

Regional Estimates of Reproduction Numbers — the ITWW model

Przemyslaw Biecek¹, Marcin Bodych², Viktor Bezborodov², Jan Pablo
Burgard³, Stefan Heyder⁴, Thomas Hotz⁴, Tyll Krüger²

¹Warsaw University of Technology, ²Wrocław University of Science and Technology, ³Universität Trier,
⁴Technische Universität Ilmenau

This work was supported by the German Federal Ministry of Education and Research (BMBF; grant 05M18SIA).

03 November 2021

recap reproduction equation

- the epidemic spread can be modeled by an reproduction equation, e.g.

$$I(t) \mid I(t-1), \dots \sim \text{Pois} \left(R(t) \sum_{\tau=1}^{\infty} I(t-\tau) w(\tau) \right)$$

where $I(t)$ is the amount of **incident cases** on day t , $R(t)$ is the **(instantaneous) reproduction number** on day t and $w(\tau)$ is the distribution of the **generation time**

- many estimators of $R(t)$ are available, we start with frequentist approach

$$\hat{R}(t) = \frac{I(t)}{\sum_{\tau=1}^{\infty} I(t-\tau) w(\tau)},$$

which works well when denominator is large, e.g. on the country level

local outbreaks: Germany in summer 2020

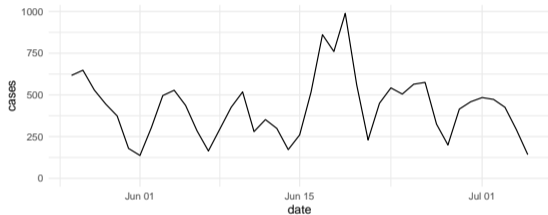


Figure: Daily reported SARS-CoV-2 infections in May – July 2020 in Germany.
Data source: Robert-Koch Institut.

local outbreaks: Germany in summer 2020

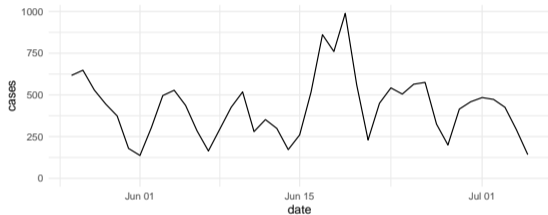


Figure: Daily reported SARS-CoV-2 infections in May – July 2020 in Germany. Data source: Robert-Koch Institut.

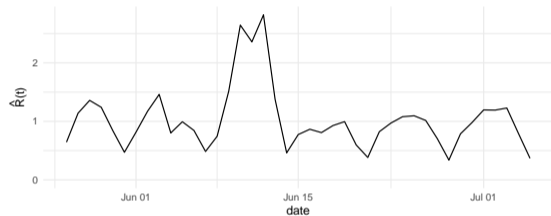


Figure: $\hat{R}(t) = I(t) / \sum_{\tau=1}^{\infty} I(t - \tau)w(\tau)$ for Germany in May – July 2020. Estimates are backdated by one week to account for reporting delay.

monitoring epidemic spread on subnational level

- large, but localized, outbreaks are regional events which may lead to undesirable estimates of $\hat{R}(t)$
 - many other aspects of an epidemic are also heterogeneous within one country:
 - immunity,
 - implemented countermeasures and
 - other socio-economic factors.
- ↪ model and estimate reproduction numbers on the county level
- county level data pose additional challenges: low case numbers, high variability and imported / exported cases between counties

model

$$I_c(t) \mid I_c(t-1), \dots \sim \text{Pois}(R_c(t)\Phi_c(t))$$

where $I_c(t)$ is the amount of incident cases in county c on day t ,

$\Phi_c(t) = \sum_{\tau=1}^{\infty} I_c(t-\tau)w(\tau)$ is the amount of currently infectious on day t in county c

model

$$I_c(t) \mid R_c(t), I_c(t-1), \dots \sim \text{Pois}(R_c(t)\Phi_c(t))$$

where $I_c(t)$ is the amount of incident cases in county c on day t ,

$\Phi_c(t) = \sum_{\tau=1}^{\infty} I_c(t-\tau)w(\tau)$ is the amount of currently infectious on day t in county c

