

# Situational awareness and forecasting

FHI COVID-19 modelling team

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## Highlights from this report:

- The situation continues to be stable at a low level of transmission.
- During the next week, we predict on average circa 15 new infections per day in Norway, with a 95% confidence interval from 0 up to 62. The prevalence of COVID-19 infections in Norway is estimated to decrease in the next three weeks, from around 95 to around 75, with a 95% confidence interval up to approx. 300. Hospitalisation is predicted to continue to drop slowly in the next three weeks. The reproduction number effective since May 11 is estimated to be 0.80, with a 95% confidence interval (0.54 - 1.01), which is stable compared to the previous week. Reproduction numbers have to be interpreted together with the low estimated prevalence.
- One year ahead predictions of hospitalisation from the changepoint model, based on the distribution of the estimated last reproduction number, shows that most likely, if the current pace is maintained, we have passed the peak already.
- According to the changepoint model, the estimated probability that the reproduction number acting from May 11 is larger than 1 is 3 %.
- Inter-municipality mobility, measured as mobility of Telenor mobile phones out from each municipality, is reduced in some counties, like Viken, Rogaland and Oslo, while it is stable in some other counties, like Agder. In Nordland it is increasing. This may be linked to the Norwegian main vacation period (fellesferie).

## 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. We seed infections imported to Norway into the model from February 26 until March 18.

### 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 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 July 26<sup>nd</sup>. 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 data, the predictions at county level can only be taken as an indication.

We assume three 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 today.

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

The basic reproductive numbers are calibrated to hospital incidence data until yesterday. Estimates of  $R_0$ ,  $R_1$ ,  $R_2$ , and  $R_3$  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 week 11 and week 17, imply that 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 with hospitalisation data leads to the following estimates figure 1 and table 1:

Table 1: Calibration results

Parameter	Mean	Median	Confidence interval (95 %)
Amplification factor	2.09	2.07	(1.23-3.11)
R <sub>0</sub>	2.66	2.65	(1.96-3.26)
R <sub>1</sub>	0.54	0.55	(0.46-0.62)
R <sub>2</sub>	0.68	0.66	(0.42-1)
R <sub>3</sub>	0.80	0.82	(0.54-1.01)

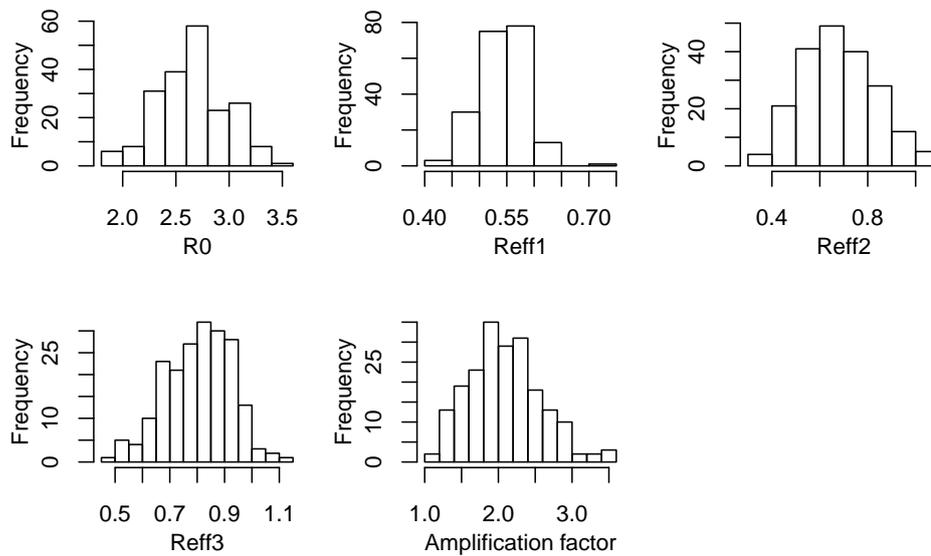


Figure 1: Estimated densities of the four parameters.

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 with the actual true data, 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.

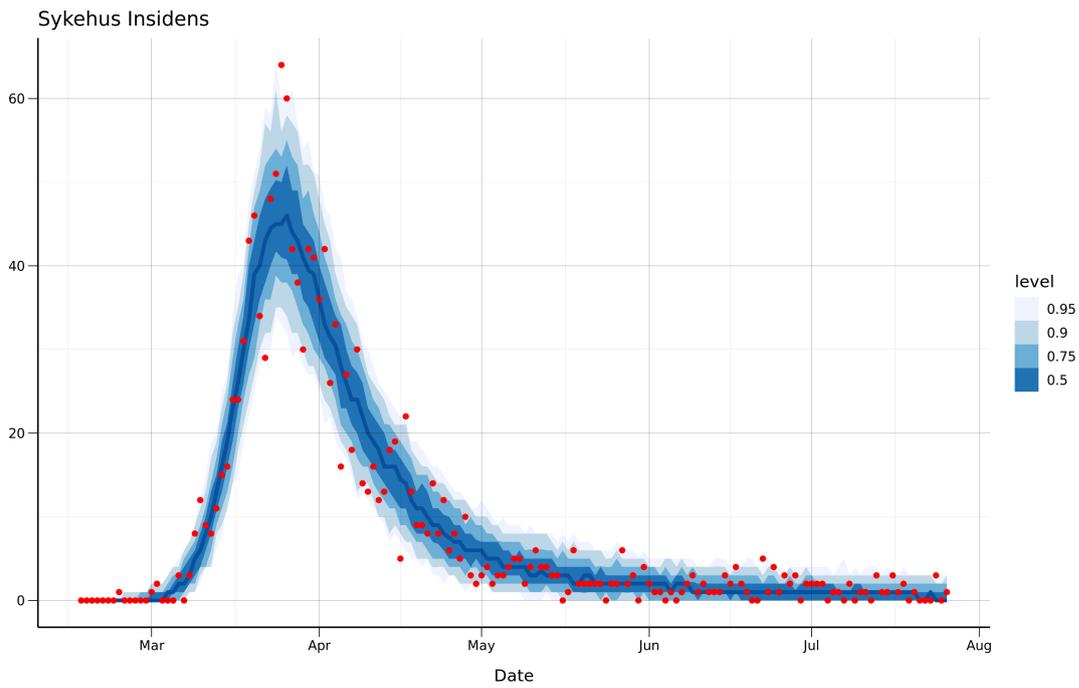


Figure 2: True total number of hospital admissions (red) and predicted values (blue)

In figure 3, we show how our model fits to the hospital prevalence data, which are not used to estimate the parameters, and can therefore be seen as a validation of the model assumptions.

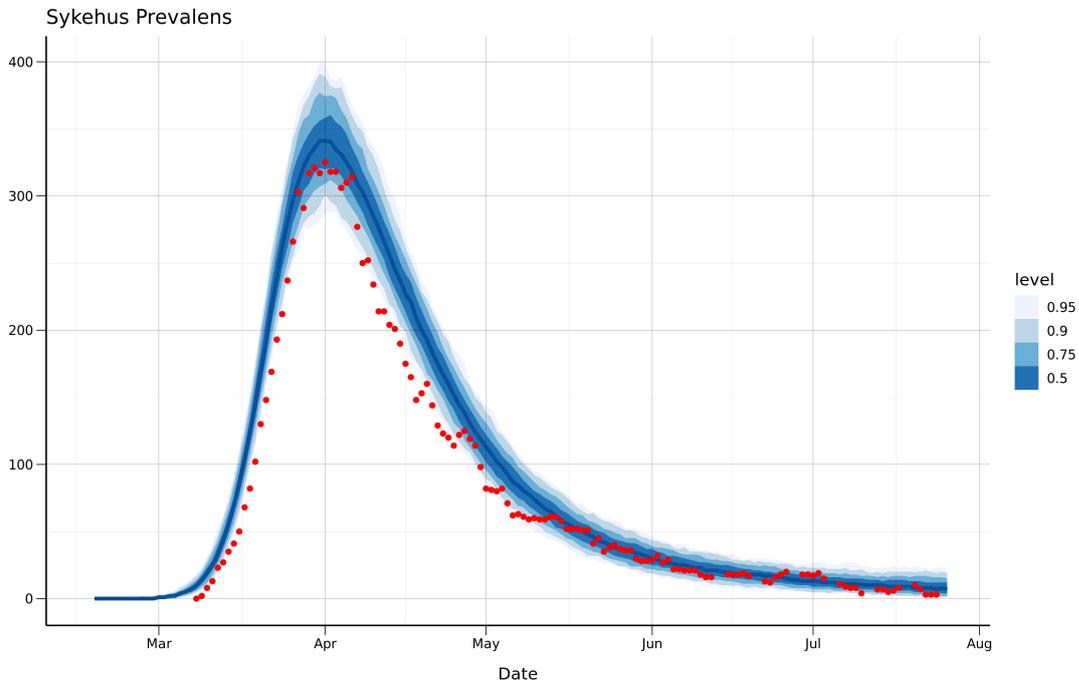


Figure 3: True total number of hospitalisations (red) and predicted values (blue)

Finally, in figure 4 we compare the true daily number of patients receiving ventilator treatment (red) with the model estimates (blue).

