NIPH
Norwegian Institute of Public Health

Situational awareness and forecasting

FHI COVID-19 modelling team

28 October 2020

Highlights from this report:

- Our models evaluate the present situation as stable. The reproduction number acting from October 1 is estimated to be 1.01 (median), with a rather narrow 95% confidence interval (0.91 - 1.13). Compared to a week ago, the estimated reproduction number is similar, with less uncertainty, because we now also use test data in addition to hospitalisation data. The estimated probability that the reproduction number R_7 is larger than 1 is 56.5 %.
- This report uses test data in addition to hospitalisation data. Until now, we have calibrated our model to daily hospital incidence. These data are reliable, as the need to be treated in hospital can be assumed to have been unchanged over time. In addition, as our main aim is precisely to provide good predictions of the hospitalisation incidence, it is advantageous to calibrate to the hospitalisation incidence. However, hospitalisation data are subject to a delay between transmission and hospitalisation, up to 14-16 days. Laboratory-confirmed cases are now also included in our calibration procedure. In this way, we include more information, in particular for the recent period, as the delay between transmission and testing is much shorter than the delay between transmission and hospitalisation. In practice, the calibration is done by simulating the number of positive tested individuals, and comparing this to the laboratory-confirmed COVID-19 cases.
- To use the test data in our report, we need to model the probability that an infected individual is detected as positive by testing. In our simulations, we assume that the number of positively tested cases can be modelled as a binomial process of the simulated daily total incidence of symptomatic and asymptomatic cases, with a time-varying detection probability which we estimate. This probability depends on the total number of tests made, both the ones resulting positive and negative. In this way we try to include in our model the time-varying efforts which have been made to find positive cases.
- What are the advantages of using also test data? With the additional information, the confidence intervals for the estimated parameters should in general become smaller. We should also be able to estimate the dynamic of the epidemic in the last two weeks better.
- The hospitalisation incidence and the number of positive and negative tests are subject to a reporting delay, meaning that in the data we have today, the incidence for the last couple of days is under-reported and will be updated a few days later. The delay in reporting is stronger during the weekends. We therefore correct for the reporting delay in our simulations, by imputing the number of missing hospitalisations and missing tests. This is done by using the information about the reporting delay from the past data. In this way, we avoid that our estimates are biased downwards in the last days because of this reporting delay. Details are provided at the end of the report.
- The model estimates the total number of infected individuals from the start of the epidemic to be just below 100.000, with a confidence interval between 87.000 and 111.000. In one week, the number of new cases per day is ca 450 and will remain at that level in three weeks. The predicted number of infected individuals in a week is about 3000 with substantial uncertainty.

- Note that the SMC model still uses only the hospitalisation incidence data. We are working on extending it to use also the test data. The SMC model estimates the 7-days averaged reproduction number two weeks ago to be 1.08 (0.63-1.63); the estimated probability that the daily reproduction number two weeks ago was larger than 1 is 59.2%.
- The estimated probability that the total number of new infections exceeds 20 per 100.000 is increasing, and is 100% in all counties.
- Hospitalisation is expected to remain stable, and we expect 61 (median) COVID-19 patients to be in hospital in a week. The 95% confidence interval is (39-91). We expect between 2 and 13 patients needing ventilator treatment in a week (95% confidence interval).
- Long-term scenario for the next 12 months, assuming that the reproduction number R_7 remains as now: the median trend is stable, slightly decreasing. The 50% quantile grows slightly until April 21, to then start decreasing. The 75% quantile has a peak in July 2021. The probability that at peak there is a need for more than 500 ventilator treatment beds is estimated to be zero. When predicting the next 12 months, we assume a constant reproduction number and a mobility as today. For the first next three weeks we use hospitalisation rates as in the rest of this report, which utilise the current age profile of positive cases. However, after the first three weeks, we use rates only based on demography, because our epidemic model does not have age classes. A discontinuity after three weeks can be seen in the figures 19 and 20.
- Long term scenarios with hypothesised and fixed reproduction numbers (1.1 , 1.2 and 1.3) have now been updated and also use hospitalisation rates only based on demography after the next three weeks.
- Inter-municipality mobility, measured as mobility of Telenor mobile phones out from each municipality is stable in the last two weeks, in most counties.
- Caveat on results per county in this report: as usual, this national report uses aggregated hospitalisation data and test data to estimate common reproduction numbers for the whole of Norway. The total number of infected individuals, hospitalised individuals, and individuals requiring ventilator treatment are then distributed to the various counties in the model simulations through use of the Telenor mobility data and age-structured demography of every municipality. The results on county level are therefore different from the ones in our regional report, where we assume that reproduction numbers can vary between counties, and where we estimate them using county-specific hospitalisation incidence and test data. We will therefore soon merge the two reports, to avoid confusion.
- There are several new figures in this report. Figure 3 shows how our model follows the reported daily number of positive cases. The fit is very good. In this figure we do not correct for the reporting delay in the last four days, so that the decay in the end is only due to such reporting delay.
- Figure 7 shows an estimate of the probability to detect a positive case. As seen in the last weeks, this probability is very stable since August, and is approximately twice as high as in in April and 30% higher than in May. In the same figure we also plot the estimated number of positive individuals infected in each month, and estimated by our model. We see that there are much less infections now compared to the spring. This is important, and shows that we are in a very different situation today compared to the last spring, despite the fact that the number of daily laboratory-confirmed cases is comparable. This is because we have a much better testing capacity and strategy today.
- Figure 8 is our best estimate of the probability to detect a positive case. This is estimated to be about 35% today and slightly growing. This means that every detected positive case, hides two additional ones, which we do not identify either because they are not tested, or they are tested, but false negative. This detection probability has increased after the summer and has slightly decreased recently. There is however so much uncertainty, that these trends are not significant, only an indication. The detection probability is estimated to be 30% higher than in May.

What this report contains:

This report presents results based on a mathematical model describing the geographical spread of COVID-19 in Norway. The model consists of three layers:

- Population structure in each municipality.
- Mobility data for inter-municipality movements (Telenor mobile phone data).
- Infection transmission model.

The model produces estimates of the current epidemiological situation at the municipality, county (fylke), and national levels, a forecast of the situation for the next three weeks, and a long term prediction.

How we calibrate the model:
The model is fitted to Norwegian COVID-19 hospital incidence data from March 10 until yesterday, and data on the laboratory-confirmed cases from May 1 until yesterday. We seed the model with infections imported to Norway from February 26 until yesterday.

How you should interpret the results:
The model is stochastic. To predict the probability of various outcomes, we run the model many times in order to represent the inherent randomness. We present the results in terms of mean values, 95% confidence intervals, medians, and interquartile ranges. We emphasise that the confidence bands might be broader than what we display, because there are several sources of additional uncertainty which we currently do not fully explore: firstly, there are uncertainties related to the natural history of SARS-CoV-2, including the importance of asymptomatic and presymptomatic infection. Secondly, there are uncertainties related to the timing of hospitalisation relative to symptom onset, the severity of the COVID-19 infections by age, and the duration of hospitalisation and ventilator treatment in ICU. We will update the model assumptions and parameters in accordance with new evidence and local data as they become available. Results can change also significantly. See more details at the end of this report.

The mobility data are updated until October 24^{th}. They account for the changes in the movement patterns between municipalities that have occurred since the start of the epidemic.

Because in this report we calibrate our model using national hospitalisation and test data, the predictions at county level can only be taken as an indication.

We assume six reproduction numbers for Norway:

- R_0 active until March 14;
- R_1 active from March 15 to April 19;
- R_2 active from April 20 until May 10.
- R_3 active from May 11 until June 30.
- R_4 active in July.
- R_5 active in August.
- R_6 active in September 1
- R_7 active in October 1

When we forecast beyond today, we use the last reproduction number for the whole future, if not explicitly stated otherwise.

The basic reproductive numbers are calibrated to hospital incidence data until yesterday. Estimates of all reproduction numbers are uncertain, and we use their distribution to assure appropriate uncertainty of our predictions. Uncertainties related to the model parameters, as well as the transient period in weeks

11 and 17, imply that the reported effective reproductive numbers should be interpreted with caution. Because patients admitted to hospital have been infected long before, there is a necessary delay of about two weeks in the estimation of reproductive numbers.

In this report, the term patient in ventilator treatment includes only those patients that require either invasive mechanical ventilation or ECMO (Extracorporeal membrane oxygenation).

1 Estimated Reproductive Numbers

Calibration of our model to hospitalisation and test data leads to the following estimates provided in figure 1 and table 1. For details on the definitions of the parameters, see the Model section at the end of the report.

Table 1: Calibration results

Parameter	Mean	Median	Confidence interval (95 %)
R0	4.06	4.07	(3.39-4.73)
R1	0.55	0.55	(0.48-0.62)
R2	0.44	0.44	(0.22-0.7)
R3	0.88	0.89	(0.67-1.04)
R4	0.90	0.88	(0.6-1.29)
R5	1.03	1.02	(0.86-1.21)
R6	1.05	1.05	(0.97-1.15)
R7	1.01	1.01	(0.91-1.13)

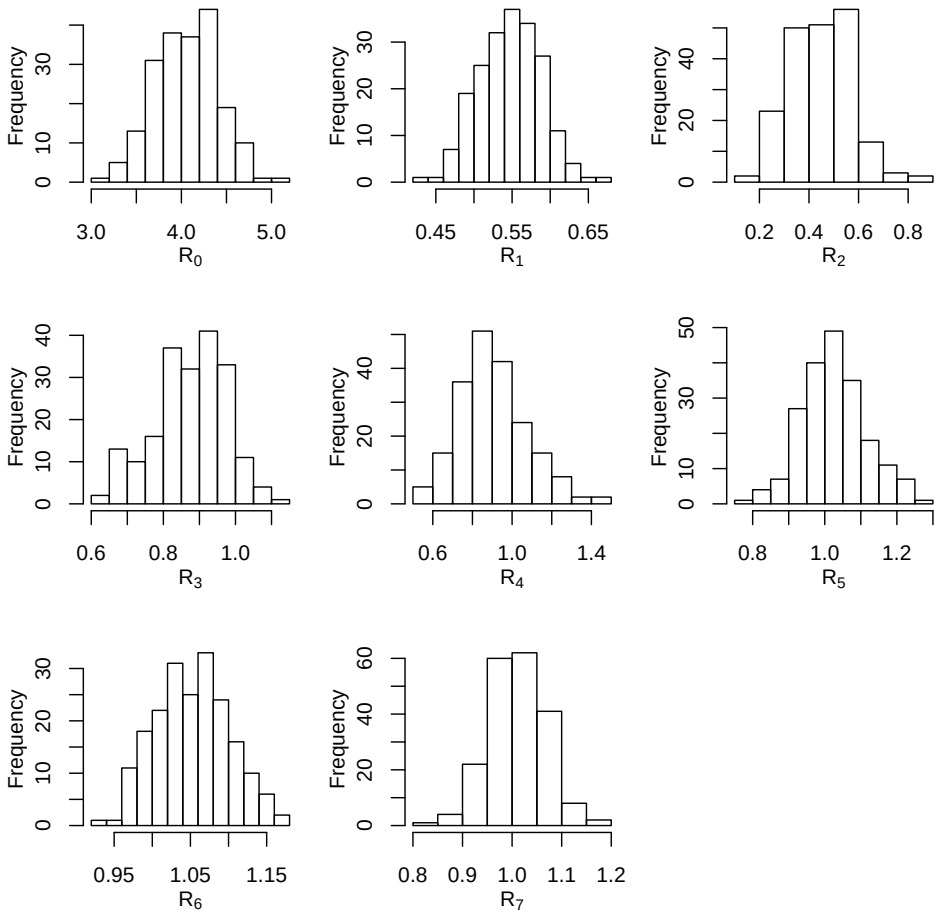

Figure 1: Estimated densities of the reproduction numbers.

Our changepoint model estimates the number of COVID-19 patients admitted daily to hospitals, plotted in figure 2 with blue median and interquartile bands, which are compared to the actual true data, provided in red. The uncertainty captures the uncertainty in the calibrated parameters in addition to the stochastic elements of our model and the variability of other model parameters.

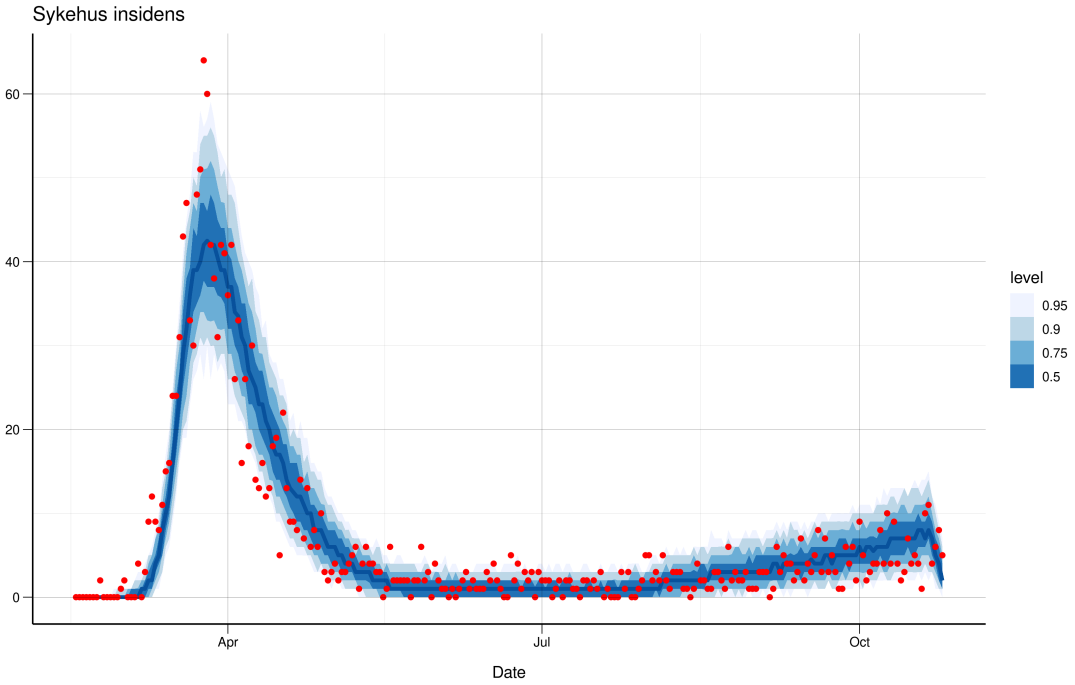

Figure 2: True total number of hospital admissions (red) and predicted values (blue)

The changepoint model is also calibrated to the number of laboratory-confirmed COVID-19 patients from May 1. We do not use data before May 1, as the testing capacity and testing criteria were significantly different in the early period. Figure 3 shows how our simulated number of positive cases, with blue median and interquartile bands, fits the actual true number of positive cases, provided in red. The uncertainty captures the uncertainty in the calibrated parameters, in addition to the stochastic elements of our model and the variability of other model parameters. Note that we do not capture all the uncertainty in the test data–our blue bands are quite narrow. This is likely because we calibrate our model parameters on a 7-days moving average window of test data, instead of daily. This is done to avoid overfitting to random daily variation. Moving averages over 7 days are less variable than the daily data.

