NIPH
Norwegian Institute of Public Health

Situational awareness and forecasting

FHI COVID-19 modelling team

12 August 2020

Highlights from this report:

- We have introduced a new change point for the reproduction number acting from July 1 in the change point model. We now report on threshold values for travel restrictions by counties in Norway. The model incorporates updated data by yesterday on infections, which are known to be imported from outside Norway.
- Compared to last week, the results from our models collectively indicate a worsening of the situation and increasing transmission.
- The reproduction number acting from July 1 is estimated to be 0.98, with a wide 95% confidence interval (0.35 - 1.5); the estimated probability that the reproduction number acting from July 1 is larger than 1 is 49 %.
- At the end of next week, we predict 84 new infections per day in Norway, with a 95% confidence interval from 0 to 303. In three weeks we expect the number of new infections to be 124, but up to 615 in the 95% confidence interval. A week ago, we estimated this upper bound to be 70, so our estimate has increased by a factor 9. We estimate a growth of new infections in the next three weeks, while a week ago, we estimated this to be stable.
- The prevalence of COVID-19 infections in Norway three weeks from today is estimated to be around 700 with a 95% confidence interval up to approximately 3000. This upper bound was about 450 a week ago, and has grown with a factor of almost 6.
- Hospitalisation, currently at a low level, is predicted to continue to slowly increase in the next three weeks. Today, 15 COVID-19 patients are hospitalised; we expect this number to increase in the next three weeks to 29, with a 95% confidence interval up to 99. For comparison, we estimated this upper bound to be 31 a week ago.
- We start to estimate the probability that the total number of new infections exceeds 20 per 100.000 inhabitants in the next two weeks. This week, the counties of Oslo, Viken, and Innlandet have largest such probability, almost 50%. The probabilities are estimated from the model based counts of new infections and not the observed lb-positive counts. The likelihood that a case is tested is not taken into account.
- Long term predictions for the next 12 months, assuming that the reproduction number R_4 remains estimated as now, show a hospitalisation peak in early 2021. The probability that more than 500 patients need ventilator treatment at peak is estimated to be 24.5% (and 21% for more than 1000). These probabilities were below 1% a week ago.
- The SMC model estimates the 7-days averaged reproduction number two weeks ago to be 1.42 (0.75-2.37); the estimated probability that the daily reproduction number two weeks ago was larger than 1 is 86%. We are still working on improving the SMC model.
- Inter-municipality mobility, measured as mobility of Telenor mobile phones out from each municipality, has been increasing in the last week, but has not reached the level of late June yet.

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 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 August 7^{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 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 June 30.
- R_4 active from July 1 until today.

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 R_0, R_1, R_2, R_3, and R_4 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 data leads to the following estimates (figure 1 and table 1):

Table 1: Calibration results

Parameter	Mean	Median	Confidence interval (95 %)
Amplification factor	2.02	2.06	(1.17-2.94)
R0	2.69	2.63	(2.1-3.4)
R1	0.54	0.54	(0.46-0.62)
R2	0.66	0.66	(0.39-0.91)
R3	0.79	0.80	(0.5-1.07)
R4	0.98	0.99	(0.35-1.5)

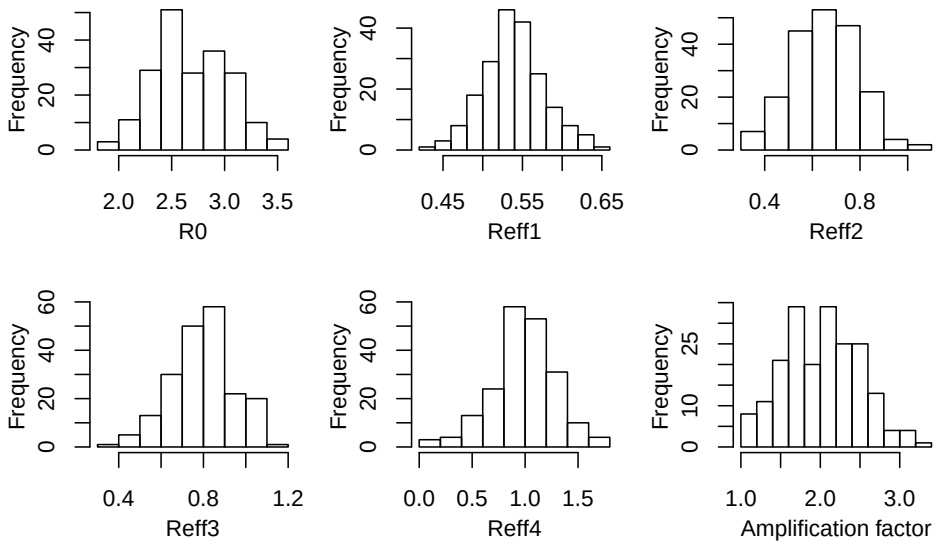

Figure 1: Estimated densities of the six parameters.

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 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.

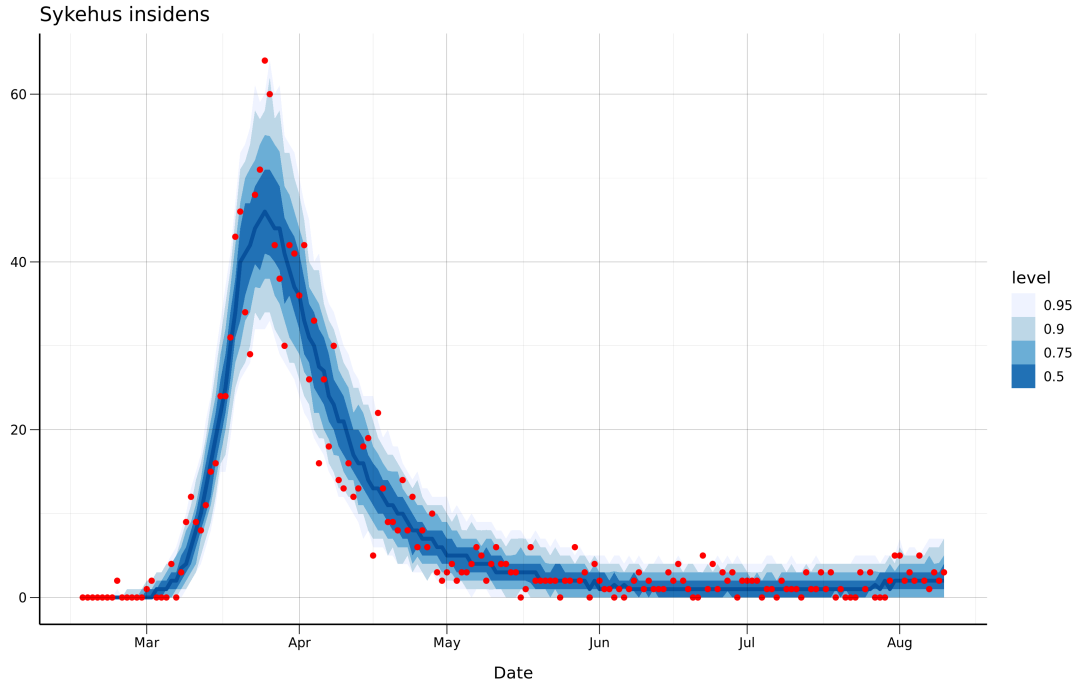

Figure 2: True total number of hospital admissions (red) and predicted values (blue)

In figure 3, 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.

