NIPH
Norwegian Institute of Public Health

Situational awareness and forecasting for Norway

FHI COVID-19 modelling team

Week 37, 15 September 2021

Highlights:

- **National epidemiological situation:** According to our changepoint model, the estimated effective reproduction number is 0.9 (median, 95% CI 0.81 - 1), on average since 27 August. Before that, from 5 August to 26 August, the estimated effective reproduction number was 1.38 (median, 95% CI 1.3-1.47). The SMC model estimates the 7-days averaged effective reproduction number during week 36 to be 0.76 (mean, 95% CI 0.61-0.95). The Epiestim model, which uses only test data, estimates the effective reproduction number as 0.9 (95% CI 0.87-0.93). We conclude that the epidemic is decreasing in recent weeks with an effective R below 1, of about 0.9. We note that our estimates presently have greater uncertainty than indicated by the uncertainty intervals due to a changing test practice in Norway. In addition, because of a data registration irregularity, the hospital data have not been fully updated the last weeks, which may impact our results.

  Since the start of the epidemic, we estimate that in total, 305.000 (95% CI 290.000- 320.000) individuals in Norway have been infected. The current estimate of the detection probability is approximately 63%. However, this estimate cannot be trusted anymore because it is based on the number of total tests performed. This quantity is presently unknown because of the massive use of home tests, where negative tests remain unreported.

- **National forecasting:** In one week, on 19 September, we estimate approximately 1700 new cases per day (median; 95% CI 1300-2100), and a prevalence (total number of presently infected individuals in Norway) of 11000 (median; 95% CI 8900 -13000). The number of COVID-19 patients in hospital (daily prevalence) on 19 September is estimated to be 85 (median 95% CI 69-101), and the number of patients on ventilator treatment is estimated to be 13 (median 95% CI 7-19). The corresponding predictions for hospital load in three weeks (3 October) are 80 (95% CI 59-105) admitted patients and 13 (95% CI 6-21) on ventilator treatment. Regarding the age profile of these predictions in three weeks (Table 4), we estimate that the age-specific hospitalisation of individuals below 30 years is very low (¡10). We also estimate no significant differences in the number of admitted patients by 10-year age groups above 30 years.

  These predictions are, as usual, under the assumption that nothing is changed since today, so no changes in interventions, no changes in mobility and in people's behaviour, no changes in future hospitalisation risks, even though the hospitalisation risks are expected to decrease further in the short term because of increased number of vaccinations. Due to intense vaccination in the last weeks in Norway, vaccine-derived immunity in the population will increase in the coming weeks, especially in younger adults. We have not been able to incorporate this effect into our three weeks predictions because it is not yet visible in the data.

  Long-term scenarios assuming the current effective reproduction numbers, and a seasonal effect of 50%, suggest a peak around March for R=0.9, with a peak prevalence of approximately 1000 hospital admissions. Assuming a 25% seasonal effect, the model suggests the peak of infections would occur earlier around October with a maximum of 100-200 people in hospital at the peak. The scenarios include vaccination of 12-15 years old children, with one dose. Note that the scenarios do not represent the likely future course of the epidemic. In the event of a severe epidemic worsening, the introduction of mitigation measures and behavioural changes in the population can limit or

reverse the wave. In both constant and control scenarios, because of vaccination, the number of people under ventilator treatment will not exceed the capacity of 500 beds.

- **Regional epidemiological situation and forecasting:** We are improving our regional changepoint model and therefore cannot provide results from it. The reason is that the situation is highly unstable and transient, due to new testing strategies, the conclusion of the vacation travelling, the effect of the delta variant on hospitalisations and the rapid vaccination campaigns. The changepoint model assumes equilibrium over several weeks (currently 5), which is not a correct assumptions at this point. The regional SMC model instead estimates a daily reproduction number and is therefore less affected by such instabilities, at a cost of large uncertainties.

  In the regional SMC model, the estimate of the effective reproduction number in the week before September 6 for Oslo is about 1, with a wide CI (0.5-1.8), for Viken also about 1 (0.6-1.6). All other counties have estimates below 1.

  Epiestim uses a very simple model and only positive test data, not corrected for imported cases from abroad, and no hospital data. The estimated reproduction numbers are: Oslo 0.9 (0.87-0.94), Viken 0.97 (0.94 - 1.0) and Vestfold og Telemark 1.08 (0.96-1.2). For the other counties, the estimates are below 1.

- **Telenor mobility data and the number of foreign visitors:** Inter-municipality mobility levels are stable in all counties. The number of foreign visitors to Norway has reached a peak and appears to be declining, with the ending of the vacation travel. Foreign roamers from from Poland and Latvia appear to have stabilised at high levels.

What this report contains:

This report presents results based on a mathematical infectious disease model describing the geographical spread of COVID-19 in Norway. We use a metapopulation model (MPM) for situational awareness and short-term forecasting and an individual-based model (IBM) for long-term predictions. The metapopulation model (MPM) consists of three layers:

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

The MPM 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. We run three different models built on the same structure indicated above: (1) a national changepoint model, (2) a regional changepoint model and (3) a national Sequential Monte Carlo model, named SMC model.

How we calibrate the model: The national changepoint model is fitted to Norwegian COVID-19 hospital incidence data from March 10 until yesterday and data on the laboratory-confirmed cases from May 1 until yesterday. We do not use data before May 1, as the testing capacity and testing criteria were significantly different in the early period.
Note that the the national changepoint model results are not a simple average or aggregation of the results of the regional changepoint model because they use different data. The estimates and predictions of the regional model are more uncertain than those of the national model. The regional model has more parameters to be estimated and less data in each county; lack of data limits the number of changepoints we can introduce in that model. In the regional changepoint model, each county has its own changepoints and therefore a varying number of reproduction numbers. Counties where the data indicate more variability have more changepoints.
The national SMC model is also calibrated to the hospitalisation incidence data (same data as described above) and the laboratory-confirmed cases.

Telenor mobility data: The mobility data account for the changes in the movement patterns between municipalities that have occurred since the start of the epidemic.

How you should interpret the results: 3-week-ahead predictions and long-term scenarios
We provide both 3-week-ahead predictions and long-term scenarios. These are simulations of the disease spread into the future, under specific assumptions.

In the 3-week-ahead predictions, we assume that all parameters are as today, and simulate disease spread 3-weeks-ahead in time. Hence, these predictions are conditional on the current situation, and specifically on the most recently estimated reproduction number. The 3-week-ahead predictions thus do not take into account changes in transmissibility that are not yet captured by the available data, for example due to the delay between transmission and positive test and/or transmission and hospitalisation. Hence one of the conditions for the predictions to be valid is that the intervention policies do not change significantly in the next weeks. Hence, it does not make sense to evaluate or use the predictions if there are big changes in factors like

- new interventions
- relaxation of interventions
- a combination of new interventions and relaxations
- a significant change in vaccination coverage
- new variants with new properties
- a significant change in the contact behaviour of individuals.

As these factors are not likely to stay constant in the long-term future, we do not produce predictions for longer than three weeks ahead in time. Hence, our 3-week-ahead predictions are predictions of what may happen in the future, if there were no significant changes in the assumptions.

In addition to the short-term predictions, we also produce different long-term scenarios. Scenarios are not predictions of how we think the future pandemic will evolve. The scenarios are based on different hypothetical assumptions, and hence cannot be validated against what we later actually observe in the data. They are not meant to be, and hence should not be interpreted as, what we believe to be the most probable future outcome.

The purpose of the scenarios is manifold. Scenarios can contribute to situational awareness, and as information in decision making and future preparedness planning. Scenarios can be used to provide a better understanding of possible future disease spread, under specific assumptions. The assumptions of the scenarios may also sometimes be unrealistic. For example, scenarios can contribute in understanding the current situation, should we not change intervention policies in the future. This does however not mean that we believe that the intervention policies will stay constant. Scenarios can also be used to compare different intervention strategies, like comparing different vaccination strategies. **Uncertainty** The model is stochastic. To predict the probability of various outcomes, we run the model multiple times to represent the inherent randomness.

We present the results in terms of mean values, 95% credibility intervals, medians, and interquartile ranges. We emphasise that the credibility 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 associated with the hospitalisation timing relative to symptom onset, the severity of the COVID-19 infections by age, and the duration of hospitalisation and ventilator treatment in ICU. We continue to update the model assumptions and parameters following new evidence and local data as they become available. A complete list of all updates can be found at the end of this report.

Estimates of all reproductive numbers are uncertain, and we use their distribution to assure appropriate uncertainty of our predictions. Uncertainties related to the model parameters imply that the reported effective reproductive numbers should be interpreted with caution.

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

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

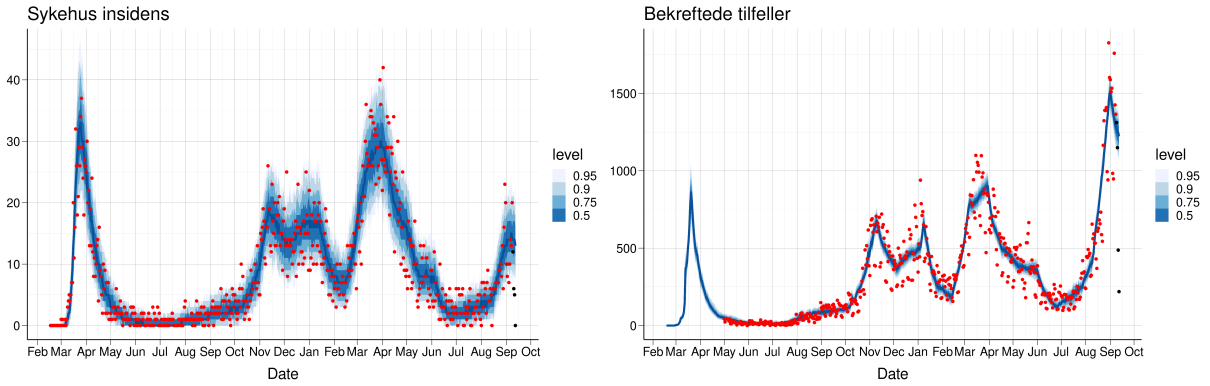
1 Estimated national reproduction numbers

Calibration of our national changepoint model to hospitalisation incidence data and test data leads to the following estimates provided in table 1. Figure 1 shows the estimated daily number of COVID-19 patients admitted to hospital (1a) and the estimated daily number of laboratory-confirmed SARS-CoV-2 cases (1b), with blue medians and interquantile 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.

Table 1: Calibration results

Reff	Period
3.21/3.22(2.71-3.77)	From Feb 17 to Mar 14
0.48/0.49(0.42-0.6)	From Mar 15 to Apr 19
0.7/0.7(0.41-0.97)	From Apr 20 to May 10
0.73/0.72(0.46-1.02)	From May 11 to Jun 30
1.16/1.16(0.62-1.62)	From Jul 01 to Jul 31
0.97/0.96(0.72-1.21)	From Aug 01 to Aug 31
0.96/0.95(0.74-1.11)	From Sep 01 to Sep 30
1.26/1.25(1.15-1.35)	From Oct 01 to Oct 25
1.29/1.3(1.14-1.49)	From Oct 26 to Nov 04
0.81/0.81(0.75-0.86)	From Nov 05 to Nov 30
1.04/1.04(1-1.1)	From Dec 01 to Jan 03
0.57/0.57(0.47-0.66)	From Jan 04 to Jan 21
0.77/0.77(0.6-0.94)	From Jan 22 to Feb 07
1.5/1.5(1.39-1.63)	From Feb 08 to Mar 01
1.04/1.04(0.99-1.09)	From Mar 02 to Mar 24
0.76/0.76(0.71-0.8)	From Mar 25 to Apr 12
0.85/0.85(0.8-0.91)	From Apr 13 to May 05
0.95/0.95(0.84-1.05)	From May 06 to May 26
0.66/0.66(0.57-0.75)	From May 27 to Jun 20
1.08/1.07(0.8-1.28)	From Jun 21 to Jul 11
0.96/0.98(0.85-1.2)	From Jul 12 to Aug 04
1.38/1.38(1.3-1.47)	From Aug 05 to Aug 26
0.9/0.9(0.81-1)	From Aug 27

Median/Mean (95% credible intervals)

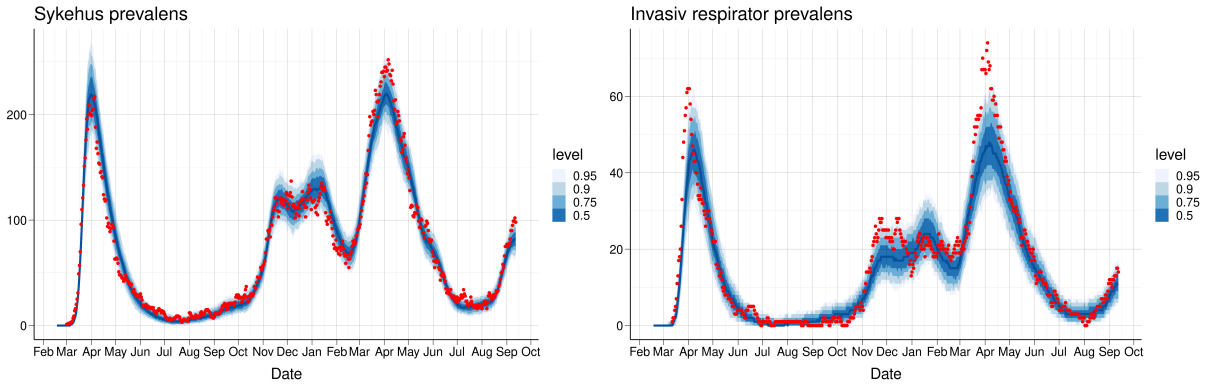


(a) Hospital admissions

(b) Test data

Figure 1: A comparison of true data (red) and predicted values (blue) for hospital admissions and test data. The last four data points (black) are assumed to be affected by reporting delay. B) Comparison of our simulated number of positive cases, with blue median and interquartile bands to the actual true number of positive cases, provided in red. The uncertainty captures the uncertainty in the calibrated parameters, in addition to the stochastic elements of our model and the variability of other model parameters. Note that we do not capture all the uncertainty in the test data–our blue bands are quite narrow. This is likely because we calibrate our model parameters on a 7-days moving average window of test data, instead of daily. This is done to avoid overfitting to random daily variation. Moving averages over 7 days are less variable than the daily data.

In figure 2, we show how our national model fits the national hospital prevalence data (2a) and the daily number of patients receiving ventilator treatment (2b). Those data sources are not used to estimate the parameters, and can therefore be seen as a validation of the model assumptions.



(a) Hospital prevalence

(b) Ventilator prevalence

Figure 2: A comparison of true data (red) and predicted values (blue) for hospital and respirator prevalence. Prevalence data is based on NIPaR and may be different to the data from Helsedirektoratet.

1.1 National SMC-model: Estimated daily reproduction numbers

In the SMC-model, we allow for estimation of a different reproduction number for each day t. To reduce spurious fluctuation, we report a 7-days moving average, $R(t)$, representing the average reproduction number for the whole week before day t. However, until March 8 we keep the reproduction number constant. By assuming a time varying reproduction number $R(t)$, we can detect changes without introducing explicit changepoints. Thus, we can easier detect unexpected changes.

