

The EpiLPS project: a new Bayesian tool for estimating the time-varying reproduction number

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28th Annual Meeting of the Royal Statistical Society of Belgium
October 22, 2021

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The Epilepsy Phenome-Genome Project

What is Epilepsy?

- ▶ Epidemiological modelling (tool) with Laplacian-P-Splines.
 - ▶ Reproduction number $R(t)$: key metric to assess disease dynamics.
 - ▶ A novel methodology for fast and flexible (approximate) Bayesian inference of $R(t)$.
 - * Laplace approximations \Rightarrow computationally very attractive.
 - * P-splines \Rightarrow flexible modeling framework with smooth estimates of the epidemic curve and $R(t)$.
 - ▶ A set of (efficient) routines with intuitive functional calls for the end user.
 - ▶ R package is currently in the pipeline.

What motivated Epilepsy?



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An approximate Bayesian approach for estimation of the reproduction number under misreported epidemic data

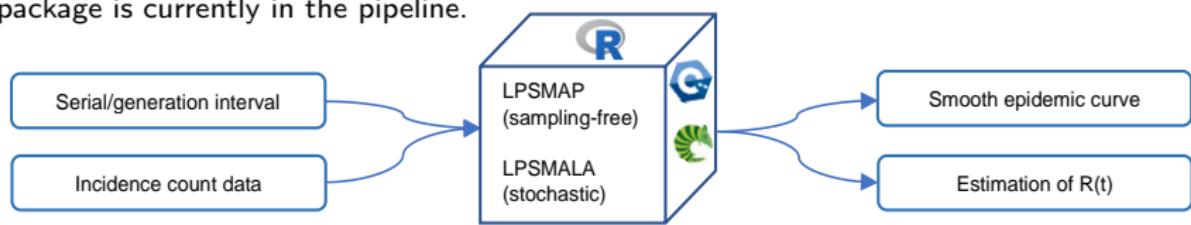
Oswaldo Gressani, Christel Faes, Niel Hens
doi: <https://doi.org/10.1101/2021.05.19.21257438>

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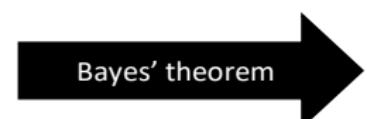
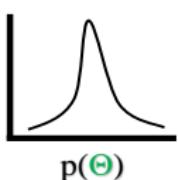
- ▶ Revisit model of Azmon et al. (2013)
 - ▶ Will Laplace approximations do the job?



Bayes' theorem and the Laplace approximation in a nutshell

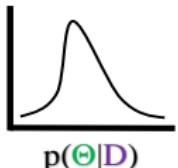
- ▶ Laplace approx. → key for making EpiLPS lightning fast, but what is it really?

Likelihood (Data) Prior beliefs



$$p(\theta|D) \propto p(D|\theta) p(\theta)$$

Posterior distribution



- ▶ Laplace approx.: simplify $p(\theta|D)$ but retain crucial features.
- ▶ Taylor expansion of $g(\theta) := \log p(\theta|D)$ around modal value $\hat{\theta}$:

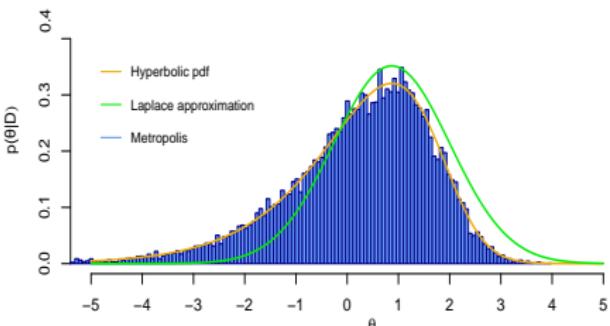
$$g(\theta) \approx g(\hat{\theta}) + \frac{1}{2}g''(\hat{\theta})(\theta - \hat{\theta})^2.$$

- ▶ Apply exponential function on both sides:

$$\begin{aligned} \tilde{p}_G(\theta|D) &\propto \exp\left(-\frac{1}{2}(-g''(\hat{\theta}))(\theta - \hat{\theta})^2\right) \\ &\Rightarrow \mathcal{N}\left(\hat{\theta}, (-g''(\hat{\theta}))^{-1}\right). \end{aligned}$$

- ▶ Ex: Hyperbolic distribution.