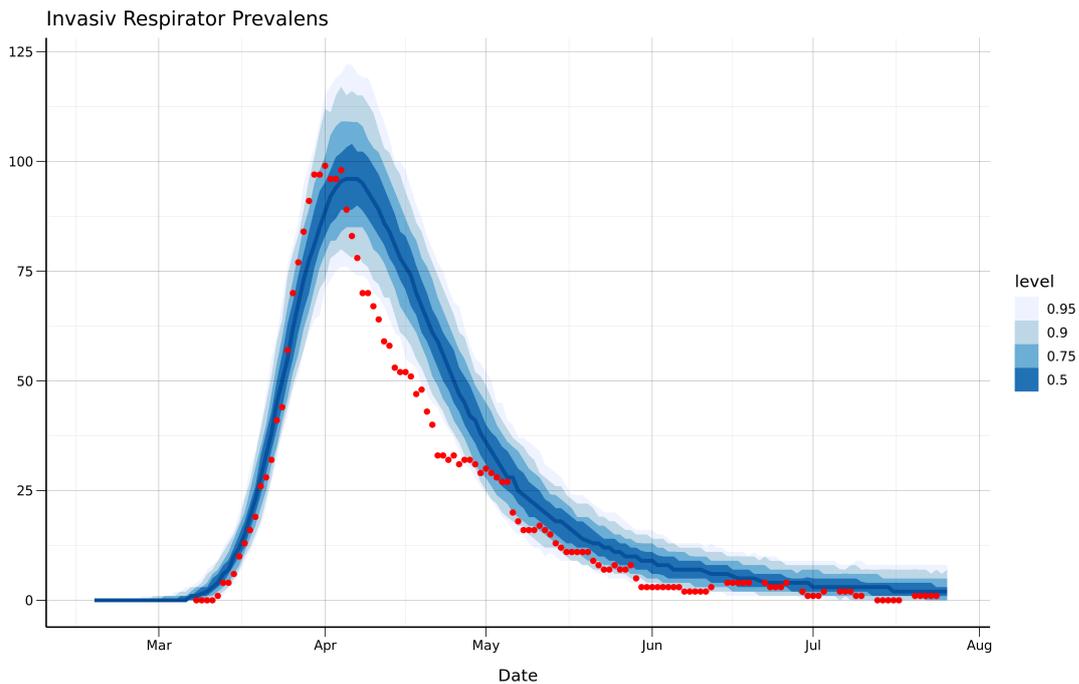


Figure 4: True total number on ventilator (red) and predicted values (blue)

## 1.1 Time varying reproduction number

We introduce a new model of the Norwegian COVID-19 pandemic, which is based on Sequential Monte Carlo, and is therefore called the SMC 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.

As for the changepoint model, we use 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 in 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  $R_3$ . For this reason, the confidence intervals were more narrow.

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 in correspondence to the lock-down. It remained stable around 0.5 until the end of April when it increased to reach 1 in the beginning of May. It then kept oscillating below and above 1, in correspondence to increases and decreases of the number of new hospitalisations.  $R(t)$  is sensitive to these oscillations in the data. An increase in hospital admissions signifies a daily reproduction number (14 days before on average) larger than 1. A decrease in hospital admissions suggests that the reproduction number was below 1 (again 14 days prior). In the last two weeks, there are less and less data which carry information about  $R(t)$ , and the uncertainty grows. We observe currently a declining trend, which is, however, not statistically significant. In the figure we plot the central 50% quantiles of the estimated posterior distribution of  $R(t)$ . The 95% confidence interval would be much larger, because of the lack of data informing the estimates.

## 1.1 Time varying reproduction number

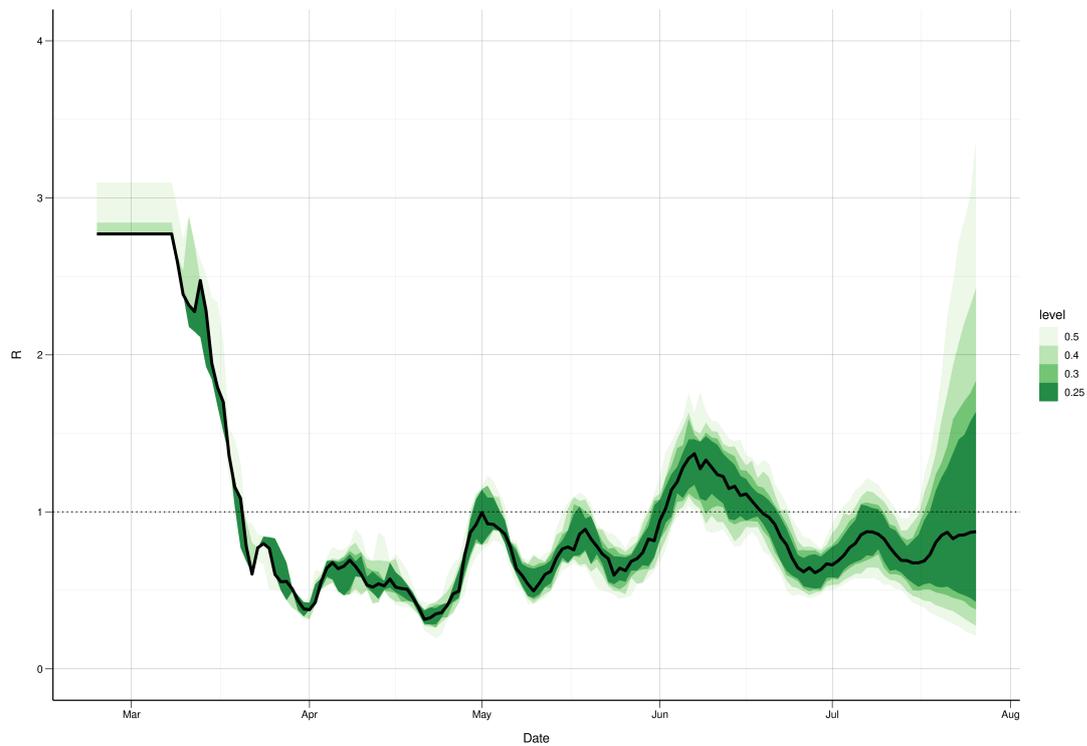


Figure 5:  $R(t)$  estimates using a Sequential Monte Carlo (SMC) approach calibrated on incidence data. The large uncertainty during the last 14 days reflects the lack of available data due to the time period between infection, symptoms onset and hospitalisation. The green band pictures the central 50% of the posterior distribution.

## 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, 2020-07-26

Region	Total	Symptomatic	No. confirmed	Fraction reported	Min. fraction
Norway	36978 (32865; 41619)	23621 (20870; 26567)	9085	25%	22%
Agder	1860 (1353; 2396)	1183 (863; 1522)	352	19%	15%
Innlandet	2939 (2357; 3600)	1893 (1521; 2327)	515	18%	14%
Møre og Romsdal	1649 (1179; 2091)	1071 (762; 1379)	160	10%	8%
Nordland	1712 (1158; 2168)	1100 (740; 1388)	130	8%	6%
Oslo	5657 (4718; 6811)	3486 (2912; 4164)	2941	52%	43%
Rogaland	4359 (3451; 5473)	2758 (2126; 3403)	453	10%	8%
Troms og Finnmark	1502 (973; 2122)	972 (629; 1378)	258	17%	12%
Trøndelag	1878 (1275; 2867)	1197 (822; 1788)	549	29%	19%
Vestfold og Telemark	3183 (2578; 3922)	2028 (1637; 2494)	301	9%	8%
Vestland	3424 (2568; 4448)	2169 (1635; 2748)	900	26%	20%
Viken	8815 (7574; 10223)	5766 (4896; 6634)	2526	29%	25%

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

### 3 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 6 and table 3.

Table 3: Predicted incidence per day.

Region	1 week prediction (02 August)	2 weeks prediction (09 August)	3 weeks prediction (16 August)
Norway	15 (0-62)	14 (0-58)	13 (0-51)
Agder	2 (0-5)	1 (0-3)	2 (0-4)
Innlandet	2 (0-5)	2 (0-5)	2 (0-6)
Møre og Romsdal	1 (0-4)	1 (0-4)	1 (0-3)
Nordland	1 (0-3)	1 (0-3)	1 (0-4)
Oslo	3 (0-9)	3 (0-9)	3 (0-9)
Rogaland	2 (0-7)	2 (0-8)	2 (0-8)
Troms og Finnmark	1 (0-7)	1 (0-4)	1 (0-5)
Trøndelag	2 (0-5)	2 (0-6)	2 (0-5)
Vestfold og Telemark	2 (0-6)	2 (0-6)	2 (0-5)
Vestland	2 (0-7)	2 (0-6)	2 (0-6)
Viken	5 (0-17)	4 (0-16)	4 (0-17)