The SMC model uses the daily number of new admissions to hospital and the daily number of positive and negative lab-confirmed tests, to estimate all its parameters. Because of the time between infection and the possibility to be detected as positive by a test, and because if a delay in reporting tests, the data contain information on the transmissibility until a week before the end of the data (today).

The parameters π_0 and π_1 related to the probability to detect a positive case by testing are estimated off-line.

Figure 3 shows the SMC estimate of the 7-day-average daily reproduction number $R(t)$ from the start of the epidemic in Norway and until today. In the figure we plot the 95% credibility interval and quantiles of the estimated posterior distribution of $R(t)$.

1.1 National SMC-model: Estimated daily reproduction numbers

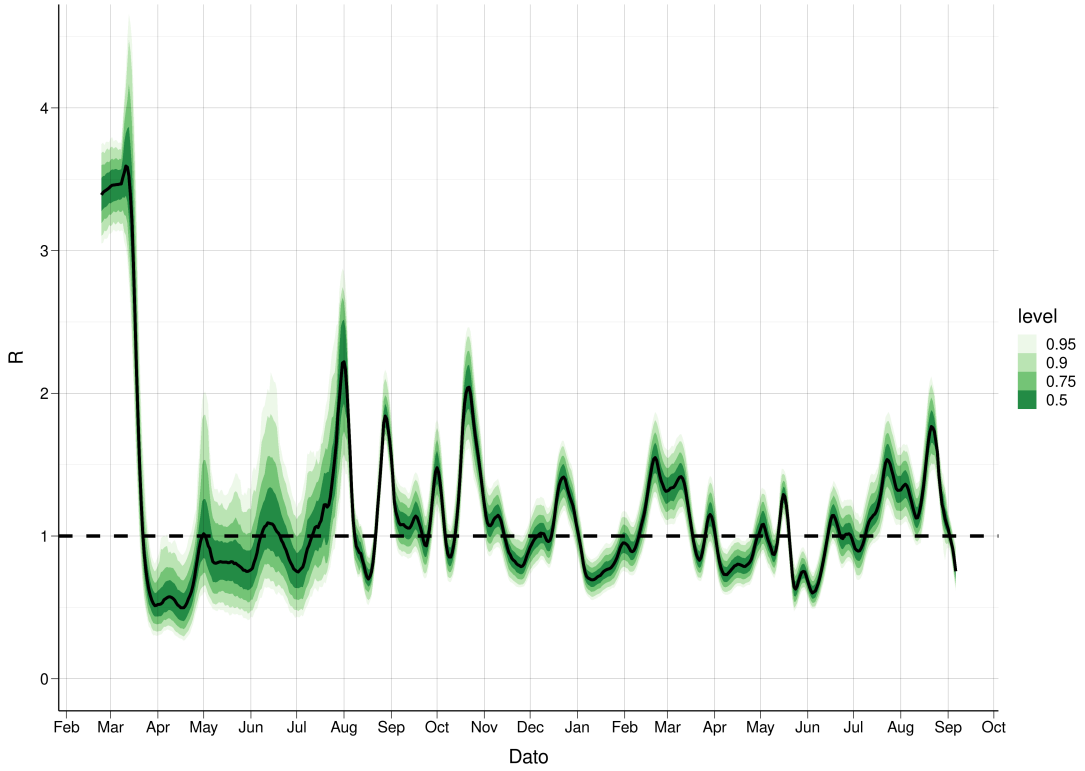


Figure 3: R(t) estimates using a Sequential Monte Carlo approach calibrated to hospitalisation incidence and test data. The large uncertainty during the last 7 days reflects the lack of available data due to the transmission delay, test delay, time between symptoms onset and hospitalisation. The green band shows the 95% posterior credibility interval. As we use test data only from 1 August, the credibility interval becomes more narrow thereafter.

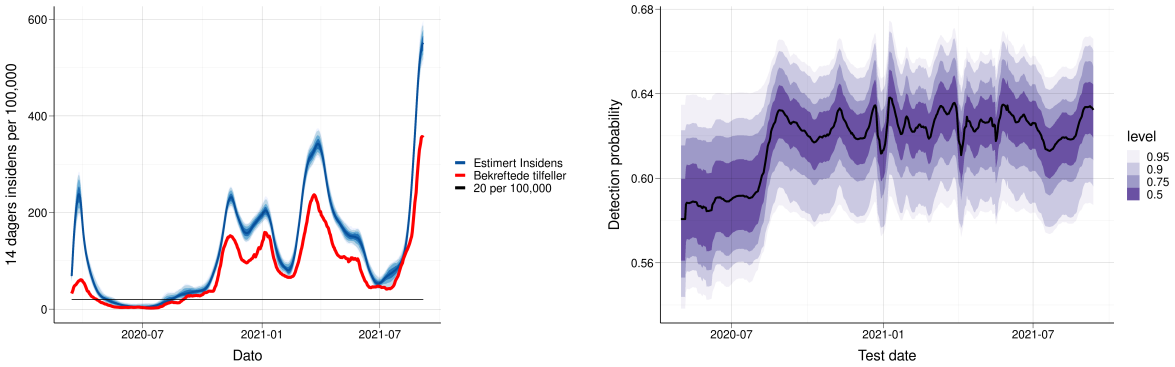
2 National estimate of cumulative (total) number of infections

The national changepoint model estimates the total number of infections and the symptomatic cases that have occurred (Table 2).
Figure 4a shows the modelled expected daily incidence (blue) and the observed daily number of laboratory-confirmed cases (red). When simulating the laboratory-confirmed cases, we also model the detection probability for the infections (both symptomatic, presymptomatic and asymptomatic), Figure 4b. There are two differences between this estimate of the detection probability and the previous one provided in figure 4a. In figure 4b, we calibrate our model to the true number of positive cases, instead of using the test data directly. Furthermore, in figure 4a we use a parametric model to estimate the detection probability that depends on the true total number of tests performed.

Table 2: Estimated cumulative number of infections, 2021-09-12

Region	Total	No. confirmed	Fraction reported	Min. fraction
Norway	305378 (290948; 320669)	169062	55%	53%

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



(a) Number of laboratory-confirmed cases vs model-based estimated number of new infected individuals

(b) Estimated detection probability for an infected case per calendar day

Figure 4

3 National 3-week predictions: Prevalence, Incidence, Hospital beds and Ventilator beds

The national changepoint model estimates the prevalence and daily incidence of infected individuals (asymptomatic, presymptomatic and symptomatic) for the next three weeks, aggregated to the whole of Norway (table 3). In addition, the table shows projected national prevalence of hospitalised patients (hospital beds) and prevalence of patients receiving ventilator treatment (ventilator beds). The projected epidemic and healthcare burden are illustrated in figure 5.

Table 3: Estimated national prevalence, incidence, hospital beds and ventilator beds. Median/Mean (CI)

	1 week prediction (Sep 19)	2 week prediction (Sep 26)	3 week prediction (Oct 03)
Prevalence	11051/11048 (8900-13391)	10139/10081 (7366-13204)	9319/9246 (6275-12999)
Daily incidence	1704/1713 (1267-2129)	1560/1524 (1100-2109)	1436/1430 (901-2116)
Hospital beds	85/85 (69-101)	85/85 (64-109)	80/79 (59-105)
Ventilator beds	13/12 (7-19)	13/13 (7-20)	13/12 (6-21)

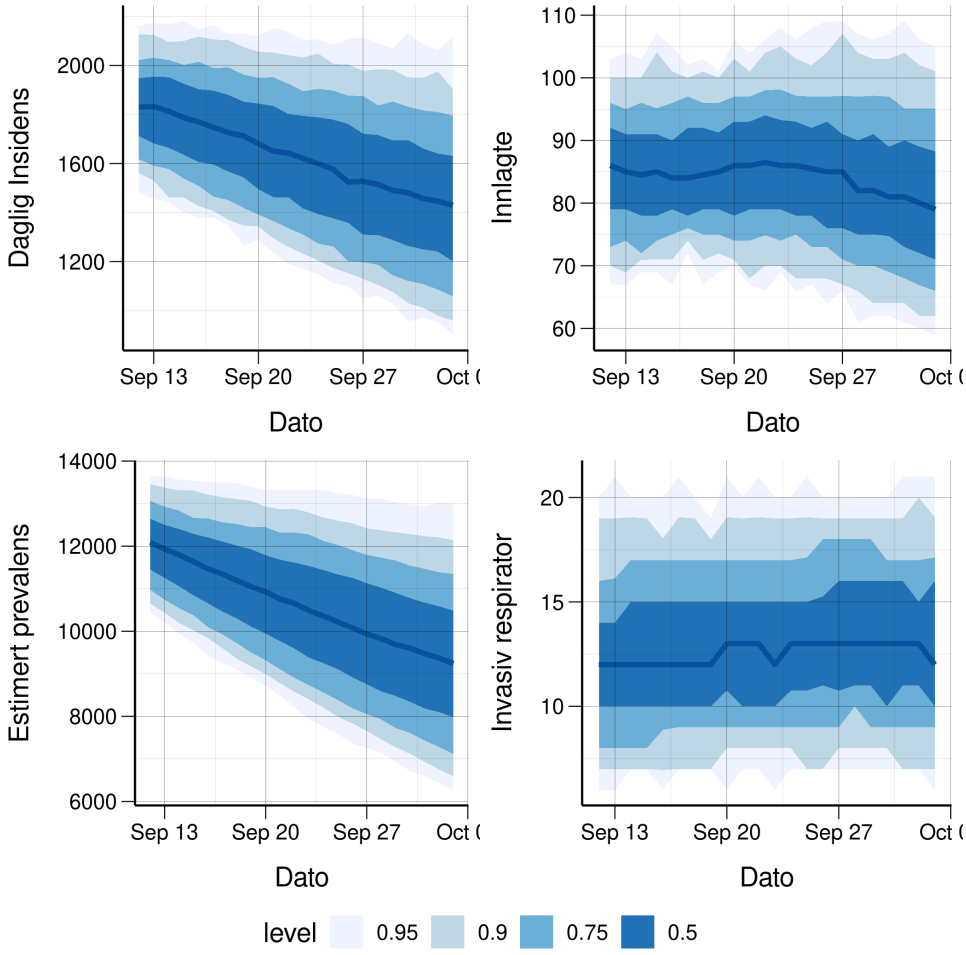


Figure 5: National 3 week predictions for incidence (top left), prevalence (bottom left), hospital beds (top right) and ventilator beds (bottom right)

3.1 Hospital and Ventilator prevalence by age

In Figures 6 and 7 we show the hospital prevalence by age group obtained from the simulations of the national model, including a 3 week forecast period. The real number of patients in each age group is also included (black dots).

In the forecast period, we assume that the age distribution of the cases in hospital and respirator beds will remain the same as today. Specific values for this projections are shown on table 4.

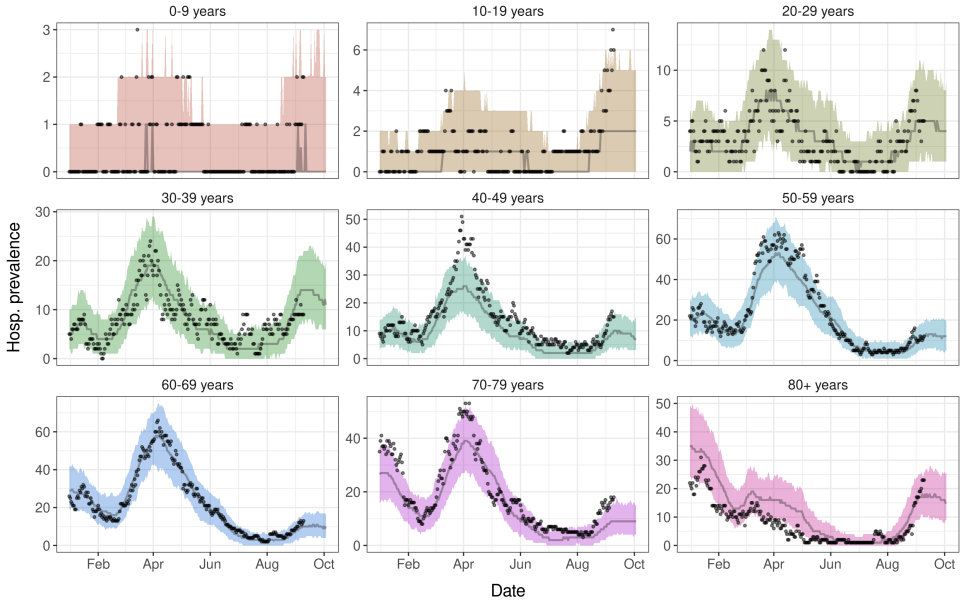


Figure 6: Simulated hospital prevalence by age group. Real data is shown as black dots

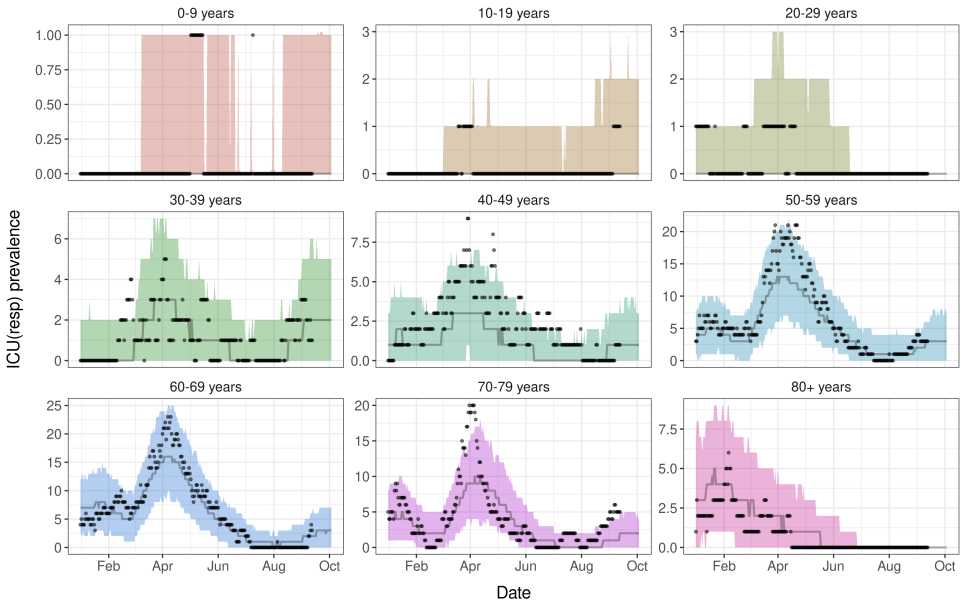


Figure 7: Simulated respirator prevalence by age group. Real data is shown as black dots

Table 4: Hospital and Respirator prevalence per age group: 3 week prediction (2021-10-03)

Age group	Hosp	Resp
0-9 years	1 (0-2)	0 (0-1)
10-19 years	2 (0-5)	1 (0-2)
20-29 years	5 (1-9)	0 (0-0)
30-39 years	13 (5-21)	2 (0-5)
40-49 years	9 (3-15)	1 (0-3)
50-59 years	13 (6-20)	4 (1-8)
60-69 years	11 (6-18)	3 (0-7)
70-79 years	10 (4-16)	2 (0-5)
+80 years	17 (10-28)	0 (0-0)

4 National long-term scenarios with vaccination plans and future interventions: Infections, hospitalisations and ventilator treatments

Note that the future course of the epidemic will depend on the national and local control measures that the authorities impose to curb the transmission in the current and future waves of the epidemic, as well as on human behaviour. These future factors cannot be anticipated by the model. In addition, the epidemiological situation is highly uncertain. Therefore, **the scenarios shown are not predictions on how the epidemic is likely to develop in the future** *but are the modelled outcomes of a specific set of assumptions.*

We present long-term scenarios from the individual-based model with vaccination.

