

Epidemiological Modeling and Hotspot Predictions of Covid-19 in Region Uppsala

Applying epidemiological modeling and using regression analysis for hotspot predictions on CRUSH Covid data prove promising in revealing the spread of Covid-19 in Region Uppsala.

VISUALIZATION

The CRUSH Covid data set consists of spatio-temporal data on positivity, tests, and cases per capita for each week and postal code area. To make this spatiotemporal data more comprehensible, an interactive visualization based on government-issued guidelines for infection spread levels is applied. This enables anyone to check out the current spread of infection in their postal code area.

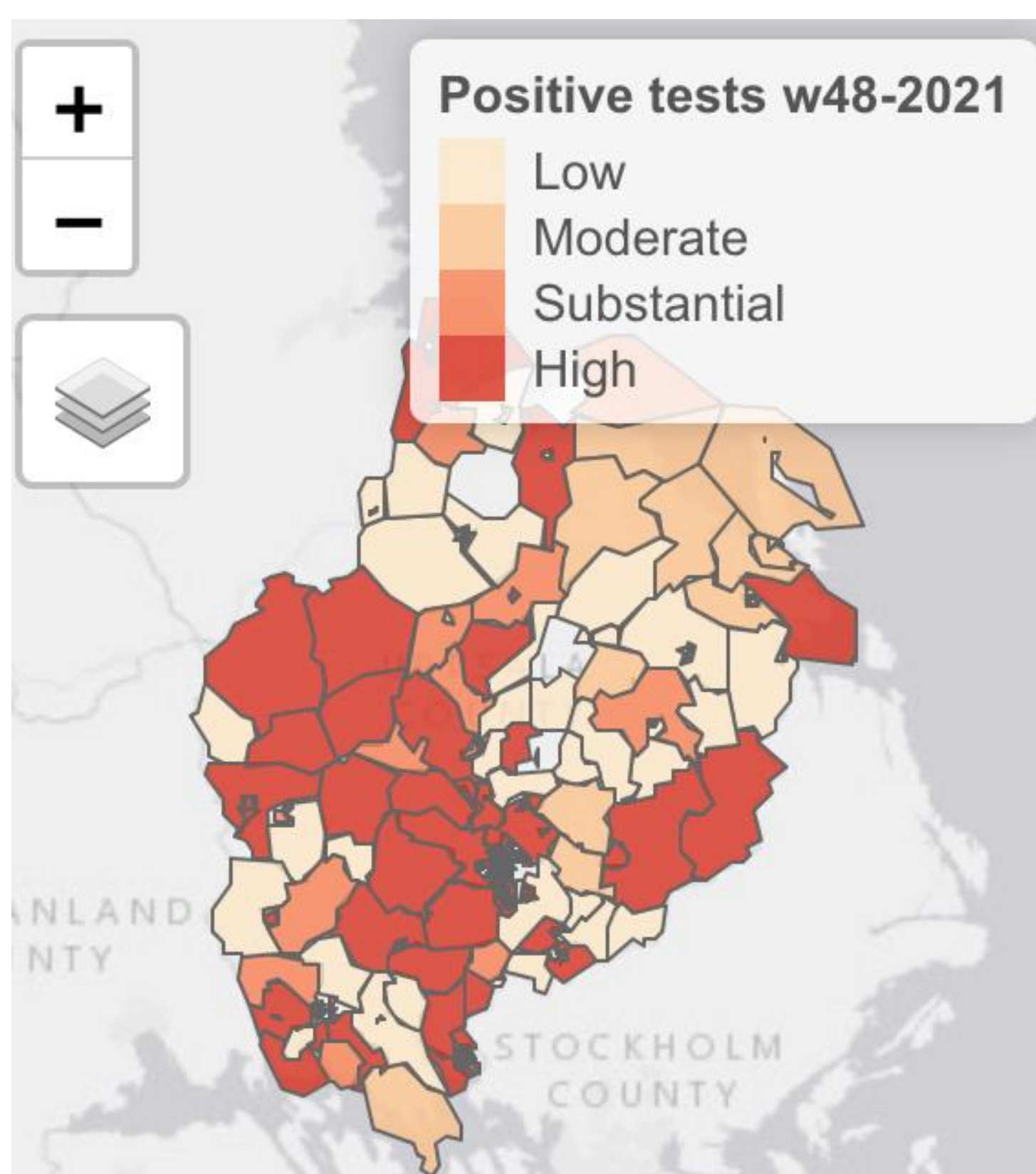
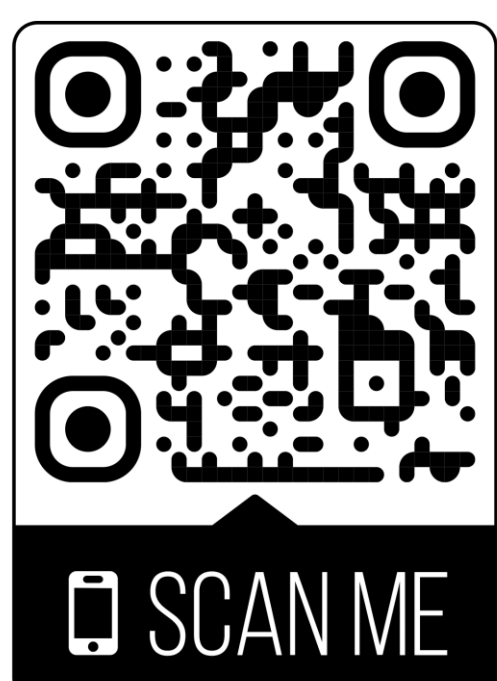