- to deal with low and highly variable case counts, we use techniques from **small-area estimation**: model $R_c(t)$ as **random with common distribution**

model

$$I_c(t) \mid R_c(t), I_c(t-1), \dots \sim \text{Pois} \left(R_c(t) \left((1 - p_t) \Phi_c(t) + \frac{p_t}{K-1} \sum_{c' \neq c} \Phi_{c'}(t) \right) \right)$$

where $I_c(t)$ is the amount of incident cases in county c on day t ,

$\Phi_c(t) = \sum_{\tau=1}^{\infty} I_c(t-\tau)w(\tau)$ is the amount of currently infectious on day t in county c

- to deal with low and highly variable case counts, we use techniques from **small-area estimation**: model $R_c(t)$ as **random with common distribution**
- to deal with imported and exported cases we add p_t , the **proportion of imported infections** which we assume to be evenly distributed among all other $K - 1$ counties
- here and in the following we tacitly condition on all past incidences

model

$$I_c(t) \mid R_c(t), I_c(t-1), \dots \sim \text{Pois} \left(R_c(t) \left((1 - p_t) \Phi_c(t) + \frac{p_t}{K-1} \sum_{c' \neq c} \Phi_{c'}(t) \right) \right)$$

- assume $R_c(t) \sim \text{Gamma}(a_t, s_t)$ with shape a_t and scale s_t such that

$$I_c(t) \mid I_c(t-1), \dots \sim \text{NegBinom}(a_t, q_t(s_t, p_t, \dots))$$

has known distribution

- assuming cond. independence we obtain maximum-likelihood estimators $(\hat{a}_t, \hat{s}_t, \hat{p}_t)$

model

$$I_c(t) \mid R_c(t), I_c(t-1), \dots \sim \text{Pois} \left(R_c(t) \left((1 - p_t) \Phi_c(t) + \frac{p_t}{K-1} \sum_{c' \neq c} \Phi_{c'}(t) \right) \right)$$

- assume $R_c(t) \sim \text{Gamma}(a_t, s_t)$ with shape a_t and scale s_t such that

$$I_c(t) \mid I_c(t-1), \dots \sim \text{NegBinom}(a_t, q_t(s_t, p_t, \dots))$$

has known distribution

- assuming cond. independence we obtain maximum-likelihood estimators $(\hat{a}_t, \hat{s}_t, \hat{p}_t)$
 \rightsquigarrow Empirical Bayes

estimated reproduction numbers

on the county level

- conditional on incidences

$$R_c(t) \mid I_c(t), I_c(t-1), \dots$$

is again gamma distributed (conjugate prior)

- estimate $\mathbb{E}(R_c(t) \mid I_c(t), I_c(t-1), \dots)$ by Plug-in using ML estimates \hat{a}_t , \hat{s}_t and \hat{p}_t

estimated reproduction numbers

on the county level

- conditional on incidences

$$R_c(t) \mid I_c(t), I_c(t-1), \dots$$

is again gamma distributed (conjugate prior)

- estimate $\mathbb{E}(R_c(t) \mid I_c(t), I_c(t-1), \dots)$ by Plug-in using ML estimates \hat{a}_t , \hat{s}_t and \hat{p}_t

on the country level

- estimate prior mean $\mathbb{E}R_c(t) = a_t s_t$ by Plug-in $\hat{a}_t \hat{s}_t$

simulation study

- simulate point process on $\mathbb{T} = \mathbb{R}^2 / (20\mathbb{Z})^2$, unit square represent counties

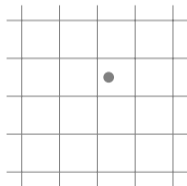


Figure: One primary case and the secondary cases it generates over time.

simulation study

- simulate point process on $\mathbb{T} = \mathbb{R}^2 / (20\mathbb{Z})^2$, unit square represent counties
- at every time t a primary case in county c with infection age τ infect $\text{Pois}(R_c(t)w(\tau))$ many secondary cases
- position of secondary cases are gaussian, centered around the position of primary case

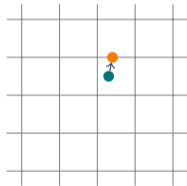


Figure: One primary case and the secondary cases it generates over time.