Posterior target distribution and its approximation



The “Epi” part: smoothing incidence count data

- ▶ Let $\{y_t, t = 1, \dots, T\}$ be a time series of incidence counts.
- ▶ Negative Binomial model for y_t , i.e. $y_t \sim \text{NegBin}(\mu(t), \rho)$ following the parameterization of [Piegorsch \(1990\)](#):

$$p(y_t | \mu(t), \rho) = \frac{\Gamma(y_t + \rho)}{\Gamma(y_t + 1)\Gamma(\rho)} \left(\frac{\mu(t)}{\mu(t) + \rho} \right)^{y_t} \left(\frac{\rho}{\rho + \mu(t)} \right)^\rho, \quad \mu(t) > 0, \quad \rho > 0.$$

- ▶ Following [Eilers and Marx \(1996\)](#), we model $\mathbb{E}(y_t) = \mu(t)$ by means of cubic B-splines with amplitudes θ_k :

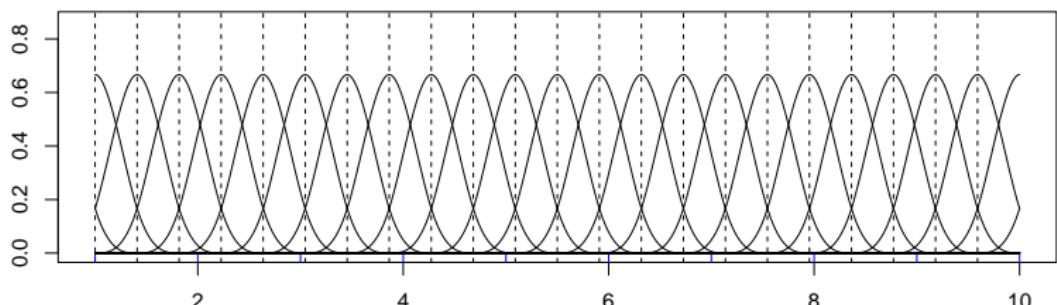
$$\log(\mu(t)) = \sum_{k=1}^K \theta_k b_k(t) = \boldsymbol{\theta}^\top \mathbf{b}(t).$$

- ▶ Idea of P-splines: Fix K large enough and counterbalance the flexibility by introducing a roughness penalty on adjacent B-spline coefficients: $\lambda \boldsymbol{\theta}^\top \mathbf{P} \boldsymbol{\theta}$.
- ▶ \mathbf{P} is a penalty matrix and $\lambda > 0$ is the roughness penalty parameter to be maximized *a posteriori* → LPSMAP.

Bayesian P-splines

- ▶ B-spline basis defined on $\mathcal{T} = [r_l, T]$, where r_l is typically the first day of the epidemic (i.e. $r_l = 1$). In the **blapsr** package:

```
> lb <- 1    # Lower bound
> ub <- 10   # Upper bound
> xdom <- seq(lb,ub)
> Bsmat <- cubicbs(xdom, lb, ub, 25)
> plot(Bsmat) # Plot the basis
```



- ▶ In the Bayesian version [Lang and Brezger \(2004\)](#), the vector of B-spline coefficients is random \Rightarrow Gaussian prior (based on random-walks).
- ▶ Also, priors on hyperparameters λ and ρ have to be specified.

Bayesian model formulation

- ▶ The Bayesian model formulation underlying EpiLPS is as follows:

$$\begin{aligned} y_t | \mu(t), \rho &\sim \text{NegBin}(\mu(t), \rho), \\ \log(\mu(t)) &= \boldsymbol{\theta}^\top \mathbf{b}(t), \\ \boldsymbol{\theta} | \lambda &\sim \mathcal{N}_{\dim(\boldsymbol{\theta})}(0, Q_\lambda^{-1}), \\ \lambda | \delta &\sim \mathcal{G}(\phi/2, (\phi\delta)/2), \\ \delta &\sim \mathcal{G}(a_\delta, b_\delta), \\ \rho &\sim \mathcal{G}(a_\rho, b_\rho). \end{aligned}$$

- ▶ We fix $\phi = 2$, $a_\delta = b_\delta = 10$ and a proper (uninformative) prior on ρ with $a_\rho = b_\rho = 10^{-4}$.
- ▶ Denote by $\boldsymbol{\eta} := (\lambda, \rho)^\top$, the vector of model hyperparameters (to be optimized).
- ▶ Laplace approximations are used to approximate the posterior of $\boldsymbol{\theta}$ in three steps.