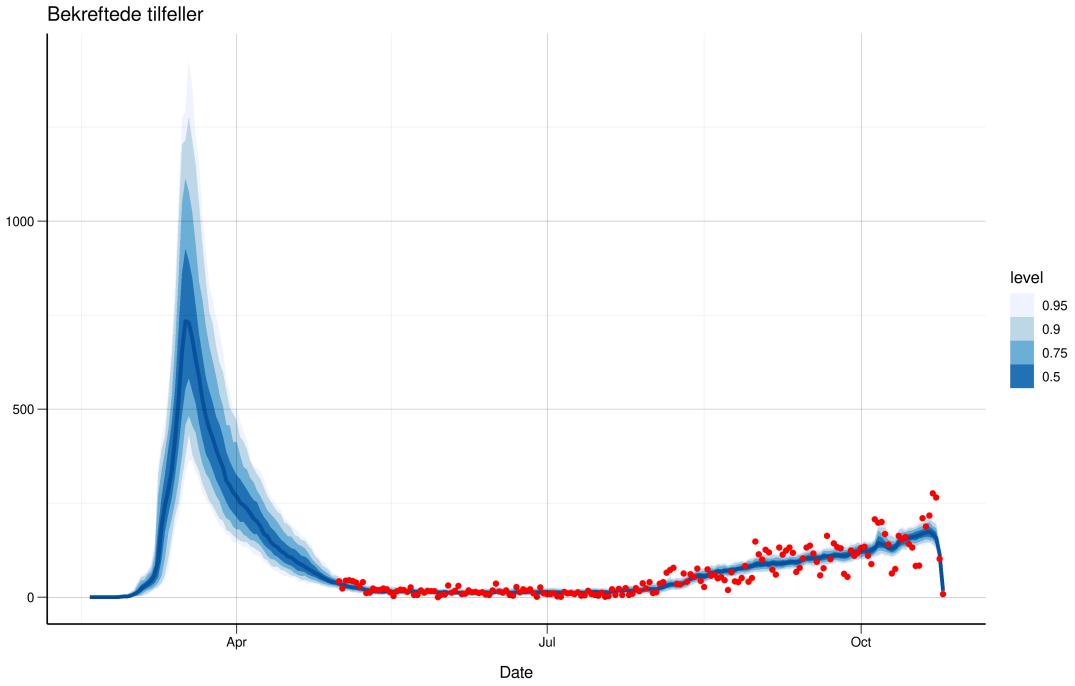

Figure 3: True total number of laboratory-confirmed cases (red) and simulated values (blue)

In figure 4, we show how our model fits the hospital prevalence data, which are not used to estimate the parameters, and can therefore be seen as a validation of the model assumptions.

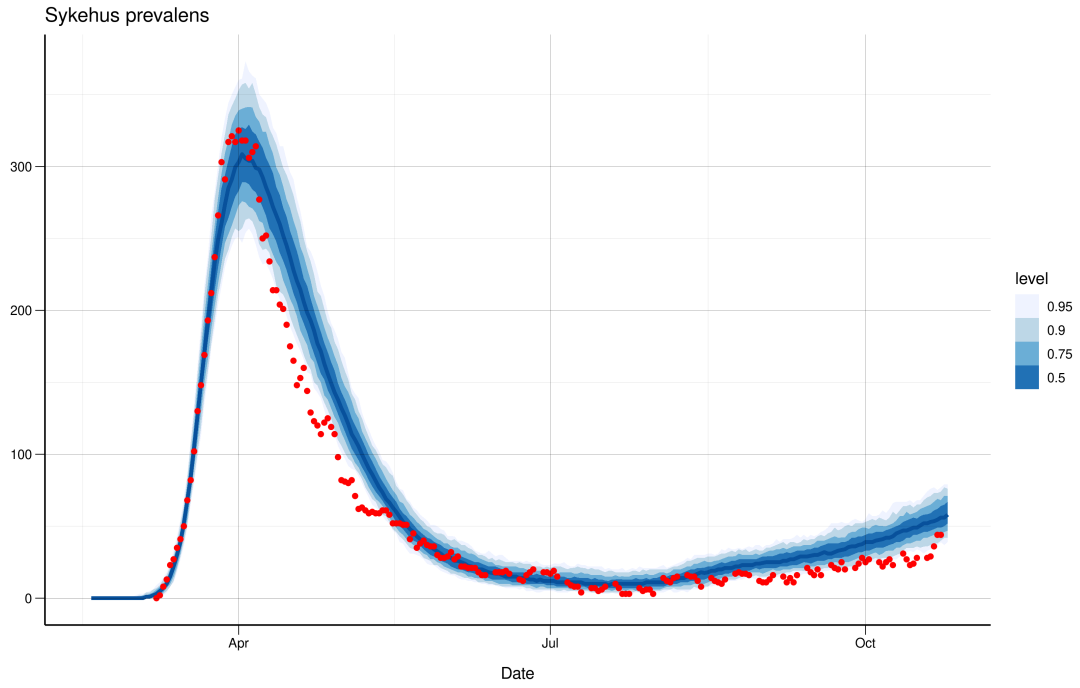

Figure 4: True total number of hospitalisations (red) and predicted values (blue)

Finally, in figure 5 we compare the true daily number of patients receiving ventilator treatment (red) with the model estimates (blue).

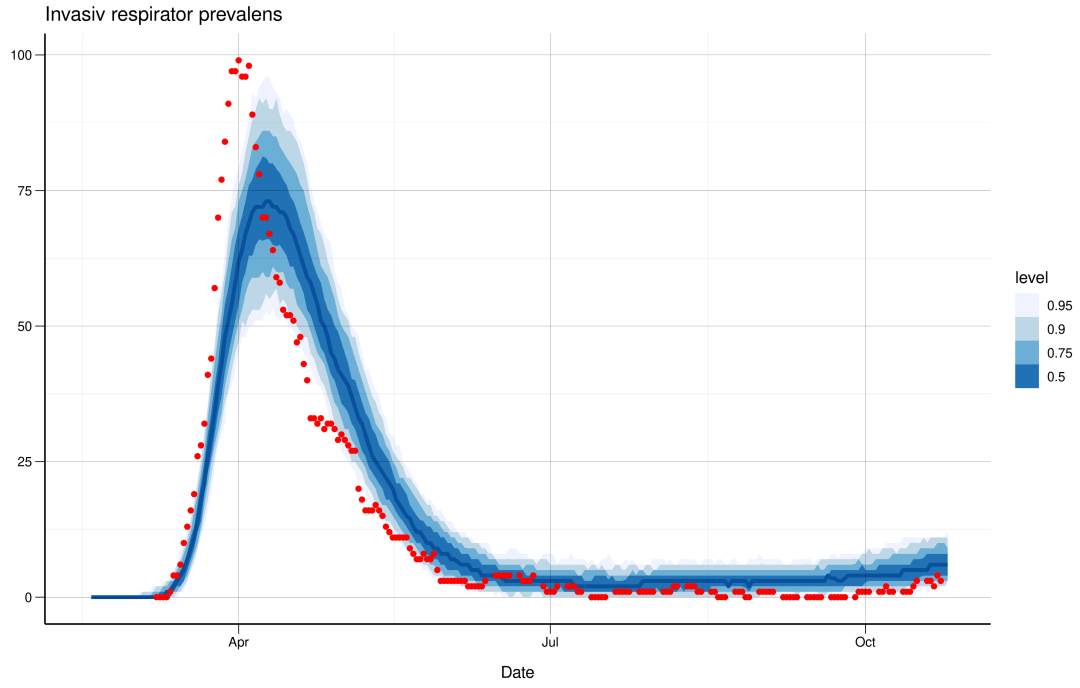

Figure 5: True total number on ventilator (red) and predicted values (blue)

1.1 Time-varying reproduction number

In addition to the changepoint model, we introduce an alternative model of the Norwegian COVID-19 pandemic, which is based on Sequential Monte Carlo, and is therefore called the SMC model. In this alternative model, we allow for a daily varying reproduction number, so that we estimate a different reproduction number for each day t. In order to reduce spurious fluctuation, we report a 7-days moving average, so that $R(t)$ represents the average reproduction number for the whole week before day t. Until March 8 we keep the reproduction number constant. (The SEIR model remains unchanged, except for the daily reproduction number, which replaces the piece-wise constant reproduction number assumed before.) By assuming a time varying reproduction number $R(t)$, we can detect changes without having to introduce explicit changepoints, which means that we can easier detect unexpected changes. However, this model requires additional parameters to be estimated, one per day. Estimating all these parameters is a difficult task, which we solve by using a method called Sequential Monte Carlo, see the Methods section at the end for details.

We use the hospitalisation incidence data to estimate all parameters. A patient hospitalised today was infected on average two weeks ago. Hence, hospitalisation data of today carry mainly information about the transmissibility 14 days ago. The estimated reproduction number of 14 days ago is thus the last one which is based on sufficient data. The estimated reproduction numbers of the days thereafter are based on diminishing information, and in particular there are no data to inform the reproduction number of today. Therefore, the uncertainty of the estimates of the reproduction numbers for the last 14 days is very large. This is also true for the reported 7-day-average reproduction numbers R_t. In the changepoint model, we are keeping the reproduction number constant after the last change point. In this way, there are more hospitalisation data points to inform the estimate of the most recent reproduction number. For this reason, the confidence intervals were more narrow. In addition, R_7 is also informed by the test data, as opposed to the current daily varying estimate.

The figure below shows the SMC estimate of the 7-day-average daily reproduction number $R(t)$ until today. We observe that $R(t)$ dropped below 1 in the middle of March, corresponding to the lockdown. It remained stable around 0.5 until the end of April, when it increased to 1 in the beginning of May. It then kept oscillating below and above 1, in accordance with increases and decreases of the number of new hospitalisations. $R(t)$ is sensitive to these oscillations in the data. An increase in hospital admissions indicates a daily reproduction number (14 days before on average) above 1. A decrease in hospital admissions suggests that the reproduction number was below 1 (again 14 days prior). In the figure we plot the 95% confidence interval and several quantiles of the estimated posterior distribution of $R(t)$.

1.1 Time-varying reproduction number

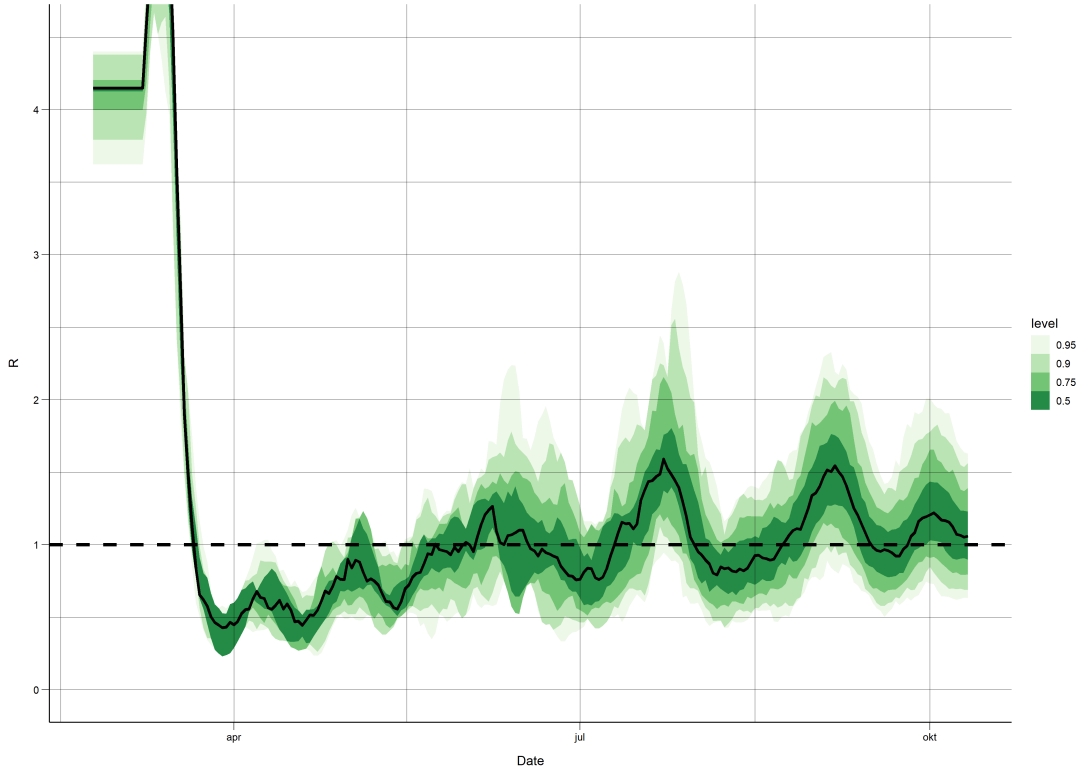

Figure 6: R(t) estimates until 14 days ago using a Sequential Monte Carlo (SMC) approach calibrated to incidence data. The large uncertainty during the last 14 days reflects the lack of available data due to the time period between infection, symptoms onset and hospitalisation. Therefore we omit the plot of the last 14 days. The green band shows the 95% posterior confidence interval.

2 Estimated cumulative number of infected individuals

The changepoint model estimates both the total number of infections and the symptomatic cases that have occurred both nationally and in each county. This result together with number of true confirmed cases can be found in table 2.

Table 2: Estimated cumulative number of infections, 2020-10-25

Region	Total	Symptomatic	No. confirmed	Fraction reported	Min. fraction
Norway	98818 (87233; 111102)	62612 (55858; 70185)	17908	18%	16%
Agder	6932 (5432; 8598)	4373 (3470; 5385)	604	9%	7%
Innlandet	7575 (6223; 8982)	4794 (3933; 5674)	847	11%	9%
Møre og Romsdal	3236 (2423; 4145)	2109 (1592; 2649)	364	11%	9%
Nordland	2411 (1768; 3468)	1547 (1151; 2175)	263	11%	8%
Oslo	16483 (13834; 19317)	10155 (8602; 11854)	5749	35%	30%
Rogaland	11295 (9331; 13205)	7113 (5869; 8240)	915	8%	7%
Troms og Finnmark	5787 (2897; 11106)	3609 (1894; 6730)	479	8%	4%
Trøndelag	4466 (3222; 5724)	2904 (2120; 3666)	834	19%	15%
Vestfold og Telemark	9416 (7937; 11073)	5989 (5036; 7050)	564	6%	5%
Vestland	8914 (6879; 11732)	5627 (4365; 7349)	2440	27%	21%
Viken	22303 (19448; 25969)	14391 (12473; 16586)	4796	22%	18%

Fraction reported=Number confirmed/number predicted; Minimal fraction reported=number confirmed/upper CI