simulation study

- simulate point process on $\mathbb{T} = \mathbb{R}^2 / (20\mathbb{Z})^2$, unit square represent counties
- at every time t a primary case in county c with infection age τ infect $\text{Pois}(R_c(t)w(\tau))$ many secondary cases
- position of secondary cases are gaussian, centered around the position of primary case

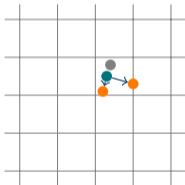


Figure: One primary case and the secondary cases it generates over time.

simulation study

- simulate point process on $\mathbb{T} = \mathbb{R}^2 / (20\mathbb{Z})^2$, unit square represent counties
- at every time t a primary case in county c with infection age τ infect $\text{Pois}(R_c(t)w(\tau))$ many secondary cases
- position of secondary cases are gaussian, centered around the position of primary case

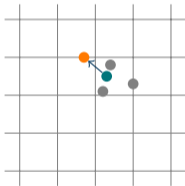


Figure: One primary case and the secondary cases it generates over time.

simulation study: results

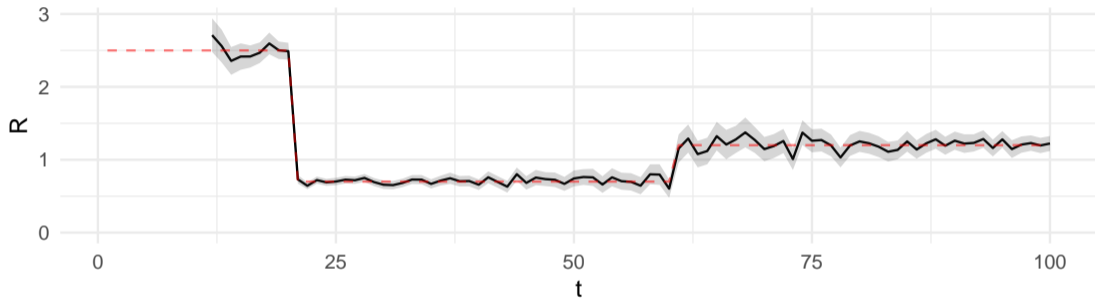


Figure: Estimated country-wide reproduction number (black) with asymptotic 95% confidence intervals (grey ribbons) and true value (dashed red line).

application to the COVID-19 epidemic in Germany

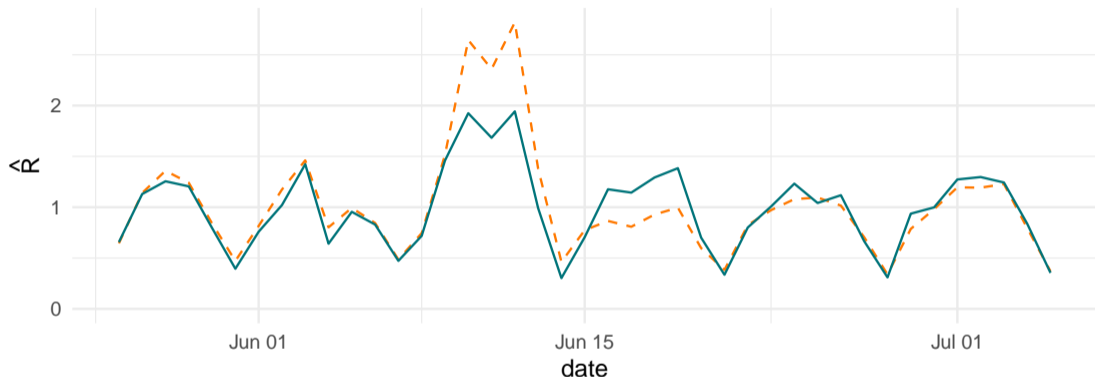


Figure: Comparison of country wide reproduction number estimates based on county and country level incidences. Estimates are backdated by one week to account for reporting delay.

application to the COVID-19 epidemic in Germany

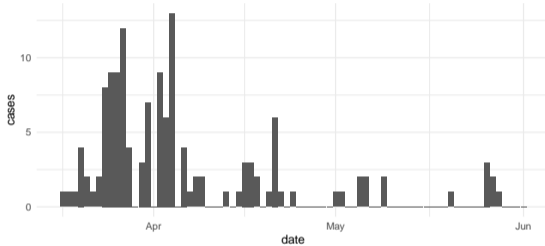


Figure: Daily reported SARS-CoV-2 cases in Ilm-Kreis county in March – June 2020 in Germany.