4.1 Assumptions

- The vaccination model includes the vaccines from Pfizer and Moderna, which are currently in the programme. In the model, the vaccines are offered to everyone 12 years or older, in line with government policy. Only one dose is given to the age-group 12-15. The vaccine uptake is assumed to be 90% in all age groups and we assume full adherence to the vaccination schedule.
- We use data from the Norwegian Immunisation Registry (SYSVAK) on the number of vaccinations carried out up until 30th August 2021 [1] to initialize the model – results here are shown starting from 13th September.
- The values of the vaccine efficacy (VE) are sampled from a flat distribution taking the Pfizer vaccine estimates as lower bound and the Moderna vaccine estimates as upper bound (Table 5).
- We assume a seasonal effect of 50% or 25%. The seasonal effect is implemented by varying the transmission rate in accordance with the mean daily temperature historically for Norway; hence, the transmission rate varies by 50% or 25% between the coldest and warmest day during the year.
- We assume the following total number of imported cases per month (the imported cases are then evenly distributed over the days of the month): September 205; October 152; November 91; December 72; January through June 2022 100.
- We assume a six-week interval between the first and second mRNA vaccine doses, for people older than 18 years of age. A ten-week interval is used for 16-17-year olds. 12-15-year olds only get one dose.
- No waning immunity after infection or vaccination is assumed.

[1] We use a two-week period from 30th August to 12th September

- The simulations do not take into account a potential reduction of the length of stay in hospital resulting from vaccination, due to lack of data on this. Thus, the prevalence of inpatients shown in the figures represents a pessimistic scenario where the vaccine does not affect hospitalization length of stay.
- We assume that the vaccines are effective against all circulating variants in the same way.
- The values of the reproduction number at the start of the simulations are based on the estimates from the national changepoint model (Table 1), the SMC model and the Epiestim model. We assume regional differences in the reproduction number by estimating a scaling factor for the national reproduction number in each municipality. The scaling factor is calculated from the proportion of the population in each municipality who has tested positive, compared to the national one. The initial conditions in the municipalities are set using the results of the regional changepoint model run until the most recent time point. The long-term scenario results are based on 100 simulations and account for stochasticity within the IBM model; however, the uncertainty in the changepoint models is not accounted for, neither the uncertainty in the estimated reproduction number, nor the uncertainty in the initial conditions.

Table 5: Vaccine effectiveness estimates for Pfizer and Moderna.

Vaccine effectiveness	**Vaccine type**	**Value % (1st dose/2nd dose)**
Against asymptomatic disease	Pfizer	25/45%
	Moderna	57/80%
Against symptomatic disease	Pfizer	50/65%
	Moderna	75/80%
Against severe disease requiring hospitalisation	Pfizer	80/90%
	Moderna	90/95%
Against death	Pfizer	85/95%
	Moderna	95/99%
Against transmission	Pfizer	65%
	Moderna	65%

4.2 Scenarios

We present results from two different scenarios:
Constant Scenario: In this scenario, we assume that the national vaccine roll-out continues as planned, that the epidemic will evolve according to the current reproduction number, and that the government/municipalities will make no changes to the current interventions. We use three different assumptions for the national reproduction number: $R \in [0.7, 0.8, 0.9]$. This is done to account for the uncertainty of the point estimates of R from the national changepoint model (0.9), SMC model (0.76) and EpiEstim model (0.9).
Controlled Scenario: In this alternative scenario, we assume that the national vaccine roll-out will continue as planned and that the national reproduction number is $R = 0.8$ on 13th September. Every two weeks, we assume that the government/municipalities choose to actively control the reopening of the society in relation to the prevalence of hospitalised patients. The model thus tunes the transmission rate between individuals up or down as a function of the hospital prevalence. The maximum allowed level of reopening corresponds to the transmission rate in the early phase of the epidemic, in February-March 2020, when no infection-control measures were implemented yet. The value of this threshold is estimated assuming a basic reproduction number of $R_0 = 4.5$ (the value takes into account the higher transmissibility of the Delta variant, currently dominating in Noway). This number is highly uncertain.

The simulation of the control mechanism is implemented at a municipality level. Therefore, the model is able to take into account regional differences in the basic reproduction number; based on the

above-defined R_0, we estimate a local R_0 for each municipality that we use to define the maximum level of reopening at the regional level.

Below are described the main control rules of the algorithm, using the national prevalence thresholds reported in Table 6. In the model these national values are translated to regional values by scaling them by the population in each municipality. Taking Oslo as an example, the three regional thresholds of the prevalence derived from Table 6 are 26, 16, and 6.

Table 6: Thresholds of national reproduction number in controlled scenario.

Prevalence of hospital admissions	Thresholds of Rt
$[200, \infty)$	0.8
$[125, 200)$	1.0
$[50, 125)$	1.05
$[0, 50)$	1.2

We set an upper threshold of 200 admitted patients nationally. If this threshold is reached, contact-reducing measures are triggered, lowering the transmission rate so that the reproduction number is reduced to 0.8 (the transmission rate and the reproductive number are closely related). We also include a lower threshold of 50 hospital admissions nationally. If the prevalence drops below this, the transmission rate is increased to give a reproduction number of 1.2, simulating a reopening. To dampen the oscillatory behaviour that arises from turning the transmission rate up and down, we also have a middle threshold of 125 hospital admissions nationally. If the prevalence of hospital admissions is between 50 and 125, we update the transmission rate by targeting a reproduction number of 1.05; while if the prevalence of hospitalised patients is between 125 and 200, we correct the transmission rate to get a reproduction number of 1.0. Note that these thresholds which trigger reopening and contact-reducing measures in the simulations have been somewhat arbitrarily chosen as an illustration of a controlled scenario.

A more detailed description of the controlled scenario dynamics is presented in the report *Modelleringsrapport til Oppdrag 346*, available online at http://www.fhi.no.

More information about the individual-based model can be found in the reports *Folkehelseinstituttets foreløpige anbefalinger om vaksinasjon mot covid-19 og om prioritering av covid-19-vaksiner, versjon 2 15. desember* and *Modelleringsrapport, delleveranse Oppdrag 8: Effekt av regional prioritering av covid-19 vaksiner til Oslo eller OsloViken samt vaksinenes effekt på transmisjon for epidemiens videre utvikling*, available online at http://www.fhi.no. The order of priority for age and risk groups can be found at https://www.fhi.no/en/id/vaccines/coronavirus-immunisation-programme/who-will-get-coronavirus-vaccine-first/.

4.3 Constant Scenario

We present scenarios until the end of June 2022 from our IBM with vaccination, showing expected prevalence (Figure 8a), hospital beds (Figure 8b) and ventilator beds (Figure 8c).

Table 7: Estimated total infections, admissions and ventilator treatments until 30th June 2022

	Seasonality	Reproduction number		
		0.7	0.8	0.9
Infections	50%	27930 (20540-43291)	193010 (87374-382135)	961280 (673943-1232463)
	25%	18832 (16204-22263)	32756 (26408-43538)	83290 (57026-135527)
Hospitalisations	50%	829 (658-1132)	3867 (1946-7302)	18094 (12677-23202)
	25%	653 (560-741)	974 (827-1228)	2027 (1463-2974)
Ventilator treatm.	50%	117 (85-157)	486 (256-920)	2326 (1605-2952)
	25%	94 (75-118)	136 (105-181)	270 (186-403)

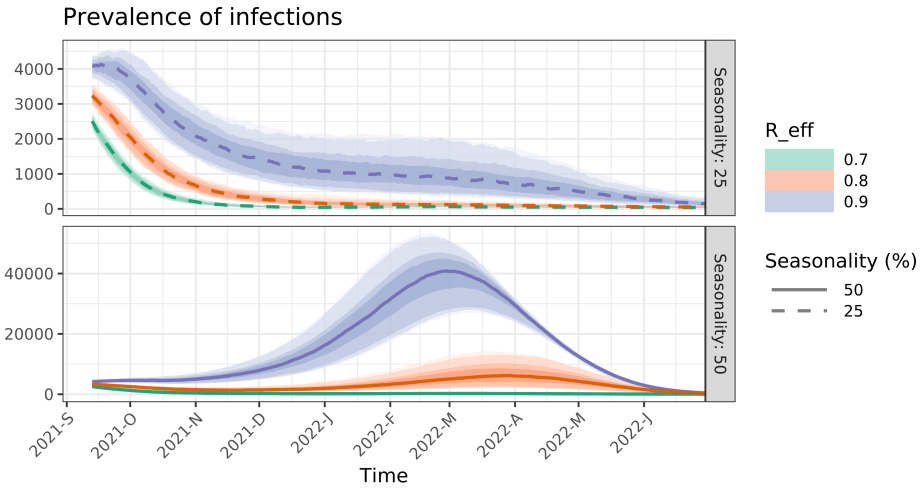
Depending on the assumed epidemiological situation (R ranging from 0.8 to 0.9) and assuming a seasonal effect of 50%, the epidemic exhibits a peak in March 2022 in case of $R = 0.9$, as seen in Figure 8. In the

4.3 Constant Scenario

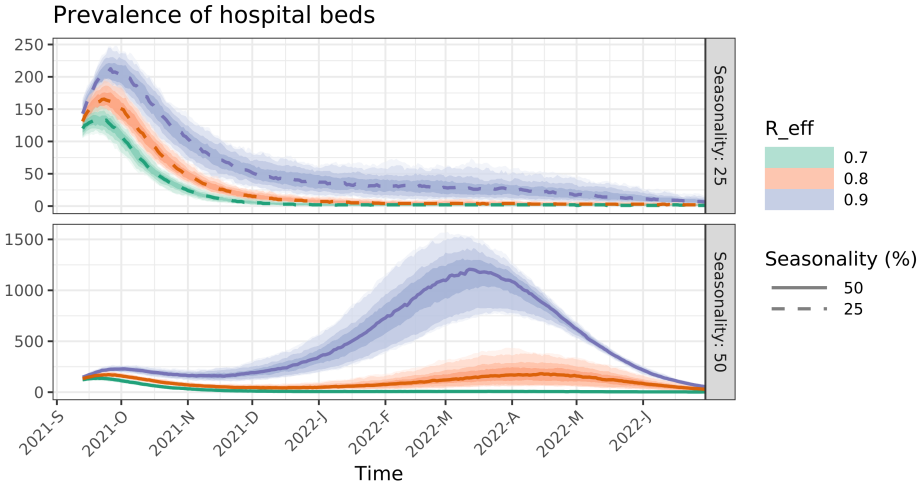
Table 8: Estimated total hospital admissions until 30th June 2022, in the constant scenarios, split on age and vaccination status. Numbers shown are median (95% CI).

R_{eff}	Seasonality	Vacc. status	Age 0-11	Age 12-17	Age 18-64	Age 65-100
0.7	25%	total	2 (0-5)	2 (0-6)	390 (314-462)	260 (208-309)
0.7	25%	unvaccinated	2 (0-5)	2 (0-5)	330 (268-384)	91 (74-108)
0.7	25%	vaccinated	0 (0-0)	0 (0-1)	60 (46-78)	168 (134-201)
0.8	25%	total	4 (1-9)	3 (0-9)	610 (492-787)	366 (304-449)
0.8	25%	unvaccinated	4 (1-9)	3 (0-8)	510 (418-657)	124 (101-156)
0.8	25%	vaccinated	0 (0-0)	0 (0-1)	100 (73-130)	242 (203-293)
0.9	25%	total	10 (3-22)	8 (4-20)	1374 (933-2091)	634 (481-859)
0.9	25%	unvaccinated	10 (3-22)	8 (4-18)	1189 (799-1849)	237 (167-358)
0.9	25%	vaccinated	0 (0-0)	0 (0-2)	184 (133-243)	398 (314-501)
0.7	50%	total	3 (0-8)	4 (1-9)	518 (394-747)	304 (232-403)
0.7	50%	unvaccinated	3 (0-8)	4 (1-8)	445 (340-650)	108 (84-155)
0.7	50%	vaccinated	0 (0-0)	0 (0-1)	73 (53-98)	196 (148-248)
0.8	50%	total	24 (8-53)	21 (7-47)	2814 (1355-5377)	970 (565-1838)
0.8	50%	unvaccinated	24 (8-53)	21 (7-45)	2582 (1214-4960)	449 (243-917)
0.8	50%	vaccinated	0 (0-0)	0 (0-2)	232 (140-417)	522 (321-921)
0.9	50%	total	140 (84-190)	112 (68-151)	13497 (9447-17163)	4408 (3067-5694)
0.9	50%	unvaccinated	140 (84-190)	110 (68-145)	12517 (8772-15881)	2266 (1563-2914)
0.9	50%	vaccinated	0 (0-0)	2 (0-6)	980 (675-1282)	2142 (1503-2780)

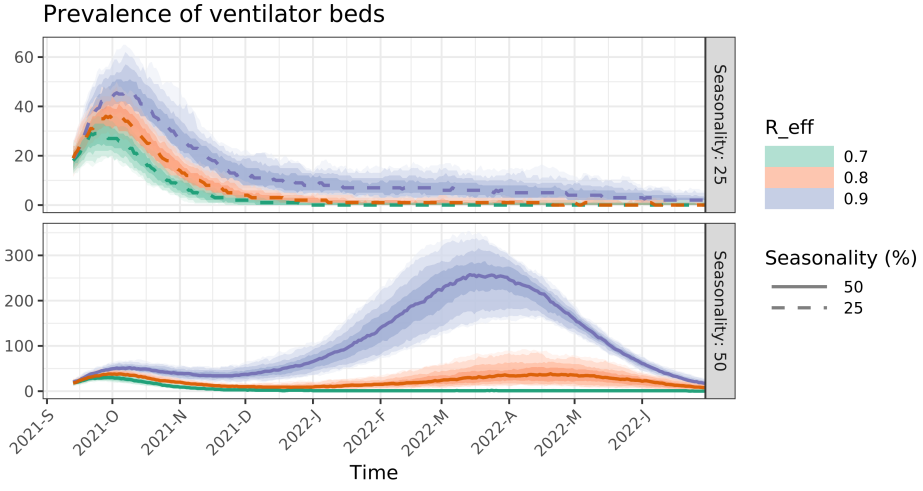
$R = 0.9$ scenario, the number of ventilator beds is lower than 300, less than the capacity need of **500 ICU** beds (Table 7). Under the assumption of a 25% seasonal effect, the peak of prevalence of infections and hospitalisations will appear in October 2021. Note that the prevalence of hospitalisation could be overestimated due to the assumption that vaccination does not reduce length of stay.



(a)



(b)



(c)

Figure 8: Long-term predictions from the constant scenario, for prevalence (a), hospital beds (b) and ventilator beds (c). Figures present both the 25% and the 50% seasonality assumption. The simulations do not take into account a potential reduction of the length of stay in hospital resulting from vaccination. Thus, the prevalence of inpatients shown in the figures may be an overestimation, and represents a pessimistic scenario where the vaccine does not affect hospitalization length of stay.