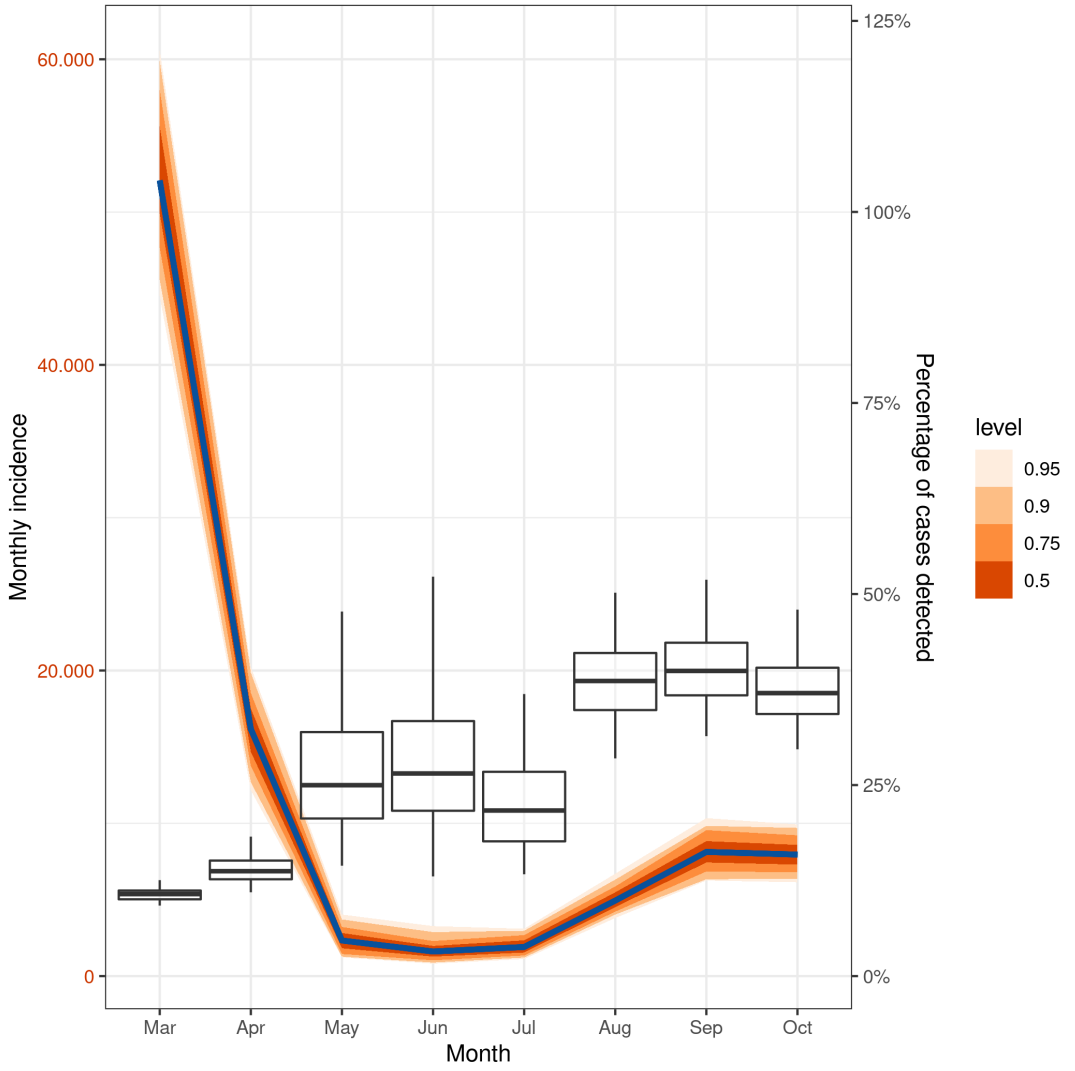

Figure 7: Here we compare the true number of positive cases detected by testing with the model-based estimated number of new infected individuals, aggregated per month. We compute a percentage of cases detected through testing according to the model over time. The randomness shown in the 95% confidence intervals accounts for the uncertainty in the estimated model-based number of cases. Test results are also prone to mistakes, which are not modelled here. The results should be interpreted with caution: the relative changes in this figure are more reliable than the absolute detection probabilities. We estimate that the detection probability has improved by a factor of circa 4.

When simulating the laboratory-confirmed cases, we also model the detection probability for the infections (both symptomatic and asymptomatic) (Figure 8). There are two differences between this estimate of the detection probability and the previous one provided in figure 7. In figure 8, we calibrate our model to the true number of positive cases, instead of using the test data directly. Furthermore, in figure 7 we use a parametric model for this detection probability that depends on the true total number of tests made.

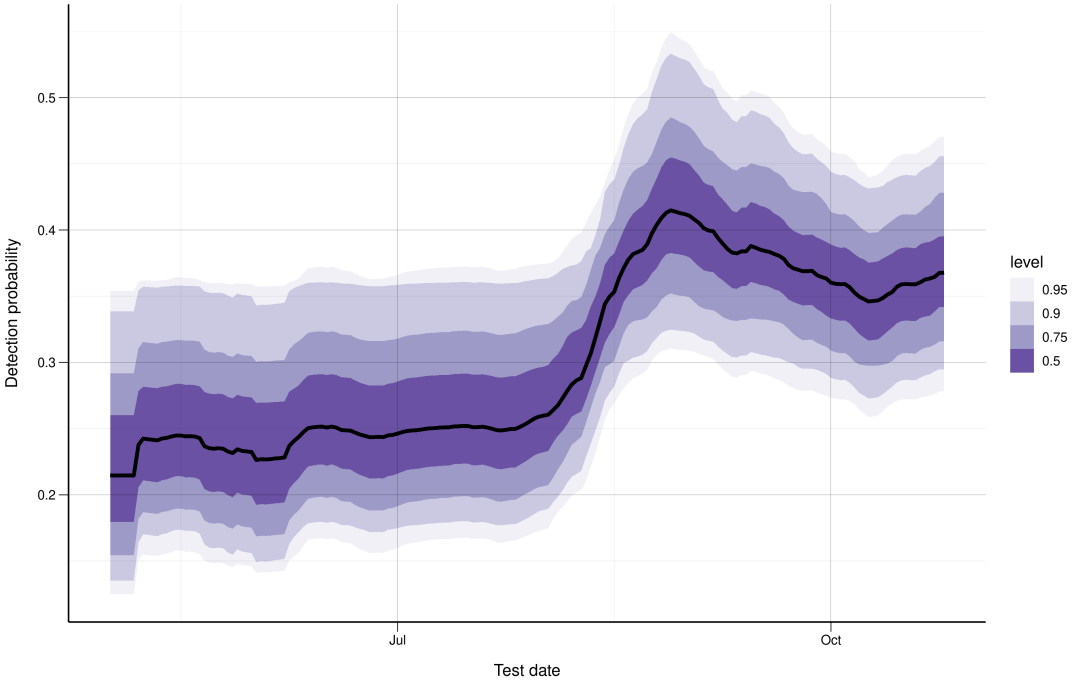

Figure 8: Estimated detection probability for an infected case per calendar day. The plot shows the mean with corresponding uncertainty bands based on the 200 parameter samples.

3 Predicted prevalence of infectious individuals, next three weeks:

The changepoint model is used to predict the daily prevalence of asymptomatic, presymptomatic and symptomatic individuals the next three weeks, aggregated to the whole of Norway, see figure 9 and table 3.

Table 3: Predicted prevalence. Number of infectious individuals (asymptomatic plus pre-symptomatic plus symptomatic) per day. Median/Mean and 95 perc. CI for three weeks prediction.

Region	01 Nov	08 Nov	15 Nov	low CI, 15 Nov	high CI, 15 Nov
Norway	2851/2929	2835.5/2929	2805/2949	1621	4986
Agder	168/180	170.5/181	173/181	79	326
Innlandet	210.5/215	203/210	196.5/209	108	333
Møre og Romsdal	154/156	154/156	150.5/158	81	298
Nordland	99/105	102.5/105	102/107	41	186
Oslo	339.5/354	346.5/363	354.5/371	187	638
Rogaland	312.5/322	308.5/316	297/312	157	560
Troms og Finnmark	85/91	89/94	89.5/98	42	191
Trøndelag	219/229	226/233	227/237	120	394
Vestfold og Telemark	212.5/226	217.5/229	218/232	108	429
Vestland	314/325	316.5/328	318.5/334	169	568
Viken	703.5/727	688.5/715	663/708	393	1206

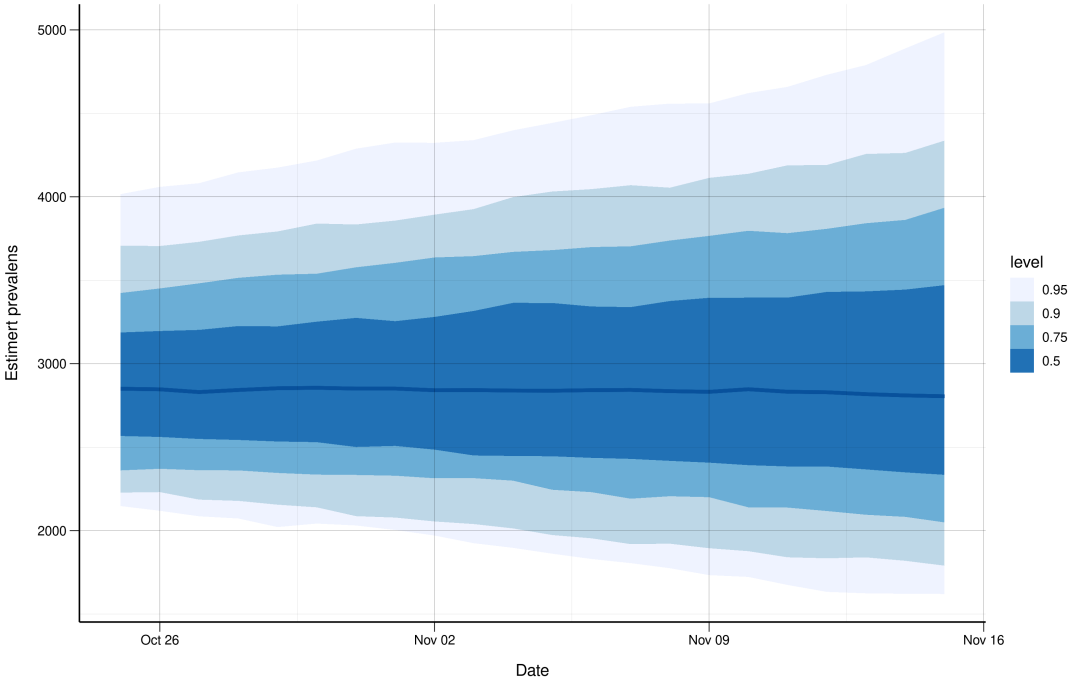

Figure 9: Predicted daily prevalence of asymptomatic, presymptomatic and symptomatic individuals, aggregated, whole Norway, (95% confidence interval).

4 Predicting prevalence on municipality level

The model is predicting prevalence on municipality level. Absolute prevalence and trend from last week are shown in figure 10. According to the mean of our simulations, today's prevalence in 288 municipalities is estimated to be equal or larger than 1.0.

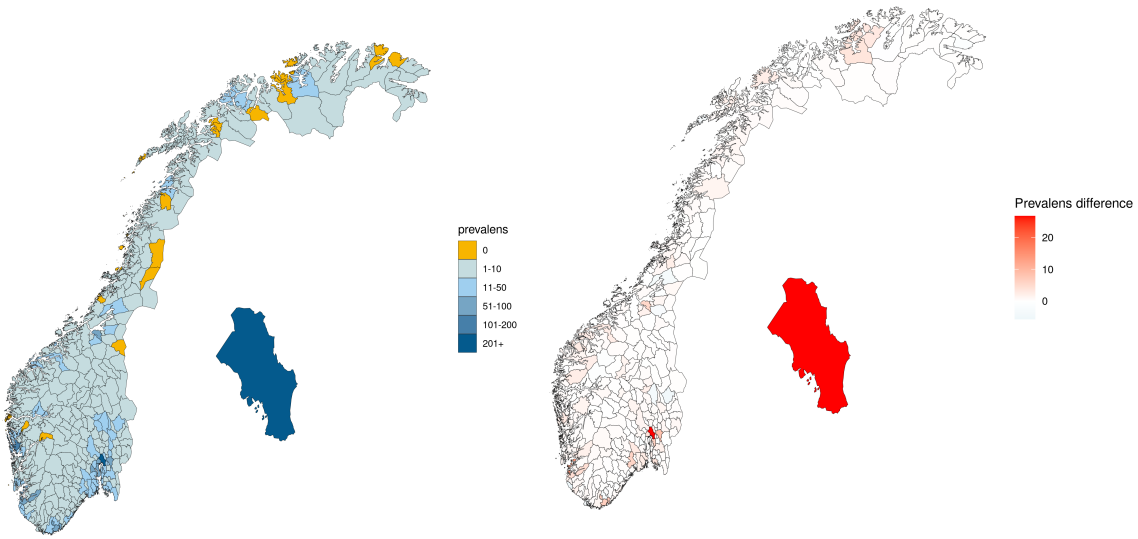

Figure 10: (Left) Map of predicted prevalence. Number of infectious individuals (asymptomatic plus presymptomatic plus symptomatic) today in each municipality. (Right) Prevalence difference compared to the previous week. Decreasing trends are shown in blue.

5 Predicted incidence of infected individuals, next three weeks

The changepoint model is used to predict the total number of infections (asymptomatic and symptomatic), see figure 11 and table 4.

Table 4: Predicted incidence per day: Median/Mean (CI)

Region	1 week prediction (01 Nov)	2 weeks prediction (08 Nov)	3 weeks prediction (15 Nov)
Norway	458/473 (310-730)	454/473 (283-763)	448/477 (250-812)
Agder	28/29 (15-53)	27/29 (13-56)	28/30 (11-53)
Innlandet	33/34 (16-57)	32/34 (17-60)	32/34 (14-61)
Møre og Romsdal	24/25 (13-43)	24/25 (12-45)	23/25 (10-50)
Nordland	17/17 (6-30)	17/17 (6-32)	16/17 (6-31)
Oslo	58/59 (31-97)	58/60 (32-101)	58/61 (30-106)
Rogaland	50/51 (29-86)	48/51 (26-91)	49/50 (21-97)
Troms og Finnmark	14/15 (6-27)	14/15 (5-33)	15/16 (5-32)
Trøndelag	36/37 (16-63)	37/37 (14-63)	36/37 (15-71)
Vestfold og Telemark	35/36 (16-65)	36/37 (16-66)	36/38 (16-72)
Vestland	51/53 (28-83)	51/52 (26-83)	51/54 (26-95)
Viken	114/116 (70-171)	111/115 (65-212)	110/114 (57-203)

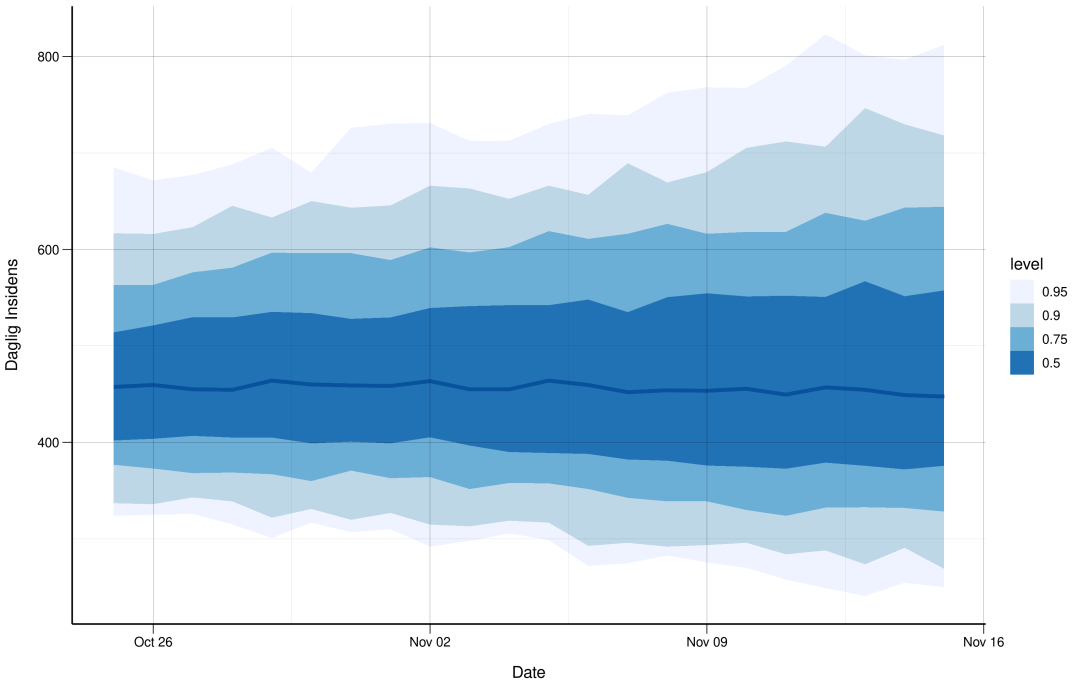

Figure 11: Predicted incidence (asymptomatic and symptomatic) for Norway per day, with confidence intervals.