application to the COVID-19 epidemic in Germany

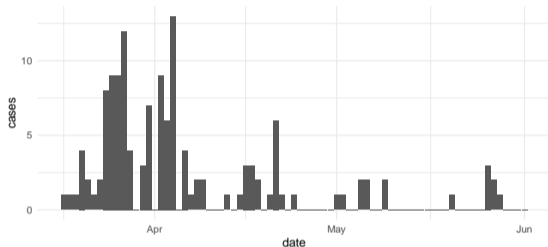


Figure: Daily reported SARS-CoV-2 cases in Ilm-Kreis county in March – June 2020 in Germany.

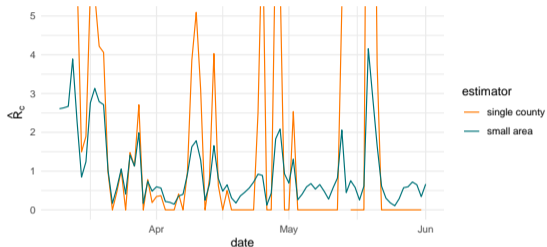
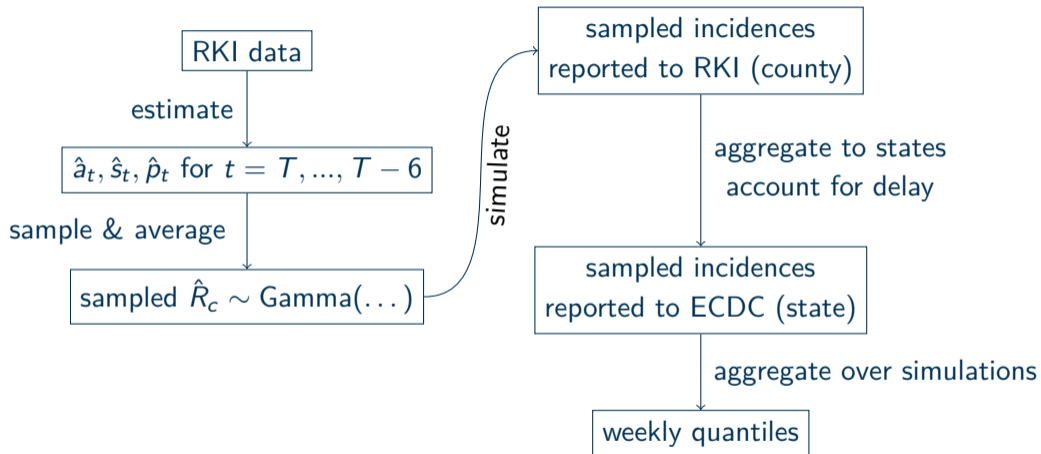
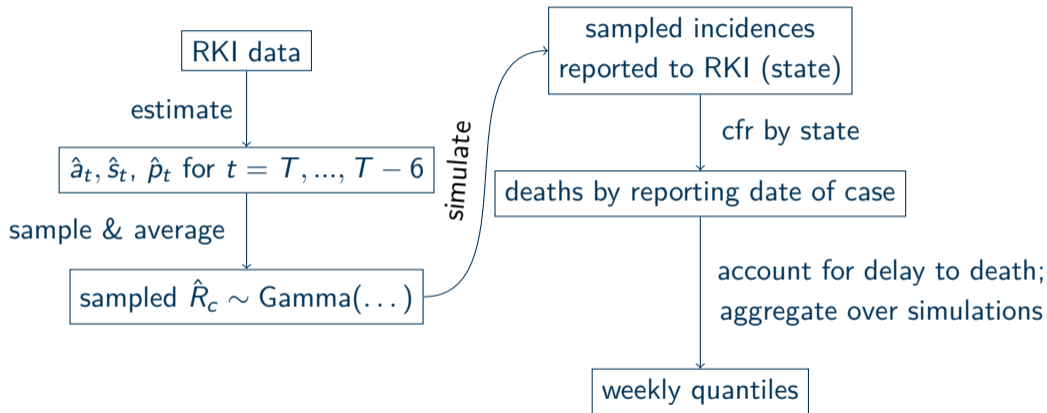