The “mechanics” of Laplacian-P-splines in 3 steps

- ▶ Objective: come up with approximated posteriors for θ and $\eta = (\lambda, \rho)^\top$.
- ▶ Gaussian prior $\theta|\eta \sim \mathcal{N}$ (LGM). Main goal is to approximate the joint posterior:

$$\begin{aligned} p(\theta|\mathcal{D}) &= \int p(\theta, \eta|\mathcal{D}) d\eta \\ &= \int p(\theta|\eta, \mathcal{D}) p(\eta|\mathcal{D}) d\eta. \end{aligned}$$

- ▶ In the philosophy of [Tierney and Kadane \(1986\)](#) and [Rue et al. \(2009\)](#):

 1. Laplace approximation to the conditional posterior:

$$p(\theta|\eta, \mathcal{D}) \rightarrow \tilde{p}_G(\theta|\eta, \mathcal{D}).$$

2. Approximation of the hyperparameter vector:

$$p(\eta|\mathcal{D}) = \frac{p(\theta, \eta|\mathcal{D})}{p(\theta|\eta, \mathcal{D})} \rightarrow \tilde{p}(\eta|\mathcal{D}) = \left. \frac{p(\theta, \eta|\mathcal{D})}{\tilde{p}_G(\theta|\eta, \mathcal{D})} \right|_{\theta=\hat{\theta}(\eta)}.$$

3. Approximation at the MAP for η (but other possibilities exist):

$$\tilde{p}(\theta|\mathcal{D}) = \mathcal{N}_{\dim(\theta)}(\theta^*(\eta^*), \Sigma^*(\eta^*)).$$

The renewal equation “plug-in” estimator

- ▶ Remember what we have so far: $\tilde{p}(\boldsymbol{\theta}|\mathcal{D}) = \mathcal{N}_{\dim(\boldsymbol{\theta})}(\boldsymbol{\theta}^*(\boldsymbol{\eta}^*), \Sigma^*(\boldsymbol{\eta}^*))$.
- ▶ Denote by $\varphi = \{\varphi_1, \dots, \varphi_k\}$ the serial interval distribution and let $\hat{\boldsymbol{\theta}} := \boldsymbol{\theta}^*(\boldsymbol{\eta}^*)$.
- ▶ Start with the renewal equation: $y_t = \sum_s R(t) \varphi_s y_{t-s}$ and write it as:

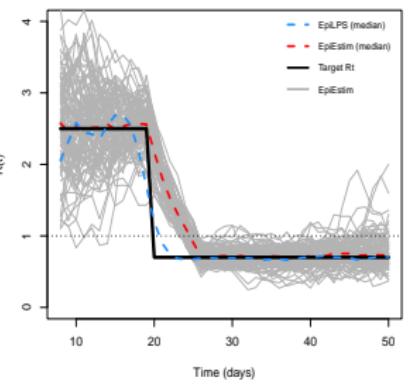
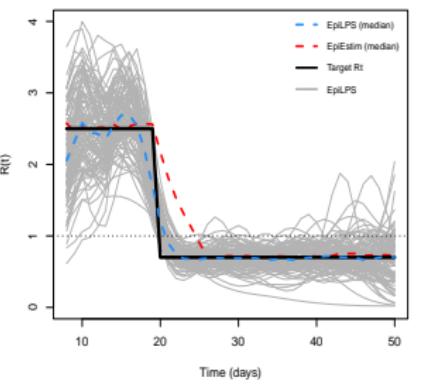
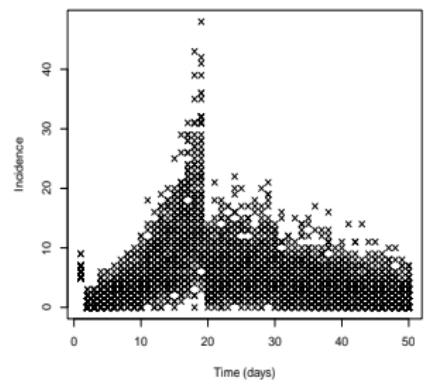
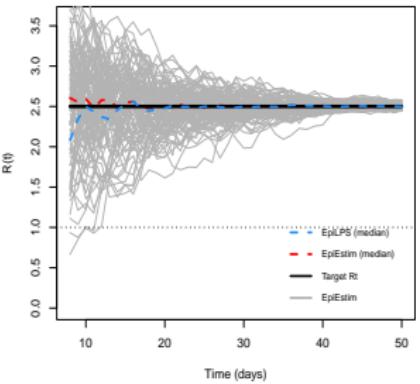
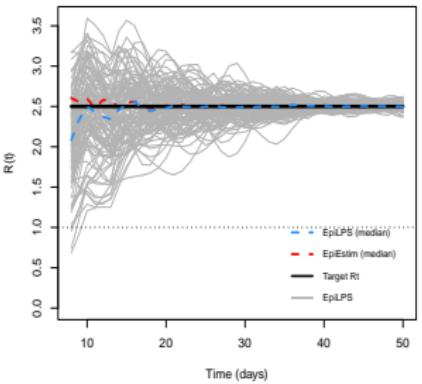
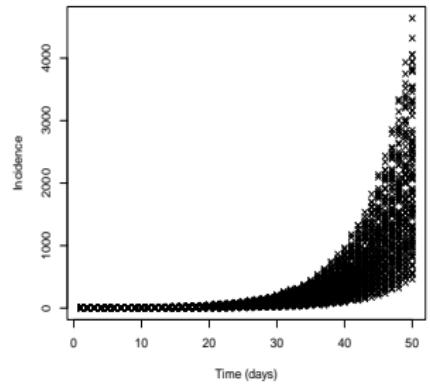
$$R(t) = \begin{cases} y_t & ; \text{for } t = 1, \\ y_t \left(\sum_{s=1}^{t-1} \varphi_s y_{t-s} \right)^{-1} & ; \text{for } 2 \leq t \leq k, \\ y_t \left(\sum_{s=1}^k \varphi_s y_{t-s} \right)^{-1} & ; \text{for } k < t \leq T. \end{cases}$$

- ▶ Replace y_t by $\hat{\mu}(t) = \exp(\hat{\boldsymbol{\theta}}^\top b(t))$ and write in compact notation:

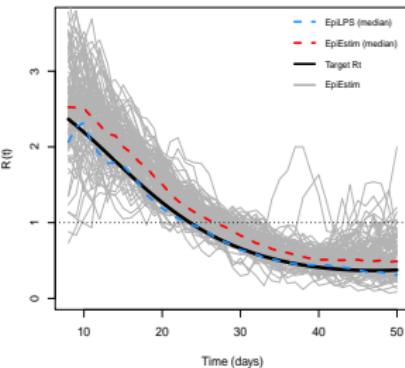
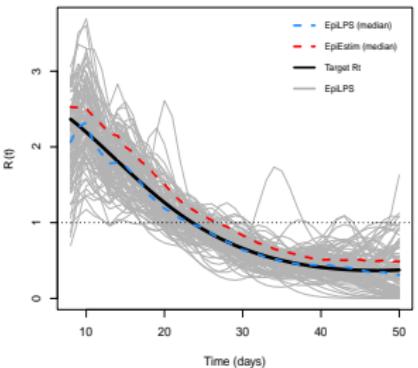
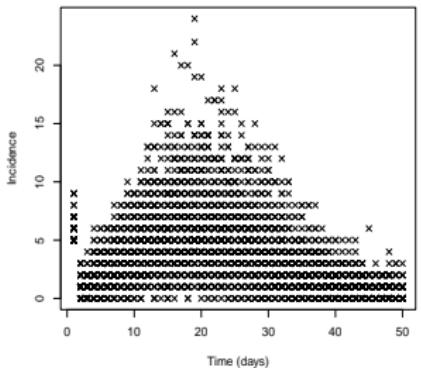
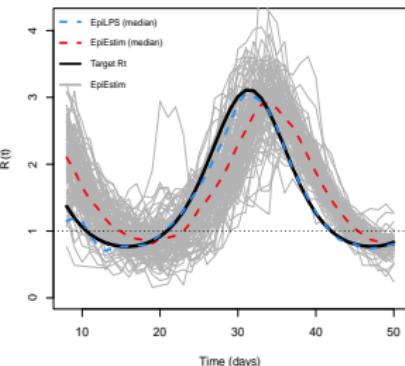
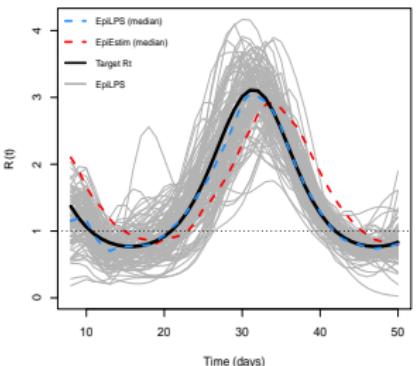
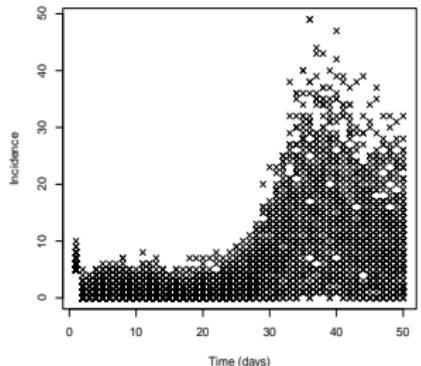
$$\begin{aligned} \hat{R}(t) &= \exp(\hat{\boldsymbol{\theta}}^\top b(t)) \left\{ \mathbb{I}(t=1) + \left(\sum_{s=1}^{t-1} \varphi_s \exp(\hat{\boldsymbol{\theta}}^\top b(t-s)) \right)^{-1} \mathbb{I}(2 \leq t \leq k) \right. \\ &\quad \left. + \left(\sum_{s=1}^k \varphi_s \exp(\hat{\boldsymbol{\theta}}^\top b(t-s)) \right)^{-1} \mathbb{I}(k < t \leq T) \right\}. \end{aligned}$$

- ▶ Consider an epidemic of $T = 50$ days.
- ▶ Data generating process based on Poisson counts and the renewal equation → repeat $S = 100$ times.
- ▶ Compare with `estimate_R()` routine of **EpiEstim** package [Cori et al. \(2013\)](#).
- ▶ For **EpiEstim**, we need to specify a sliding window, (here 7 days).
- ▶ Four different scenarios:
 - ▶ Scenario 1: constant $R(t)$.
 - ▶ Scenario 2: assess impact of intervention, step function for $R(t)$.
 - ▶ Scenario 3: curved $R(t)$.
 - ▶ Scenario 4: decaying $R(t)$.