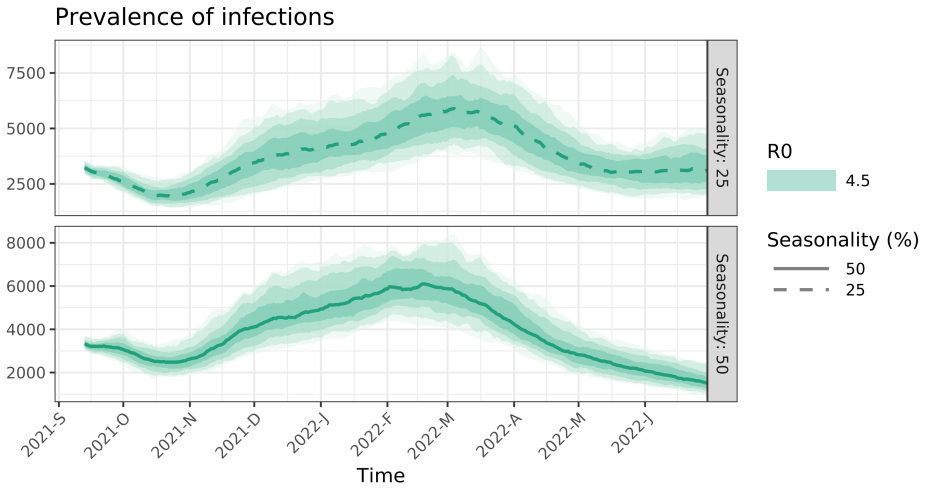
4.4 Controlled Scenario

We next present long-term projections using the controlled scenarios described above, showing expected prevalence (Figure 9a), hospital beds (Figure 9b) and ventilator beds (Figure 9c).
Figure 10 shows at a national level the relative average contact rate compared to an open society with "normal" social interaction. To estimate the level of contact corresponding to a fully open community, we first calculate the transmission rate in each region during the period before the lockdown in March 2020, from the estimated basic reproduction number, R_0.
The transmission rate, the so-called beta parameter, is the product of the contact rate multiplied with the probability of transmission given contact. We can think of the transmission rate as an effective contact rate, relevant to the spread of the SARS-CoV-2 virus.
Note that the reopening is simulated locally and that the degree of reopening may differ in the various regions of the country.

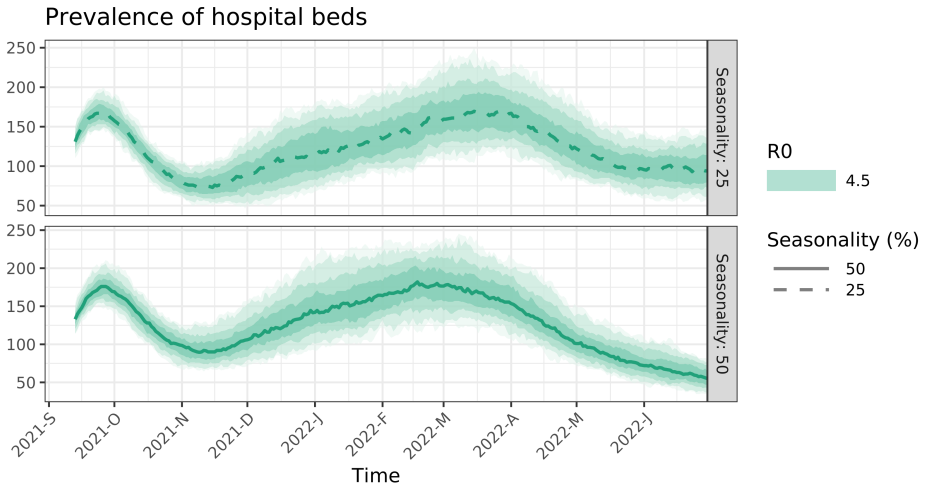
Table 9: Estimated total number of infections, hospitalisations and ventilator treatments until 30th June 2022

Total	Seasonality	Maximum reproduction number 4.5
Infections	50%	242952 (208283-279227)
	25%	240379 (203156-287741)
Hospitalisations	50%	4839 (4199-5476)
	25%	4704 (4060-5583)
Ventilator treatm.	50%	624 (526-709)
	25%	596 (515-717)

Table 9 shows a controlled scenario with hospital admissions as steering parameter. There are no significant differences in the total numbers between the 25% and 50% seasonality scenarios. Figure 10 indicates that in the scenarios assuming a maximum reproduction number at 4.5 a gradual reopening could start from 2022. Note that, due to the assumption that vaccination does not reduce hospital length-of-stay, the modelled prevalence may be an overestimation. This could in turn lead to the model being more conservative in its reopening strategy.



(a)



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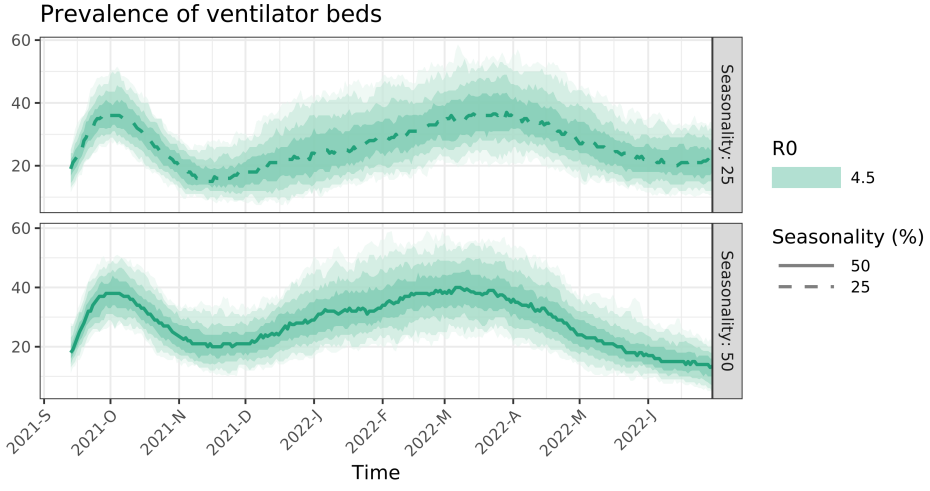


(c)

Figure 9: Long-term predictions from the controlled scenario, for prevalence (a),hospital beds (b) and ventilator beds (c). Figures present both the 25% and the 50% seasonality assumption. The simulations do not take into account a potential reduction of the length of stay in hospital resulting from vaccination.

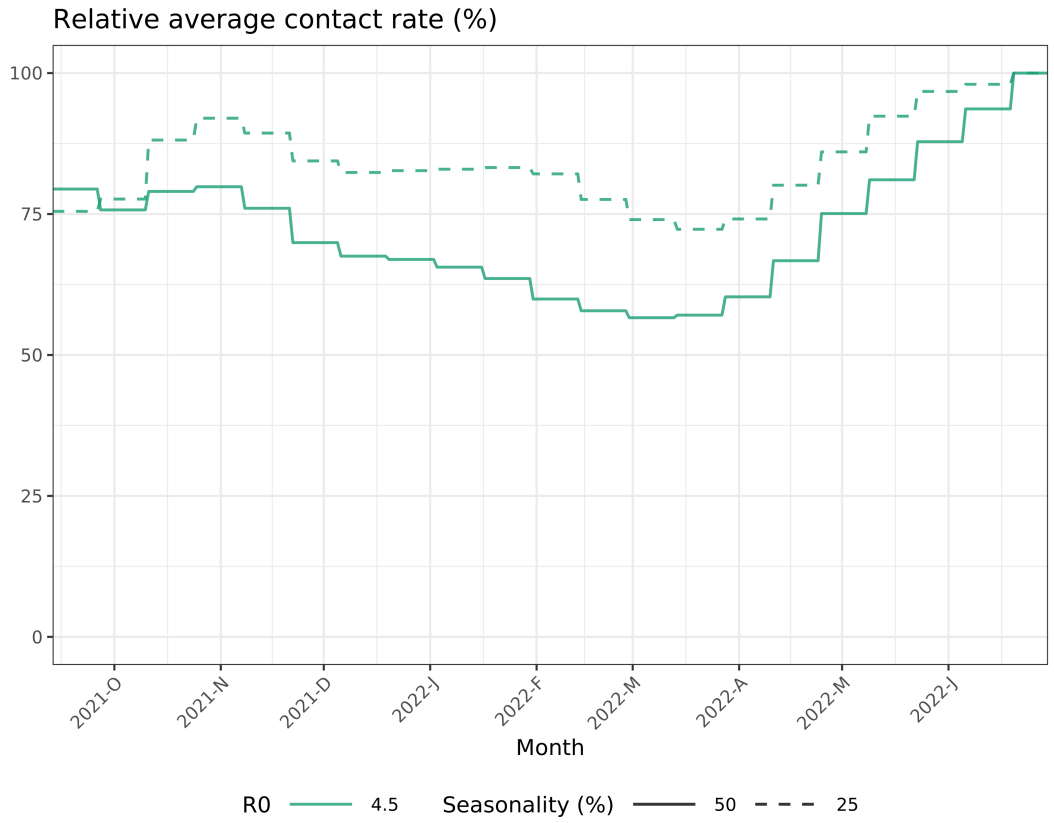


Figure 10: Relative average national contact rate compared to a fully open society using a reopening factor to determine the maximum level of reopening in the controlled scenario. The line represents the reopening factor and is normalized by its own maximum contact rate. The contact rate is a population-weighted average in all municipalities, updated every two weeks to simulate gradual reopening by evaluating the number of hospital admissions. Both the 25% and 50% seasonality assumptions are shown.

5 Estimated regional reproduction numbers

Also this week we are not presenting results from the regional changepoint model. The reason is that we are updating the model in several directions, as we found this needed to cope with a more complicated situation. The regional testing in the most populated municipalities is particularly influenced by the self-testing. Because negative results are not recorded, the number of tests is highly under-reported. Vaccination is also happening in various age groups unevenly in the country, which leads to less susceptible quite rapidly, more than what we see from the positive test data (which should decrease, if we would have the same efforts in detecting them by testing). We are also updating several parameters in our model, related to the basic assumptions of the transmission, because of the delta variant. The changepoint model produces estimates which are valid for a longer period (some weeks), within which we assume transmission to be stable and the epidemic to be in equilibrium. This is particularly difficult to assume now. Therefore we publish our regional SMC model, which has a daily reproduction number, with all the caveats being however valid, about data and dynamics of the epidemics.

6 14-day trend analysis of confirmed cases and hospitalisations by county

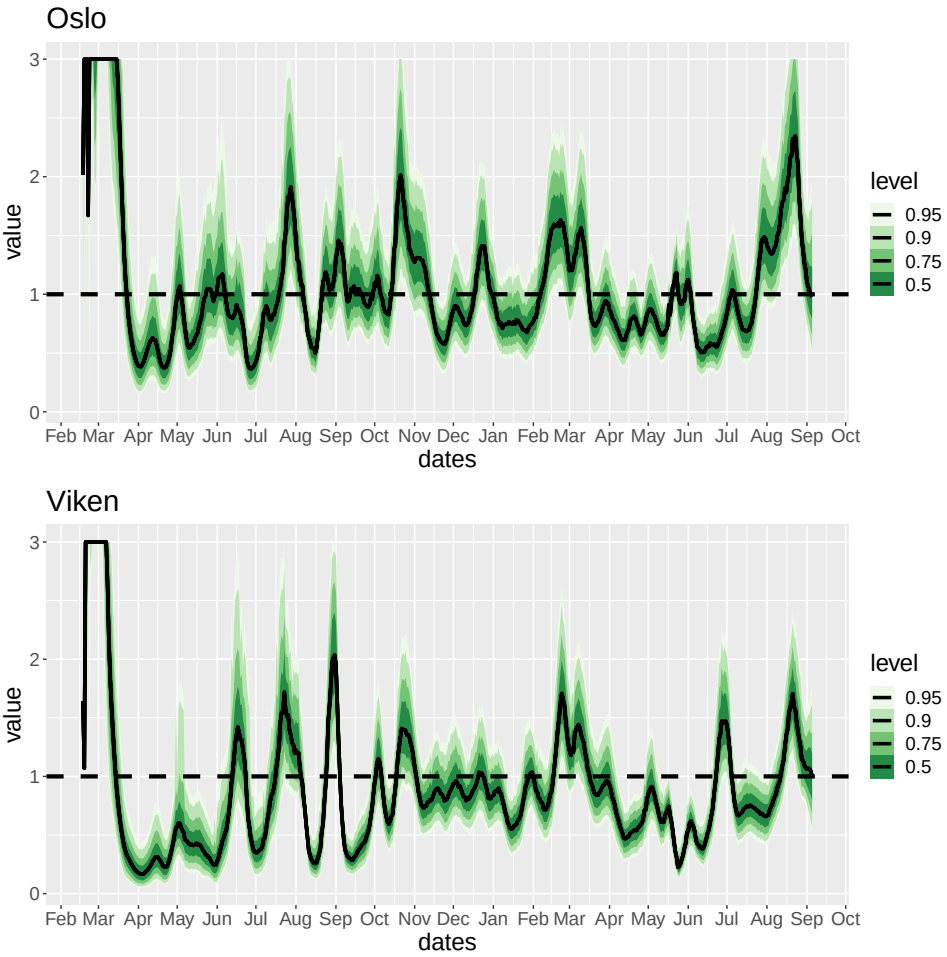
To estimate recent trends in hospitalisation and number of positive tests, we present results in table 10 based on a negative binomial regression where we account for weekend effects. We exclude the last three days to avoid problems of reporting delay and fit the model using data from 17 days to 3 days before the current date. We fit a separate trend model for confirmed cases and for hospital incidence. We only fit a trend model if there has been more than 5 cases or hospitalisations in the 14-day period.