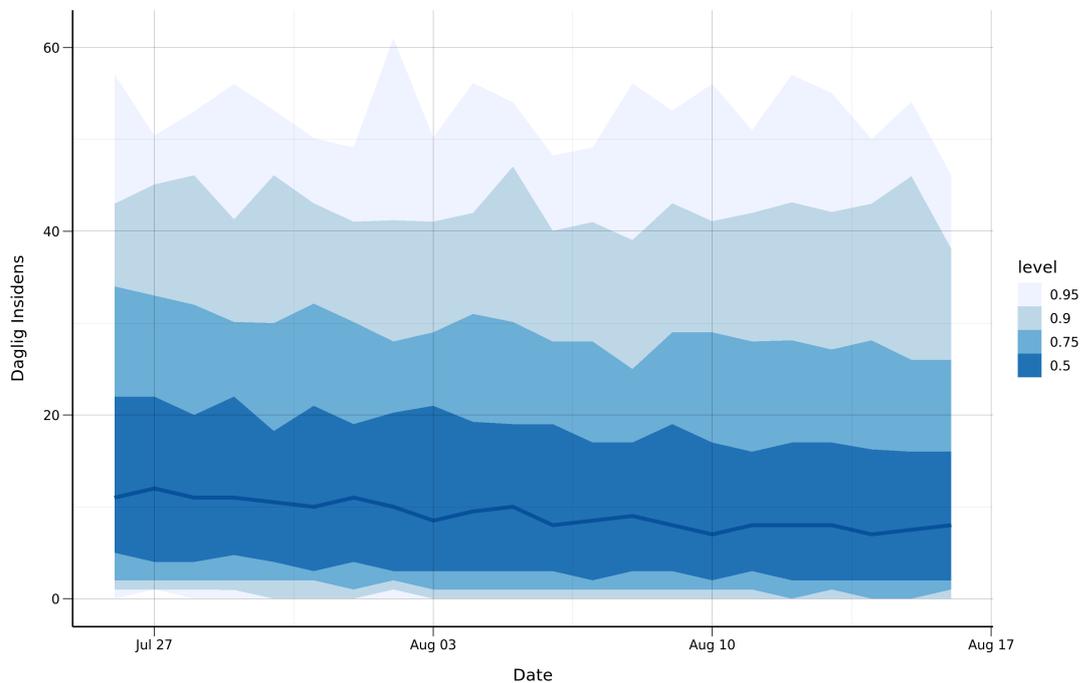


Figure 6: Predicted incidence (asymptomatic and symptomatic) for Norway per day, with confidence intervals.

## 4 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 7 and table 4.

Table 4: Number of hospitalisation beds occupied by Covid-19 patients.

Region	1 week prediction (02 August)	2 weeks prediction (09 August)	3 weeks prediction (16 August)
Norge	8 (0-24)	7 (0-22)	6 (0-23)
Agder	1 (0-3)	1 (0-3)	0 (0-2)
Innlandet	1 (0-3)	1 (0-4)	1 (0-3)
Møre og Romsdal	0 (0-3)	0 (0-3)	0 (0-2)
Nordland	0 (0-3)	0 (0-2)	0 (0-3)
Oslo	1 (0-5)	1 (0-3)	1 (0-3)
Rogaland	1 (0-3)	1 (0-3)	0 (0-3)
Troms og Finnmark	0 (0-3)	0 (0-3)	0 (0-2)
Trøndelag	0 (0-3)	0 (0-4)	0 (0-3)
Vestfold og Telemark	1 (0-5)	1 (0-3)	1 (0-5)
Vestland	1 (0-5)	1 (0-3)	1 (0-4)
Viken	2 (0-6)	2 (0-8)	2 (0-9)

Yesterday's real value for Norway: 3

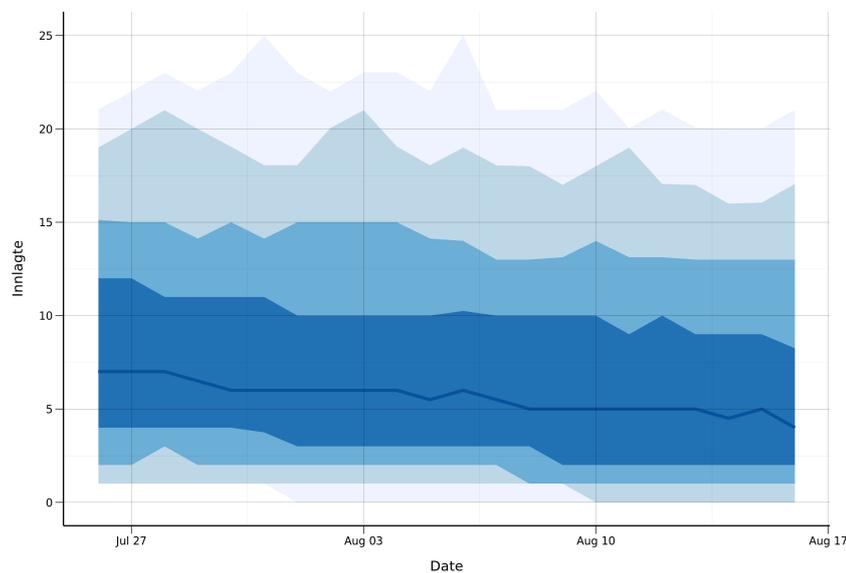


Figure 7: Predicted daily number of COVID-19 patients in hospital in Norway (95% confidence intervals and interquartile range), next three weeks, including patients ventilator treatment.

## 5 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 8 and table 5.

Table 5: Number of ICU beds occupied by Covid-19 patients.

Region	1 week prediction (02 August)	2 weeks prediction (09 August)	3 weeks prediction (16 August)
Norge	2 (0-8)	2 (0-7)	2 (0-7)
Agder	0 (0-1)	0 (0-1)	0 (0-1)
Innlandet	0 (0-1)	0 (0-1)	0 (0-1)
Møre og Romsdal	0 (0-1)	0 (0-1)	0 (0-1)
Nordland	0 (0-1)	0 (0-1)	0 (0-1)
Oslo	0 (0-2)	0 (0-1)	0 (0-1)
Rogaland	0 (0-1)	0 (0-1)	0 (0-1)
Troms og Finnmark	0 (0-1)	0 (0-1)	0 (0-1)
Trøndelag	0 (0-1)	0 (0-1)	0 (0-1)
Vestfold og Telemark	0 (0-2)	0 (0-1)	0 (0-2)
Vestland	0 (0-2)	0 (0-1)	0 (0-1)
Viken	0 (0-2)	0 (0-3)	0 (0-3)

Yesterday's real value for Norway: 1

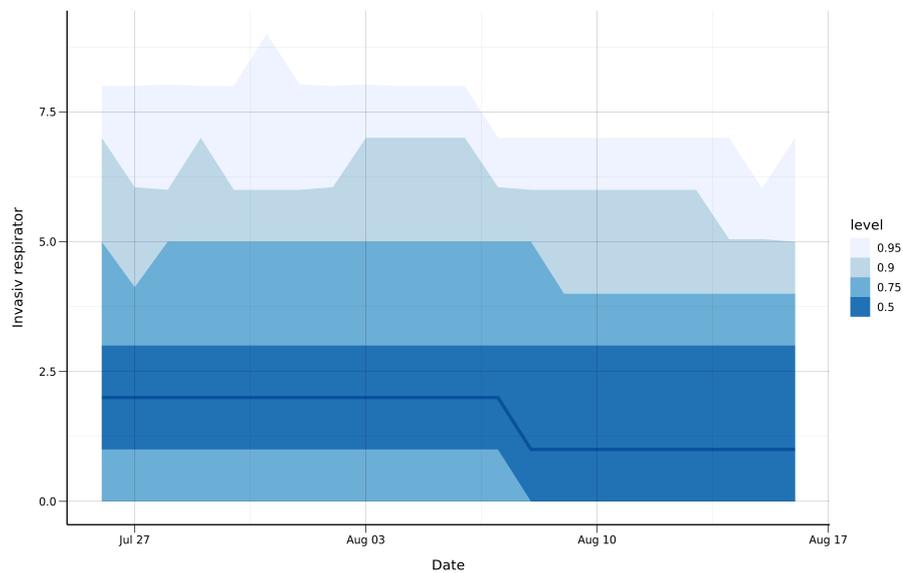


Figure 8: Predicted daily number of COVID-19 patients in ventilator treatment in Norway (95% confidence intervals and interquartile range), next three weeks.

## 6 Predicted prevalence of infectious individuals, next three weeks:

The changepoint model is used to predict the daily prevalence of asymptomatic, presymptomatic and symptomatic individuals, aggregated for the whole of Norway the next three weeks, see figure 9 and table 6.

Table 6: Predicted prevalence. Number of infectious individuals (asymptomatic plus pre-symptomatic plus symptomatic) per day. Means and 95 perc. CI for three weeks prediction.