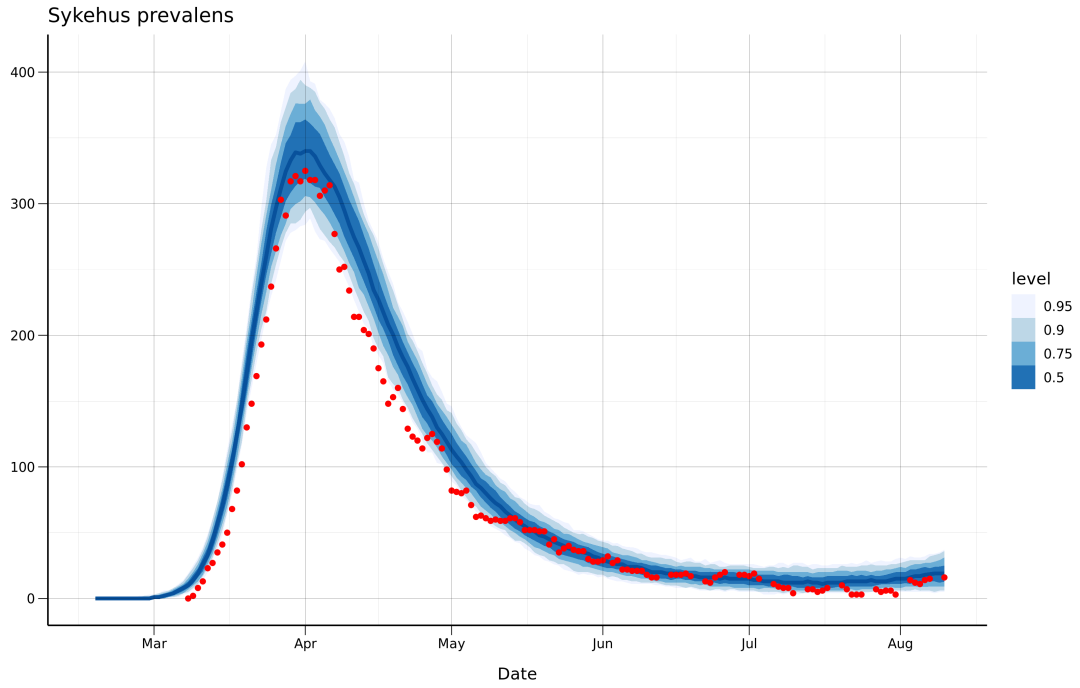

Figure 3: True total number of hospitalisations (red) and predicted values (blue)

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

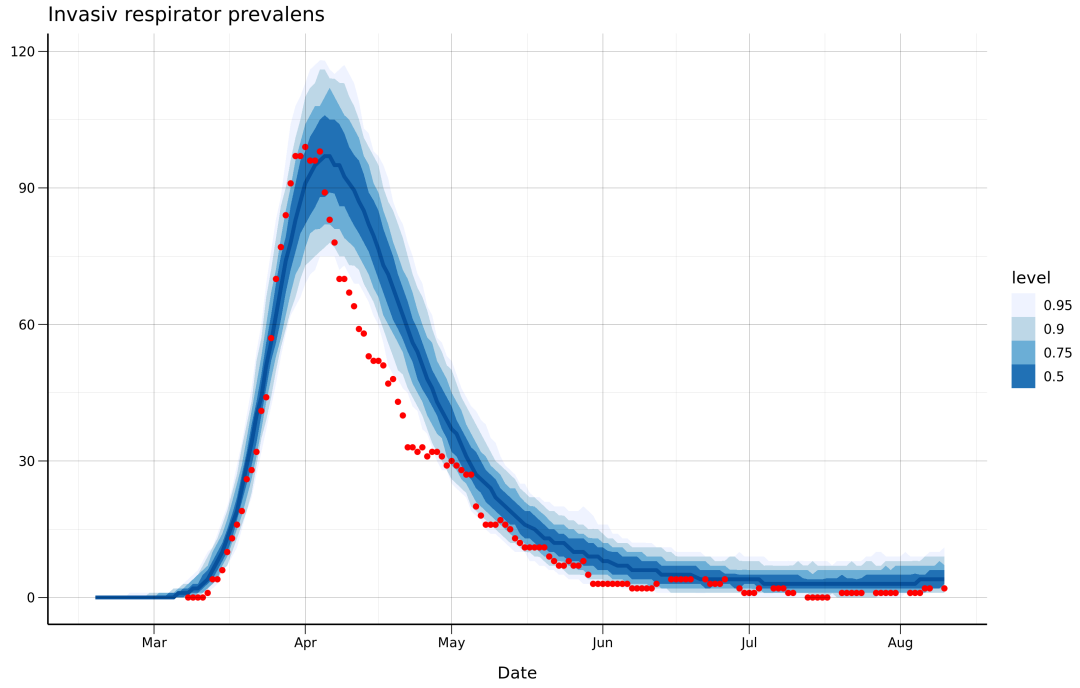

Figure 4: True total number on ventilator (red) and predicted values (blue)

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 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 R_4. 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, 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

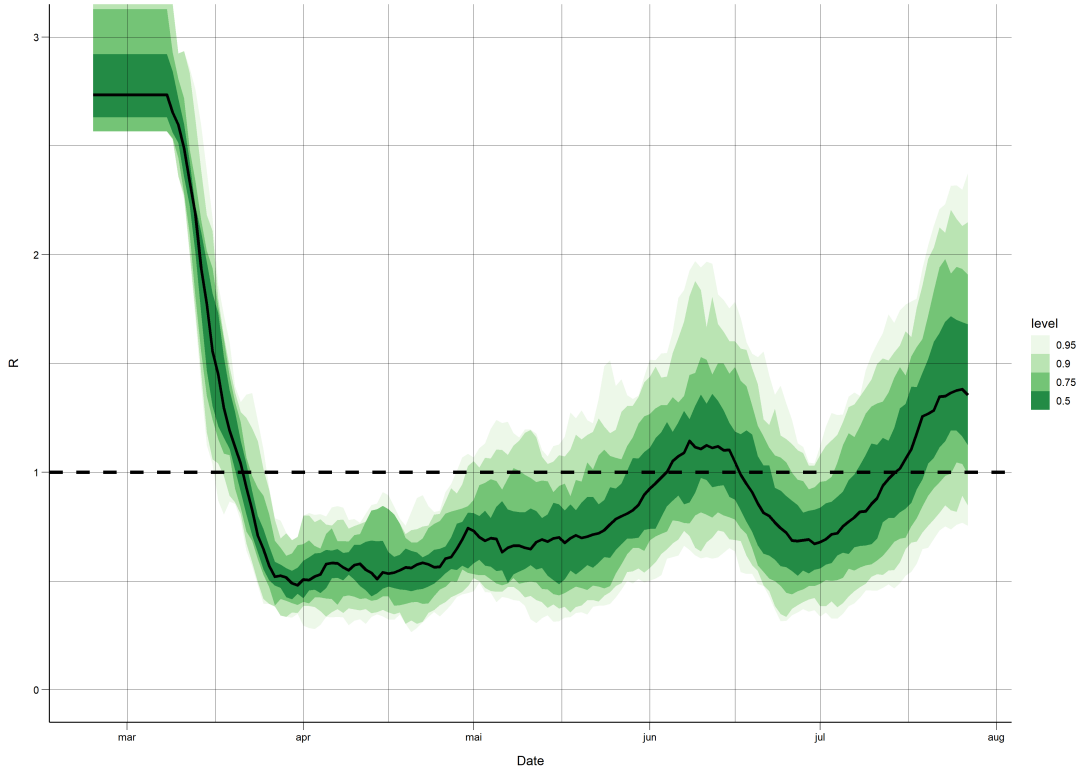

Figure 5: R(t) estimates until 14 days ago using a Sequential Monte Carlo (SMC) approach calibrated to incidence data. The large uncertainty during the last 14 days reflects the lack of available data due to the time period between infection, symptoms onset and hospitalisation. Therefore we omit the 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, 2020-08-10

Region	Total	Symptomatic	No. confirmed	Fraction reported	Min. fraction
Norway	38591 (34058; 43903)	24659 (21645; 27870)	9682	25%	22%
Agder	2634 (2057; 3299)	1697 (1329; 2104)	358	14%	11%
Innlandet	2538 (2001; 3213)	1627 (1288; 2063)	528	21%	16%
Møre og Romsdal	1988 (1566; 2603)	1294 (1015; 1660)	165	8%	6%
Nordland	1174 (805; 1685)	750 (531; 1064)	138	12%	8%
Oslo	5894 (4933; 6898)	3630 (3068; 4251)	3122	53%	45%
Rogaland	3966 (3071; 4834)	2501 (1956; 3032)	485	12%	10%
Troms og Finnmark	1717 (1173; 2524)	1114 (768; 1568)	300	17%	12%
Trøndelag	2301 (1576; 3298)	1469 (1016; 2093)	580	25%	18%
Vestfold og Telemark	2709 (2115; 3579)	1729 (1334; 2248)	328	12%	9%
Vestland	4370 (3515; 5350)	2768 (2237; 3345)	943	22%	18%
Viken	9300 (7898; 10662)	6080 (5114; 6954)	2735	29%	26%