The table 5 shows the probability that the bi-weekly cumulative incidence for each county exceeds 20 cases per 100.000 population.

Table 5: Probability of exceeding 20 cases per 100.000 population as cumulative incidence during the next two weeks according to our simulations.

County	Prob. exceeding 20 cases per 100.000 population
Agder	1
Innlandet	1
Møre og Romsdal	1
Nordland	1
Oslo	1
Rogaland	1
Troms og Finnmark	1
Trøndelag	1
Vestfold og Telemark	1
Vestland	1
Viken	1

6 Predicted hospitalisation, next three weeks, including patients in ventilator treatment

The changepoint model is used to predict the daily number of COVID-19 patients in hospital in Norway (95% confidence intervals and interquartile range), next three weeks, including patient's ventilator treatment, see figure 12 and table 6.

Table 6: Number of hospitalisation beds occupied by Covid-19 patients: Median/Mean (CI)

Region	1 week prediction (01 Nov)	2 weeks prediction (08 Nov)	3 weeks prediction (15 Nov)
Norge	61/63 (39-91)	62/64 (39-101)	64/65 (34-101)
Agder	4/5 (1-11)	3/4 (0-10)	3/4 (0-10)
Innlandet	5/5 (1-12)	4/5 (1-13)	4/5 (1-13)
Møre og Romsdal	3/4 (0-9)	3/3 (0-9)	2/3 (0-9)
Nordland	2/3 (0-7)	2/2 (0-8)	2/2 (0-9)
Oslo	8/8 (2-16)	8/8 (2-16)	8/8 (2-17)
Rogaland	7/7 (2-14)	7/7 (1-16)	7/7 (1-16)
Troms og Finnmark	2/2 (0-7)	2/2 (0-6)	2/2 (0-7)
Trøndelag	4/5 (0-11)	4/5 (1-11)	4/5 (1-12)
Vestfold og Telemark	4/5 (1-12)	4/5 (1-12)	4/5 (1-14)
Vestland	6/6 (1-13)	7/7 (2-14)	7/7 (1-16)
Viken	12/13 (4-24)	14/15 (7-26)	15/15 (5-28)

Yesterday's real value for Norway: 54

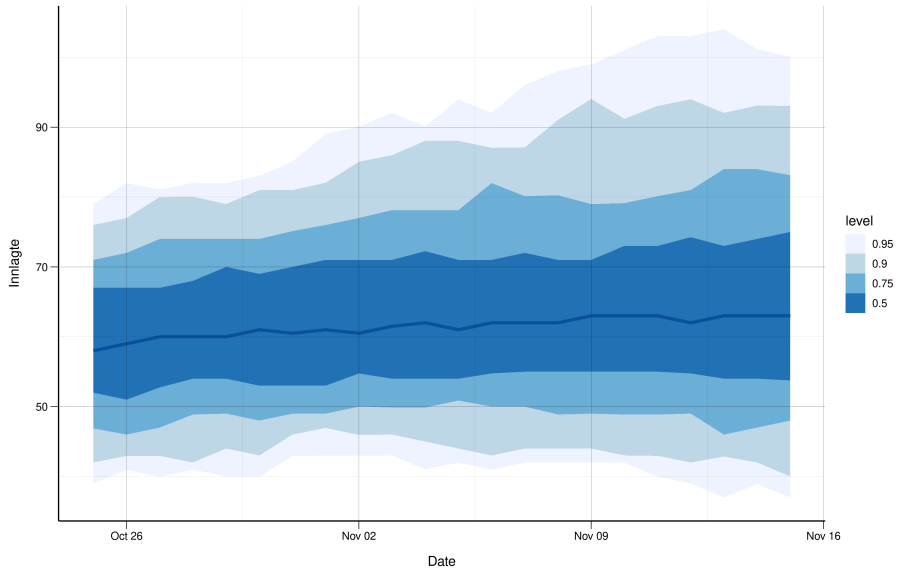

Figure 12: Predicted daily number of COVID-19 patients in hospital in Norway (95% confidence intervals and interquartile range), next three weeks, including patients ventilator treatment.

7 Predicted number of patients in ventilator treatment: next three weeks

The changepoint model is used to predict the daily number of COVID-19 patients needing ventilator treatment in Norway (95% confidence intervals and interquartile range), the next three weeks, see figure 13 and table 7.

Table 7: Number of ICU beds occupied by Covid-19 patients: Median/Mean (CI)

Region	1 week prediction (01 Nov)	2 weeks prediction (08 Nov)	3 weeks prediction (15 Nov)
Norge	7/7 (2-13)	7/7 (3-14)	8/8 (3-14)
Agder	0/1 (0-2)	0/1 (0-2)	0/1 (0-2)
Innlandet	0/1 (0-2)	0/1 (0-3)	0/1 (0-3)
Møre og Romsdal	0/0 (0-2)	0/0 (0-2)	0/0 (0-2)
Nordland	0/0 (0-1)	0/0 (0-2)	0/0 (0-2)
Oslo	1/1 (0-3)	1/1 (0-3)	1/1 (0-3)
Rogaland	1/1 (0-3)	1/1 (0-3)	1/1 (0-3)
Troms og Finnmark	0/0 (0-1)	0/0 (0-1)	0/0 (0-2)
Trøndelag	0/0 (0-2)	0/0 (0-2)	0/1 (0-2)
Vestfold og Telemark	0/1 (0-2)	0/1 (0-2)	0/1 (0-3)
Vestland	1/1 (0-2)	1/1 (0-2)	1/1 (0-2)
Viken	1/2 (0-4)	2/2 (0-5)	2/2 (0-4)

Yesterday's real value for Norway: 3

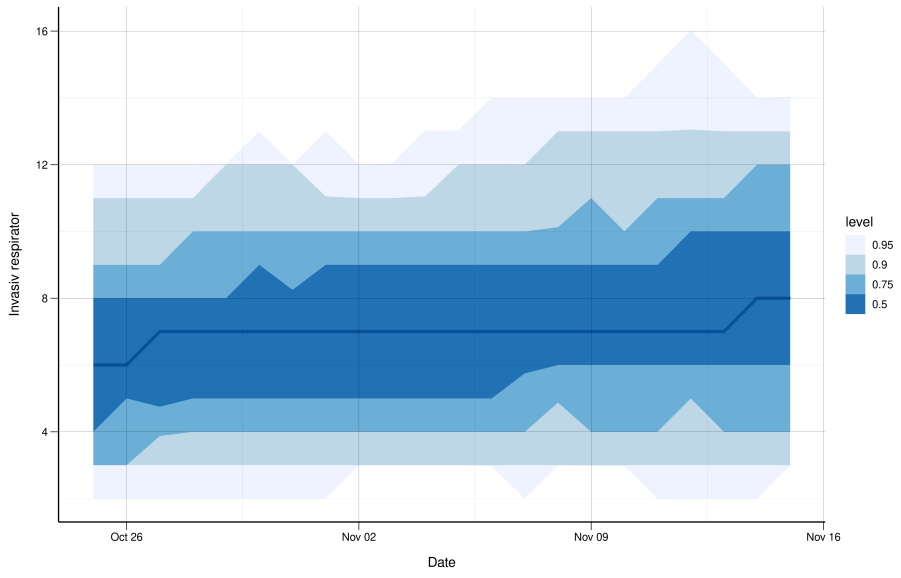

Figure 13: Predicted daily number of COVID-19 patients in ventilator treatment in Norway (95% confidence intervals and interquartile range), next three weeks.

8 Mobility between municipalities

Number of trips out from each municipality during each day is based on Telenor mobility data. We observed a large reduction in inter-municipality mobility in March (with minimum reached on Tuesday 17 March), and thereafter we see an increasing trend in the mobility lasting until vacation time in July. The drop in mobility in July coincides with the three-week "fellesferie" in Norway, and during August the mobility resumes approximately the same levels as pre-vacation time.

See Figure 14 for an overview of the mobility since March for the 20 largest municipalities, and Figure 15 for Norway's counties (fylker). Figure 16 and 17 are zooming in on the mobility since June 29, for municipalities and counties, respectively.

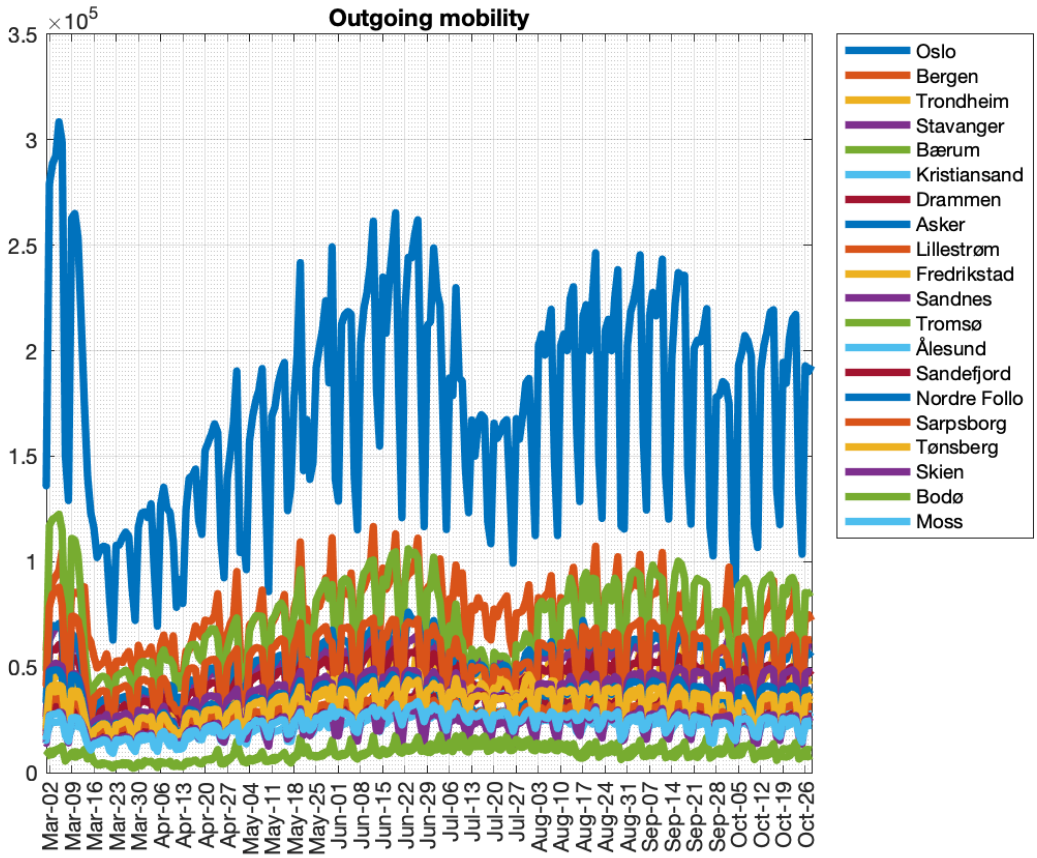

Figure 14: Inter-municipality mobility from week 10 until today.

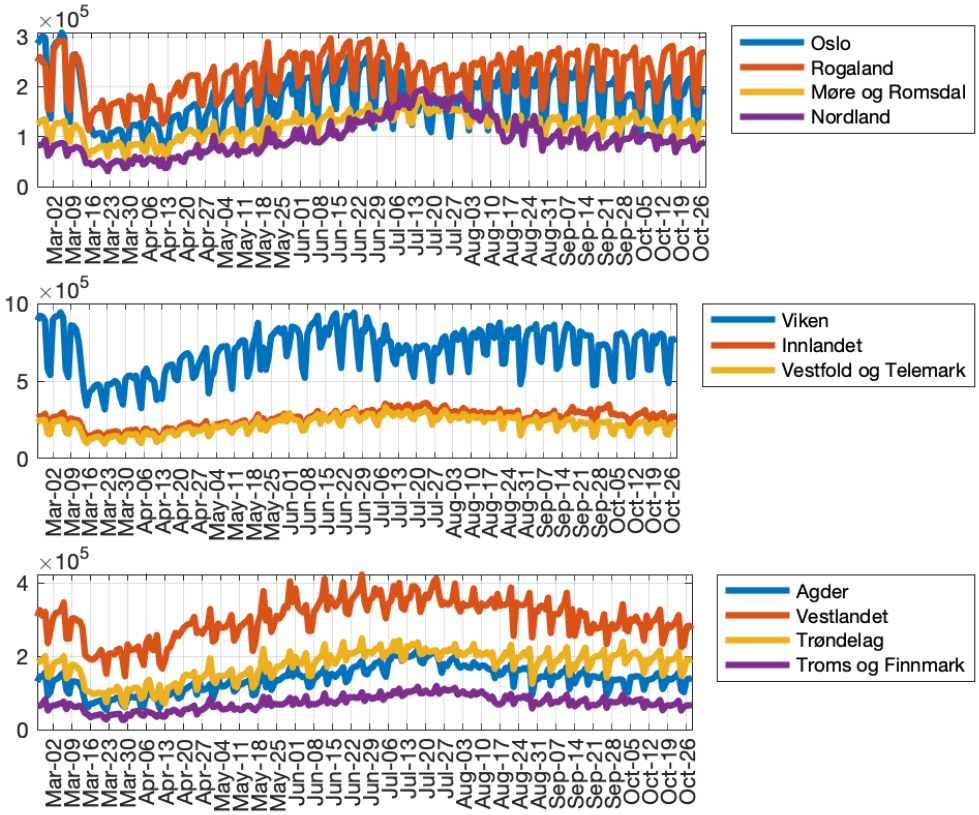

Figure 15: Inter-county mobility from week 10 until today.

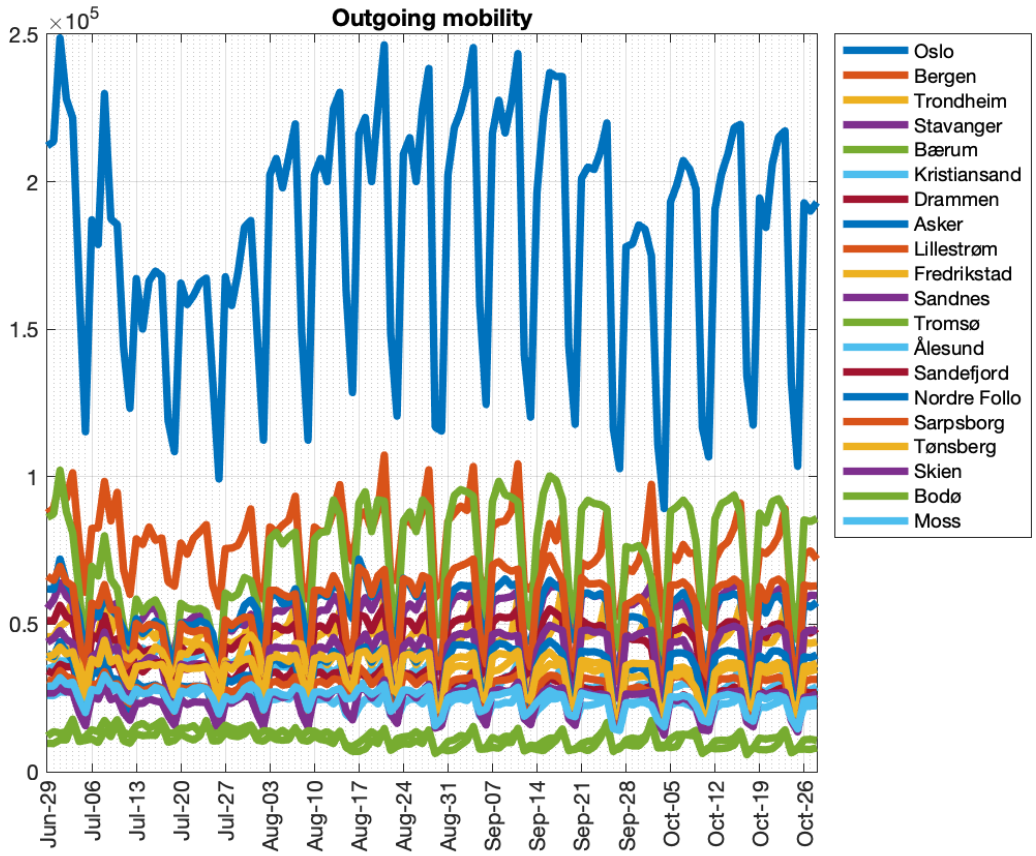

Figure 16: Zoom: Inter-municipality mobility from June 29 until today.