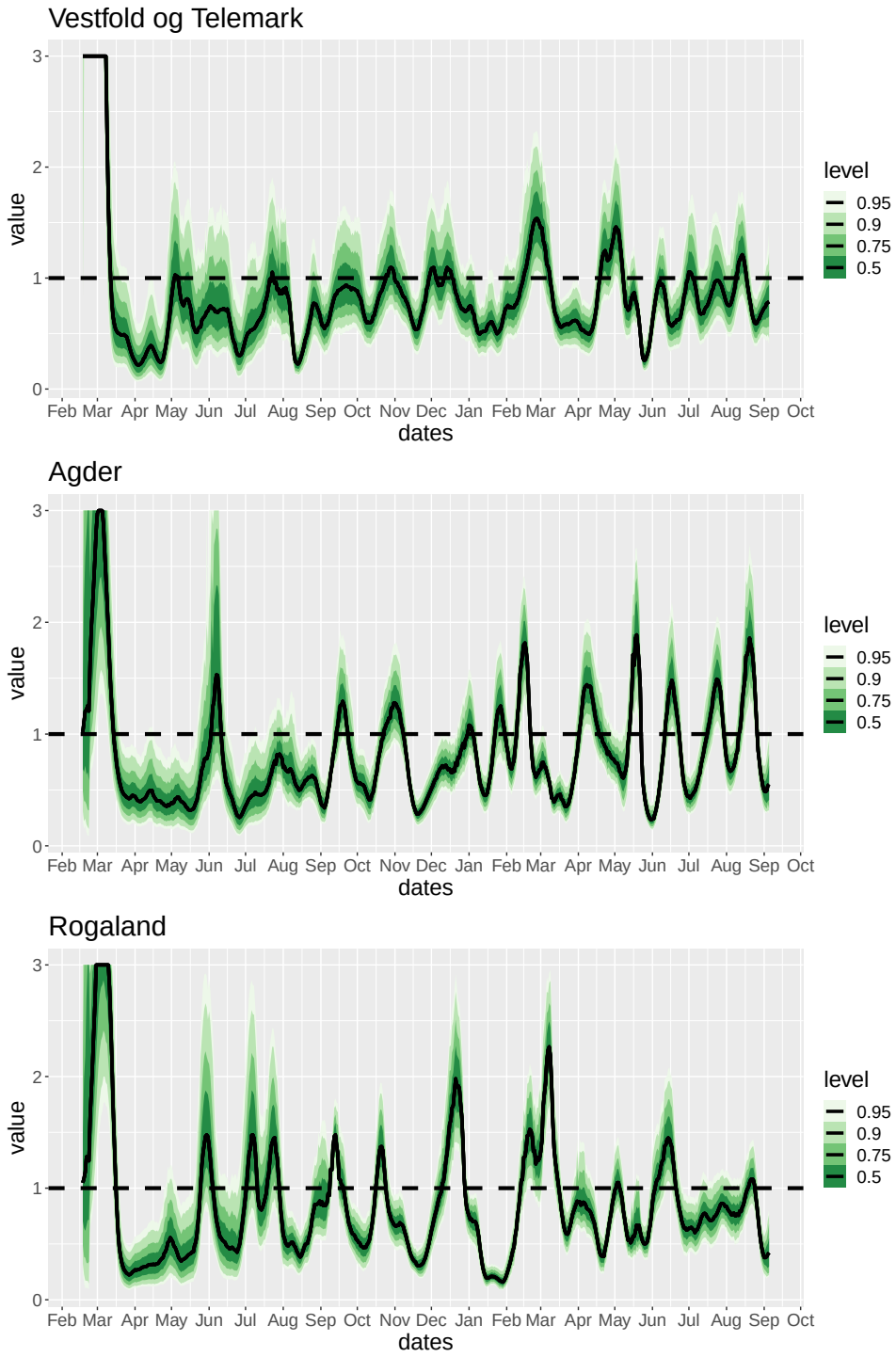
Table 10: Trend analysis for the last 14 days

	Average daily increase last 14 days		Doubling Time (days)	
County	Hospitalisations	Cases	Hospitalisations	Cases
Agder	11.3 (-4.6, 32.1) %	-6.1 (-7.8, -4.3) %	6.5 (-14.8, 2.5)	-11.1 (-8.5, -15.7)
Innlandet	-2.8 (-20.1, 17.4) %	-4 (-7.9, 0.1) %	-24.6 (-3.1, 4.3)	-17 (-8.4, 793.8)
Møre og Romsdal	Not enough data	-3.5 (-6.3, -0.6) %	Not enough data	-19.5 (-10.6, -115.5)
Nordland	Not enough data	-1.6 (-6.3, 3.3) %	Not enough data	-42.7 (-10.7, 21.6)
Norge	-0.9 (-5.2, 3.7) %	-2.6 (-3.7, -1.5) %	-80.4 (-12.9, 19)	-26.1 (-18.3, -45.4)
Oslo	-2.7 (-9.6, 4.5) %	-2.5 (-3.8, -1.2) %	-24.9 (-6.9, 15.8)	-27.1 (-17.9, -55.5)
Rogaland	Not enough data	-8.8 (-11.5, -6.1) %	Not enough data	-7.5 (-5.6, -11.1)
Troms og Finnmark	Not enough data	-0.1 (-3, 3) %	Not enough data	-1246.5 (-22.8, 23.6)
Trøndelag	Not enough data	-4.2 (-6.6, -1.8) %	Not enough data	-16.2 (-10.2, -38.5)
Vestfold og Telemark	18.9 (0.4, 46.2) %	2.1 (0.1, 4.1) %	4 (176.5, 1.8)	33.3 (668.3, 17.1)
Vestland	Not enough data	-6.8 (-9.3, -4.2) %	Not enough data	-9.8 (-7.1, -16)
Viken	-11 (-23, 1.8) %	-1.2 (-2.8, 0.4) %	-6 (-2.7, 38.5)	-58.1 (-24.5, 156.5)

7 Regional SMC-model: Estimated daily reproduction numbers

As we do for the national SMC-model (section 1.1), we now allow for a different reproduction number for each day and for each county. The model uses the daily number of new admissions to hospital and the daily number of positive and negative lab-confirmed tests fpr each county, to estimate all parameters. Because of the time between infection and the possibility to be detected as positive by a test, and because of a delay in reporting tests, the data contain information on the transmissibility until a week before the end of the data used. We therefore stop the estimates one week ago. As for the national SMC model, the figures below shows the SMC estimate of the 7-day-average daily reproduction number for each fylke. In the figure we plot the 95% credibility interval and quantiles of the estimated posterior distribution of the reproduction numbers. For some counties, uncertainty is large towards the most recent time, because there are very few data and possibly reporting delays which are different in each county.

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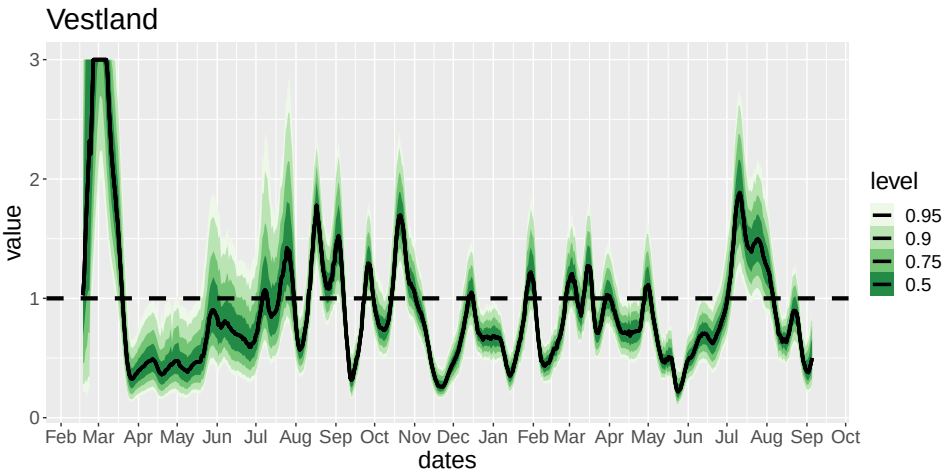
Agder
Rogaland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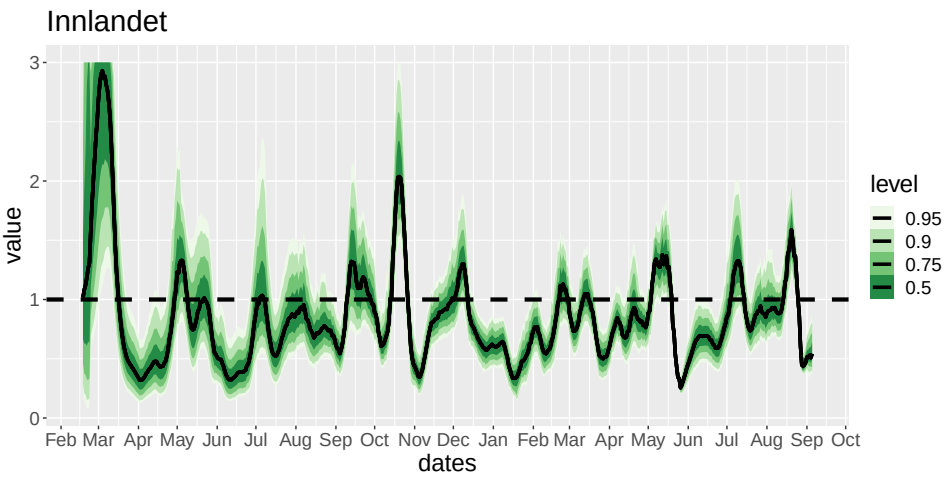
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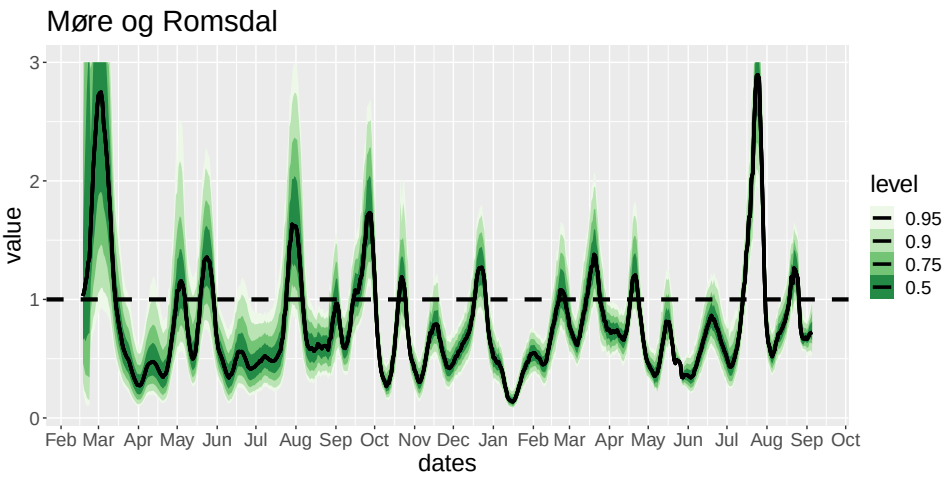
Møre og Romsdal
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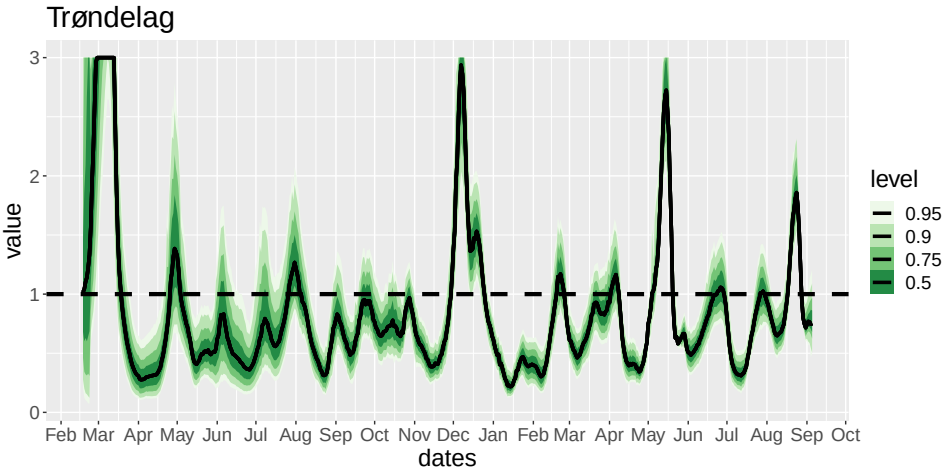
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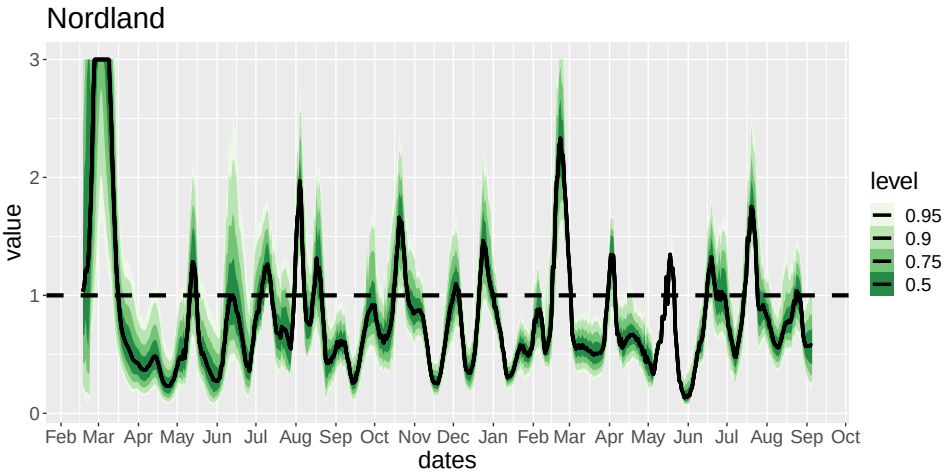
Nordland
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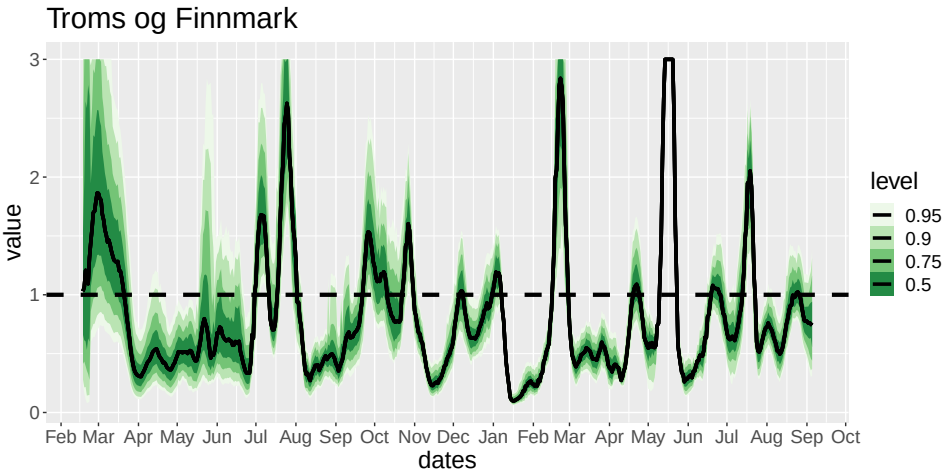
Troms og Finnmark
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Feb Mar Apr May Jun Jul Aug Sep Oct Nov Dec Jan Feb Mar Apr May Jun Jul Aug Sep Oct

	Median	5%	95%	Prob>1
Oslo	0.981	0.535	1.772	0.479
Rogaland	0.421	0.224	0.762	0.003
Møre og Romsdal	0.723	0.551	0.975	0.041
Nordland	0.575	0.263	1.011	0.058
Viken	0.997	0.566	1.606	0.498
Innlandet	0.542	0.393	0.806	0.007
Vestfold og Telemark	0.786	0.460	1.224	0.179
Agder	0.549	0.316	0.943	0.031
Vestland	0.499	0.284	0.830	0.013
Trøndelag	0.751	0.505	1.089	0.098
Troms og Finnmark	0.742	0.370	1.311	0.223

Table 11: Regional estimates at Sep 5

8 Mobility

Number of trips out from each municipality during each day is based on Telenor mobility data. We observed a large reduction in inter-municipality mobility in March 2020 (with minimum reached on Tuesday 17 March 2020), and thereafter we see an increasing trend in the mobility lasting until vacation time in July 2020. The changes in mobility in July 2020 coincides with the three-week "fellesferie" in Norway, and during August the mobility resumes approximately the same levels as pre-vacation time. There is however a significant regional variation.

The reference level is set to 100 on March 2nd 2020 for all the figures in this section, and we plot the seven-day, moving average of the daily mobility. Figure 11 shows an overview of the mobility since March 2020 for the largest municipalities in each county, and Figure 12 shows the total mobility out from all municipalities in each county, including Oslo. Figure 13 and 14, zooms in on mobility from April 19 2021, for municipalities and counties, respectively.