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 (17 August)	2 weeks prediction (24 August)	3 weeks prediction (31 August)
Norway	84 (1-303)	100 (0-407)	124 (0-615)
Agder	5 (0-22)	7 (0-24)	8 (0-39)
Innlandet	8 (0-27)	9 (0-44)	11 (0-58)
Møre og Romsdal	4 (0-18)	5 (0-24)	7 (0-40)
Nordland	3 (0-16)	4 (0-26)	5 (0-31)
Oslo	14 (0-53)	16 (0-71)	19 (0-104)
Rogaland	7 (0-28)	8 (0-35)	10 (0-43)
Troms og Finnmark	3 (0-14)	4 (0-18)	5 (0-31)
Trøndelag	9 (0-31)	10 (0-46)	13 (0-65)
Vestfold og Telemark	8 (0-28)	9 (0-39)	11 (0-66)
Vestland	9 (0-39)	11 (0-39)	13 (0-58)
Viken	23 (0-86)	27 (0-131)	32 (0-196)

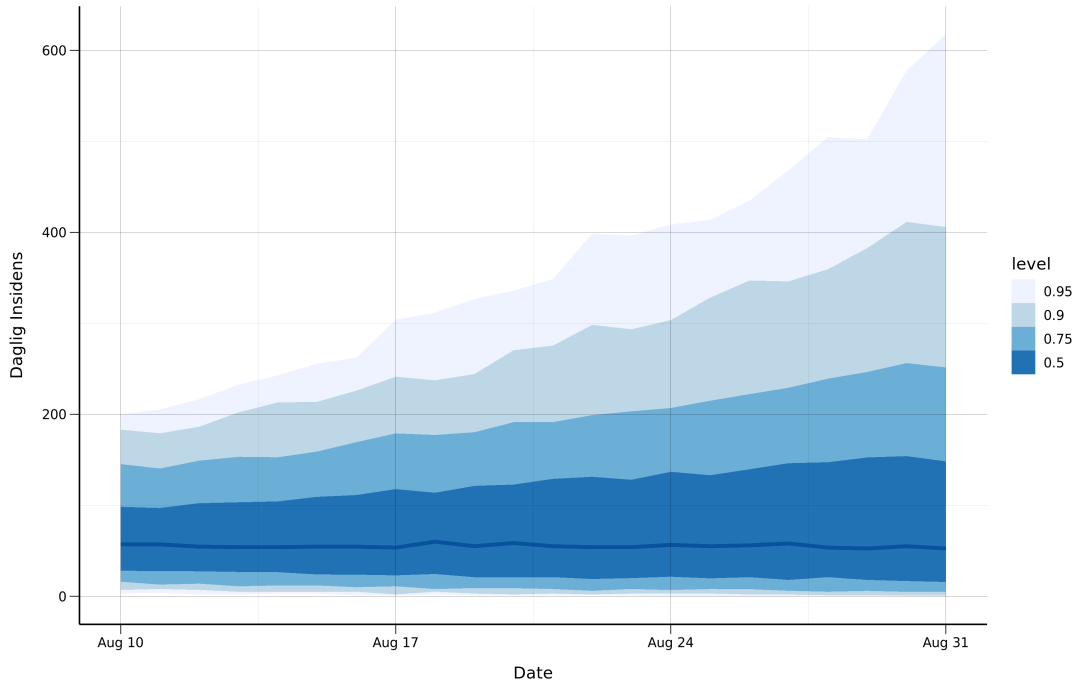

Figure 6: Predicted incidence (asymptomatic and symptomatic) for Norway per day, with confidence intervals.

The table 4 shows the probability that the bi-weekly cumulative incidence for each county exceeds 20 cases per 100.000 population.

Table 4: 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	0.38
Innlandet	0.44
Møre og Romsdal	0.26
Nordland	0.24
Oslo	0.46
Rogaland	0.33
Troms og Finnmark	0.22
Trøndelag	0.38
Vestfold og Telemark	0.40
Vestland	0.33
Viken	0.46

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 5.

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

Region	1 week prediction (17 August)	2 weeks prediction (24 August)	3 weeks prediction (31 August)
Norge	22 (4-48)	25 (1-71)	29 (1-99)
Agder	1 (0-7)	2 (0-7)	2 (0-7)
Innlandet	2 (0-9)	3 (0-12)	3 (0-12)
Møre og Romsdal	1 (0-5)	1 (0-6)	1 (0-7)
Nordland	1 (0-4)	1 (0-6)	1 (0-6)
Oslo	3 (0-11)	3 (0-11)	4 (0-13)
Rogaland	1 (0-6)	1 (0-6)	2 (0-9)
Troms og Finnmark	1 (0-6)	1 (0-5)	1 (0-7)
Trøndelag	2 (0-8)	2 (0-9)	3 (0-11)
Vestfold og Telemark	2 (0-8)	3 (0-10)	3 (0-11)
Vestland	2 (0-7)	3 (0-9)	3 (0-14)
Viken	5 (0-15)	6 (0-18)	7 (0-28)

Yesterday's real value for Norway: 15

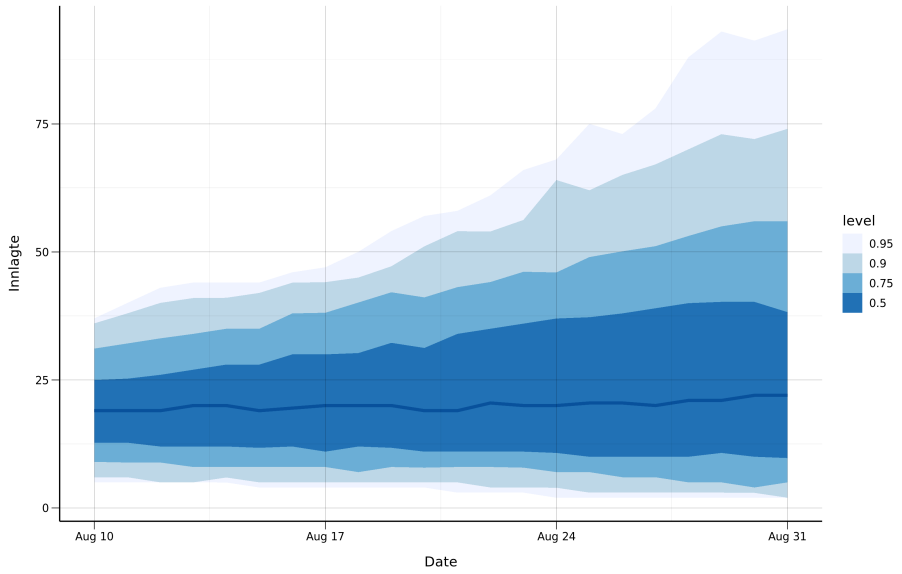

Figure 7: Predicted daily number of COVID-19 patients in hospital in Norway (95% confidence intervals and interquartile range), next three weeks, including patients ventilator treatment.

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 6.

Table 6: Number of ICU beds occupied by Covid-19 patients.

Region	1 week prediction (17 August)	2 weeks prediction (24 August)	3 weeks prediction (31 August)
Norge	5 (1-11)	6 (0-15)	7 (0-22)
Agder	0 (0-2)	0 (0-2)	0 (0-2)
Innlandet	1 (0-3)	1 (0-3)	1 (0-3)
Møre og Romsdal	0 (0-2)	0 (0-2)	0 (0-2)
Nordland	0 (0-1)	0 (0-2)	0 (0-2)
Oslo	1 (0-3)	1 (0-3)	1 (0-4)
Rogaland	0 (0-2)	0 (0-2)	0 (0-2)
Troms og Finnmark	0 (0-2)	0 (0-1)	0 (0-1)
Trøndelag	0 (0-3)	1 (0-3)	1 (0-3)
Vestfold og Telemark	1 (0-3)	1 (0-3)	1 (0-3)
Vestland	0 (0-2)	1 (0-2)	1 (0-3)
Viken	1 (0-4)	1 (0-4)	2 (0-7)

Yesterday's real value for Norway: 2

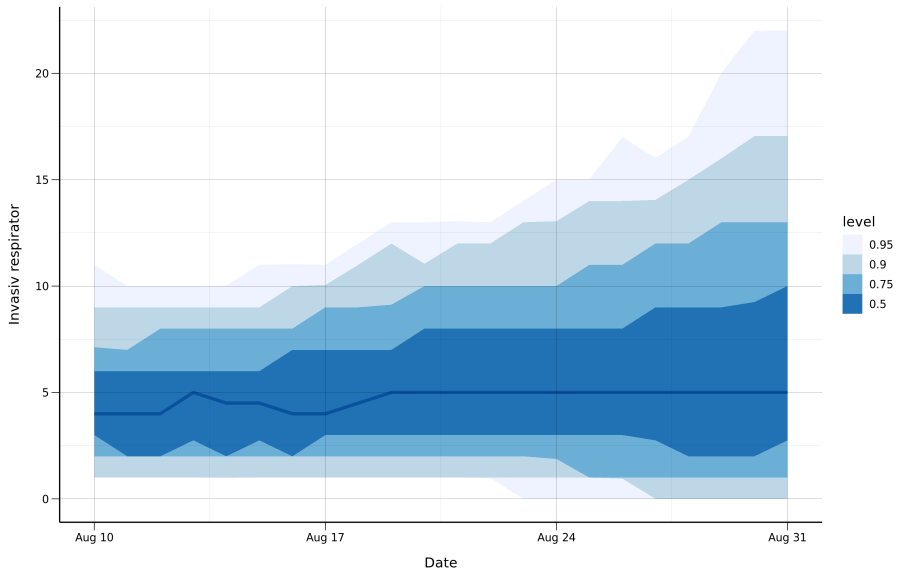

Figure 8: Predicted daily number of COVID-19 patients in ventilator treatment in Norway (95% confidence intervals and interquartile range), next three weeks.