Scenarios 1 and 2



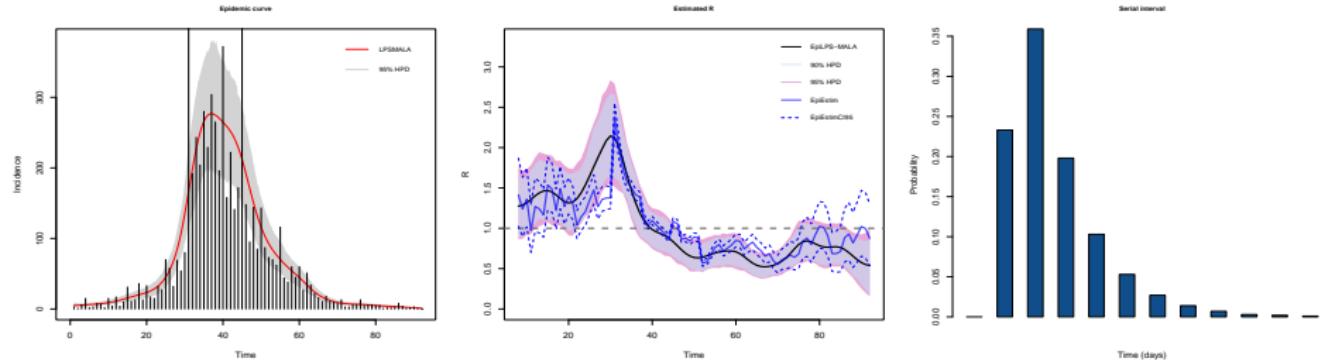
Scenarios 3 and 4



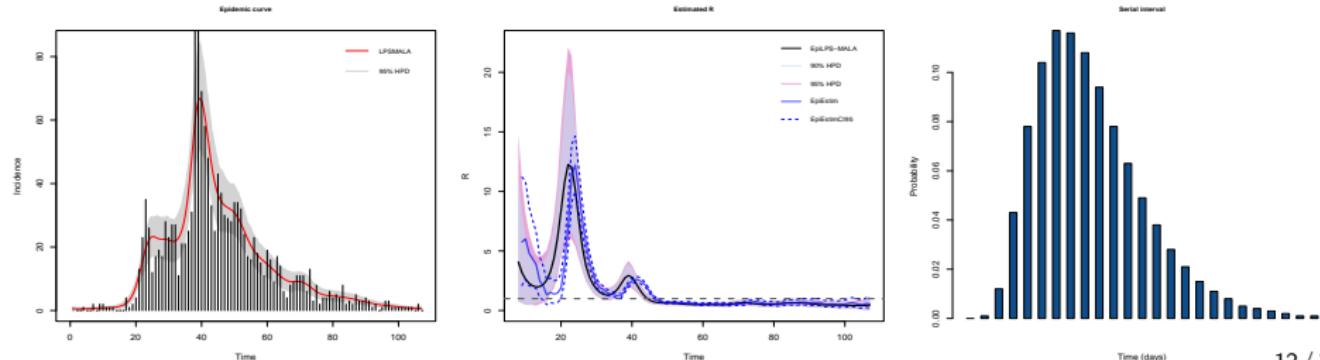
Real data applications with LPSMALA

We revisited historical outbreaks analyzed in [Cori et al. \(2013\)](#) with LPSMALA.

► Influenza pandemic in Baltimore (1918)



► SARS epidemic in Hong Kong (2003)



EpiLPS vs EpiEstim

Main methodological differences between EpiLPS and EpiEstim:

- ▶ EpiLPS extracts a signal from the epidemic curve (smoothed version of mean incidence counts) and injects it into the renewal equation. Priors imposed on overdispersion parameter and smoothing parameter.
- ▶ EpiEstim imposes a (conjugate) Gamma prior on $R(t)$, so that *a posteriori* $R(t)$ is also Gamma distributed. In [Cori et al. \(2013\)](#), they assume a Gamma prior with mean 5 and standard deviation 5.
- ▶ In EpiLPS, we show that *a posteriori* $R(t)$ has a log-normal distribution.
- ▶ EpiEstim uses a Poisson distribution to model transmissions, while EpiLPS uses a Negative Binomial model (accounts for overdispersion).
- ▶ In EpiLPS no need to choose a time window, simply estimate $R(t)$ over the whole time interval of interest. EpiEstim requires a specification of a time window as an input (what is the optimal sliding window?).

Concluding remarks and take home message

- ▶ EpiLPS is a novel methodology for fast and flexible approximate Bayesian inference of the epidemic curve and the time-varying reproduction number $R(t)$.
- ▶ The computational efficiency is mainly due to Laplace approximations and its associated routine coded in C++ and integrated via Rcpp.
- ▶ The Bayesian P-splines framework allows to get smooth estimates of the epidemic curve and the latter information is used in conjunction with the epidemic renewal equation to provide a smooth estimate of $R(t)$.
- ▶ Credible intervals of $R(t)$ can be efficiently computed via the delta method.
- ▶ EpiLPS provides both a sampling-free approach (LPSMAP) and a fully stochastic approach based on Langevin diffusions (LPSMALA) to estimate $R(t)$.

Acknowledgments: This project is funded by the European Union's Research and Innovation Action under the H2020 work programme, EpiPose (grant number 101003688).

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