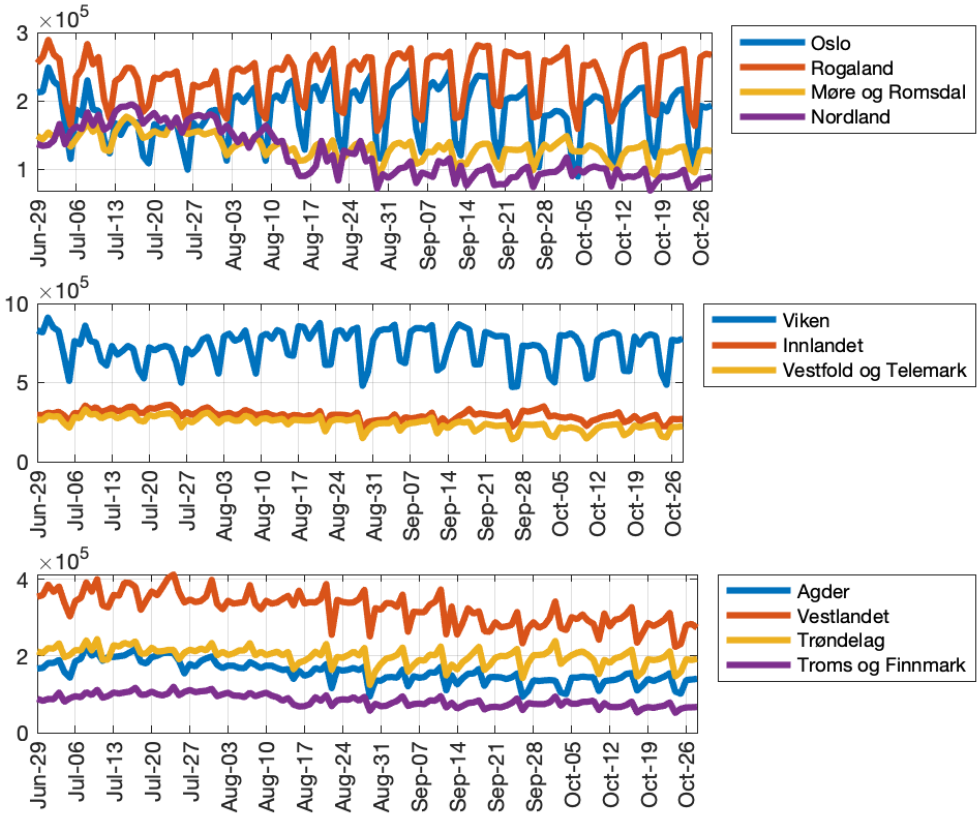

Figure 17: Zoom: Inter-municipality mobility from June 29 until today.

The reduction in movements the last ten days is compared to movements in week 10: Mondays are compared to Monday March 2nd (last Monday before restrictions); Tuesdays are compared to Tuesday March 3rd, etc. until Sundays are compared to Sunday March 8th. For municipalities see Table 8, and for counties see Table 9.

Table 8: Percentage reduction in total mobility out from each municipality.

	19 Oct 2020 Mandag	20 Oct 2020 Tirsdag	21 Oct 2020 Onsdag	22 Oct 2020 Torsdag	23 Oct 2020 Fredag	24 Oct 2020 Lørdag	25 Oct 2020 Søndag	26 Oct 2020 Mandag	27 Oct 2020 Tirsdag	28 Oct 2020 Onsdag
Hele Norge	5.8%	12.8%	9.4%	9.5%	7.7%	2.8%	4.6%	8.1%	10.7%	10.9%
Oslo	30.3%	36.1%	29.6%	30.3%	27.3%	12.3%	19.7%	30.9%	34.2%	34.0%
Bergen	12.7%	18.0%	18.4%	16.5%	15.3%	14.6%	15.8%	14.3%	17.0%	22.8%
Trondheim	-4.4%	1.8%	3.1%	1.1%	-0.3%	-1.1%	2.0%	-2.7%	2.1%	2.6%
Stavanger	6.7%	10.4%	13.0%	9.9%	10.2%	-1.6%	-2.6%	7.1%	9.5%	13.4%
Bærum	25.2%	29.8%	24.4%	24.4%	23.2%	1.8%	5.9%	27.1%	29.4%	29.1%
Kristiansand	0.7%	6.1%	5.3%	5.1%	4.3%	-3.5%	-7.7%	3.1%	4.0%	4.8%
Drammen	14.6%	22.3%	14.8%	17.3%	14.0%	6.0%	6.6%	15.3%	19.6%	16.5%
Asker	14.6%	23.0%	15.0%	15.5%	15.0%	0.4%	-3.9%	16.2%	20.1%	16.9%
Lillestrøm	20.3%	31.2%	25.2%	25.6%	20.6%	12.2%	20.1%	19.6%	25.6%	26.7%
Fredrikstad	5.1%	9.9%	9.4%	8.3%	3.7%	-5.0%	1.1%	7.8%	8.5%	8.3%
Sandnes	4.0%	5.7%	7.5%	4.6%	6.1%	-6.3%	-7.7%	3.5%	4.6%	8.2%
Tromsø	10.9%	12.5%	23.0%	11.6%	-9.9%	-17.4%	3.6%	9.0%	11.1%	19.8%
Ålesund	1.2%	9.0%	4.7%	1.9%	3.2%	5.3%	5.7%	1.0%	6.9%	6.1%
Sandefjord	10.1%	16.2%	13.3%	14.4%	10.2%	12.1%	11.5%	10.7%	14.2%	13.6%
Nordre Follo	17.8%	21.8%	15.9%	15.7%	13.3%	-3.3%	2.7%	18.4%	20.2%	18.7%
Sarpsborg	4.0%	11.2%	9.4%	8.6%	5.9%	5.1%	9.1%	7.7%	10.1%	9.8%
Tønsberg	8.8%	15.0%	12.7%	10.6%	11.5%	8.3%	8.8%	10.2%	13.2%	11.2%
Skien	3.5%	4.2%	4.3%	8.0%	4.9%	4.6%	4.4%	7.9%	7.4%	4.7%
Bodø	-11.0%	-8.9%	-5.7%	-2.1%	-22.2%	-29.9%	-12.5%	-5.5%	-8.0%	1.6%
Moss	4.9%	10.5%	7.9%	9.1%	3.8%	-2.6%	2.3%	10.4%	11.6%	11.5%

Table 9: Percentage reduction in total mobility out from each county.

	19 Oct 2020 Mandag	20 Oct 2020 Tirsdag	21 Oct 2020 Onsdag	22 Oct 2020 Torsdag	23 Oct 2020 Fredag	24 Oct 2020 Lørdag	25 Oct 2020 Søndag	26 Oct 2020 Mandag	27 Oct 2020 Tirsdag	28 Oct 2020 Onsdag
Hele Norge	5.8%	12.8%	9.4%	9.5%	7.7%	2.8%	4.6%	8.1%	10.7%	10.9%
Oslo	30.3%	36.1%	29.6%	30.3%	27.3%	12.3%	19.7%	30.9%	34.2%	34.0%
Rogaland	3.5%	6.1%	8.0%	5.8%	5.5%	-4.9%	-7.1%	3.5%	5.1%	8.5%
Møre og Romsdal	-5.0%	2.0%	0.6%	-3.7%	-1.3%	-2.3%	-6.7%	-5.4%	-0.5%	0.7%
Nordland	-10.3%	-6.0%	-4.7%	-5.8%	-16.2%	-18.0%	-0.7%	-5.8%	-3.6%	-3.8%
Viken	11.4%	19.4%	13.7%	14.6%	12.7%	2.6%	7.5%	13.8%	16.6%	15.3%
Innlandet	-8.7%	5.1%	-1.7%	-0.1%	0.7%	6.7%	10.6%	-1.7%	0.6%	-1.0%
Vestfold og Telemark	3.1%	10.3%	6.8%	8.4%	6.1%	5.7%	2.9%	7.2%	8.8%	6.8%
Agder	-4.6%	1.3%	0.9%	1.8%	0.3%	-0.7%	-4.4%	-2.4%	-1.4%	0.5%
Vestlandet	6.4%	12.7%	10.7%	9.7%	10.0%	9.7%	6.6%	8.2%	10.9%	14.3%
Trøndelag	-7.8%	-3.0%	-2.5%	-3.8%	-5.8%	-5.5%	-6.9%	-7.7%	-3.2%	-3.0%
Troms og Finnmark	-1.4%	2.1%	2.8%	0.7%	-3.0%	7.3%	12.8%	-0.1%	0.2%	4.1%

9 Long-term prediction results

Predicted daily number of COVID-19 patients in hospital and receiving ventilator treatment in Norway until the end of April 2021, in addition to prevalence. The figures are made using the 200 candidate models, where the reproductive numbers are varying according to their estimated uncertainty as estimated today with the changepoint model.
The confidence intervals reflected in the plots are two-tailed around the median, and therefore the upper 95 % level shows the 97.5 % boundary, see figure 18 for estimated prevalence, figure 19 for estimated number of hospitalisations, and figure 20 for estimated number of patients needing ventilator treatment.

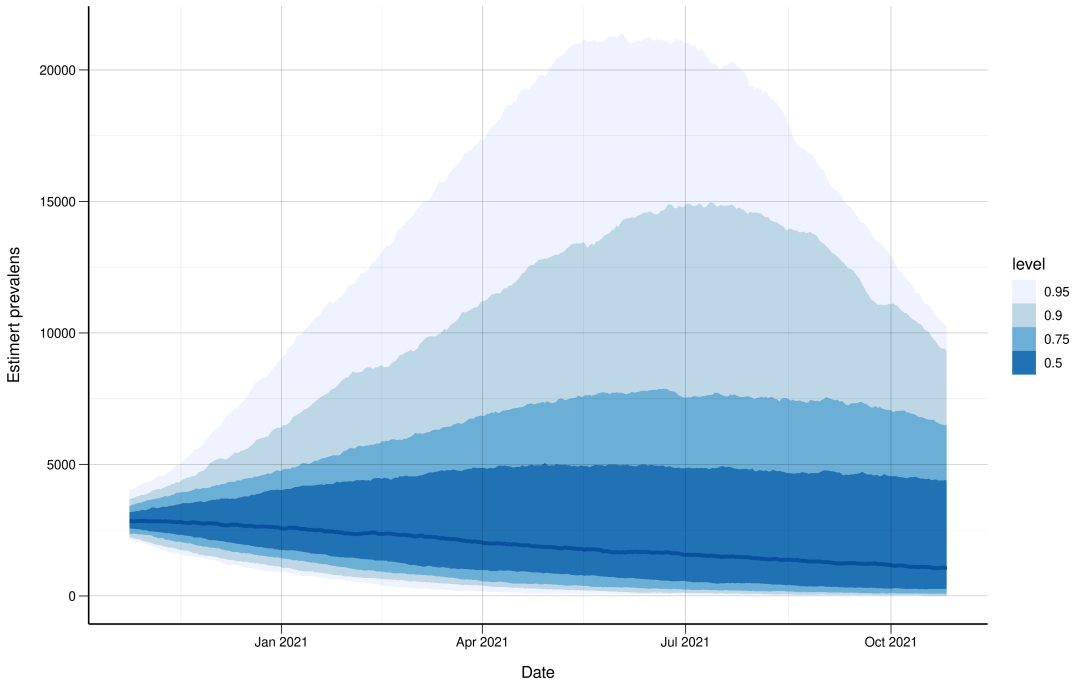

Figure 18: Predicted prevalence of COVID-19 based on 200 candidate models where the reproductive number used for simulation varies according to the estimated uncertainty.

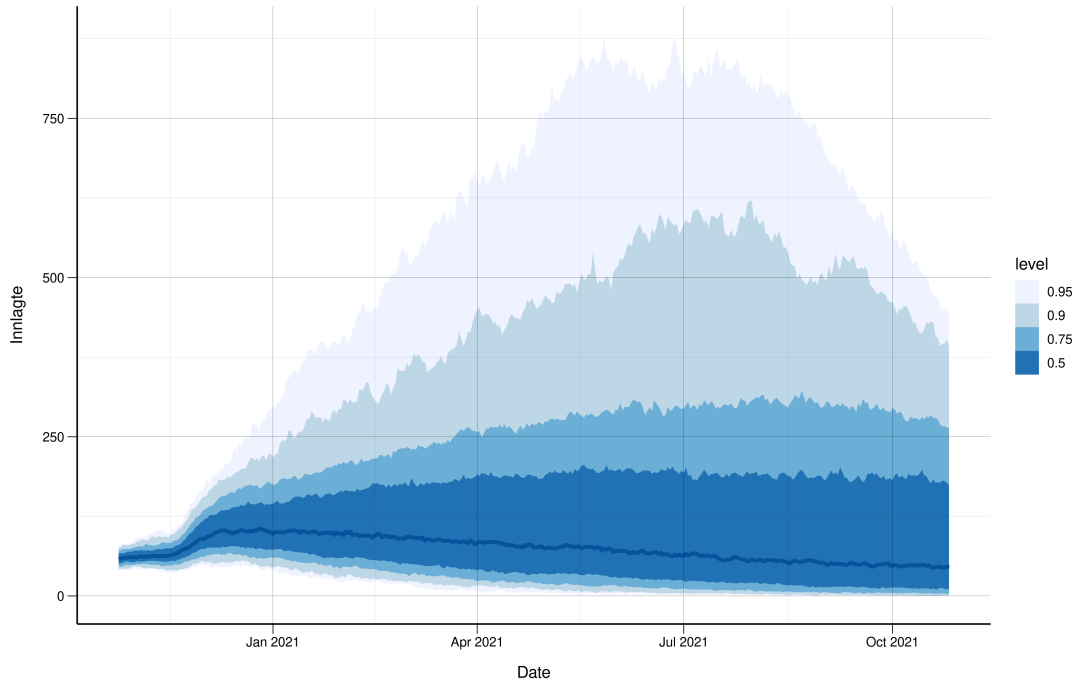

Figure 19: Predicted number of COVID-19 patients in hospital based on 200 candidate models where the reproductive number used for simulation varies according to the estimated uncertainty.