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 the next three weeks, aggregated to the whole of Norway, see figure 9 and table 7.

Table 7: 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, 17 August	Mean, 24 August	Mean, 31 August	low CI, 31 August	high CI, 31 August
Norway	473	564	694	3	3097
Agder	27	33	40	0	185
Innlandet	39	46	56	0	263
Møre og Romsdal	20	25	33	0	175
Nordland	15	19	24	0	152
Oslo	75	89	104	1	473
Rogaland	35	41	52	0	207
Troms og Finnmark	14	17	21	0	161
Trøndelag	45	53	65	0	294
Vestfold og Telemark	38	46	58	0	273
Vestland	47	57	71	0	295
Viken	127	150	180	0	807

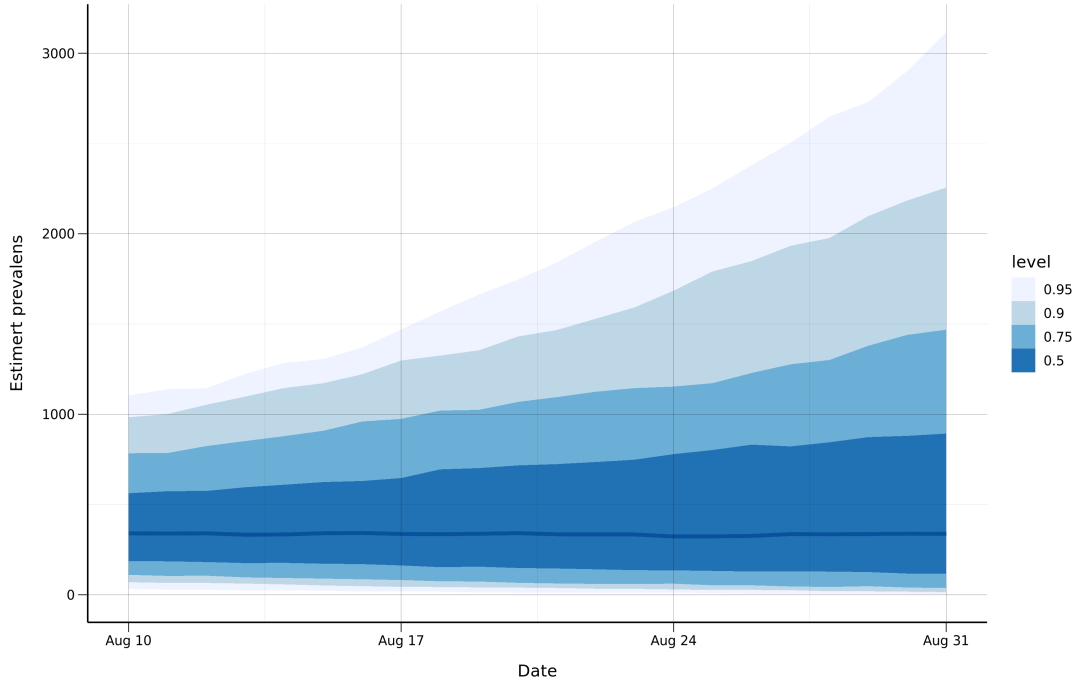

Figure 9: Predicted daily prevalence of asymptomatic, presymptomatic and symptomatic individuals, aggregated, whole Norway, (95% confidence interval).

7 Predicting prevalence on municipality level

The model is predicting prevalence on municipality level. Absolute prevalence and trend from last week are shown in figure 10. According to the mean of our simulations, today's prevalence in 82 municipalities is estimated to be equal or larger than 1.0.

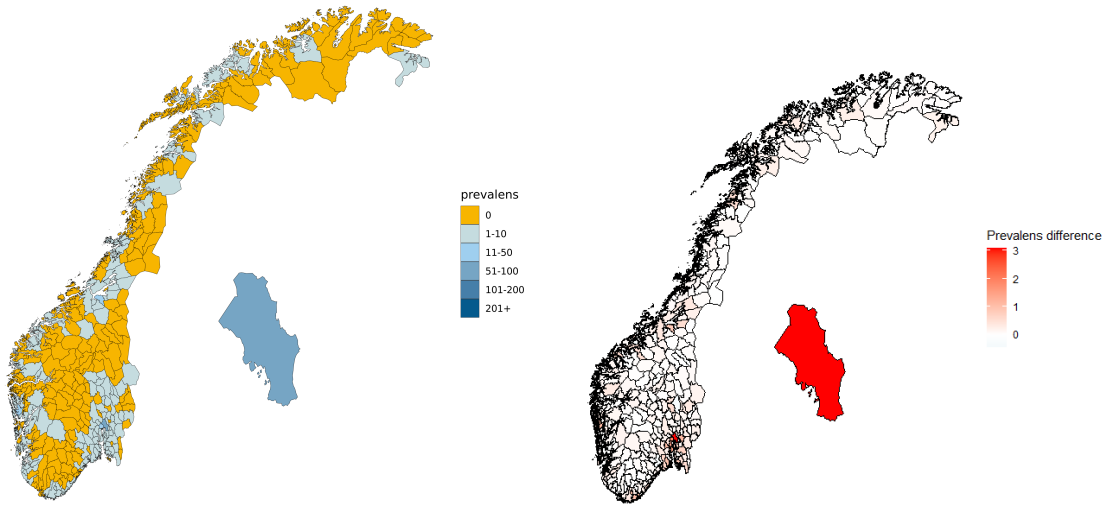

Figure 10: (Left) Map of predicted prevalence. Number of infectious individuals (asymptomatic plus presymptomatic plus symptomatic) today in each municipality. (Right) Prevalence difference compared to the previous week. Decreasing trends are shown in blue.

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).

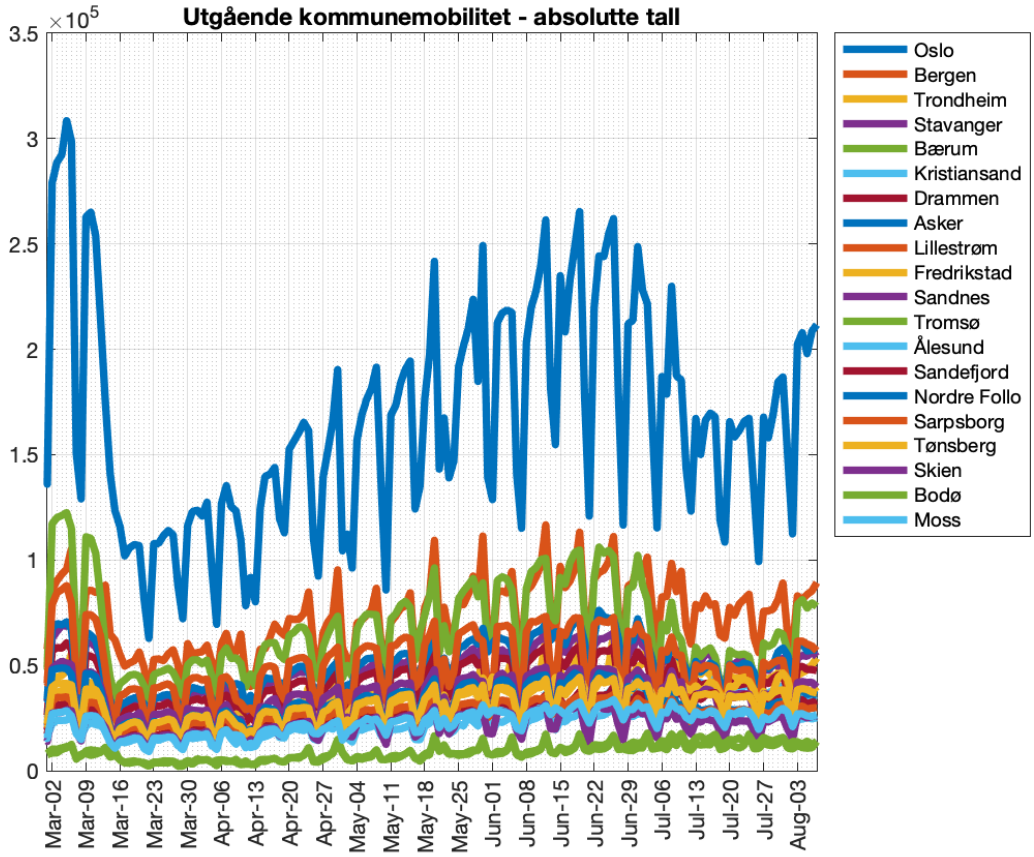

Figure 11: Inter-municipality mobility from week 10 until today.