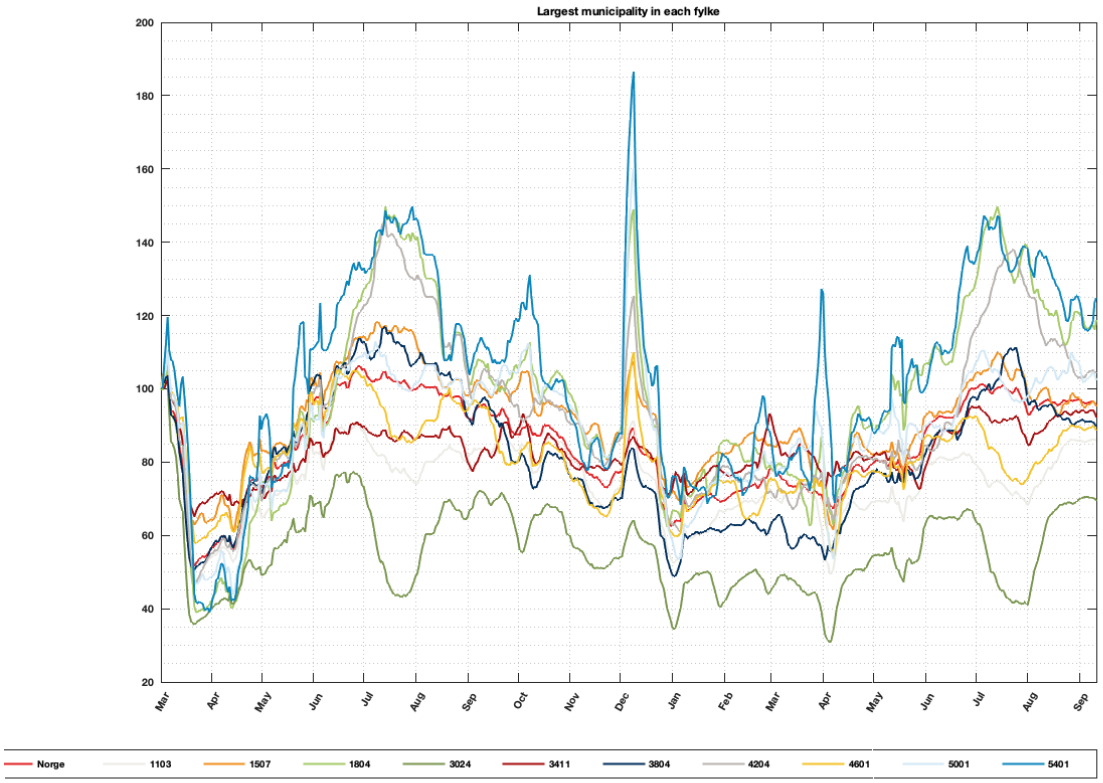


Figure 11: Mobility for selected municipalities since March 2020: Nationally (Norge), Stavanger (1103), Ålesund (1507), Bodø (1804), Bærum (3024), Ringsaker (3411), Sandefjord (3804), Kristiansand (4204), Bergen (4601), Trondheim (5001), Tromsø (5401).

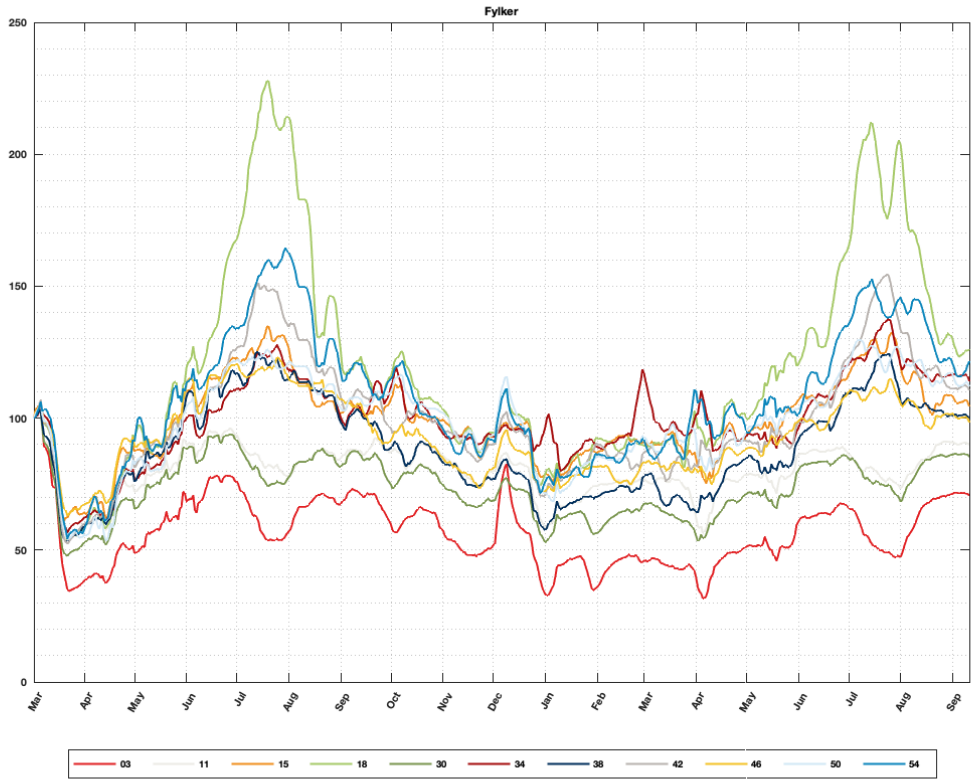


Figure 12: Mobility for fylker since March 2020: Oslo (03), Rogaland (11), Møre og Romsdal (15), Nordland (18), Viken (30), Innlandet (34), Vestfold og Telemark (38), Agder (42), Vestland (46), Trøndelag (50), Troms og Finmark (54).

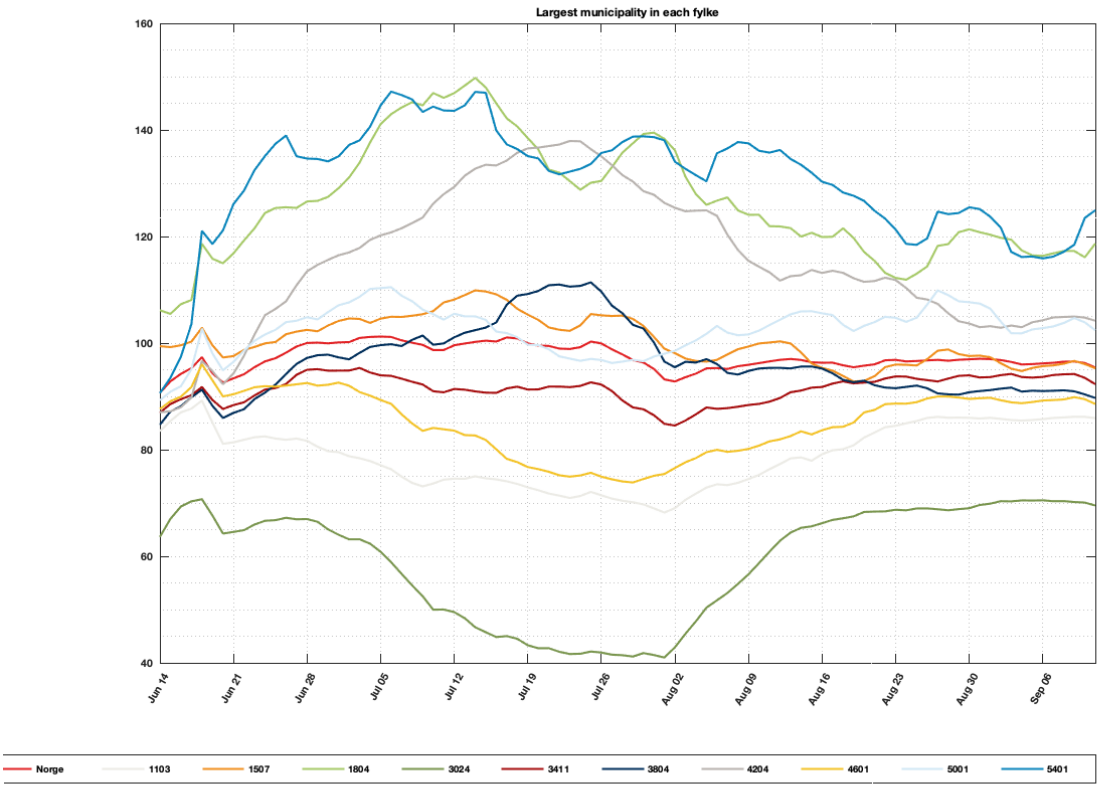


Figure 13: Zoom: Mobility from April 19, 2021 and onwards: Nationally (Norge), Stavanger (1103), Ålesund (1507), Bodø (1804), Bærum (3024), Ringsaker (3411), Sandefjord (3804), Kristiansand (4204), Bergen (4601), Trondheim (5001), Tromsø (5401).

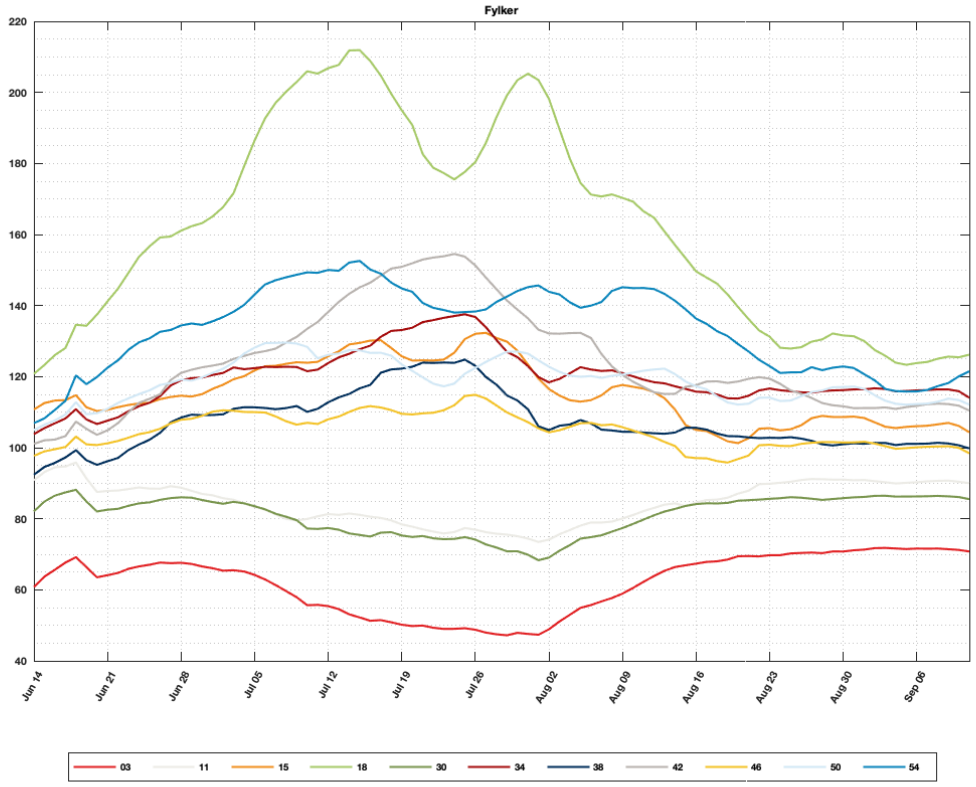


Figure 14: Zoom: Mobility from April 19, 2021 and onwards, per fylker: Oslo (03), Rogaland (11), Møre og Romsdal (15), Nordland (18), Viken (30), Innlandet (34), Vestfold og Telemark (38), Agder (42), Vestland (46), Trøndelag (50), Troms og Finnmark (54).

	33	34	35	36	37
Norge	95.9	96.3	96.8	97.0	96.2
Stavanger	74.5	79.2	84.5	86.0	85.7
Ålesund	99.4	95.3	96.0	97.6	95.7
Bodø	124.1	119.9	112.2	121.3	116.4
Bærum	56.6	66.2	68.7	69.0	70.5
Ringsaker	88.4	91.8	93.8	94.0	93.7
Sandefjord	94.8	95.2	91.5	90.8	91.0
Kristiansand	115.4	113.2	111.8	103.7	104.3
Bergen	80.1	83.7	88.7	89.5	89.2
Trondheim	101.6	105.6	104.8	107.7	102.8
Tromsø	137.5	130.3	121.3	125.5	115.9

Table 12: Municipalities

	33	34	35	36	37
Oslo	58.9	67.4	69.8	70.8	71.6
Rogaland	80.1	84.6	89.8	91.0	90.3
Møre og Romsdal	117.7	105.0	105.5	108.6	106.0
Nordland	170.3	149.6	131.2	131.6	123.8
Viken	77.4	84.1	85.6	85.8	86.3
Innlandet	121.0	115.8	116.6	116.2	116.1
Vestfold og Telemark	104.5	105.6	102.8	101.0	101.1
Agder	120.5	117.6	119.4	111.6	111.8
Vestlandet	105.8	97.1	100.8	101.5	100.1
Trøndelag	120.6	117.3	114.1	117.1	112.3
Troms og Finnmark	145.2	136.3	123.0	122.9	115.8

Table 13: Counties

Weekly mobility for Norway and selected municipalities is displayed in Table 12 and mobility for counties is displayed in Table 13. The percentages in the tables are to be interpreted towards the reference level of 100 for week 10 in March 2020. The color-coding encodes the following: 'Green' monotonic decrease in mobility, 'Yellow' almost monotonic decrease or flat mobility trend, 'Red' increasing mobility.

8.1 Foreign roamers on Telenor's network in Norway

An analysis of foreign roamers in Norway from January 2020 has been carried out, to better understand the potential virus importation. In Figure 15 the total number of roamers per day per county are displayed. We can see an approximate 40% drop in the number of visiting roamers after the lock-down in March 2020. The number of visiting roamers recover during the Summer of 2020, and there is a spike of visitors in August followed by a drop again. During October and November 2020 the levels of visiting, foreign roamers to Norway have reached quite high levels, just 10% short of the all-year high for 2020, and Oslo and Viken have seen big increases in visitors. There is a reduction in visitors during Christmas, and in January 2021 we see an increasing trend again.

Figure 16 shows the levels of roamers from the following countries: Poland, Lithuania, Sweden, Netherlands, Denmark, Latvia, Germany, Spain, Finland and the rest of the world. These levels represent the total number of foreign, visiting roamers from each of the countries per day in Norway, since April 19 2021.