Fig. 1: Positive tests per capita for all postal codes in Region Uppsala



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HOTSPOT PREDICTION

Using Machine Learning approaches for predicting hotspots of Covid-19 in Region Uppsala.

The implemented regression models for performing one-week ahead predictions are Random Forest (RF), Quantile Regression (QR) and Quantile Random Forest (QRF).

RF and QRF returns the mean respective quantile of the decision trees' outputs and QR can model any quantile of the response variable's distribution.

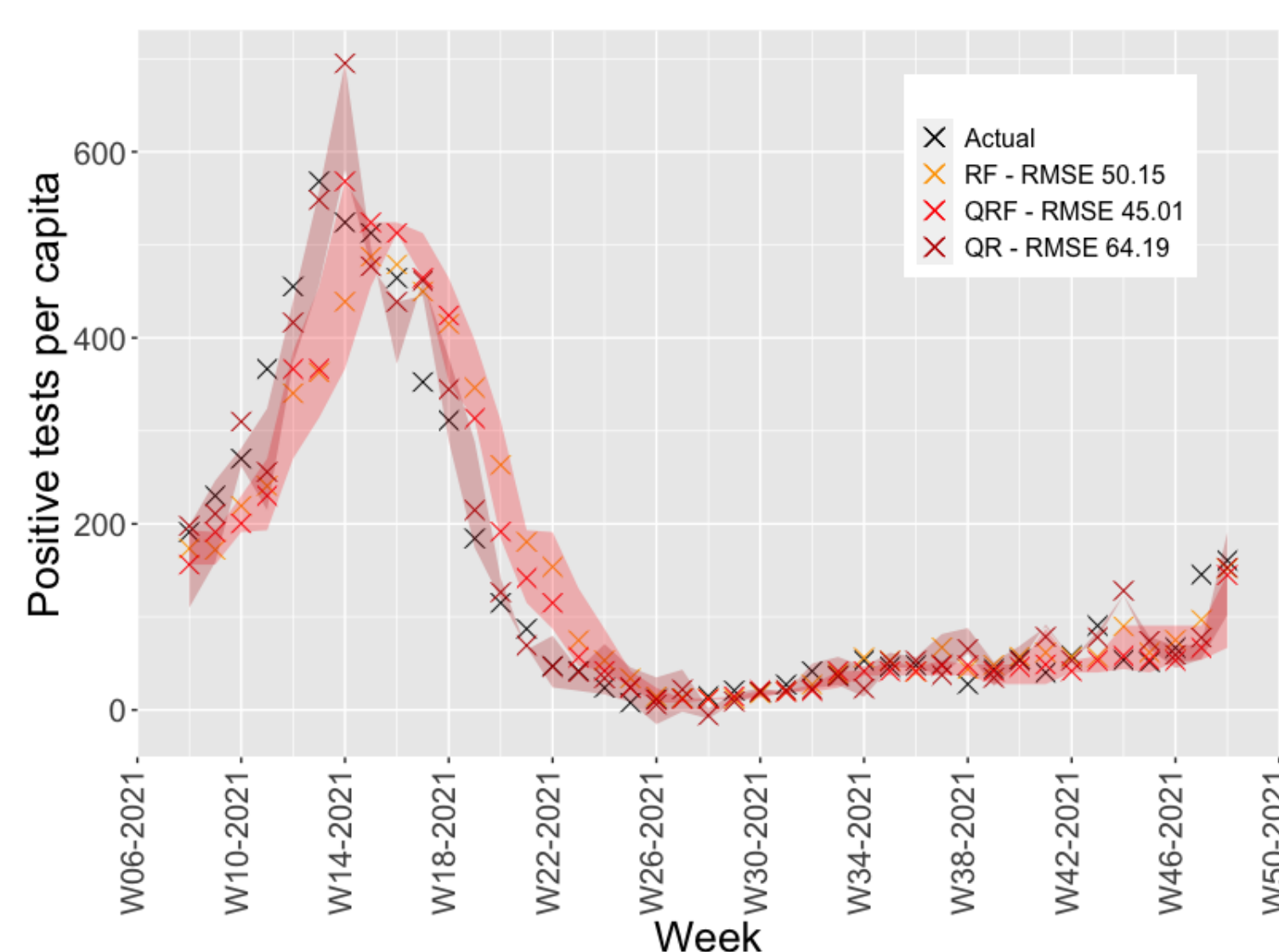


Fig. 2: Validation predictions on positive tests per capita in Uppsala municipality

In Fig. 2, validation predictions for all weeks, starting from week 6 2021, are plotted against actual data for Uppsala municipality. All models capture the actual data.