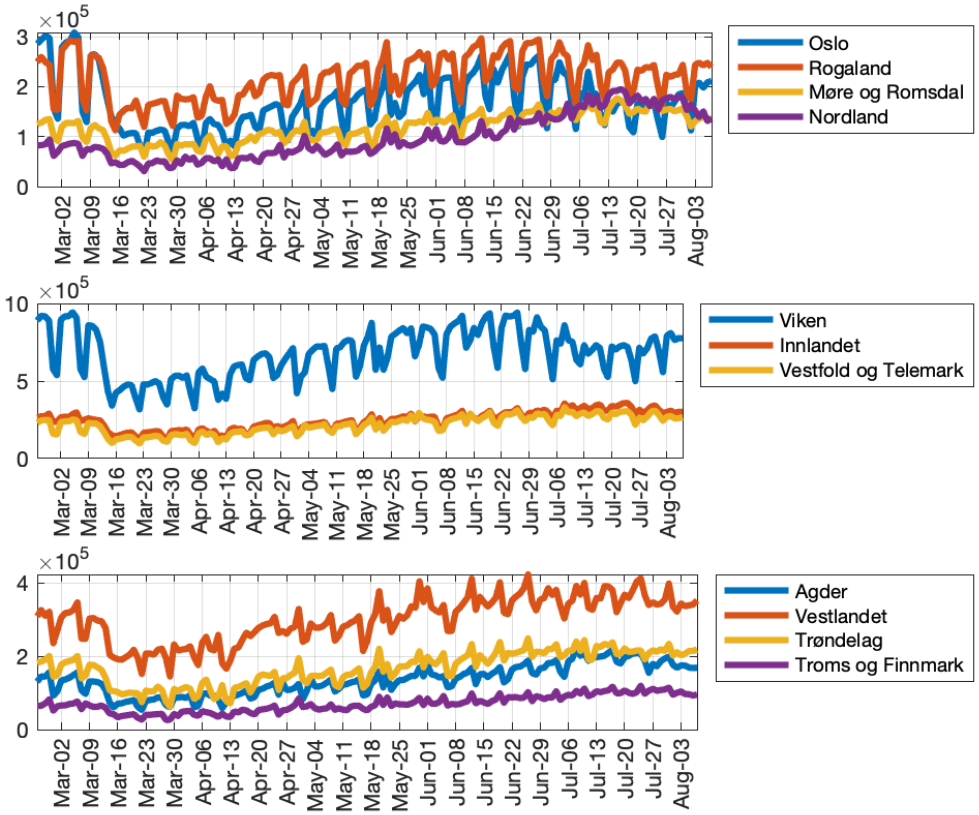

Figure 12: Inter-county mobility from week 10 until today.

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 8, and for counties see Table 9.

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

	29 Jul 2020 Onsdag	30 Jul 2020 Torsdag	31 Jul 2020 Fredag	01 Aug 2020 Lørdag	02 Aug 2020 Søndag	03 Aug 2020 Mandag	04 Aug 2020 Tirsdag	05 Aug 2020 Onsdag	06 Aug 2020 Torsdag	07 Aug 2020 Fredag
Hele Norge	2.4%	0.2%	-3.6%	-34.5%	-26.8%	-3.0%	-0.8%	2.5%	5.0%	4.6%
Oslo	42.0%	40.2%	37.5%	1.2%	12.9%	27.5%	28.0%	32.3%	32.4%	29.2%
Bergen	17.7%	15.1%	15.4%	1.5%	1.0%	3.2%	9.9%	10.4%	10.9%	15.2%
Trondheim	1.0%	3.2%	5.2%	-23.9%	-16.5%	-6.0%	-4.6%	-6.0%	-5.0%	3.9%
Stavanger	27.0%	27.7%	23.3%	-4.2%	-6.4%	15.1%	17.3%	21.3%	17.7%	22.3%
Bærum	50.2%	46.2%	43.6%	4.7%	14.8%	32.6%	32.4%	36.3%	35.0%	32.2%
Kristiansand	-26.3%	-26.3%	-12.0%	-66.9%	-98.7%	-27.0%	-23.4%	-17.9%	-12.7%	0.0%
Drammen	24.8%	25.2%	20.7%	-3.7%	-2.2%	13.8%	15.3%	17.4%	20.9%	17.5%
Asker	27.0%	20.2%	13.1%	-27.1%	-19.2%	13.0%	13.6%	17.7%	19.0%	14.3%
Lillestrøm	40.4%	40.4%	34.1%	10.1%	15.3%	21.9%	27.2%	30.1%	32.7%	28.3%
Fredrikstad	0.7%	-16.0%	-27.8%	-75.9%	-55.5%	-5.3%	-7.7%	4.2%	1.6%	-10.0%
Sandnes	30.5%	29.5%	23.7%	3.8%	-6.4%	14.0%	16.0%	19.4%	17.8%	21.0%
Tromsø	-17.7%	-17.7%	-21.9%	-96.9%	-30.9%	-42.7%	-29.1%	-5.7%	-0.3%	-11.3%
Ålesund	-9.9%	-13.5%	-4.3%	-18.9%	-13.1%	-9.5%	-2.6%	-5.8%	-2.4%	2.6%
Sandefjord	-5.8%	-11.0%	-16.3%	-50.0%	-49.0%	-9.9%	-8.5%	-1.7%	0.7%	-3.8%
Nordre Follo	35.0%	32.6%	28.7%	-2.2%	6.9%	22.2%	21.0%	25.7%	24.5%	21.9%
Sarpsborg	19.4%	11.4%	4.2%	-25.6%	-13.6%	8.6%	11.9%	15.5%	15.3%	8.8%
Tønsberg	10.7%	8.2%	5.6%	-24.8%	-19.0%	3.3%	5.8%	6.9%	9.9%	9.2%
Skien	11.6%	11.1%	11.5%	-8.4%	-7.1%	3.4%	5.3%	9.5%	11.1%	7.5%
Bodø	-31.5%	-31.3%	-36.2%	-112.0%	-98.7%	-33.8%	-24.2%	-29.6%	-7.9%	-20.4%
Moss	9.4%	0.7%	-13.7%	-57.0%	-41.1%	0.1%	1.8%	6.5%	9.4%	-2.0%

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

	29 Jul 2020 Onsdag	30 Jul 2020 Torsdag	31 Jul 2020 Fredag	01 Aug 2020 Lørdag	02 Aug 2020 Søndag	03 Aug 2020 Mandag	04 Aug 2020 Tirsdag	05 Aug 2020 Onsdag	06 Aug 2020 Torsdag	07 Aug 2020 Fredag
Hele Norge	2.4%	0.2%	-3.6%	-34.5%	-26.8%	-3.0%	-0.8%	2.5%	5.0%	4.6%
Oslo	42.0%	40.2%	37.5%	1.2%	12.9%	27.5%	28.0%	32.3%	32.4%	29.2%
Rogaland	23.4%	22.4%	16.5%	-6.2%	-13.8%	10.8%	12.5%	17.0%	14.6%	17.9%
Møre og Romsdal	-18.2%	-20.8%	-18.8%	-42.6%	-34.6%	-9.2%	-6.8%	-9.4%	-6.7%	-2.7%
Nordland	-104.7%	-106.8%	-106.4%	-150.2%	-117.3%	-87.5%	-66.9%	-74.7%	-50.3%	-59.9%
Viken	22.5%	18.0%	13.1%	-19.8%	-6.0%	11.4%	11.8%	16.7%	17.7%	14.6%
Innlandet	-16.2%	-16.7%	-15.4%	-30.0%	-17.3%	-12.6%	-14.4%	-10.0%	-5.3%	-0.9%
Vestfold og Telemark	-12.4%	-19.8%	-25.0%	-63.7%	-53.4%	-14.6%	-14.3%	-7.5%	-3.5%	-7.6%
Agder	-32.2%	-30.1%	-27.6%	-65.8%	-73.2%	-30.5%	-27.7%	-19.7%	-12.9%	-8.2%
Vestlandet	-7.5%	-8.8%	-14.8%	-35.3%	-29.9%	-12.5%	-5.7%	-6.1%	-4.5%	-1.5%
Trøndelag	-17.3%	-12.9%	-16.5%	-44.9%	-42.8%	-14.0%	-12.6%	-14.7%	-12.9%	-8.8%
Troms og Finnmark	-54.4%	-53.8%	-49.1%	-71.1%	-40.1%	-58.4%	-46.1%	-37.9%	-30.7%	-24.9%

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 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 $R_4 > 1$ which result in 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.

