{matrix} 0_{\mathrm{k}} \\ \Gamma_{\mathrm{t}}(\mathrm{X_t} \vee 0) \end{matrix} \right)$$

Given this assumption we have, by Eatonxxx,

$$\hat{X}_{t|t} = I_{t-1} + \hat{X}_{t|t-1} + L_t\left(Y_t - \hat{Y}_{t|t-1}\right)$$
$$L_t \stackrel{\text{def}}{=} V_{t|t-1}^{XY}(V_{t|-1}^{YY})^{-1} = W_{t|t-1}F^T D_t^{-1}, \qquad D_t = FW_{t|t-1}F^T + \operatorname{diag}(\Gamma_t\hat{X}_{t|t-1})$$

$$W_{t|t} = V_{t|t-1}^{XX} - V_{t|t-1}^{XY}(V_{t|t-1}^{YY})^{-1}V_{t|t-1}^{YX} = W_{t|t-1} - W_{t|t-1}F^T D_t^{-1} F W_{t|t-1}$$

Note that L_t may be seen as a conditional version of a Kalman gain matrix.

As for the estimation itself, assume that $F = F(\Theta_0)$,$P_t = P_t(\Theta_0)$, $G_t = G_t(\Theta_0)$, $\Gamma_t = \Gamma_t(\Theta_0)$ and $I_t = I_t(\Theta_0)$ where $\Theta_0 \in \mathbb{R}^r$ is an unknown parameter. For its estimation, it is possible to to use either nonlinear least squares, i.e.

$$\hat{\Theta} = \arg\min \sum_t (Y_t - \hat{Y}_{t|t}(\Theta))^T D(\Theta)_t^{-1} (Y_t - \hat{Y}_{t|t}(\Theta))$$

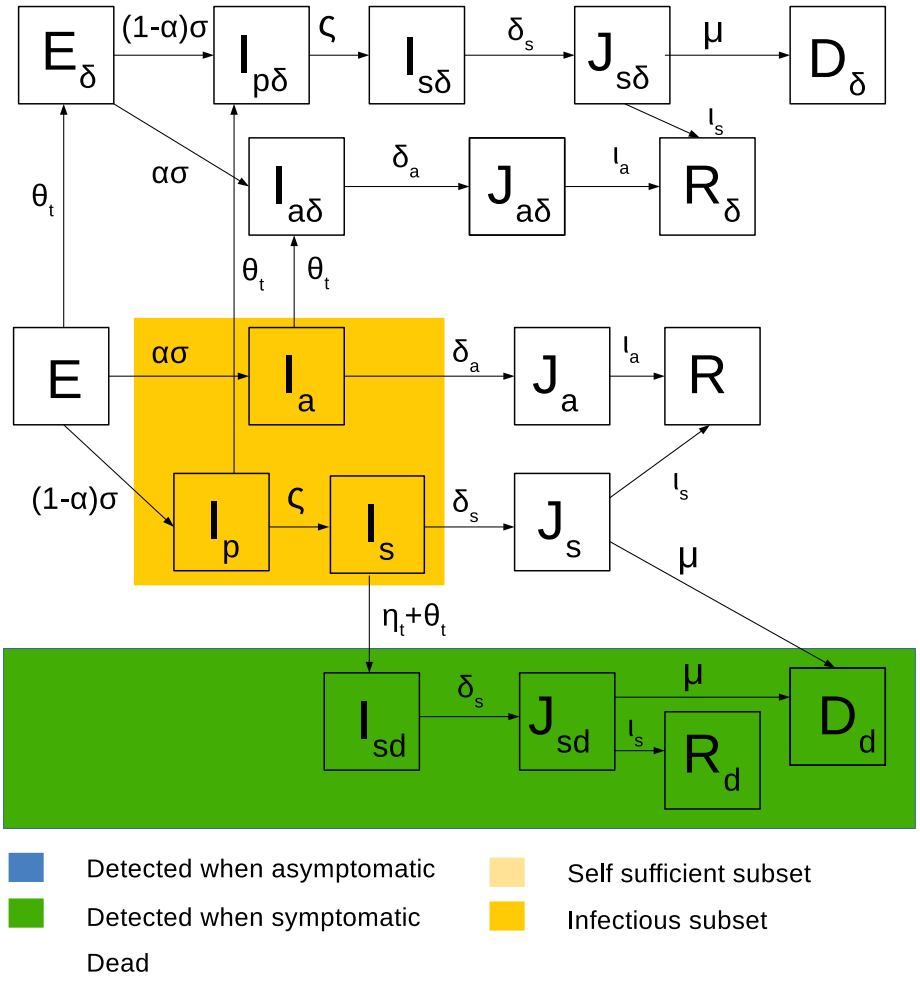
or maximum likelihood

$$\tilde{\Theta} = \arg\min \sum_t \varphi((Y_t - \hat{Y}_{t|t}(\Theta)), D_t(\Theta)), \qquad \varphi(x, v) = -\frac{k \ln 2\pi + \ln\det(v) + x^T v^{-1} x}{2}$$