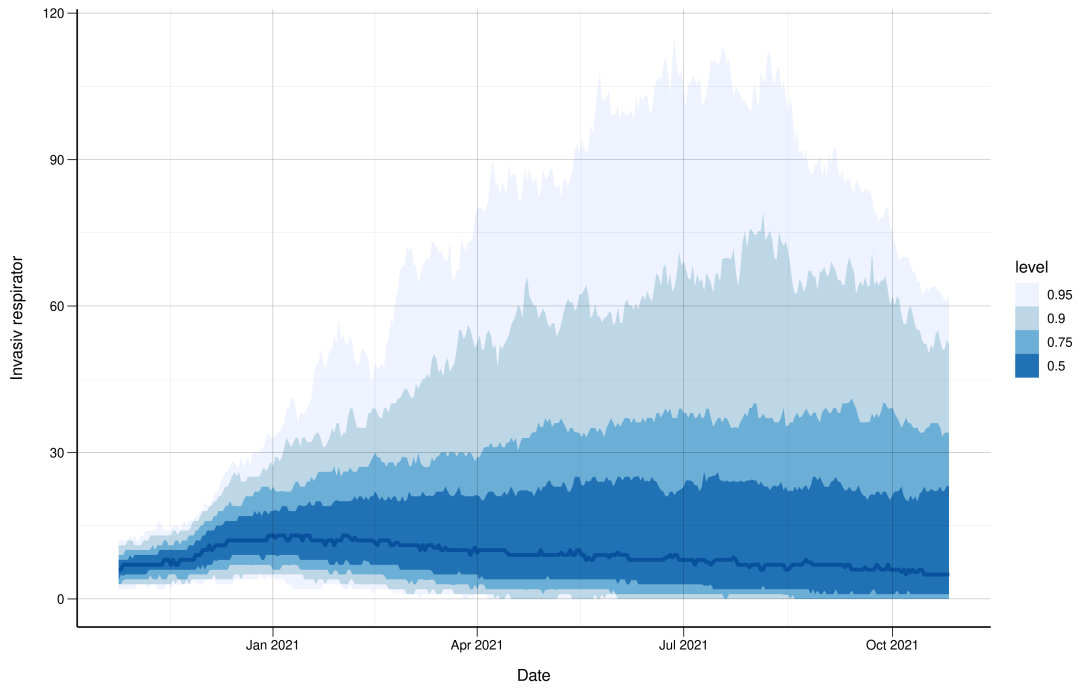

Figure 20: Predicted prevalence of COVID-19 patients needing ventilator treatment based on 200 candidate models where the reproductive number used for simulation varies according to the estimated uncertainty.

None of the simulations exceeded the surge capacity need of **500 ventilator treatments**.

10 Long-term scenario results

Here we show how the epidemic will develop, from October 25, under three assumed scenarios. We assume that until October 25 we follow our estimated reproduction numbers, but from October 26, we fix a new effective reproductive number. We show three cases, with this effective reproduction number equal to 1.1, 1.2 or 1.3. We show the daily number of COVID-19 patients in hospital (including with ventilator treatment), see figure 21, and the daily number of patients with ventilator treatment, figure 22. Note that for the hospitalisation risks, we have decided to base them on demography after 21 days, as it is not reasonable to assume that the age profile of the cases will remain as today into the long future. In table 10 we also report the number of totally infected individuals under these three scenarios. We indicate the number of patients estimated to need hospitalisation and ventilator treatment in total and at peak time. We show 95% confidence intervals. The reproduction number determines the prevalence and incidence at the peak, while the number in ICU and in hospital is in addition strongly dependent on the probability of being hospitalised and the probability of needing ventilator treatment.

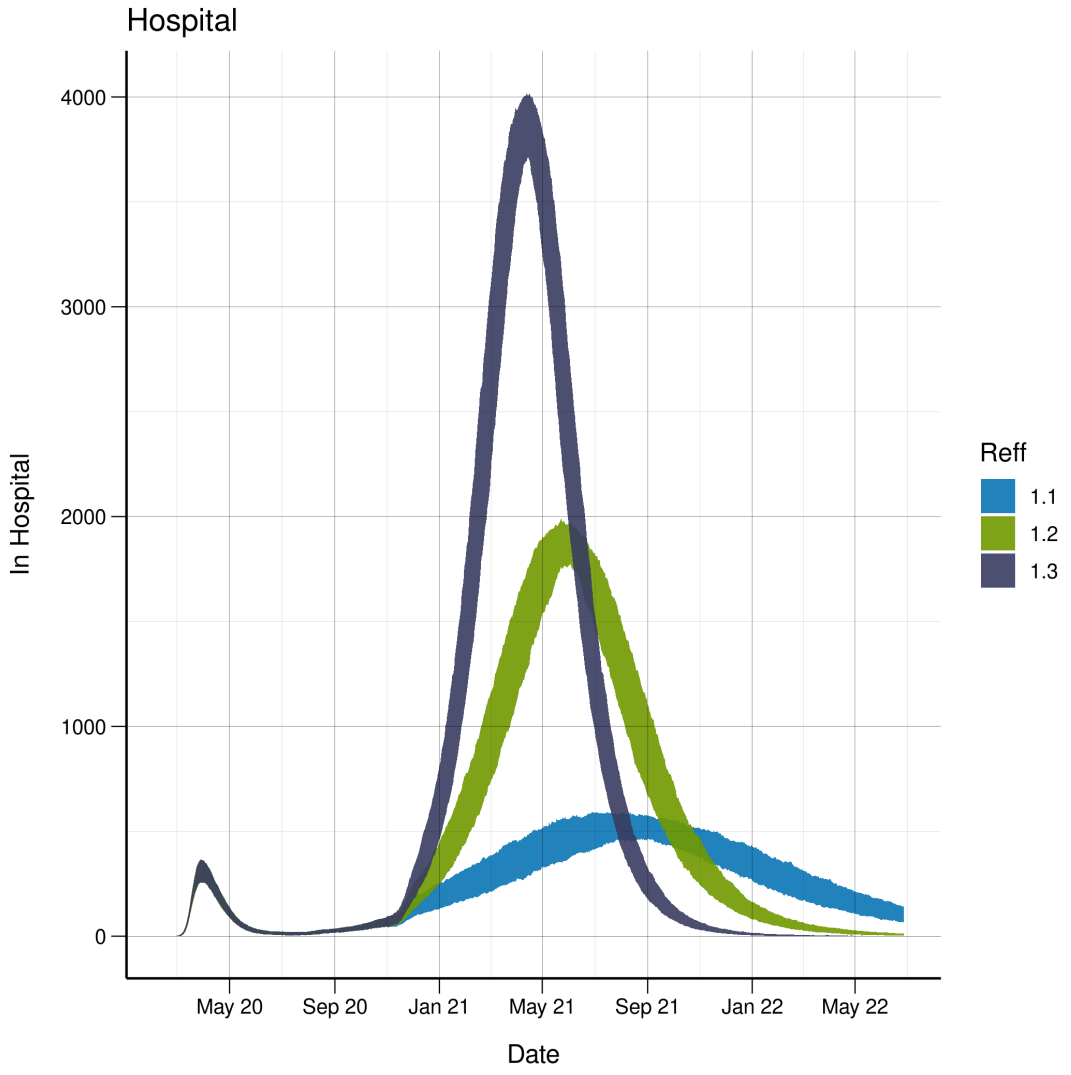

Figure 21: Predicted number of COVID-19 patients in hospital based on three different scenarios with R effective equal to 1.1, 1.2 and 1.3.

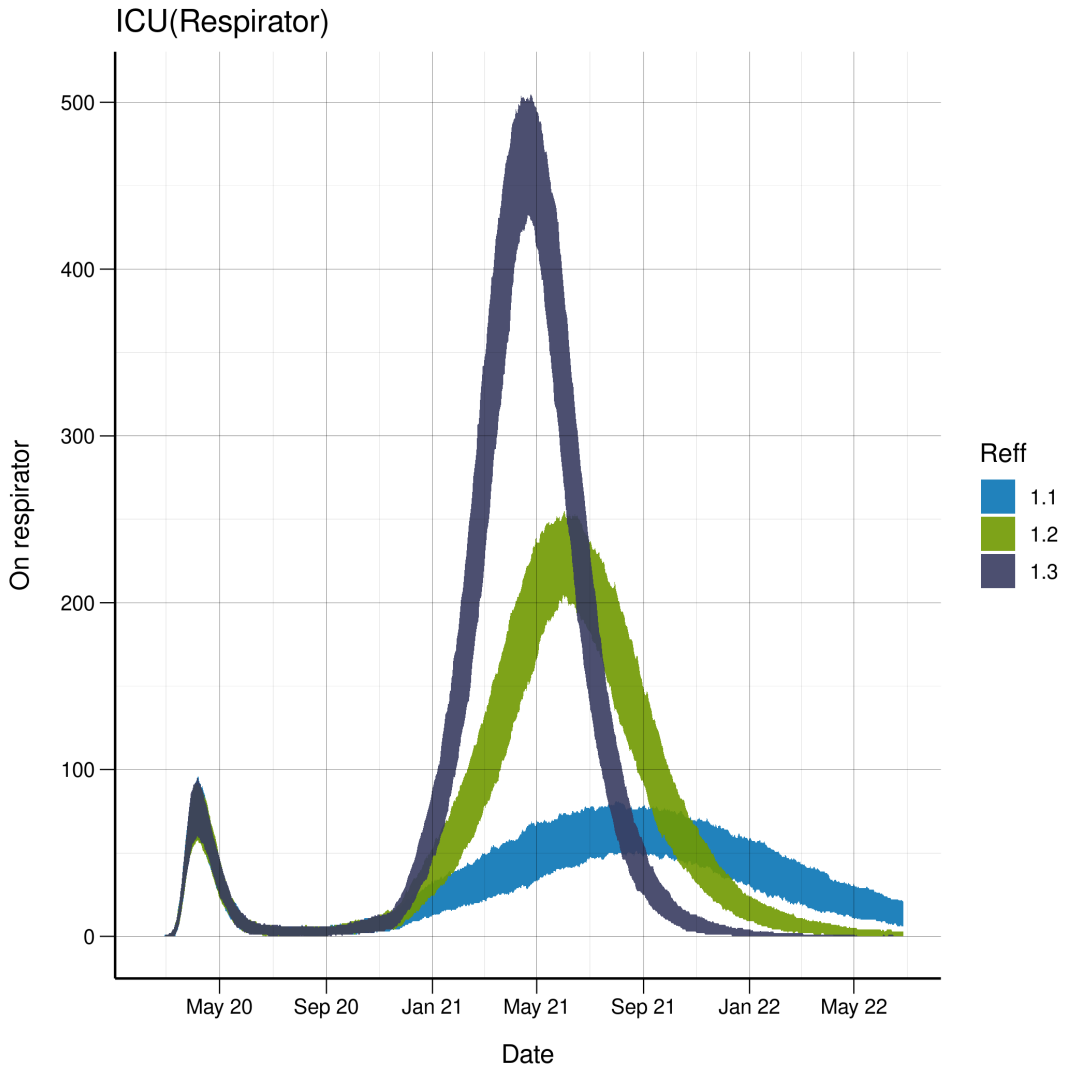

Figure 22: Predicted number of COVID-19 patients needing ventilator treatment based on three different scenarios with R effective equal to 1.1, 1.2 and 1.3.

Table 10: Predicted numbers of total infected, total number of hospitalisations, total number needing ventilator treatment, and the predicted peak number in ward (not in respirator), hospitalised (both with and without ventilator treatment) and ventilated treatments based on three different scenarios with R effective equal to 1.1, 1.2 and 1.3.

	Reff=1.1	**Reff=1.2**	**Reff=1.3**
Total infected	903.000(865.000 - 931.000)	1.640.000(1.620.000 - 1.660.000)	2.220.000(2.210.000 - 2.240.000)
Total Hospital	27.200(25.900 - 28.100)	50.300(49.600 - 51.000)	68.700(68.000 - 69.400)
Total on respirator	1.770(1.660 - 1.840)	3.150(3.070 - 3.250)	4.260(4.150 - 4.360)
Ward[1] at peak	510(459 - 550)	1.700(1.640 - 1.780)	3.480(3.370 - 3.600)
Hospital[2] at peak	576(517 - 625)	1.930(1.860 - 2.020)	3.950(3.820 - 4.070)
Respirator at Peak	84(73 - 97)	247(228 - 265)	488(461 - 523)

[1]In hospital not on respirator
[2]Includes both patients receiving respiratory treatment and patients who do not.

Model

We use a metapopulation model to simulate the spread of COVID-19 in Norway in space and time. The model consists of three layers: the population structure in each municipality, information about how people move between different municipalities, and local transmission within each municipality. In this way, the model can simulate the spread of COVID-19 within each municipality, and how the virus is transported around in Norway.

Transmission model

We use an SEIR (Susceptible-Exposed-Infected-Recovered) model without age structure to simulate the local transmission within each area. Mixing between individuals is assumed to be random. Demographic changes due to births, immigration, emigration and deaths are not considered. The model distinguishes between asymptomatic and symptomatic infection, and we consider presymptomatic infectiousness among those who develop symptomatic infection. In total, the model consists of 6 disease states: Susceptible (S), Exposed, infected, but not infectious (E), Presymptomatic infected (E2), Symptomatic infected (I), Asymptomatic infected (Ia), and Recovered, either immune or dead (R). A schematic overview of the model is shown in figure 23.

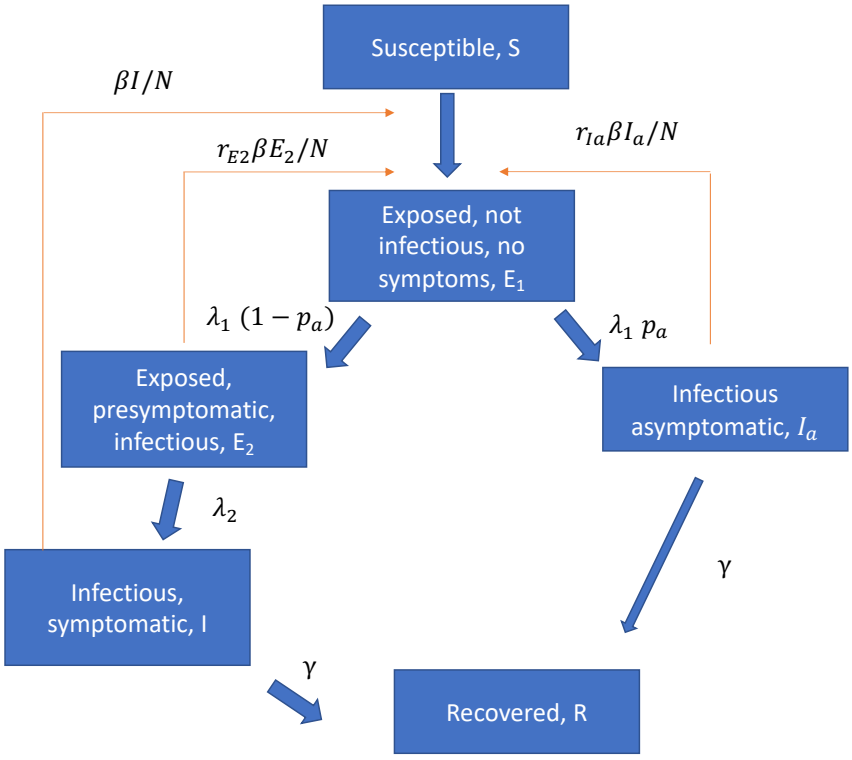

Figure 23: Schematic overview of the model.

Movements between municipalities:

We use 6-hourly mobility matrices from Telenor to capture the movements between municipalities. The matrices are scaled according to the overall Telenor market share in Norway, estimated to be 48%. Since week 8, we use the actual daily mobility matrices to simulate the past. In this way, alterations in the mobility pattern will be incorporated in our model predictions. To predict future movements, we use the latest weekday measured by Telenor. We follow closely the development in the mobility matrices, and weekend patterns will be introduced if necessary.

Healthcare utilisation

Based on the estimated daily incidence data from the model and the population age structure in each municipality, we calculated the hospitalisation using a weighted average. We correct these probabilities by a factor which represents the over or under representation of each age group among the lab confirmed positive cases. The hospitalisation is assumed to be delayed relative to the symptom onset. We calculate the number of patients admitted to ventilator treatment from the patients in hospital using age-adjusted probabilities and an assumed delay.