Region	Mean, 02 August	Mean, 09 August	Mean, 16 August	low CI, 16 August	high CI, 16 August
Norway	93	84	77	1	291
Agder	6	5	5	0	23
Innlandet	8	8	7	0	27
Møre og Romsdal	5	4	4	0	15
Nordland	4	4	4	0	16
Oslo	13	12	11	0	55
Rogaland	9	8	8	0	38
Troms og Finnmark	5	4	4	0	28
Trøndelag	8	7	6	0	30
Vestfold og Telemark	9	8	7	0	34
Vestland	10	9	9	0	34
Viken	25	23	21	0	87

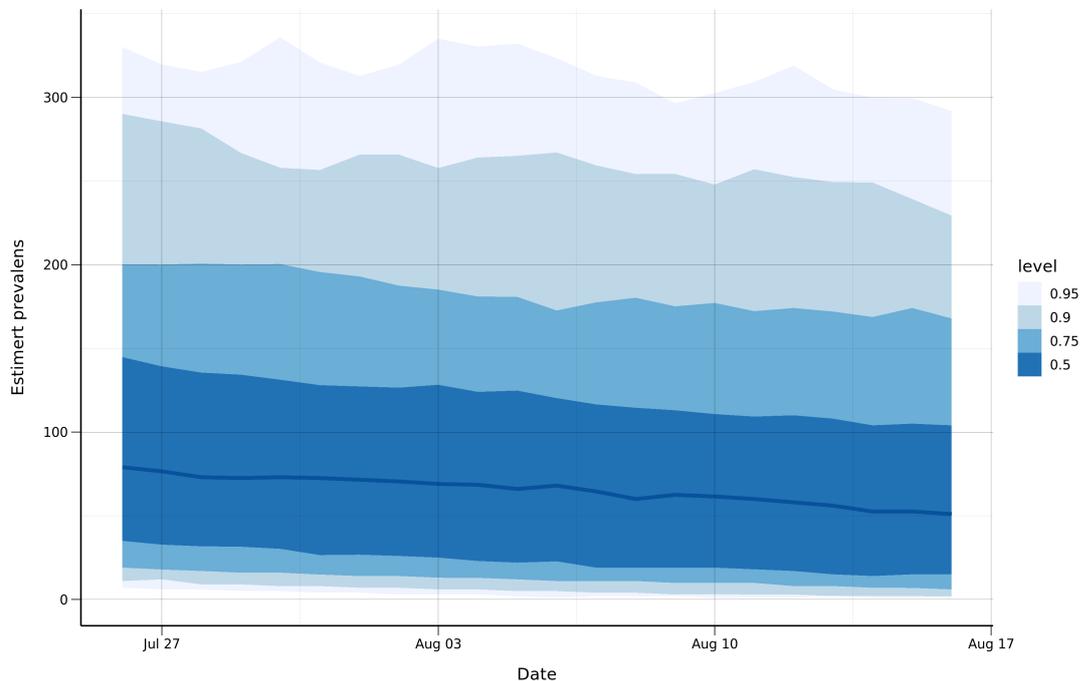


Figure 9: Predicted daily prevalence of asymptomatic, presymptomatic and symptomatic individuals, aggregated, whole Norway, (95% confidence interval).

## 7 Predicting prevalence on municipality level

The model is predicting prevalence on municipality level, which can be found in Figure 10.

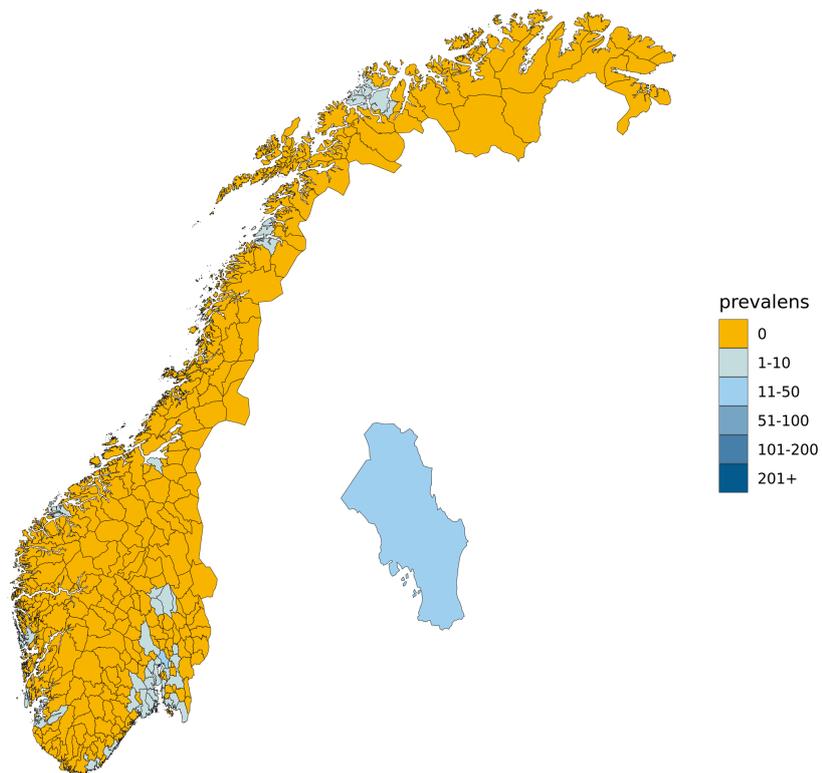


Figure 10: Map of predicted prevalence. Number of infectious individuals (asymptomatic plus presymptomatic plus symptomatic) today in each municipality.

## 8 Mobility between municipalities

Number of trips out from each municipality during each day, based on Telenor mobility data. We have observed a large reduction in inter-municipality mobility in week 11 (around March 11), with a minimum reached on Tuesday 17 March. The reduction with respect to the weeks before (week 10, which we use as reference) is on average 50%. Thereafter, we observe a slight increasing trend: in Oslo, for example, out-mobility has increased of roughly 2% per day in the three weeks 12, 13 and 14. Weekends have a lower mobility, indicating that there is still commuting-to-job during weekdays. On Tuesday April 14th, after Easter, nationwide mobility was only reduced by 38% compared to week 10. On Monday April 20th, when kindergarten started to re-open, the nationwide reduction was only 23% compared to week 10. The nationwide mobility experienced a 27% reduction on Monday April 27 compared to week 10, which is the week where grades 1 to 4 in elementary school re-opened, see Figure 11 for the 20 largest municipalities and Figure 12 for Norway's counties (fylker).

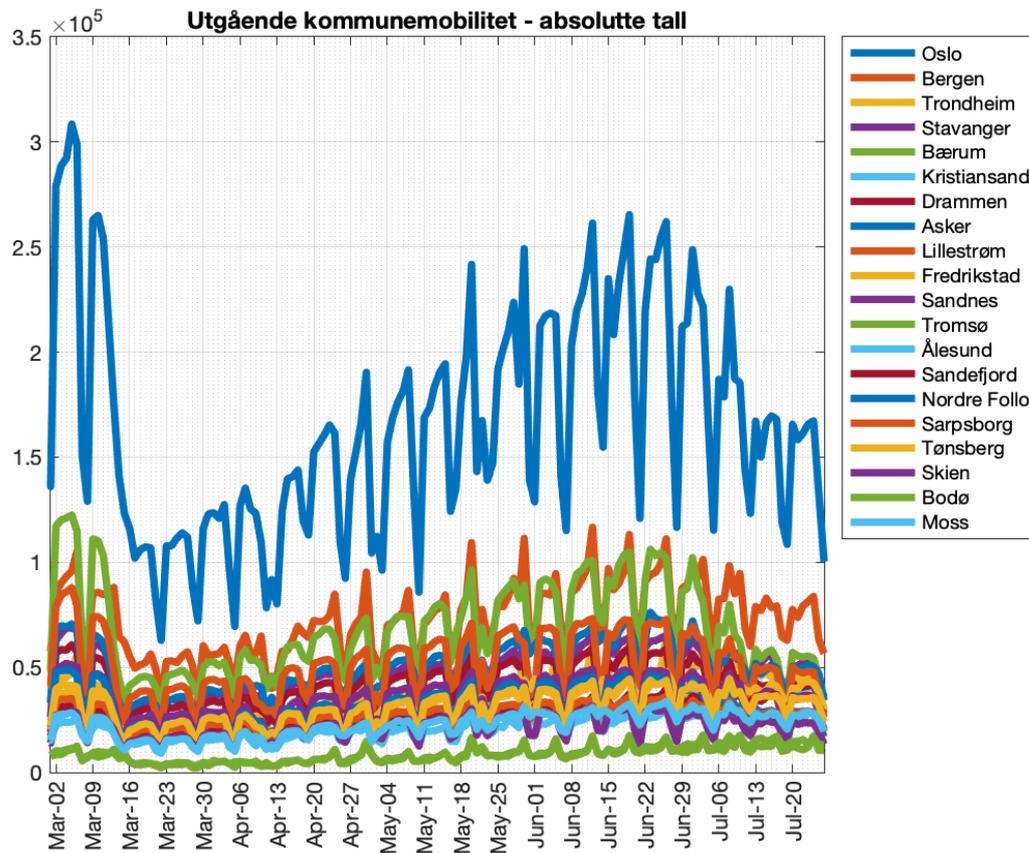


Figure 11: Inter-municipality mobility from week 10 until today.