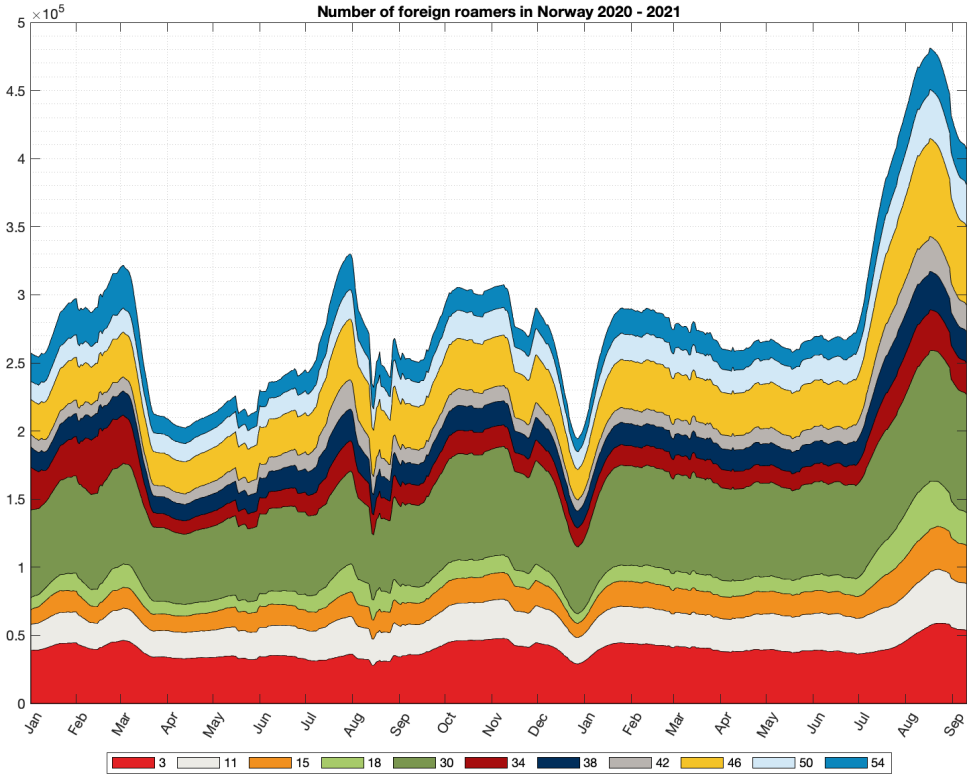


Figure 15: The total number of foreign roamers in Norway broken down on different fylker: Oslo (3), Rogaland (11), Møre og Romsdal (15), Nordland (18), Viken (30), Innlandet (34), Vestfold og Telemark (38), Agder (42), Vestland (46), Trøndelag (50), Troms og Finnmark (54).

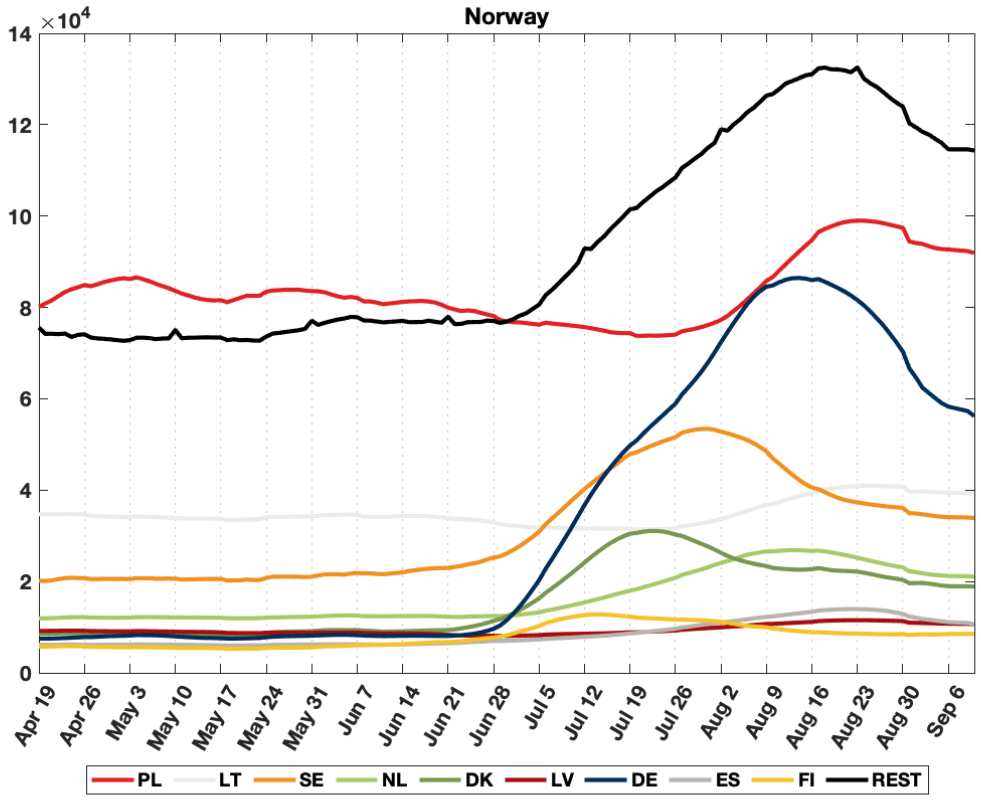
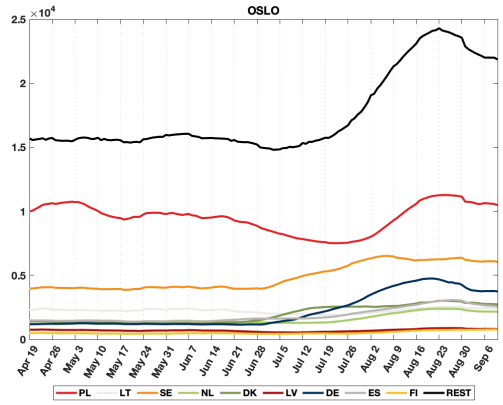
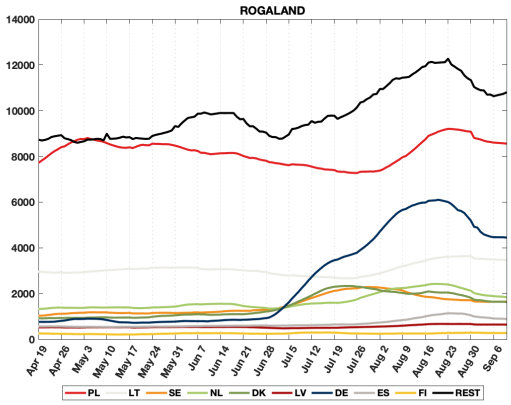
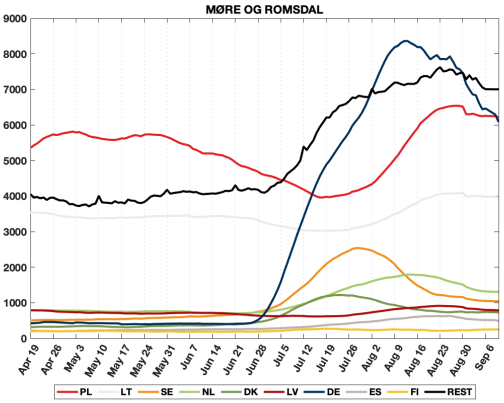


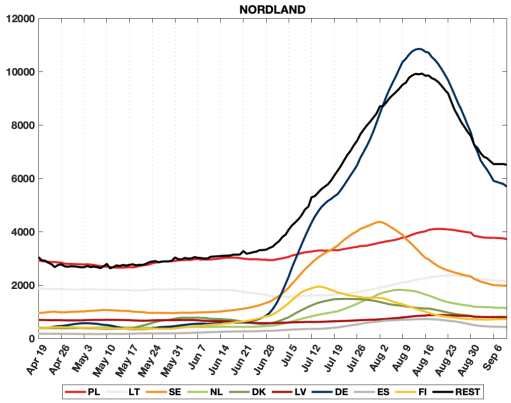
Figure 16: National overview of total number of foreign, visiting roamers from Poland, Lithuania, Sweden, Netherlands, Denmark, Latvia, Germany, Spain, Finland and the rest of the world.

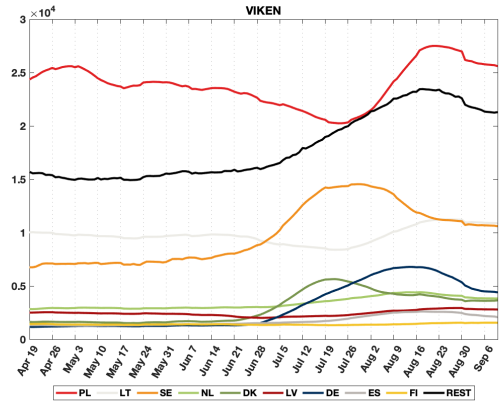
8.2 Foreign roamers per county (fylke) in Norway

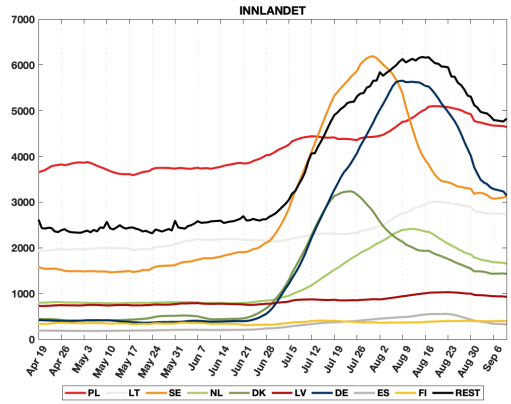




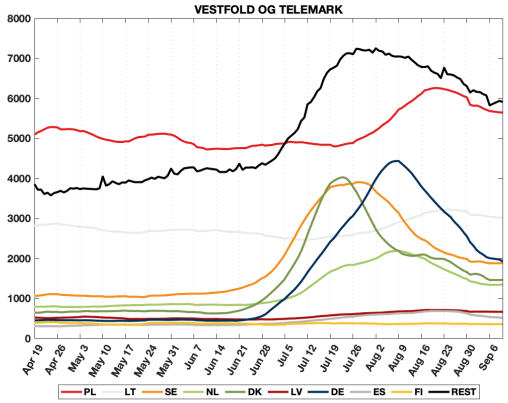


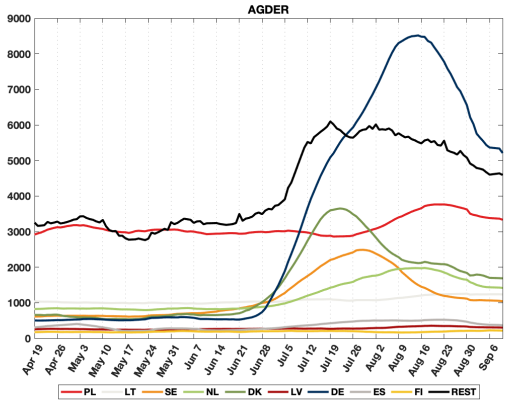


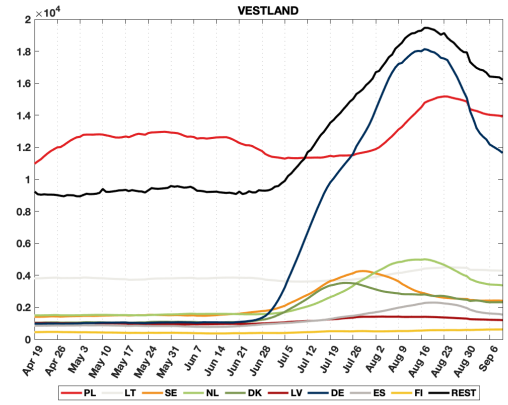


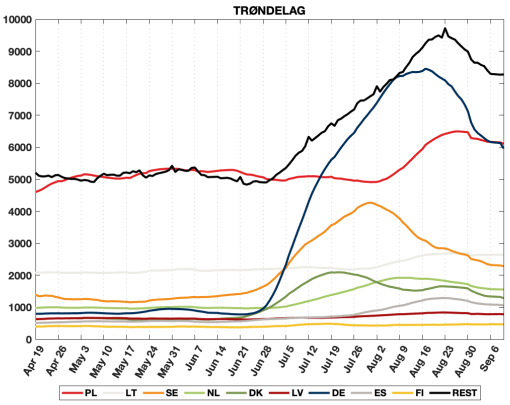


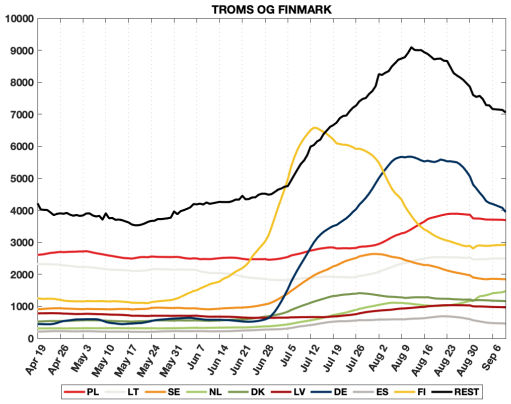
8.2 *Foreign roamers per county (fylke) in Norway*











9 Methods

9.1 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.

9.1.1 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 within each area 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_1), Presymptomatic infected (E_2), Symptomatic infected (I), Asymptomatic infected (I_a), and Recovered, either immune or dead (R). A schematic overview of the model is shown in figure 19.

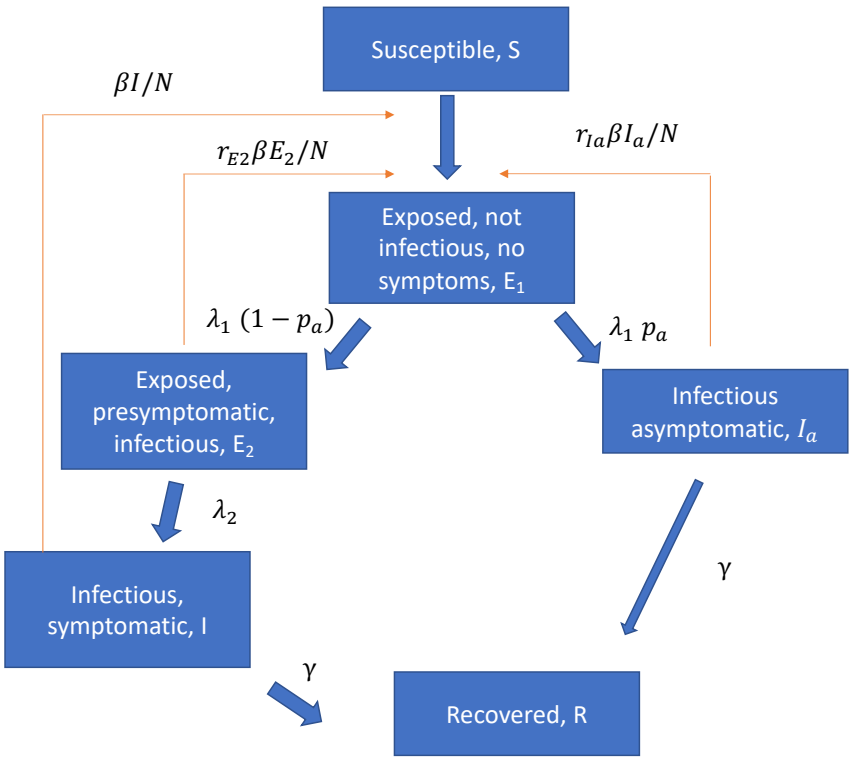


Figure 19: Schematic overview of the model.

9.2 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, regularised to be balanced in total in- and outgoing flow for each municipality.

9.3 Healthcare utilisation

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

9.4 Seeding

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

9.5 Calibration

Estimation of the parameters of the model: the reproduction numbers, the amplification factor for the imported cases, the parameters of the detection probability and the delay between incidence and test, is done using Sequential Monte Carlo Approximate Bayesian Computation (SMC-ABC), as described in Engebretsen et al. (2020): https://royalsocietypublishing.org/doi/10.1098/rsif.2019.0809, where the algorithm can be found in the supplement.