The models' performance was analyzed using the widely used forecasting metric *Root Mean Square Error*, which revealed that QRF has the lowest error.

EPIDEMIOLOGICAL MODELING

The SimInf package was used to create a stochastic time dynamic SIS model to describe the outbreak of Covid-19 in Region Uppsala. The SIS model contains two compartments, the Susceptible (S) and the Infected (I), where the rate of recovery is denoted by γ and the rate of infection is divided into four or five periods denoted by β_t . The models also allow for modeling of multiple nodes, denoting the different municipalities of Region Uppsala.

A Bayesian method has been implemented where the parameters prior distribution are initially set as uniform. Approximate Bayesian computation with sequential Monte Carlo sampling (ABC-SMC) was used to calculate the posterior distribution.

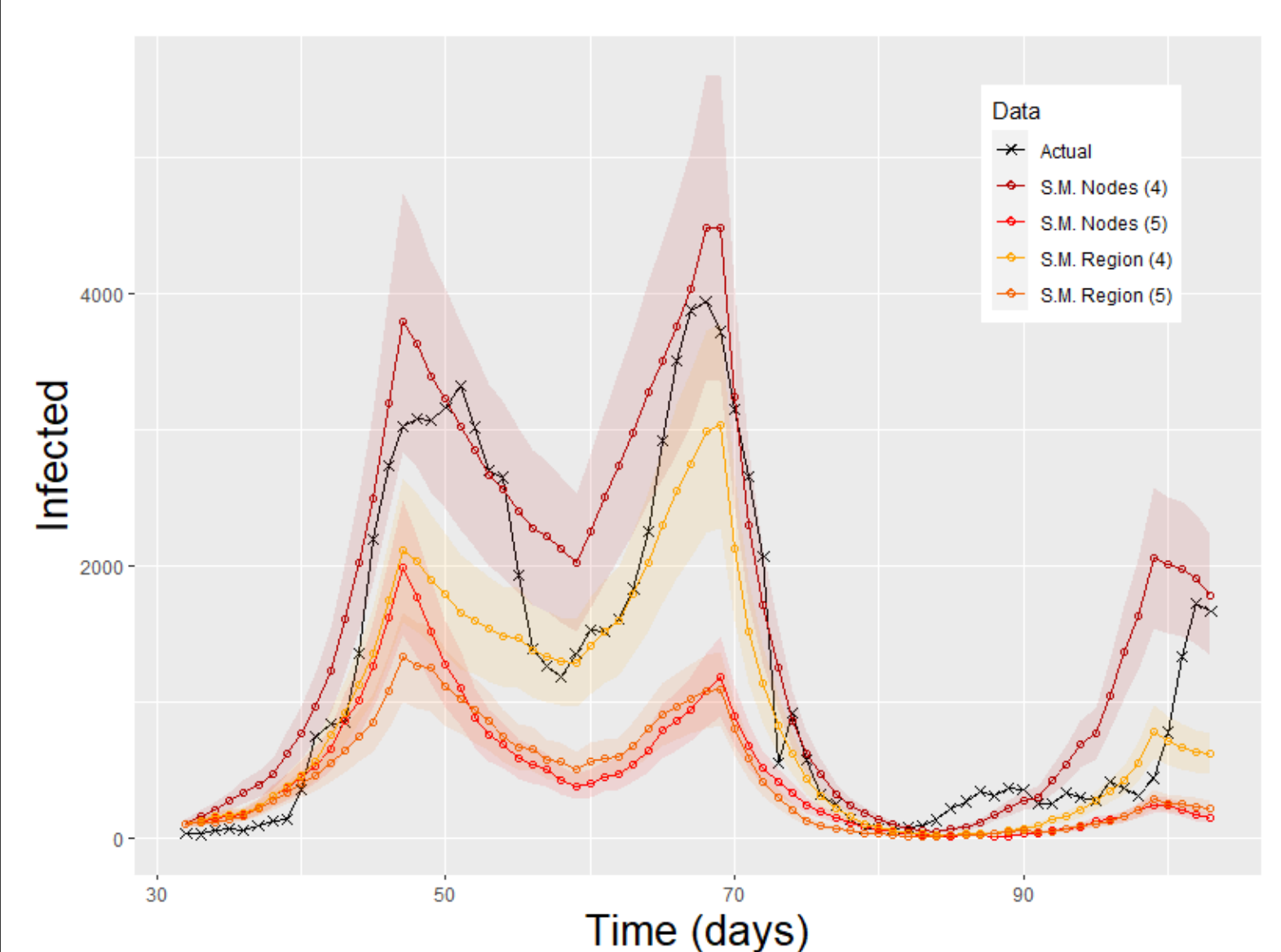


Fig. 3: Model predictions of infected

In Fig. 3, actual infected data from Region Uppsala are plotted against simulated data and predictions from four SIS models. The models approximate the actual data and make reasonable predictions.