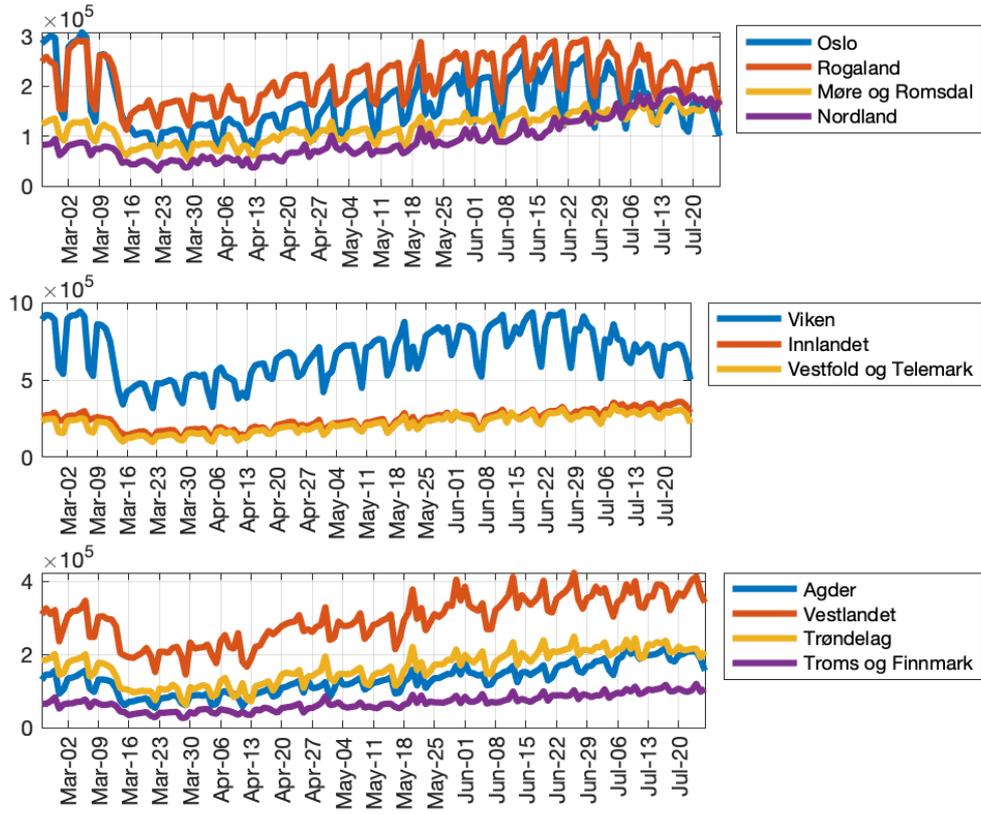


Figure 12: Inter-county mobility from week 10 until today.

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 7, and for counties see Table 8.

Table 7: Percentage reduction in total mobility out from each municipality.

	17 Jul 2020	18 Jul 2020	19 Jul 2020	20 Jul 2020	21 Jul 2020	22 Jul 2020	23 Jul 2020	24 Jul 2020	25 Jul 2020	26 Jul 2020
	Fredag	Lørdag	Søndag	Mandag	Tirsdag	Onsdag	Torsdag	Fredag	Lørdag	Søndag
Hele Norge	-1.0%	-27.3%	-30.8%	-5.5%	0.3%	-1.7%	-0.8%	-1.8%	-35.0%	-23.8%
Oslo	43.8%	20.9%	15.9%	40.6%	45.2%	44.8%	46.3%	44.0%	11.7%	22.2%
Bergen	24.7%	0.2%	-6.5%	9.6%	18.2%	15.1%	15.0%	20.4%	2.0%	4.2%
Trondheim	10.4%	-25.3%	-17.3%	-5.1%	1.1%	3.1%	3.2%	13.6%	-21.2%	-16.6%
Stavanger	26.9%	-1.4%	-22.8%	19.1%	23.6%	23.9%	23.2%	22.2%	-11.3%	-5.9%
Bærum	53.1%	29.5%	24.2%	51.3%	53.9%	54.6%	54.8%	52.8%	23.5%	27.8%
Kristiansand	-22.4%	-81.2%	-117.7%	-40.4%	-33.5%	-28.4%	-27.9%	-14.4%	-66.6%	-84.5%
Drammen	28.7%	6.7%	1.1%	25.6%	31.0%	30.0%	32.1%	26.5%	2.0%	3.6%
Asker	25.8%	3.1%	-7.5%	25.6%	29.0%	28.0%	27.7%	24.9%	-9.0%	-2.0%
Lillestrøm	38.9%	19.7%	22.9%	36.3%	43.3%	44.9%	45.3%	39.7%	17.0%	25.6%
Fredrikstad	-12.6%	-47.6%	-47.2%	-10.3%	-6.8%	-12.9%	-13.5%	-17.1%	-55.8%	-40.9%
Sandnes	27.9%	6.4%	-19.4%	24.9%	28.8%	29.7%	28.5%	27.7%	-1.0%	3.4%
Tromsø	-29.1%	-84.1%	-34.8%	-51.4%	-36.4%	-5.9%	-11.6%	-38.9%	-91.8%	-33.6%
Ålesund	-6.8%	-23.6%	-36.6%	-18.6%	-12.3%	-8.3%	-15.9%	-10.5%	-29.6%	-33.6%
Sandefjord	-15.6%	-43.3%	-61.5%	-14.8%	-11.4%	-12.9%	-9.9%	-11.7%	-47.9%	-41.6%
Nordre Follo	38.2%	18.1%	16.4%	39.3%	40.6%	40.5%	40.0%	38.0%	13.7%	18.4%
Sarpsborg	14.2%	-4.6%	-10.3%	13.8%	20.0%	16.7%	17.7%	12.9%	-9.1%	-5.8%
Tønsberg	10.3%	-25.4%	-22.1%	10.3%	15.7%	15.2%	15.2%	12.3%	-23.5%	-13.3%
Skien	17.1%	-5.3%	-11.6%	10.5%	17.3%	14.7%	18.5%	17.4%	-7.0%	5.5%
Bodø	-48.3%	-125.1%	-88.7%	-44.1%	-44.5%	-44.5%	-15.5%	-43.4%	-124.2%	-89.1%
Moss	-6.9%	-35.4%	-38.4%	-1.4%	2.6%	-1.4%	-0.9%	-8.1%	-41.9%	-32.4%

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

	17 Jul 2020	18 Jul 2020	19 Jul 2020	20 Jul 2020	21 Jul 2020	22 Jul 2020	23 Jul 2020	24 Jul 2020	25 Jul 2020	26 Jul 2020
	Fredag	Lørdag	Søndag	Mandag	Tirsdag	Onsdag	Torsdag	Fredag	Lørdag	Søndag
Hele Norge	-1.0%	-27.3%	-30.8%	-5.5%	0.3%	-1.7%	-0.8%	-1.8%	-35.0%	-23.8%
Oslo	43.8%	20.9%	15.9%	40.6%	45.2%	44.8%	46.3%	44.0%	11.7%	22.2%
Rogaland	20.6%	-4.2%	-26.5%	14.4%	18.2%	18.1%	17.8%	16.6%	-12.5%	-6.0%
Møre og Romsdal	-23.8%	-48.1%	-66.5%	-30.2%	-18.9%	-17.8%	-31.5%	-28.3%	-57.5%	-70.3%
Nordland	-121.4%	-171.8%	-132.5%	-124.9%	-104.2%	-103.8%	-84.7%	-105.6%	-150.0%	-128.8%
Viken	21.5%	-0.7%	-0.2%	19.2%	23.4%	21.3%	22.4%	20.6%	-9.8%	4.3%
Innlandet	-17.1%	-28.5%	-23.2%	-27.4%	-24.1%	-29.4%	-24.8%	-20.4%	-38.8%	-14.3%
Vestfold og Telemark	-22.7%	-53.4%	-59.1%	-24.9%	-19.3%	-24.9%	-20.8%	-23.3%	-64.6%	-38.1%
Agder	-39.6%	-73.4%	-85.2%	-46.9%	-46.8%	-46.9%	-39.9%	-33.4%	-75.8%	-59.4%
Vestlandet	-9.5%	-29.2%	-39.3%	-20.5%	-12.6%	-18.9%	-23.6%	-18.9%	-48.0%	-38.0%
Trøndelag	-18.5%	-47.9%	-39.8%	-24.8%	-15.2%	-13.8%	-13.4%	-7.6%	-37.5%	-41.5%
Troms og Finnmark	-52.9%	-77.4%	-39.5%	-62.5%	-51.4%	-39.3%	-43.8%	-56.2%	-75.5%	-49.0%

## 9 Long-term prediction results

Predicted daily number of COVID-19 patients in hospital and receiving ventilator treatment in Norway until the end April, 2021, in addition to prevalence. The figures are made using 200 candidate models, where the reproductive numbers are varying according to their estimated uncertainty as estimated today with the changepoint model. There are some candidate models for which  $R3 > 1$  which induce the appearance of a peak in the future. The interpretation of the figures should be made with this in mind. 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 13 for estimated prevalence, figure 14 for estimated number of hospitalisations, and figure 15 for estimated number of patients needing ventilator treatment.