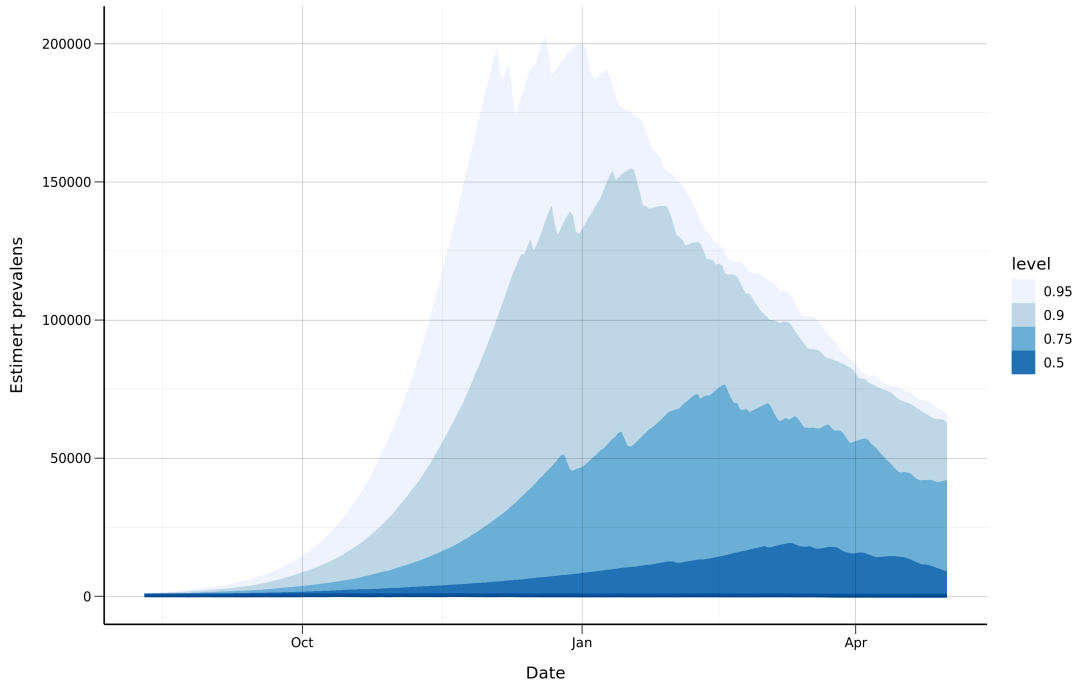

Figure 13: Predicted prevalence of COVID-19 based on 200 candidate models where the reproductive number used for simulation varies according to the estimated uncertainty.

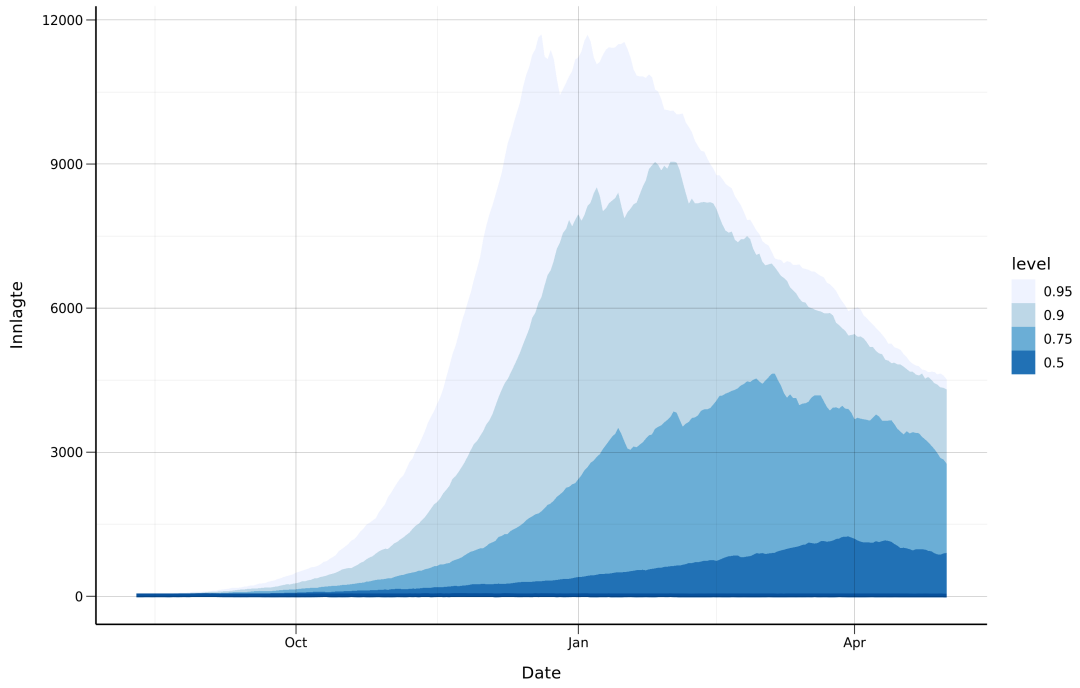

Figure 14: Predicted number of COVID-19 patients in hospital based on 200 candidate models where the reproductive number used for simulation varies according to the estimated uncertainty.

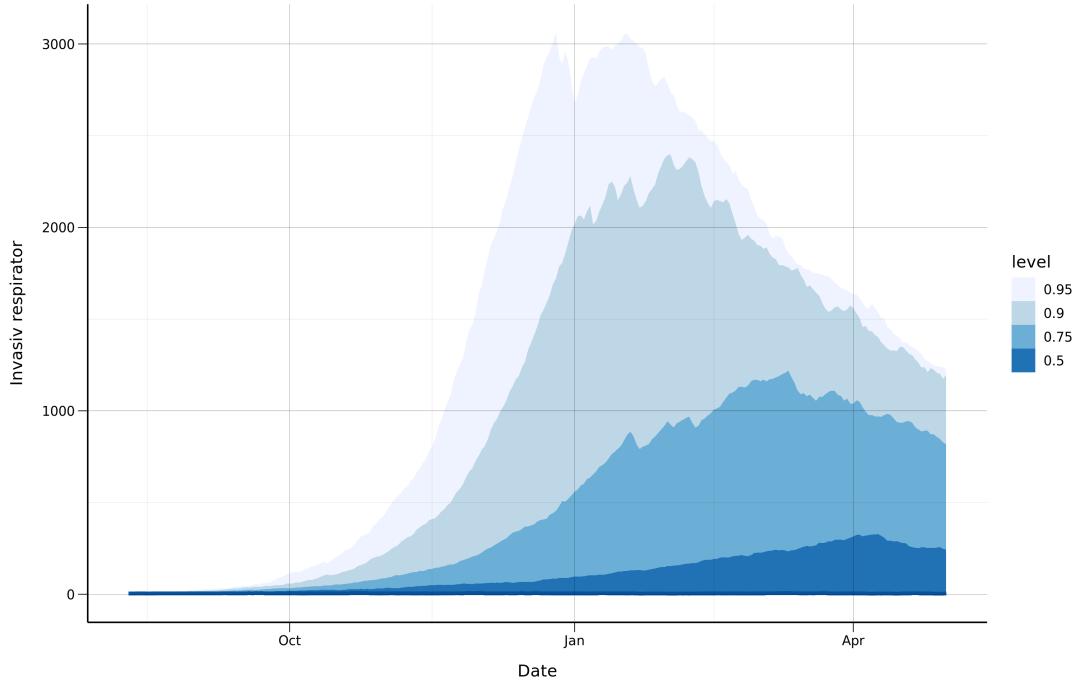

Figure 15: Predicted prevalence of COVID-19 patients needing ventilator treatment based on 200 candidate models where the reproductive number used for simulation varies according to the estimated uncertainty.

