**Appendix**

**Parameter estimation procedure**

Parameters of the model $θ$ include the prior mean of $R\_{0}$ for the three different lockdown conditions $\left(β\_{0},β\_{1},β\_{2}\right)$, as well the expected value of the log-infected population at initial point $x\_{i}\left(r\right)$. Parameters were fitted from the data by maximum likelihood estimation, using an expectation-maximization procedure. The procedure also allowed to recover the posterior distribution of true cases $p\left(I|y;θ\right)$ for each day and autonomous community. We convert the infected population to the log-scale, defining $x\left(r,d\right)=logI\left(r,d\right)$:

$$x\left(r,d+1\right)=x\left(r,d\right)-\left(R\_{0}\left(r,d\right)-1\right)γ$$

This can be turned into:

$$x\left(r,d\right)=x\_{i}\left(r\right)+γ\left(\sum\_{t<d}^{}R\_{0}\left(r,d\right)-d\right)$$

In vectorial terms, we have $x=T\left[x\left(0,r\right),R\_{0}\left(r,:\right)\right]$, where $T$ is an upper triangular matrix of 1 that implements the summing operation. Since both $x\_{i}\left(r\right)$ and $R\_{0}\left(r,:\right)$ have multivariate normal prior distribution, the prior over $x$ is normal itself with mean $μ\_{r}=T\left[x\_{i}\left(r\right),Φβ\right]$ and covariance $K\_{x}=T\tilde{K}T'$ where $Φ$ is an $D$-by-3 indicator matrix indicating the lockdown state for each day, and $\tilde{K}$ is block diagonal with submatrices $σ\_{0}^{2}$ and $K$. In the Expectation step, we estimate the posterior distribution over log-infected population using a Laplace approximation $p\left(x|y,θ\right)≈N\left(m,V\right)$. We first identified the maximum-a-posteriori variable *m* through gradient search, and then computed *V* as the inverse of the negative of the hessian joint-log-probability evaluated at *m*.

Parameters were updated in the M-step by maximizing the objective function analytically. We run the EM 10 times with different initial values for the parameters to avoid falling into local maxima of the log-likelihood. Confidence intervals for parameters were estimated using parametric bootstrapping using 20 bootstraps. All analyses were implemented in Matlab with custom codes, which will be uploaded on a public repository upon publication of the manuscript.