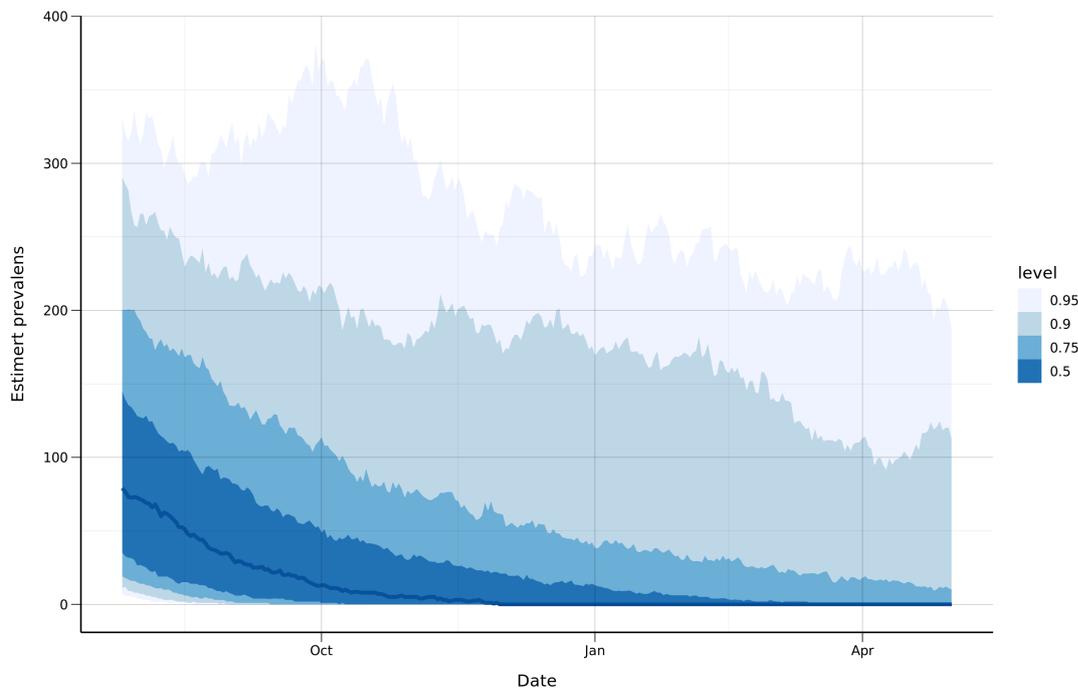


Figure 13: Predicted prevalence of COVID-19 based on 200 candidate models where the reproductive number used for simulation varies according to their estimated uncertainty.

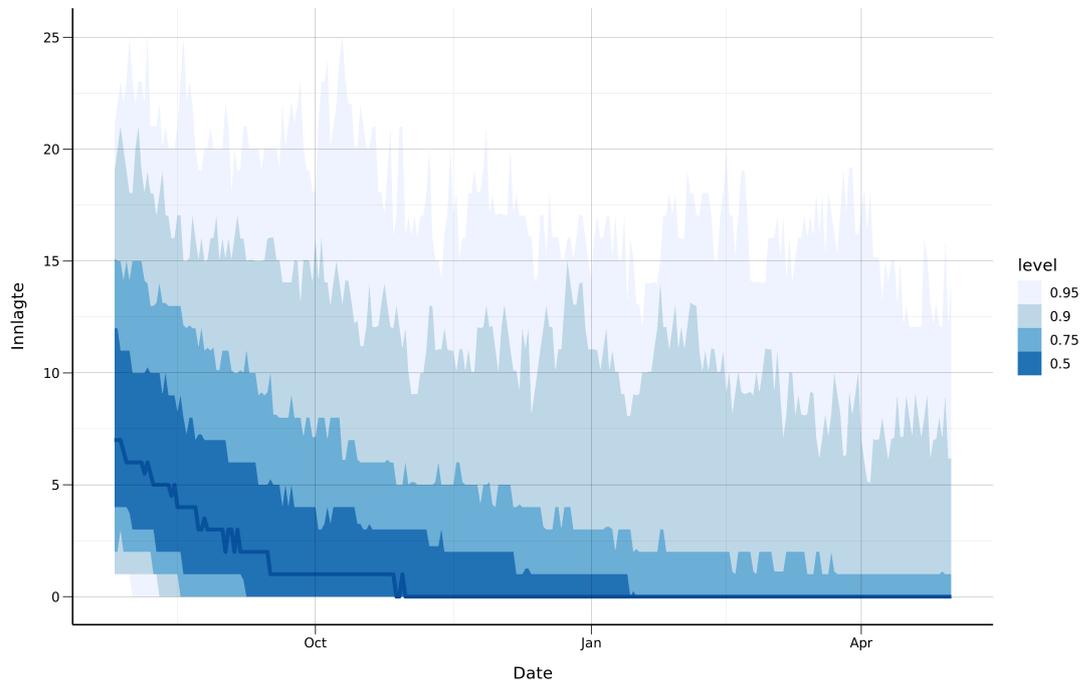


Figure 14: Predicted number of COVID-19 patients in hospital based on 200 candidate models where the reproductive number used for simulation varies according to their estimated uncertainty.

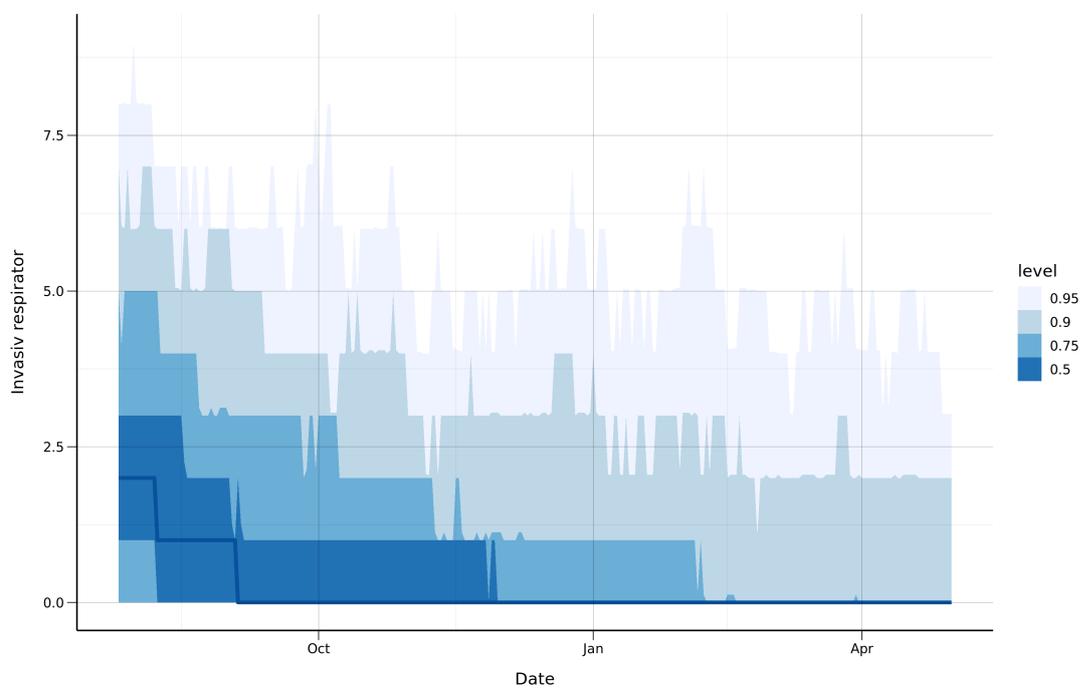


Figure 15: Predicted prevalence of COVID-19 patients needing ventilator treatment based on 200 candidate models where the reproductive number used for simulation varies according to their estimated uncertainty.

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 July 23rd, under three assumed scenarios. We assume that until July 23rd we follow our estimated reproductions numbers, but from July 24th, we fix a new effective reproduction 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 16, and the daily number of patients with ventilator treatment, figure 17. In table 9 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 probability of being hospitalised and the probability of needed ventilator treatment.