We estimate the probability of a surge capacity need above **1000 ICU** beds to be equal to **21 %**.The probability of a surge capacity need above **500 ICU** beds is **24.5 %**.

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 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 16, and the daily number of patients with ventilator treatment, figure 17. 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.

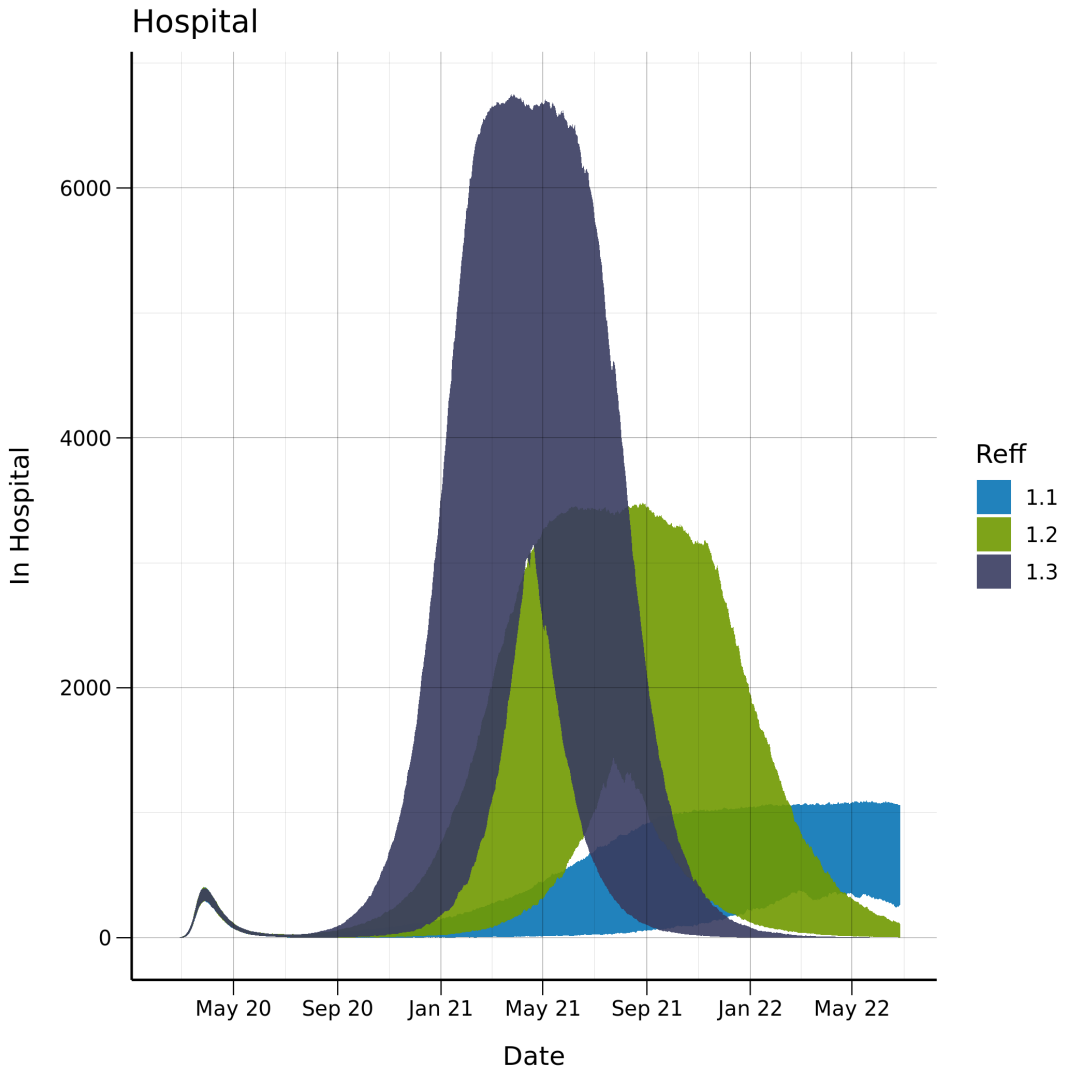

Figure 16: Predicted number of COVID-19 patients in hospital based on three different scenarios with R effective equal to 1.1, 1.2 and 1.3.

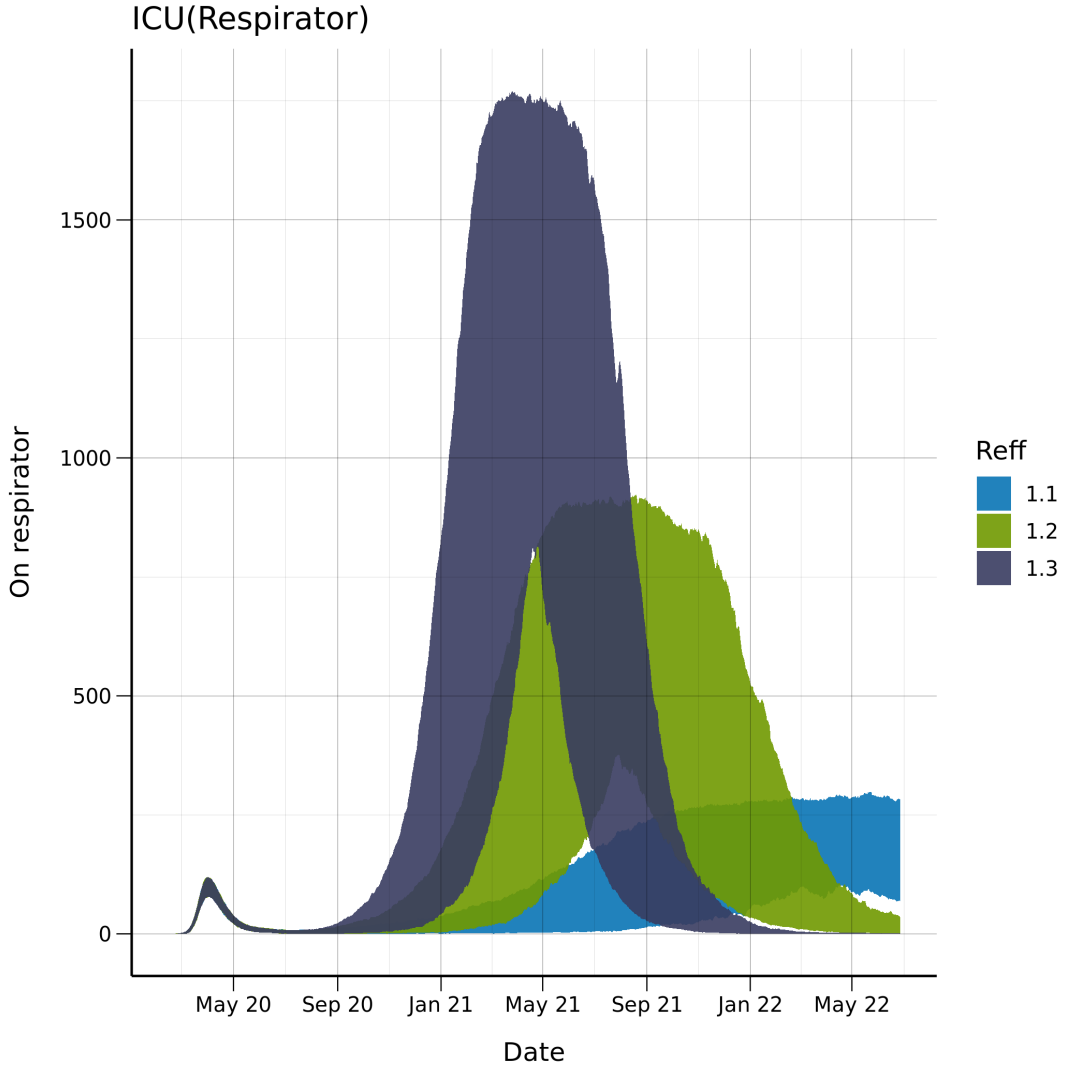

Figure 17: Predicted number of COVID-19 patients needing ventilator treatment based on three different scenarios with R effective equal to 1.1, 1.2 and 1.3.

Table 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	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[1] at peak	802(660 - 867)	2.560(2.440 - 2.680)	4.990(4.800 - 5.130)
Hospital[2] 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)

[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 18.