Seeding

At the start of each simulation, we locate 5.367.580 people in the municipalities of Norway according to data from SSB per January 1. 2020. All confirmed Norwegian imported cases with information about residence municipality and test dates are used to seed the model, using the data available until yesterday. For each case, we add an additional random number of infectious individuals, in the same area and on the same day, to account for asymptomatic imported cases who were not tested or otherwise missed. We denote this by the amplification factor.

Reproduction number and calibration

We assume a first reproduction number R_0 until March 14, a second reproduction number R_1 until April 19, a third reproduction number R_2 until May 10, a fourth reproduction number R_3 until June 30, R_4 until July 31, R_5 until August 31, R_6 from September 1 until September 30, and a seventh reproduction number until today. This last reproduction number is used for the future. The changepoints follow the change in restrictions introduced. We estimate the reproduction numbers so that the predicted number of hospitalised individuals is closest to the true number of hospitalised individuals, from March 10 until the last available data point, and the simulated positive tests are closest to the data on laboratory-confirmed COVID-19 cases from May 1 until the latest available data point. We use a method called sequential ABC which tests millions of combinations of R_0, R_1, R_2, R_3, R_4, R_5, R_6, R_7 and the amplification factor, to determine the 200 ones that lead to the best fits to the hospitalisation incidence. The algorithm is described in Engebretsen et al. (2020) https://royalsocietypublishing.org/doi/10.1098/rsif.2019.0809.

Calibration to test data

We include the laboratory-confirmed cases in the calibration procedure, as these contain additional information about the transmissibility, and the delay between transmission and testing is shorter than the delay between transmission and hospitalisation. Therefore, we simulate also the number of detected positive cases in our model. We assume that the number of detected positive cases can be modelled as a binomial process of the simulated daily total incidence of symptomatic and asymptomatic cases, with a success probability π_t, which changes every day. We also assume a delay d between the day of test and the day of transmission. In the ABC procedure we thus use two summary statistics, one is the distance between the simulated hospitalisation incidence and the observed incidence, and the other is the distance between the observed number of laboratory-confirmed cases and the simulated ones. As the two summary statistics are not of the same scale, we use two separate tolerances in the ABC-procedure, ensuring that we get a good fit to both data sources.

The data on the number of positive cases are more difficult to use, as the test criteria and capacity have changed multiple times. We take into account these changes by using the total number of tests performed on each day, as a good proxy of capacity and testing criteria. Moreover, we choose not to calibrate to the test data before May 1, because the test criteria and capacity were so different in the early period. The detection probability is modelled as

$$\pi_t = \exp(\pi_0 + \pi_1 \cdot k_t)/(1 + \exp(\pi_0 + \pi_1 \cdot k_t)),$$

where k_t is the number of tests actually performed on day t, and π_0 and π_1 are two parameters that we estimate, assuming positivity of π_1. We also estimate the delay d. We choose to use a 7-days backwards

moving average for the covariate k_t, and to calculate the distance between the observed number of positive tests and the simulated ones using a 7-days backwards moving average. We do this to take into account potential day-of-the-week-effects. For example, it could well be that the testing criteria are different on weekends and weekdays. However, using instead the number of tests and calibrating on a daily basis would lead to a larger day-to-day variance. This is likely why we find that the uncertainty in the simulated positive cases seems somewhat too low, and that we do not capture all the variance in the daily test data. Moreover, the binomial assumption could be too simple, and a beta-binomial distribution would allow more variance. A limitation of our current model for the detection probability, is that we only capture the changes in the test criteria that are captured in the total number of tests performed.

Update notes: what is new in this report.

Here we list aspects of the model or of the input parameters which have changed compared to previous reports, and we explain the reason for these changes. Some changes will have big effects on some of our estimates.

– 14 April: **Hospitalisation risk:** Our model requires the specification of the proportion of symptomatic and asymptomatic patients requiring hospitalisation. Previously we used estimates from Verity et al. (2020) based on Chinese data, adapted to the Norwegian demography, and to the reduced mobility of elderly patients living in elderly homes. We summarised this proportion to be 5.6%. Under these assumptions, our model estimates a cumulative number of infected individuals of ca. 14.000. As we have had ca 135 confirmed deaths in Norway, this corresponds to an Infection Fatality Ratio (IFT) of roughly 1%. However, international studies indicate that the IFT should be around 0.3% (https://www.cebm.net/COVID-19/global-COVID-19-case-fatality-rates/). We therefore calibrate our model to this IFT (in addition to calibrate the model to the hospitalisation data), by adjusting the hospitalisation risk in our model, reducing it by a third, to 1.85%. The effect of this change is visible on the estimated cumulative number of infected individuals, which is now approximately 45.000. A further effect of this change is that the reproductive numbers are different, with R_0 larger and R_{eff} smaller than before, when we had a higher hospitalisation risk.

– 14 April: **Change point for the reproductive number:** On March 12, a number of contact restrictions were implemented. During that week 11, mobility was reduced significantly, and appears to stabilize on Monday March 16th. Between the 11th and 16th of March we expect a reduction of the reproduction rate. We model this change as a sudden jump from a first reproduction rate R_0 to a second and lower reproduction rate R_{eff}, through a change in the model parameter β. We have chosen Monday March 15 as the changepoint for the reproductive number because it gives the best fit to the hospitalisation data. If we move the changepoint to March 14, or assume a continuous linear reduction during week 11, the fit deteriorates. We also notice that the best changepoint depends on the assumed time between symptoms appearance and hospitalisation, which is assumed to have mean 8 days in this report. The optimal changepoint also depends on the assumed hospitalisation risk.

– 20 April: **Change in parameter estimation method:** We use sequential ABC instead of iterative parameter calibration. Estimation of the reproduction numbers and of the amplification factor in the seeding of the epidemic at the start is done using Approximate Bayesian Computation (ABC), as described in Engebretsen et al. (2020)[3]. Sequential ABC avoids to calibrate R_0 first on part of the data and then, given the best values of such R_0, to find the best fitting R_{eff}, which might not lead to optimal estimation and is based on more ad-hoc choices. We also do not weigh the last part of the data more than the rest. Sequential ABC takes more time to run: therefore the daily report might use only the hospitalisation until yesterday.

[3]https://www.medrxiv.org/content/10.1101/2020.03.11.20033555v1

– 3 May: **New reproduction number active from 20 April:** We introduce a new changepoint in the reproduction number, so that R_1 is active until 19 April and R_2 from 20 April. This is the day the kindergarten reopened. On April 27 also part of primary school reopened, and we will see if a further change point will be useful to fit the data best.

– 15 May: **New parameters related to hospitalisation risk:** Our model requires the specification of the proportion of symptomatic and asymptomatic patients requiring hospitalisation. Previously we used estimates from Verity et al. (2020) based on Chinese data, adapted to the Norwegian demography and to the reduced mobility of elderly patients living in elderly homes, and calibrated to obtain a Infection Fatality Ratio (IFT) of roughly 0.3%. We adjust again the hospitalisation risk in our model based on Salje et al Science 13 May 2020[4], again adapted to Norwegian demography and to the reduced mobility of elderly in elderly homes. The effect of this change is visible on the estimated cumulative number of infected individuals, which is now approximately 35.000. The infection fatality rate in this study is 0.7%

– 15 May: **Change of the data we use, from occupied beds to new admissions to hospital:** We use the daily number of lab-confirmed COVID-19 patients admitted to hospitals in Norway to estimate the reproduction numbers and the amplification factor. Before we were using the daily number of beds occupied by lab-confirmed COVID-19 cases. We have moved from hospital prevalence to hospital incidence. The prevalence is influenced by the length of stay in hospital for the patients, while incidence is not. In this sense the incidence data should carry a clearer signal of the infection strengths in the country. However, both data capture this signal with a delay, which we estimate to have an expectation of 14 days. The incidence data are less smooth in time (more irregular) and are more difficult to fit well, as can be seen in Figure 2. The estimated hospital prevalence (Figure 4) is fitted in a satisfying way. The incidence data are available at hospital level.

– 15 May: **New parameter value related to periods of stay in hospital:** Our model requires the specification of several lengths of stay in hospital: time spent in hospital for patients not requiring ventilator treatment; time spent with ventilator treatment; etc. We also need the time between onset of symptoms and hospitalisation. See the graph at the end of this report for a full specification. We have now estimated the distributions of all these lengths, and of the probability of requiring ventilator treatment if hospitalised, from data covering almost all patients hospitalised in Norway so far. Previously, we used parameters published in Fraser et al. which were not based on the Norwegian epidemic. A note which documents the way we estimate the new parameters is in preparation. We will regularly re-estimate these parameters on the basis of additional new hospitalised patients.

– 20 May: **New estimated period in ward after ICU stay :** We have estimated that patients stay on average 7.7 days in a non-ICU ward in hospital, after being off from ventilator treatment.

– 26 June: **New reproduction number active from 11 May:** We introduce a new change point in the reproduction number, so that R_2 is active until 10 May and R_3 from 11 May. This is the day of the last ease of restrictions before summer.

– 29 June: **Time-varying reproduction number and Sequential Monte Carlo estimation** We assume a daily varying reproduction number (after March 9). In this way we are able to automatically detect changes in the reproduction number with no need to introduce changepoints explicitly. However, estimating many more parameters (one for each day) is much harder than the three reproduction numbers we assume in the changepoint model. We developed a method and an algorithm to estimate the daily reproduction numbers based on Sequential Monte Carlo (Doucet and Johansen, A tutorial on particle filtering and smoothing: Fifteen years later, Handbook of nonlinear filtering, 2009). To stabilise our estimates, we run a 7-days moving window, so that R_t is the average of the reproduction numbers over the 7 previous days. We quantify the uncertainty of our estimates by simulation. The disadvantage of this approach is that the estimated R_t for the last two weeks,

[4]https://science.sciencemag.org/content/early/2020/05/12/science.abc3517.abstract

and in particular for the last days, is very uncertain. Therefore we look two weeks back in time to determine sensible reproduction numbers. We compute the posterior probability of the time-varying reproduction number and plot the central 50% of this distribution to sketch the uncertainty. This band can be interpreted as the one which we predict to contain the daily reproduction number with 50% of posterior probability. We also compute the posterior probability that the reproduction number is above 1.

– 1 July: **Imported cases until June** We incorporate confirmed imported cases now until June 26. They are placed in their municipality of residence. We assume a unique amplification factor for all imported cases during the whole epidemic, and estimate it.

– 10 August: **Imported cases until yesterday** We incorporate confirmed imported cases until the day before ("yesterday") and continue to assume a single amplification factor which is re-estimated every time we have new data.

– 10 August: **New reproduction number active from 1 July:** We introduce a new change point in the reproduction number, so that R_3 is active until 11 May and R_4 from 1 July. We plan to add a new change point every first day of the month, but start to estimate it only from the 21 of the same months, as we need three weeks of data to get a good estimate.

– 10 August: **Improved Sequential Monte Carlo estimation** We have reported an estimate of the daily reproduction number (7-days moving window average) R_t in the last month and observed that our estimate was too sensitive to small changes in the daily hospital incidence. This produced visible oscillations in R_t, which we think are not realistic. We have therefore changed the likelihood of the hospital incidence, so that small variations can more easily seen as noisy variations. We use now a beta-binomial likelihood (with $\alpha = 8$, but will optimise this parameter further in the next days).

– 12 August: **Reporting expected probability that the total number of new cases per 100.000 inhabitants will exceed 20** For each county, we estimate this probability in the next two weeks, using estimated number of cases.

– 17 August: **New seeding data set** We change the source of the seeding data. Before, we used the first day with symptoms for every imported case. Now instead, we use the date of positive testing. The reason is that most imported cases might have been abroad when the symptoms appeared, while we are sure that they are in Norway on the day they test. The positive test data is also a more sure data point, compared to the first day with symptoms. This change makes a difference in March and April, as can be seen in the figure 24, where we show a comparison between the previous seeding (red) and the new one (black).

– 24 August: **New reproduction number active from 1 August:** We introduce a new changepoint in the reproduction number, so that R_4 is active until July 31 and R_5 from August 1. We start to estimate the new reproduction number approximately three weeks after, when some data informing it are available.

– 24 August: **Predicted medians instead of means** We report posterior medians as point predictions, instead of means, because of the strong skewness of the posterior distributions.

– 1 September: **Revised hospitalisation probabilities** We have changed the probability that an infected individual (symptomatic or asymptomatic) is hospitalised. In the last weeks it has become apparent that the age profile of the individuals who test positive does not follow the demography of the Norwegian population, with a much stronger representation of the age group between 20 and 29 years. Therefore we had to change our assumptions, namely that age of infected individuals was following the demographic age profile of the Norwegian population. Instead we learn the distribution of ages of the infected from the Norwegian data of who tested positive. We computed a correction factor for each age group, consisting of the ratio between the proportion tested of each group divided by the demographic proportion in the overall Norwegian population. We computed the percentage of each age group among all positive tests taken from May 1 until the last available data. For the

age group 20-29 this percentage was on 1 September 26%, while in the general population, this age group consists of only 15%, and is therefore highly overrepresented. This correction influences the overall probability for an infected individual to be hospitalised. Before we used 3.9%. This percentage becomes now 2.26% using the new correction factors. The correction factors multiplied by the hospitalisations probabilities from Saljie at al 2020, in the 9 age groups are: $0.459 * 0.002, 0.874 * 0.002, 1.954 * 0.006, 1.480 * 0.013, 1.128 * 0.017, 1.005 * 0.035, 0.479 * 0.071, 0.331 * 0.1130, 0.373 * 0.27$.

– 1 September: **Percentage of detected cases each month** We add a new figure in section 2, where we represent the percentage of detected cases, among the positive cases that our model estimates. This is done for the whole period in Table 2, and for each month in the figure.

– 10 September: **New probabilities of being hospitalised when infected, per age group** Salje at al. 2020 updated their results on the basis of better outcomes of some of the patients in their cohort. Therefore their estimates of the probability of being hospitalised if infected per age group are reduced. We use the new values from today. For the 9 age groups, the new (and old) probabilities are: 0.1% (0.092%), 0.1% (0.2%), 0.5% (0.6%), 1.1% (1.3%), 1.4% (1.7%), 2.9% (3.5%), 5.8% (7.1%), 9.3% (11.3%), 22.3% (27%).

– 14 September: **New probability of requiring ventilator treatment if hospitalised**, from May 1 updated to 8.7% from previously 15.1% based on analysis of registry data on patients hospitalised in Norway from May-September.

– 21 September: **New reproduction number active from 1 September:** We introduce a new changepoint in the reproduction number, so that R_5 is active until August 31 and R_6 from September 1. We start to estimate the new reproduction number approximately three weeks after, when some data informing it are available.

– 5 October **Updated hospitalisation parameters:** We have updated the hospitalisation parameters (time to hospitalisation, length of stay, etc.) based on more recent data. In particular, we introduce a changepoint in the hospitalisation parameters on 1 April, where the data before and after 1 April are used to estimate the different parameters. See figures in the next section.

– 12 October **Included reporting delay for hospital admissions:** We have implemented a reporting delay of new hospitalisations. We estimated it from all data since April using time from admissions to reporting in the BeredtC19 registry. The reporting delay is implemented as a probability that an admission which happened on a certain day is actually reported with a delay of one to four days. We estimated these delay probabilities for the last four days from "today" and have different delay probabilities on Monday compared to the rest of the week, because the delay is more pronounced for admissions happening in the weekend. The probabilities are listed in Table 12, Assumptions.

–19 October **Using test data:** We include the test data in the calibration procedure of the changepoint model. Before, we have calibrated our model to hospital incidence only. In our simulations, we assume that the number of positively tested cases can be modelled as a binomial process of the simulated daily total incidence of symptomatic and asymptomatic cases, with a time-varying detection probability which we estimate.See in the model description above all details on the model we use for the detection probability and the way we actually perform the calibration. The estimated parameters of the detection probability are listed in Table 11.