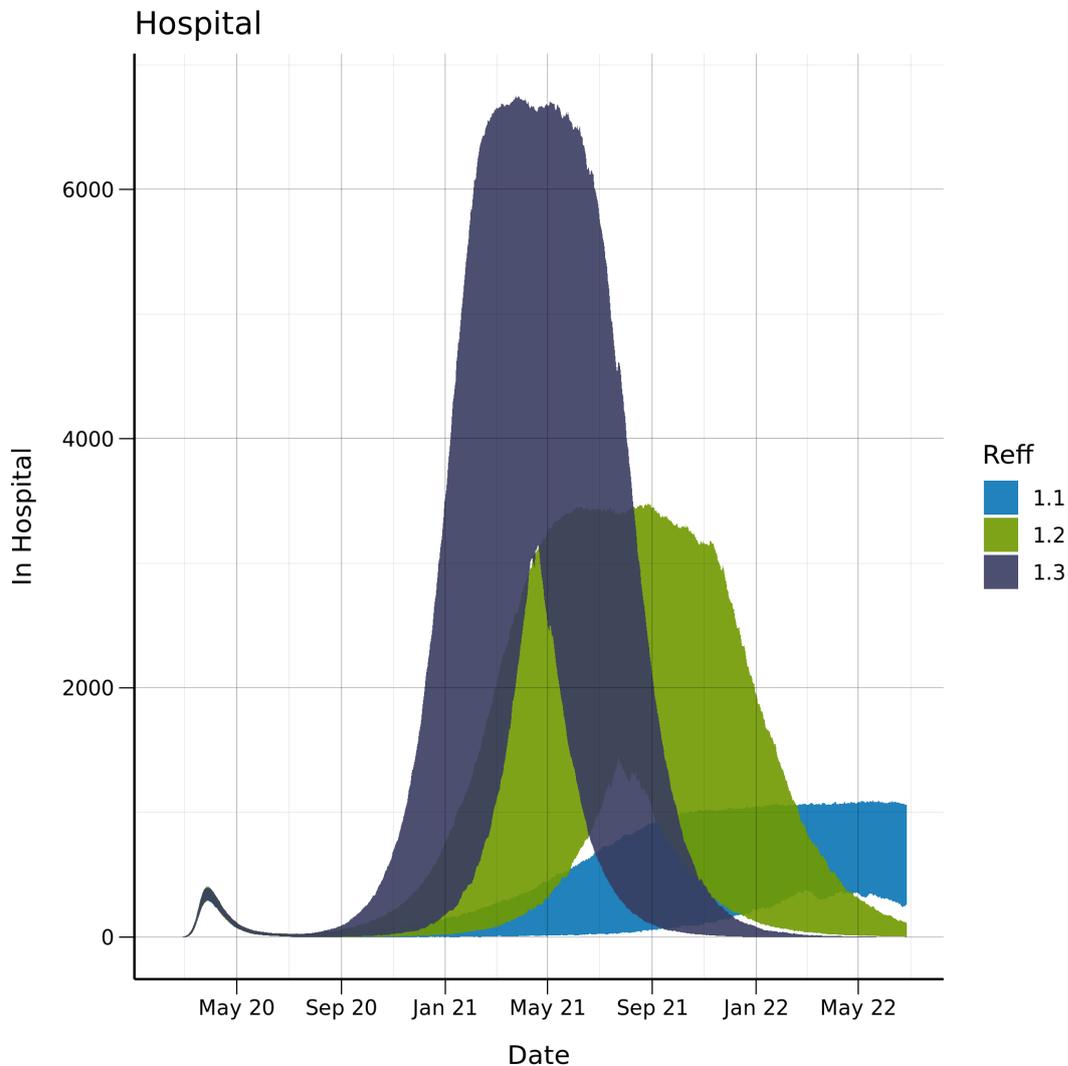


Figure 16: Predicted number of COVID-19 patients in hospital based on three different scenarios with R effective equal to 1.1, 1.2 and 1.3.

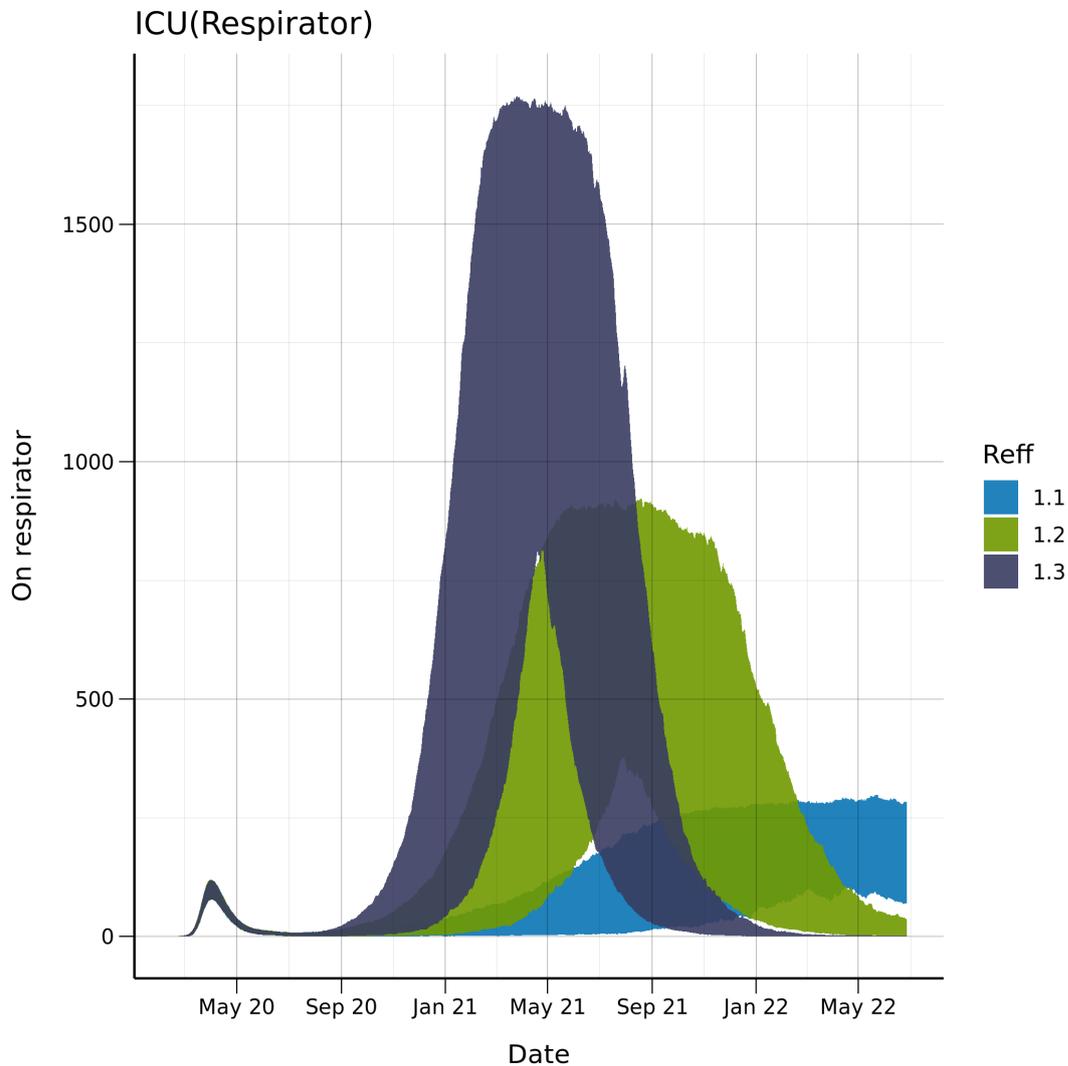


Figure 17: Predicted number of COVID-19 patients needing ventilator treatment based on three different scenarios with R effective equal to 1.1, 1.2 and 1.3.

Table 9: Predicted numbers of total infected, total number of hospitalizations, total number needing ventilator treatment and the predicted peak number of 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.

	<b>Reff=1.1</b>	<b>Reff=1.2</b>	<b>Reff=1.3</b>
Total infected	849.000(376.000 - 981.000)	1.790.000(1.760.000 - 1.840.000)	2.380.000(2.350.000 - 2.420.000)
Total Hospital	33.100(14.100 - 38.300)	69.700(68.200 - 72.200)	92.100(90.900 - 94.300)
Total on respirator	4.980(2.060 - 5.770)	10.600(10.200 - 11.000)	13.900(13.700 - 14.300)
Ward <sup>1</sup> at peak	802(660 - 867)	2.560(2.440 - 2.680)	4.990(4.800 - 5.130)
Hospital <sup>2</sup> at peak	1.070(884 - 1.160)	3.440(3.300 - 3.610)	6.710(6.450 - 6.900)
Respirator at Peak	285(222 - 316)	912(857 - 964)	1.760(1.680 - 1.830)

<sup>1</sup>In hospital not on respirator

<sup>2</sup>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 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: Susceptibles (S), Exposed, infected, but not infectious (E), Presymptomatic infected (E<sub>2</sub>), Symptomatic infected (I), Asymptomatic infected (I<sub>a</sub>), and Recovered, either immune or dead (R). A schematic overview of the model is shown in figure 18.

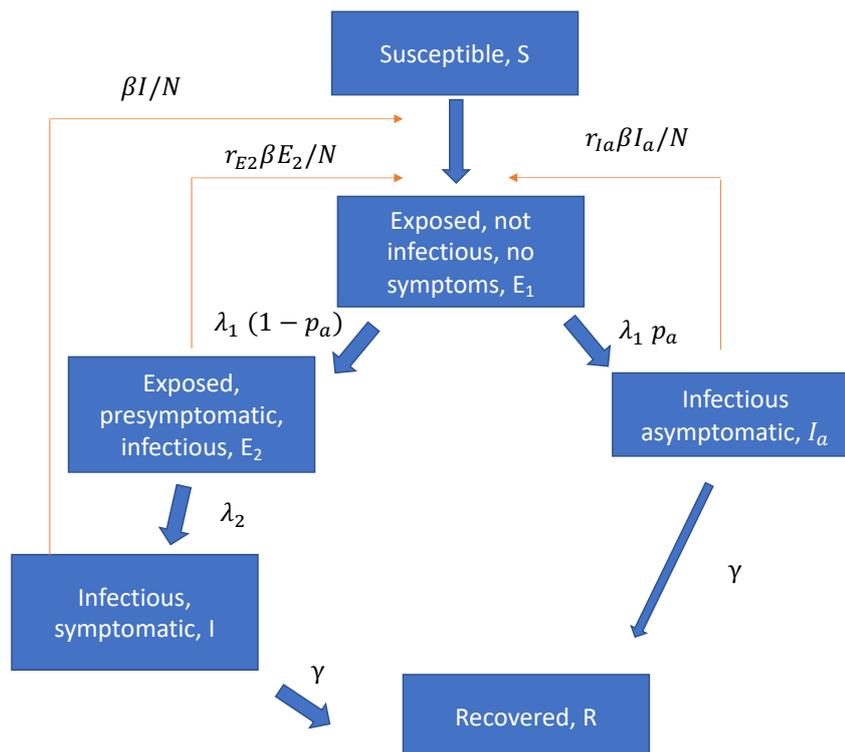


Figure 18: Schematic overview of the model.