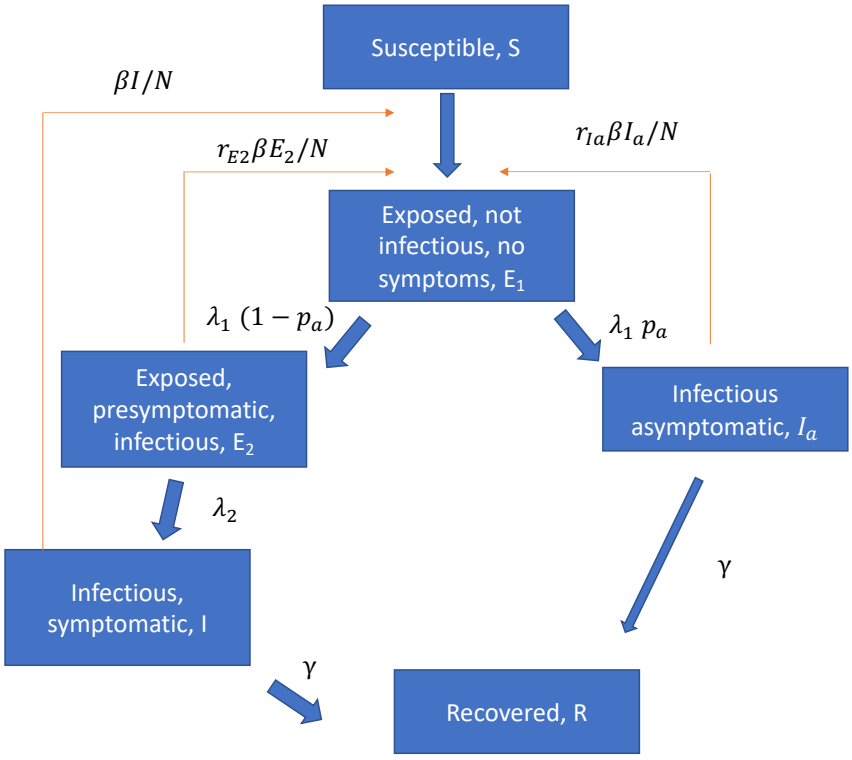

Figure 18: Schematic overview of the model.

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 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. 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, 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, and a fifth 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. We use a method called sequential ABC which tests thousands of combinations of R_0, R_1, R_2, R_3, R_4 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.

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 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 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.

[3] https://www.medrxiv.org/content/10.1101/2020.03.11.20033555v1
[4] 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 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, 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.

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.

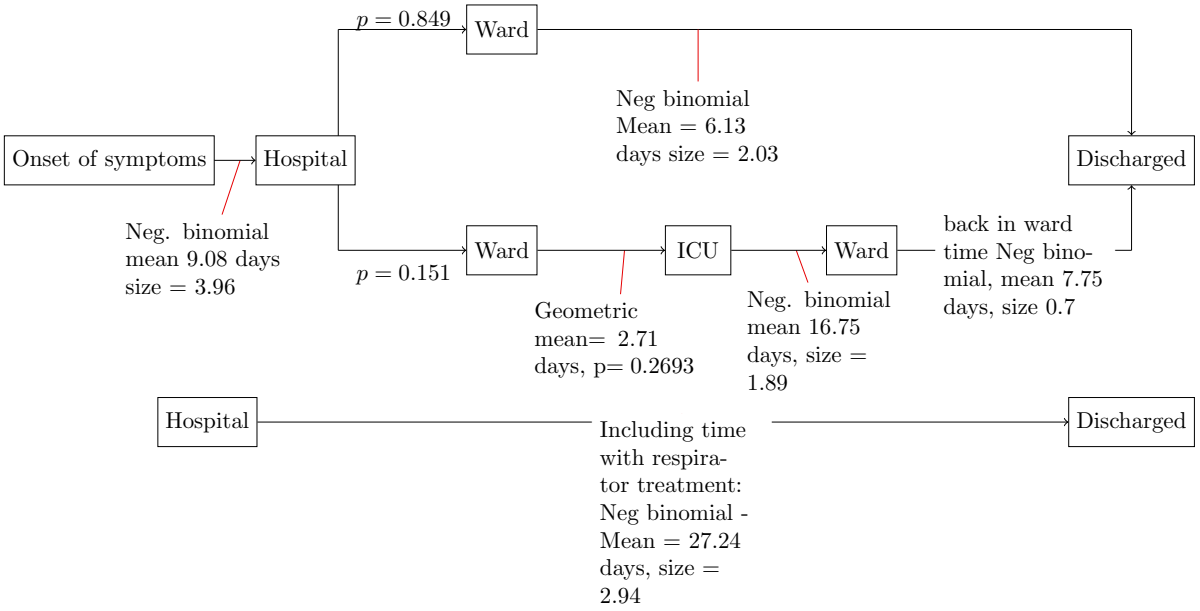

Figure 19: Hospital assumptions and parameters

Table 11: Assumptions I

Assumptions	Mean	Distribution	Reference
Seeding			
Scaling factor on imported cases	Min. 1.10 1st Qu. 1.66 Median 2.06 Mean 2.02 3rd Qu. 2.37 Max. 3.26	random	Calibrated to hospitalisations
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
R_0, until March 14	Min. 1.90 1st Qu. 2.43 Median 2.63 Mean 2.69 3rd Qu. 2.93 Max. 3.49	random	Calibrated to hospitalisations
R_1, from 15 March until 19 April	Min. 0.43 1st Qu. 0.52 Median 0.54 Mean 0.54 3rd Qu. 0.56 Max. 0.65	random	Calibrated to hospitalisations
R_2, from 20 April until 10 May	Min. 0.34 1st Qu. 0.57 Median 0.66 Mean 0.66 3rd Qu. 0.75 Max. 1.06	random	Calibrated to hospitalisations
R_3, from 11 May until 30 June	Min. 0.37 1st Qu. 0.70 Median 0.80 Mean 0.79 3rd Qu. 0.89 Max. 1.10	random	Calibrated to hospitalisations
R_4, from 1 July until today	Min. 0.16 1st Qu. 0.83 Median 0.99 Mean 0.98 3rd Qu. 1.17 Max. 1.80	random	Calibrated to hospitalisations

Table 12: Assumptions II

Assumptions	Mean	Distribution	Reference
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	 0.2% 0.2% 0.6% 1.3% 1.7% 3.5% 7.1% 11.3% 27%	Fixed	Saljie et al 2020 corrected for: % of elderly living in of elderly living in Norway (last two age groups).
% hospitalized patients requiring ICU Feb - March April May -	 20% 10% 15.1 %	Fixed	Estimated from "Beredskapsregistret BeredtC19"
Overall hospitalization risk	3.9%	Fixed	Saljie et al 2020 (adapted to Norwegian population)
Mobile phone mobility			
Until August 7th	Measured Telenor mobility		
Data used in the predictions	August 7	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 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 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.

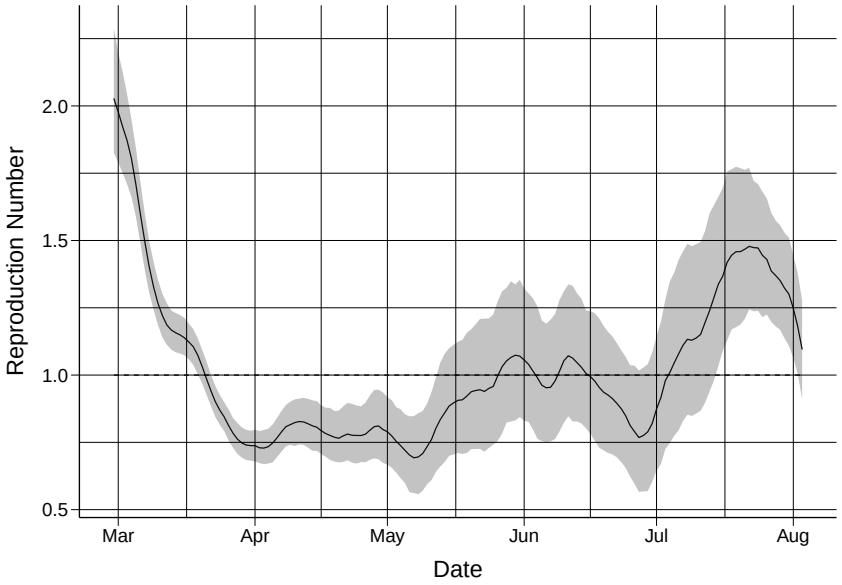

Figure 20: Reproduction number estimated using the R package EpiEstim.

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