–19 October **Included reporting delay for test data:** As for the hospitalisation data, we take into account the reporting delay of the test data for the last four days. Details are provided in the Model chapter of the report. The reporting delay probabilities are listed in Table 12, Assumptions.

–20 October **Three new figures** Figure 3 shows how our model follows the reported daily number of positive cases. In this figure we do not correct for the reporting delay in the last four days, so that the decay in the end is only due to such delay. Figure 7 also shows the estimated number of positive individuals infected in each month, and estimated by our model. Figure 8 is a daily varying estimate of the probability to detect a positive case. This is based on a logit model with intercept and total number of tests as covariate.

–27 October **Long term predictions use hospitalisation rates based only on demography.** When predicting the next 12 months, we assume a constant reproduction number distribution and a mobility matrix as today. For the first next three weeks we use hospitalisation rates, which utilise also the current age profile of positive cases. However, after the first three weeks, we use rates only based on demography. This is because our compartmental model does not have age classes, and in the long term the number of immune per age class does matter. A discontinuity after three weeks can be seen in the figures 19 and 20. This is also used for the scenario simulations.

–27 October listing anymore additions of changepoints. Approximately around the 21st of every month, we add a new change point in the reproduction number, acting from the start of the month. We do not list such changes anymore in this diary of changes.

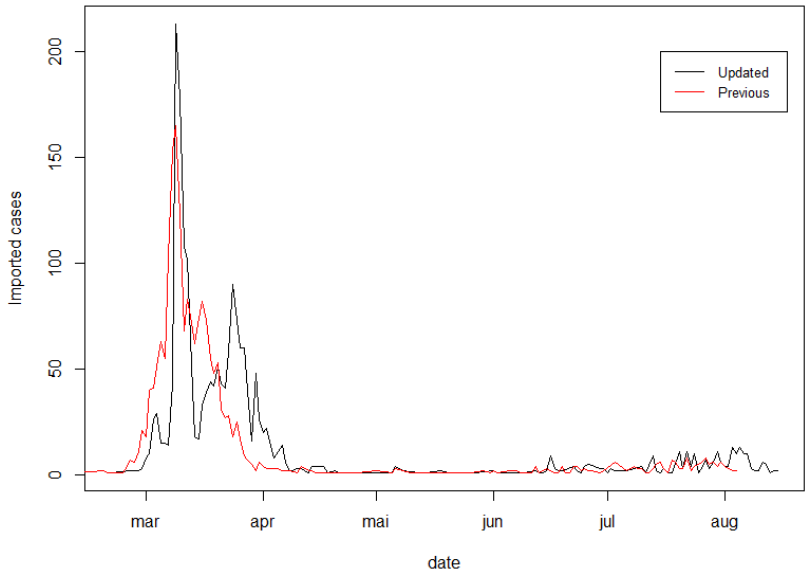

Figure 24: Comparison between the number of imported cases on the day of declared appearance of symptoms (red) and on the date of positive test, which is used from now on (black).

Parameters used today

Figures 25 and 26 indicate which assumptions we make in our model, related to hospitalisation. We obtained estimates from Norwegian data, namely NPR data linked with MSIS data. These estimates will be regularly updated, on the basis of new data.

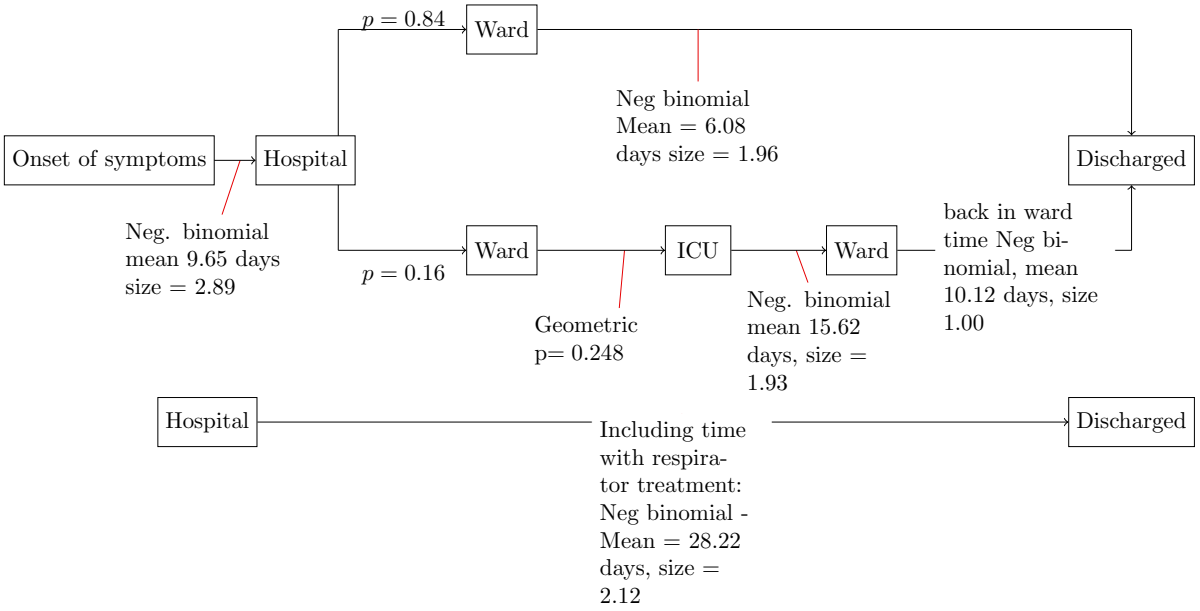

Figure 25: Hospital assumptions and parameters used before 1 August

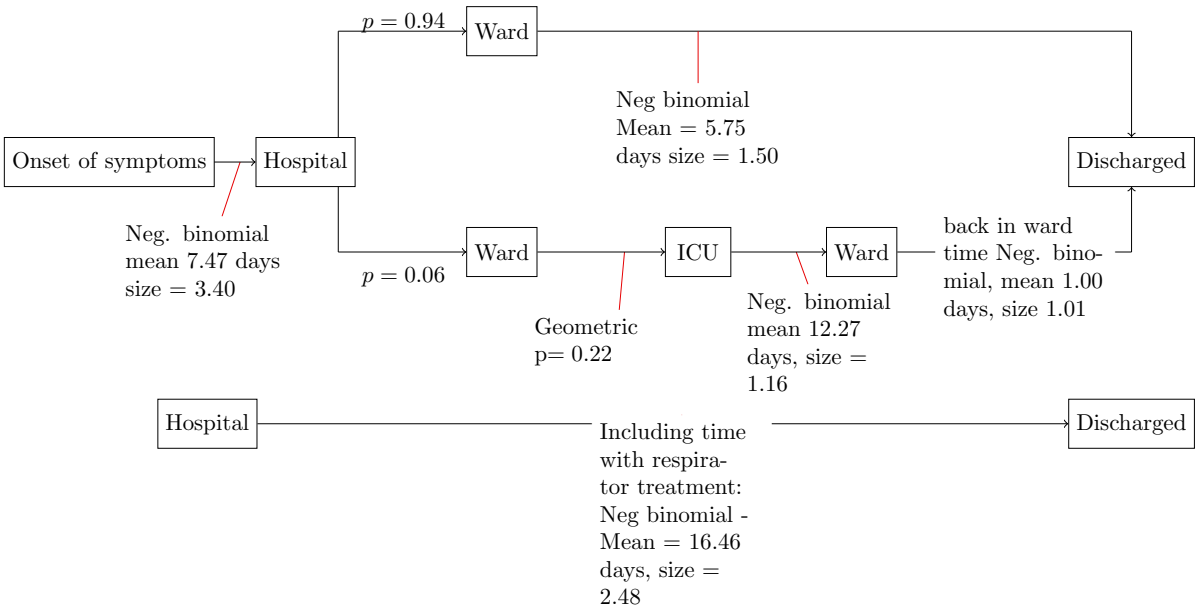

Figure 26: Hospital assumptions and parameters used after 1 August

Table 11: Estimated parameters

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	Period
R0s	3.129	3.808	4.066	4.058	4.291	5.001	Until March 14
R1s	0.436	0.519	0.547	0.548	0.577	0.674	From March 15 to April 19
R2s	0.123	0.346	0.436	0.445	0.533	0.846	From April 20 until May 10
R3s	0.617	0.812	0.885	0.875	0.948	1.103	From May 11 until June 30
R4s	0.52	0.787	0.883	0.902	1.001	1.473	From July 1 until July 31
R5s	0.797	0.973	1.021	1.026	1.083	1.252	From Aug 1 until Aug 31
R6s	0.926	1.017	1.052	1.052	1.083	1.164	From Sept 1 until Sept 30
R7s	0.845	0.972	1.009	1.011	1.05	1.17	From Oct 1
AMPs	1.88	2.771	3.195	3.158	3.525	4.425	From February
π_0	-2.316	-1.616	-1.393	-1.371	-1.102	-0.534	-
π_1	7.2e-06	5.4e-05	7.4e-05	7.6e-05	9.5e-05	1.7e-04	-
delays	0	0	1	1.215	2	5	-

Table 12: Assumptions I

Assumptions	Mean	Distribution	Reference
Seeding			
Telenor coverage	48%		https://ekomstatistikken.nkom.no/
Model parameters			
Exposed period ($1/\lambda_1$)	3 days	Exponential	Feretti et al 2020
Pre-symptomatic period ($1/\lambda_2$)	2 days	Exponential	Feretti et al 2020
Symptomatic infectious period ($1/\gamma$)	5 days	Exponential	Feretti et al 2020
Asymptomatic, infectious period ($1/\gamma$)	5 days	Exponential	Feretti et al 2020
Infectiousness asympt. (r_{I_a})	0.1	Fixed	Feretti et al 2020
Infectiousness presymp (r_{E_2})	1.25	Fixed	guided by Feretti et al 2020
Prob. asymptomatic infection (p_a)	0.4		Feretti et al 2020
Healthcare			
Time sympt. onset to hospitalisation	9 days	Neg. binomial	
Fraction asymptomatic infections	40%	Fixed	Mizumoto et al 2020 20% for the old population, Diamond Princess
% symptomatic and asymptomatic infections requiring hospitalization: 0-9 years 10 - 19 years 20 - 29 years 30 - 39 years 40 - 49 years 50 - 59 years 60 - 69 years 70 - 79 years 80+ years	 0.476*0.1% 0.896 *0.1% 2.044 *0.5% 1.45*1.1% 1.098*1.4% 0.975*2.9% 0.468*5.8% 0.337*9.3% 0.346*22.3%	Fixed	Saljie et al 2020 corrected for: % of elderly living in elderly homes in Norway (last two age groups) and corrected for presence among positive tested since May 1.
% hospitalized patients requiring ICU Feb - March April May -	 20% 10% 8.7 %	Fixed	Estimated from "Beredskapsregistret BeredtC19"
Overall hospitalization risk	2.26%	Fixed	Corrected Saljie et al 2020 (adapted to Norwegian population and adapted to positive tested)
Probability that an admission has been reported on Monday From Sunday From Saturday From Friday From Thursday	 32% 49% 68% 86%	Fixed	Estimated from "Beredskapsregistret BeredtC19"
Probability that an admission has been reported From one day before From two days before From three days before From four days before	 53% 77% 82% 91%	Fixed	Estimated from "Beredskapsregistret BeredtC19"
Probability that a positive laboratory test has been reported From one day before From two days before From three days before From four days before	 10% 66% 90% 97%	Fixed	Estimated from MSIS
Probability that a negative laboratory test has been reported From one day before From two days before From three days before From four days before	 16% 74% 92% 98%	Fixed	Estimated from MSIS
Mobile phone mobility			
Until October 24th	Measured Telenor mobility		
Data used in the predictions	October 23th	Fixed	Corrected to preserve population

Supplementary analysis: Instantaneous reproduction number based on lab-confirmed cases

To complement the results of the metapopulation model, we present estimates of the temporal evolution of the reproduction number in Norway based on an analysis of laboratory-confirmed cases. The primary purpose of this analysis is to provide a more comprehensive perspective on the epidemic situation, taking into account several data sources.
The hospitalisation data are a less biased information source for the number of infections compared to case data because the testing criteria in Norway has changed. For this reason, the present results should be interpreted with caution. During the early part of the period, testing of individuals was mainly based on travel history to areas with an ongoing outbreak. Since the middle of March, testing is recommended for people with an acute respiratory infection. From early May, the testing criteria have been expanded to include less severe symptoms. The analysis of laboratory-confirmed cases does not take into account the effect of imported cases during the early outbreak in Norway; the early results are less reliable than later results when the impact of importations is negligible. Overall, the reproduction numbers estimated by this method gives a similar conclusion to the analysis based on the metapopulation model from the middle of March onwards.

EpiEstim method and assumptions

We estimate the instantaneous reproduction number using the procedure outlined in Thompson et al. (2019). This method, implemented in the EpiEstim R-package, uses a Bayesian approach to estimate the instantaneous reproduction number smoothed over a sliding window of 5 days, see figure 27. For the results to be comparable to those of the metapopulation model, we use the same natural history parameters. We estimate the date of infection for each confirmed case by first estimating the date of symptom onset and then subtracting 5 days for the incubation period. We estimate the date of symptom onset from the empirical delay between onset and testing in the first reported cases. For each case, we draw 100 possible onset dates from the delay distribution; this gives us 100 epi-curves that we use to estimate the reproduction number. The displayed results are the combined results from all these 100 simulated epi-curves. The serial interval was assumed to be 5 days with uncertainty; the serial interval refers to the time between symptom onset between successive cases in a chain of transmission (see https://www.medrxiv.org/content/10.1101/2020.02.03.20019497v2). To account for censoring of observations with onset dates in the last few days we correct the observed data by the mean of a negative binomial distribution with observation probability given by the empirical cumulative distribution of the onset to reporting date distributions. Due to this correction, the results from the last few days are uncertain, as indicated by increasing credible intervals.

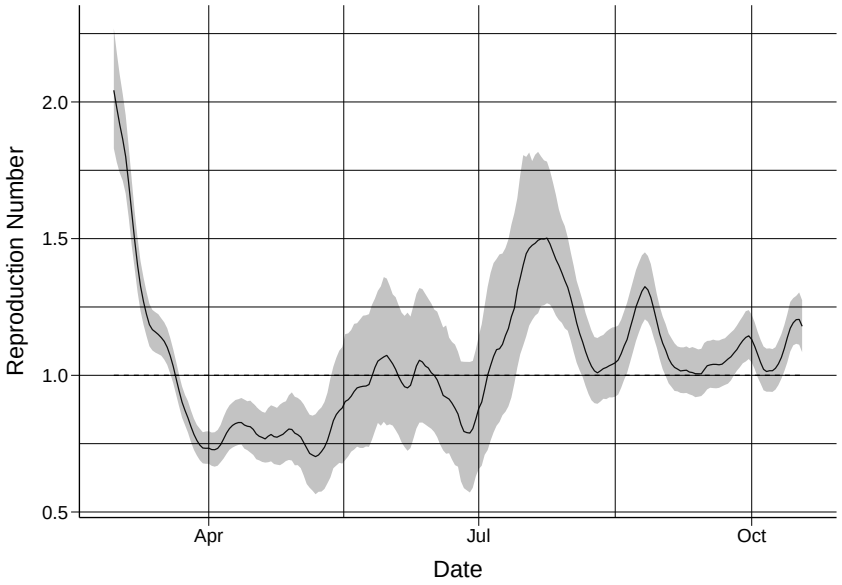

Figure 27: Reproduction number estimated using the R package EpiEstim.

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