### 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 at 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 needed.

## Healthcare utilisation

Based on the estimated daily incidence data from the model and the population age structure in each municipality, we calculated the hospitalization using a weighted average. The hospitalisation is assumed delayed relative to 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, until 18th March. 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 others missed. This is called 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, and a fourth reproduction number  $R_3$  thereafter. This last reproduction number is used in the future. The change points follow the change of 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. We use a method called sequential ABC which tests thousands of combinations of  $R_0, R_1, R_2, R_3$  and the amplification factor, to determine the 200 ones that lead to the best fits of hospitalisations. The algorithm is described in Engebretsen et al. (2020) <https://royalsocietypublishing.org/doi/10.1098/rsif.2019.0809>.

## 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  $\beta$ . 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)<sup>3</sup>. 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 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<sup>4</sup>, 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 3) 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.

<sup>3</sup><https://www.medrxiv.org/content/10.1101/2020.03.11.20033555v1>

<sup>4</sup><https://science.sciencemag.org/content/early/2020/05/12/science.abc3517.abstract>

- 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 in 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, and in particular for the last days, is very uncertain. Therefore we look two weeks back in time to determine safe 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.

## Parameters used today

Figure 19 indicates 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.

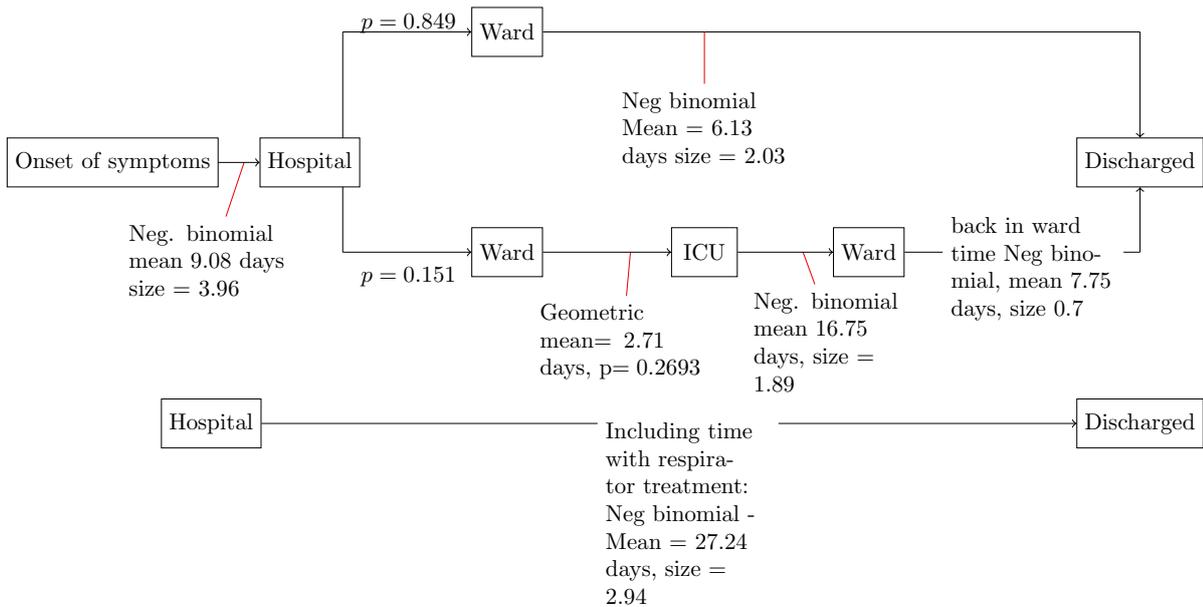


Figure 19: Hospital assumptions and parameters

Table 10: Assumptions I

Assumptions	Mean	Distribution	Reference
<b>Seeding</b>			
Scaling factor on imported cases	Min. 1.09 1st Qu. 1.76 Median 2.07 Mean 2.09 3rd Qu. 2.39 Max. 3.50	random	Calibrated to hospitalisations
Telenor coverage	48%		<a href="https://ekomstatistikken.nkom.no/">https://ekomstatistikken.nkom.no/</a>
<b>Model parameters</b>			
Exposed period ( $1/\lambda_1$ )	3 days	Exponential	<a href="#">Feretti et al 2020</a>
Pre-symptomatic period ( $1/\lambda_2$ )	2 days	Exponential	<a href="#">Feretti et al 2020</a>
Symptomatic infectious period ( $1/\gamma$ )	5 days	Exponential	<a href="#">Feretti et al 2020</a>
Asymptomatic, infectious period ( $1/\gamma$ )	5 days	Exponential	<a href="#">Feretti et al 2020</a>
Infectiousness asympt. ( $r_{I_a}$ )	0.1	Fixed	<a href="#">Feretti et al 2020</a>
Infectiousness presymp ( $r_{E_2}$ )	1.25	Fixed	<a href="#">guided by Feretti et al 2020</a>
Prob. asymptomatic infection ( $p_a$ )	0.4		<a href="#">Feretti et al 2020</a>
$R_0$ , until March 14	Min. 1.89 1st Qu. 2.43 Median 2.65 Mean 2.66 3rd Qu. 2.85 Max. 3.46	random	Calibrated to hospitalisations
$R_1$ , from 15 March until 19 April	Min. 0.43 1st Qu. 0.51 Median 0.55 Mean 0.54 3rd Qu. 0.57 Max. 0.70	random	Calibrated to hospitalisations
$R_2$ , from 20 April until 10 May	Min. 0.36 1st Qu. 0.56 Median 0.66 Mean 0.68 3rd Qu. 0.79 Max. 1.08	random	Calibrated to hospitalisations
$R_3$ , from 11 May until today	Min. 0.50 1st Qu. 0.72 Median 0.82 Mean 0.80 3rd Qu. 0.90 Max. 1.11	random	Calibrated to hospitalisations

Table 11: Assumptions II

Assumptions	Mean	Distribution	Reference
<b>Healthcare</b>			
Time sympt. onset to hospitalisation	9 days	Neg. binomial	
Fraction asymptomatic infections	40%	Fixed	<a href="#">Mizumoto et al 2020</a> 20% for the old population, Diamond Princess
% symptomatic and asymptomatic infections requiring hospitalization:			<a href="#">Saljie et al 2020</a> corrected for: % of elderly living in of elderly living in Norway (last two age groups).
0-9 years	0.2%	Fixed	
10 - 19 years	0.2%		
20 - 29 years	0.6%		
30 - 39 years	1.3%		
40 - 49 years	1.7%		
50 - 59 years	3.5%		
60 - 69 years	7.1%		
70 - 79 years	11.3%		
80+ years	27%		
% hospitalized patients requiring ICU			
Feb - March	20%	Fixed	Estimated from "Beredskapsregistret BeredtC19"
April	10%		
May -	15.1 %		
Overall hospitalization risk	3.9%	Fixed	<a href="#">Saljie et al 2020</a> (adapted to Norwegian population)
<b>Mobile phone mobility</b>			
Until July 26nd	Measured Telenor mobility		
Data used in the predictions	July 23	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 lab-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 hospitalization data are a less biased estimator of 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 20. 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 at 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.

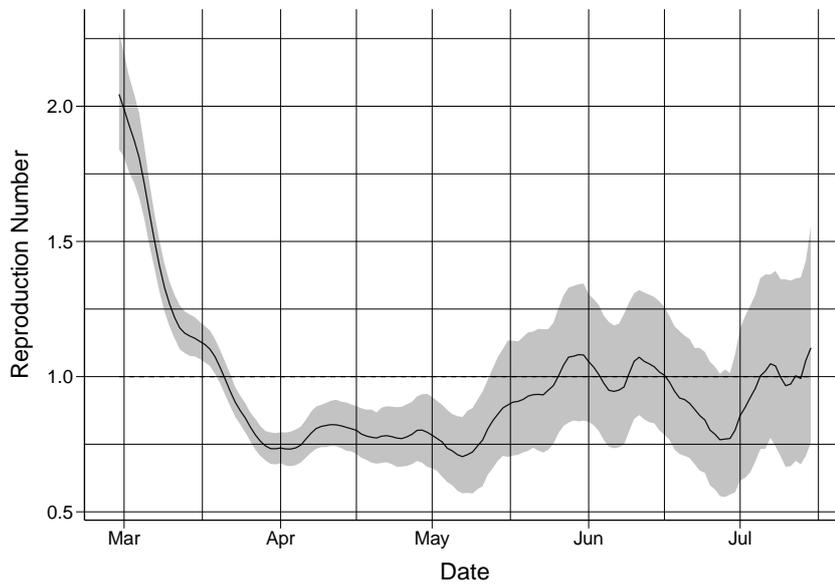


Figure 20: Reproduction number estimated using the R package EpiEstim.

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