Both these estimators are consistent and asymptotically normal under some conditions, see *G*acob, *G*acob respectively (footnote one dim), verifying these conditions for our model is, however, beyond the scope of this short research letter and remains as topic of a future research. Mote also, that our proof of Proposition 1 is not valid for the approximate model, as ξ is not necessarily positive here

The COVID Pandemics in Czech Republic

We applied our model to the data from the first and second wave of the pandemics in the Czech Republic, starting from Feb 27, 2020. In addition to the states from 2 and, in addition, we considered their "detected" versions, distinguish detection in when being asymptomatic (subscript δ) and when being symptomatic (subscript d). Further, for both the symptomatic and the asymptomatic course, we added the states in which the individuals are RNA positive, but not infectious (denoted by J) and we distinguish two "removed" states: recovered (R) and dead (D). All the J and R states have three versions: undetected, detected when asymptomatic. Finally, we assume that once the undetected course ends by death, the detection takes place before the time of death. See Figure and the Table,



Similarly as in the Example, we assumed equal infectiousness γ_t for all the infectious states E, I_a, I_p, I_s, fulfilling

$$\gamma_t = \beta c_t p_t s_t \tag{3}$$

where β is an (estimated) constant, c_t is the contact reduction (with $c_0 = 1$), p_t is the reduction caused by personal protection and s_t is a (possible) seasonal element. Reflecting the weekly pattern of reporting, we assume

$$\theta_t = \phi_t \theta, \qquad \eta_t = \phi_t \eta$$

where ϕ_t is the adjustment for the day of the week.

We took three data series as observations: the daily numbers of detected, distinguished between symptomatic (S) asymptomatic (A) and daily numbers of dead (D), i.e.

$$Y_t = \begin{bmatrix} A_t \\ S_t \\ D_t \end{bmatrix},$$

with F_{1i}, F_{2i} and F_{3i} is one/zero if the state i is/is not *detected asymptomatic*, *detected symptomatic*,, respectively (see Figure). Assuming imports only to the state E, we took

$$I_t = r_t R_{t+8}$$

where R_t is the number of detected with the indicated infection abroad and r_t is a multiplication factor, in particular, we took r_t as an unknown parameter in the first month, which allows to reflect the the excess numbers of dead in comparison with the detected, that many of the cases remained unnoticed in the beginning of the pancemics. For the next months of the pandemics, we took $r_t = \frac{1}{1-\alpha}$??.

To compute c_t and p_t we used [Dan]. As the total estimated number of risk contacts C_t is one of the values monitored by the study, we could estimatd $c_t = \frac{C_t}{C_0}$. With the personal protection, the situation is more compicated, as the study monitors observance of several protective measures. If we assume that the i-th measure reduces the probability of infection λ_i, we get that, given observance P_t^i of the measure, the average reduction brought by the the measure will be $(1 - P_t^i) \times 1 + P_t^i(1 - \lambda^i) = 1 - P_t^i \lambda^i$. Consequently, the total reduction will be

$$p_t = \prod_{i=1}^{q} (1 - P_t^i \lambda^i).$$

Unfortunately, λ_i are unknown and their estimation would bring a serious danger of over-fitting and/or co-linearity (series $p_t^\bullet$ are almost perfectly co-related). To overcome this difficulty, we applied factor analysis to $(C_t, P_t^1, \ldots, P_t^q)$ on the respondent level, treating the responses in different times as separate observations. As a result, we extracted two main factors, the first strongly related to contact reduction, the second lacking connection with C. Thus, having C already used in (3), we approximated each compliance by

$$P_t^i \doteq \overline{P}_t^i + \nu_t F_t$$

where $\overline{P}_t^i$ is the average of P_t^i over time and respondents, ν_t is a constant and F_t is average of the second factor over respondents at t. Having that. we could

approximate

$$p_t \doteq \prod_{i=1}^{q}(1-\lambda^i(\overline{P}_t^i+\nu_t F_t)) = \exp\left\{\sum_{i=1}^{q}\ln(1-\lambda^i(\overline{P}_t^i+\nu_t F_t))\right\}$$
$$\doteq \exp\left\{\sum_{i=1}^{q}\left[-\lambda^i(\overline{P}_t^i+\nu_t F_t) - \frac{(\lambda^i(\overline{P}_t^i+\nu_t F_t))^2}{2}\right]\right\} = a\exp\left\{-bF_t - cF_t^2\right\}$$

where $b \geq 0$, $c \geq 0$.