Figure: Estimated reproduction numbers for Ilm-Kreis county between March and June 2020.

forecasting incidences in Germany



forecasting deaths in Germany



dealing with overconfidence

- recall that under our modelling assumptions, $R_c(t)|I_c(t), \dots \sim \text{Gamma}(a_t + I_c(t), \dots)$
- sampling $R_c(t)$ independently in each county yields narrow prediction intervals on state and country level
- to introduce more variation, use copula for reproduction numbers of counties within one state:
sample for each state l a probability $Q_l \sim \text{Unif}(0, 1)$ i.i.d. and for any county c in state l set

$$R_c(t) = F^{-1}(Q_l; \hat{a}_t + I_c(t), \dots)$$

for the inverse cdf $F^{-1}(\cdot; a, s)$ of the gamma distribution $\text{Gamma}(a, s)$

Model Performance - 2 week ahead forecasts

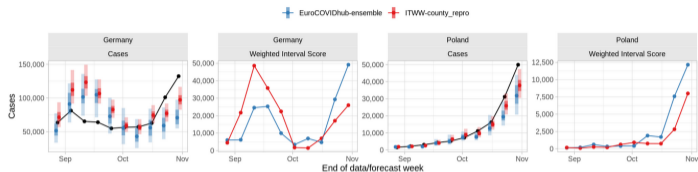


Figure: ECDC ForecastHub performance over time: cases

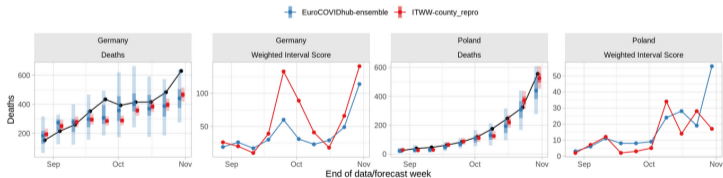


Figure: ECDC ForecastHub performance over time: deaths

Model Performance - State level

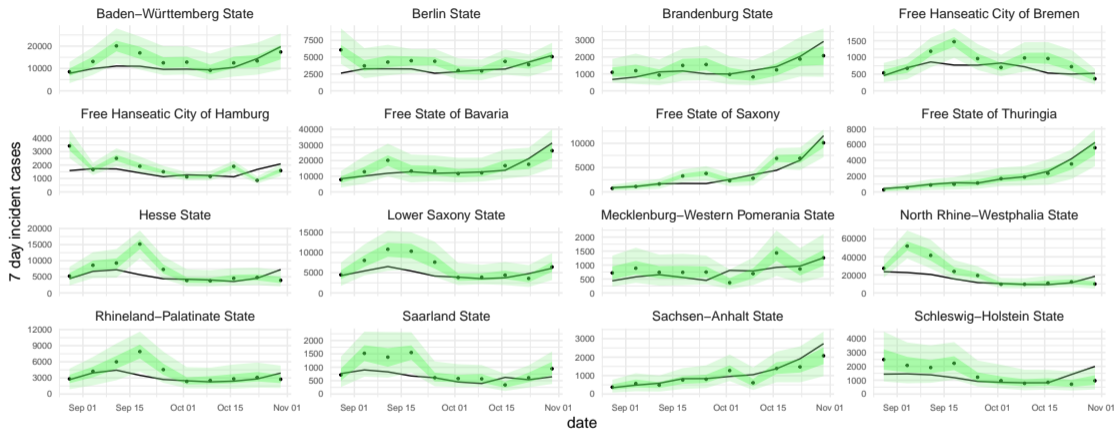


Figure: 95% and 50% prediction intervals, point forecast for 2 week ahead case forecasts on the state level in Germany

conclusion

- sub-national perspective allows to account for heterogeneity in spread
- good performance during phases of exponential growth
- problems: overshooting at peaks & overconfidence

conclusion

- sub-national perspective allows to account for heterogeneity in spread
- good performance during phases of exponential growth
- problems: overshooting at peaks & overconfidence

future research

- allow other prior distributions for $R_c(t)$: computationally intensive
- investigate and account for impact of socio-economic factors, week-day effects on $R_c(t)$