The idea behind ABC is to try out different parameter sets, simulate using these, then compare how much the simulations deviate from the observations in terms of summary statistics. We thus test millions of combinations of the different reproductive numbers, the amplification factor, and the parameters for the positive tests, to determine the ones that lead to the best fits to the true number of hospitalised individuals, from March 10 2020 until the last available data point, and the laboratory-confirmed COVID-19 cases from May 1 until the latest available data point.

In the ABC procedure we thus use two summary statistics, one is the distance between the simulated hospitalisation incidence and the observed incidence, and the other is the distance between the observed number of laboratory-confirmed cases and the simulated ones. As the two summary statistics are not on the same scale, we use two separate tolerances in the ABC-procedure, ensuring that we get a good fit to both data sources.

9.5.1 Calibration to hospitalisation data

In order to calibrate to the hospitalisation data, we need to simulate hospital incidence. The details on how we simulate hospitalisations are described in Section 9.3, using the parameters provided in Section 10, which are estimated from individual-level Norwegian data, and updated regularly. As our distance measure, we calculate the squared distance over each time point and each county.

9.5.2 Calibration to test data

We include the laboratory-confirmed cases in the calibration procedure, as these contain additional information about the transmissibility, and the delay between transmission and testing is shorter than the delay between transmission and hospitalisation. Therefore, we simulate also the number of detected positive cases in our model. We assume that the number of detected positive cases can be modelled as a binomial process of the simulated daily total incidence of symptomatic and asymptomatic cases, with a

success probability π_t, which changes every day. We also assume a delay d between the day of test and the day of transmission.

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

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

where k_t is the number of tests actually performed on day t, and π_0 and π_1 are two parameters that we estimate, assuming positivity of π_1. We also estimate the delay d. We choose to use a 7-days backwards moving average for the covariate k_t. To calculate the distance between the observed number of positive tests and the simulated ones we also use a 7-days backwards moving average. We do this to take into account potential day-of-the-week-effects. For example, it could well be that the testing criteria are different on weekends and weekdays. However, using instead the number of tests and calibrating on a daily basis would lead to a larger day-to-day variance. This is likely why we find that the uncertainty in the simulated positive cases seems somewhat too low, and that we do not capture all the variance in the daily test data. Moreover, the binomial assumption could be too simple, and a beta-binomial distribution would allow more variance. A limitation of our current model for the detection probability, is that we only capture the changes in the test criteria that are captured in the total number of tests performed.

9.6 Specifications for the national changepoint model

In the national changepoint model, we assume a first reproduction number R_0 until March 14, a second reproduction number R_1 until April 19, a third reproduction number R_2 until May 10, a fourth reproduction number R_3 until June 30, R_4 until July 31, R_5 until August 31, R_6 from September 1 until September 30, R_7 from October 1 until October 26, R_8 until November 4, R_9 from November 5th until November 30th, R_{10} from December 1st until January 4, a twelfth reproduction number R_{11} from January 4 until January 21, a thirteenth reproduction number from January 22 to February 7 and a fourteenth reproduction number from February 8. This last reproduction number is used for the future. The changepoints follow the changes in restrictions introduced. In the calibration procedure, we obtain 200 parameter sets that we use to represent the distributions of parameters.

After we have obtained the estimated parameters, we run the model with these 200 parameter sets again, from the beginning until today, plus three weeks into the future (or for an additional year). In this way, we obtain different trajectories of the future, allowing us to investigate different scenarios, with corresponding uncertainty.

9.7 Specifications for the regional changepoint model

In the regional changepoint model, each county has its own reproduction numbers, assumed constant in different periods, just like the national changepoint model. As there are more parameters in the regional changepoint model, we obtain 1000 parameter sets in the ABC-SMC.

Calibrating regional reproduction numbers is a more difficult estimation problem than calibrating national reproduction numbers, as we have a lot more parameters, and in addition less data in each county. Therefore, we cannot include the same amount of changepoints in the regional model as we can for the national model.

After we have obtained the estimated parameters, we run the model with these 1000 parameter sets again, from the beginning until today, plus three weeks into the future (or for an additional year). In this way, we obtain different trajectories of the future, allowing us to investigate different scenarios, with corresponding uncertainty.

10 Parameters used today

Figures 20 to 24 indicate which assumptions we make in our national model, related to hospitalisation. We obtained data from the Norwegian Pandemiregister. These estimates will be regularly updated, on the basis of new data.

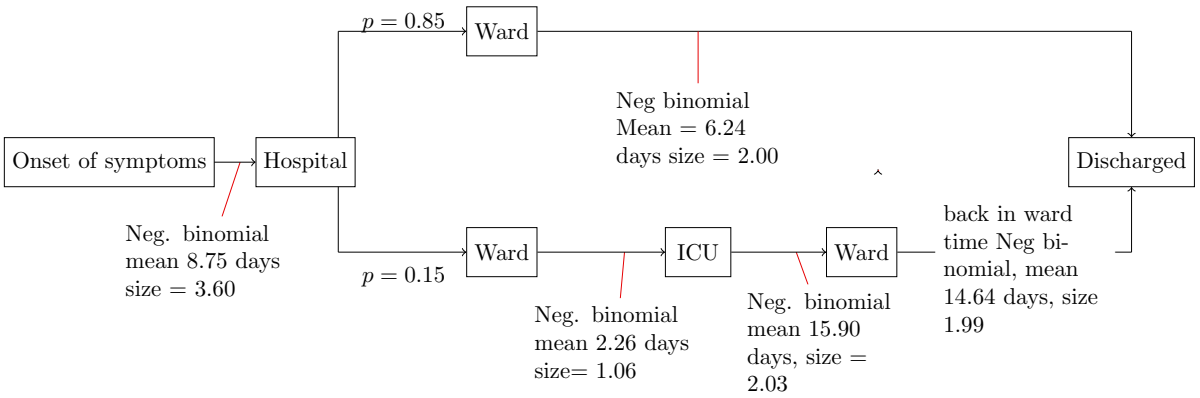


Figure 20: Hospital assumptions and parameters used before 1 June 2020

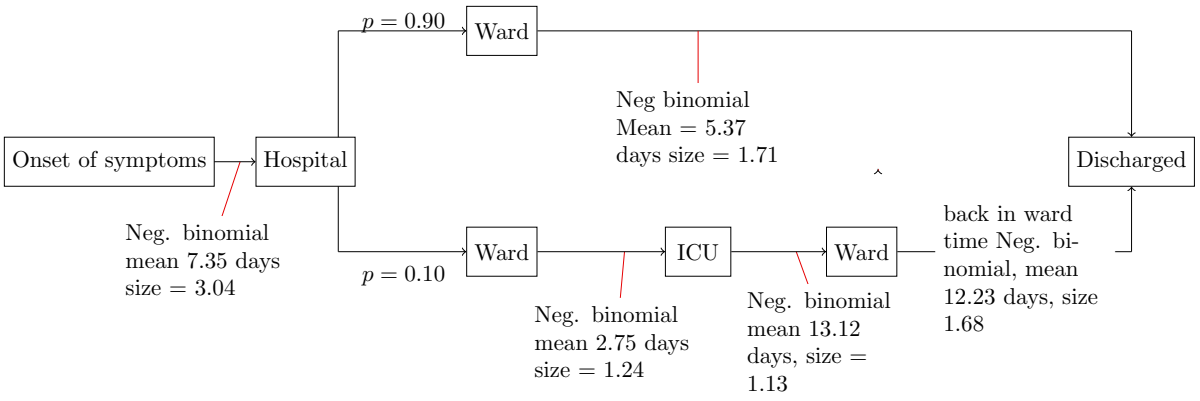


Figure 21: Hospital assumptions and parameters used between 1 June 2020 and 1 January 2021

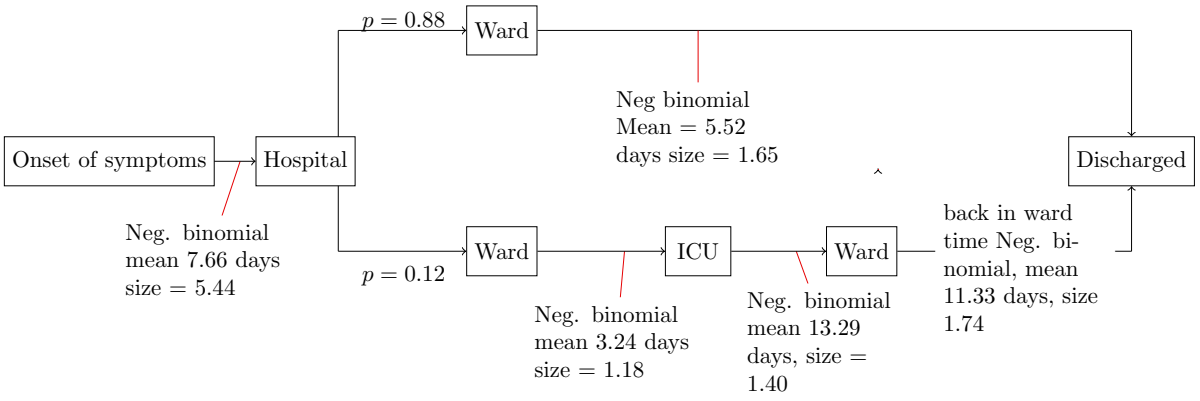


Figure 22: Hospital assumptions and parameters used between 1 January 2021 and 1 March 2021

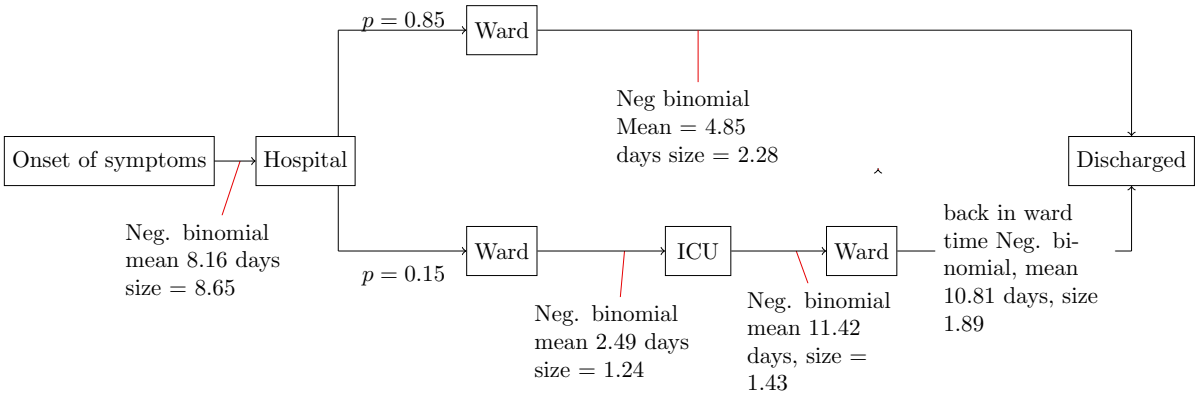


Figure 23: Hospital assumptions and parameters used between 1 March 2021 and 1 June 2021

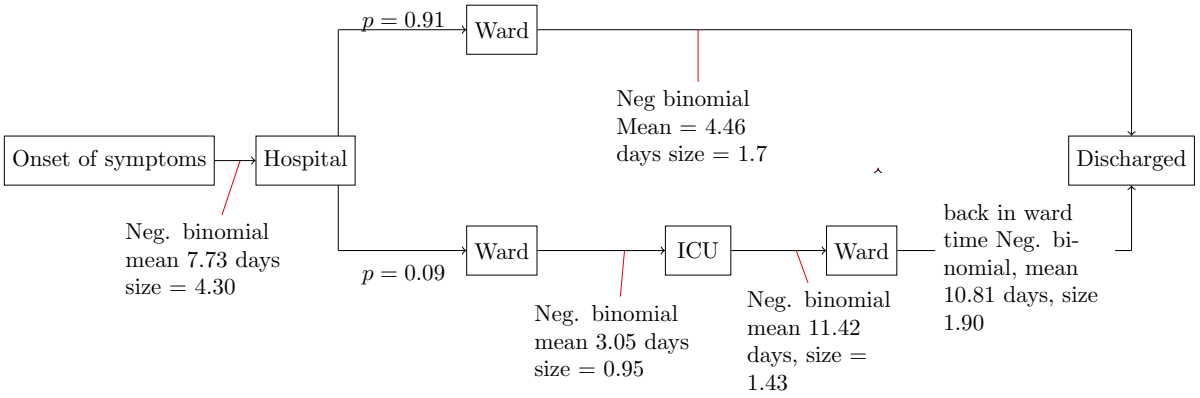


Figure 24: Hospital assumptions and parameters used from 1 June 2021

Table 14: Estimated parameters

	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	Period
R0s	2.498	2.995	3.215	3.222	3.439	3.979	Until March 14
R1s	0.375	0.46	0.485	0.49	0.51	0.649	From 15 March to 19 April
R2s	0.212	0.615	0.698	0.702	0.792	1.068	From 20 April to 10 May
R3s	0.239	0.617	0.726	0.719	0.813	1.209	From 11 May to 30 June
R4s	0.483	0.99	1.164	1.16	1.358	1.897	From 01 July to 31 July
R5s	0.604	0.856	0.973	0.961	1.056	1.321	From 01 August to 31 August
R6s	0.718	0.886	0.961	0.954	1.017	1.163	From 01 September to 30 September
R7s	1.097	1.212	1.255	1.251	1.287	1.38	From 01 October to 25 October
R8s	1.017	1.236	1.293	1.298	1.356	1.547	From 26 October to 04 November
R9s	0.732	0.792	0.812	0.809	0.825	0.877	From 05 November to 30 November
R10s	0.989	1.025	1.035	1.04	1.051	1.103	From 01 December to 03 January
R11s	0.426	0.528	0.571	0.571	0.616	0.7	From 04 January to 21 January
R12s	0.579	0.702	0.77	0.772	0.842	0.999	From 22 January to 07 February
R13s	1.372	1.46	1.501	1.503	1.544	1.695	From 08 February to 01 March
R14s	0.981	1.028	1.043	1.043	1.06	1.099	From 02 March to 24 March
R15s	0.695	0.744	0.76	0.759	0.775	0.814	From 25 March to 12 April
R16s	0.762	0.829	0.848	0.851	0.874	0.928	From 13 April to 05 May
R17s	0.809	0.914	0.95	0.948	0.986	1.097	From 06 May to 26 May
R18s	0.517	0.619	0.658	0.659	0.697	0.807	From 27 May to 20 June
R19s	0.713	0.989	1.082	1.071	1.167	1.366	From 21 June to 11 July
R20s	0.784	0.914	0.96	0.975	1.009	1.231	From 12 July to 04 August
R21s	1.253	1.353	1.381	1.382	1.41	1.53	From 05 August to 26 August
R22s	0.783	0.87	0.902	0.903	0.935	1.051	From 27 August
AMPs	1.176	1.796	2.067	2.035	2.252	2.881	-
π_0	0.091	0.222	0.308	0.314	0.389	0.626	-
π_1	1.2e-08	1.0e-05	1.6e-05	1.5e-05	2.1e-05	3.1e-05	-
delays	2	3	4	3.565	4	4	-

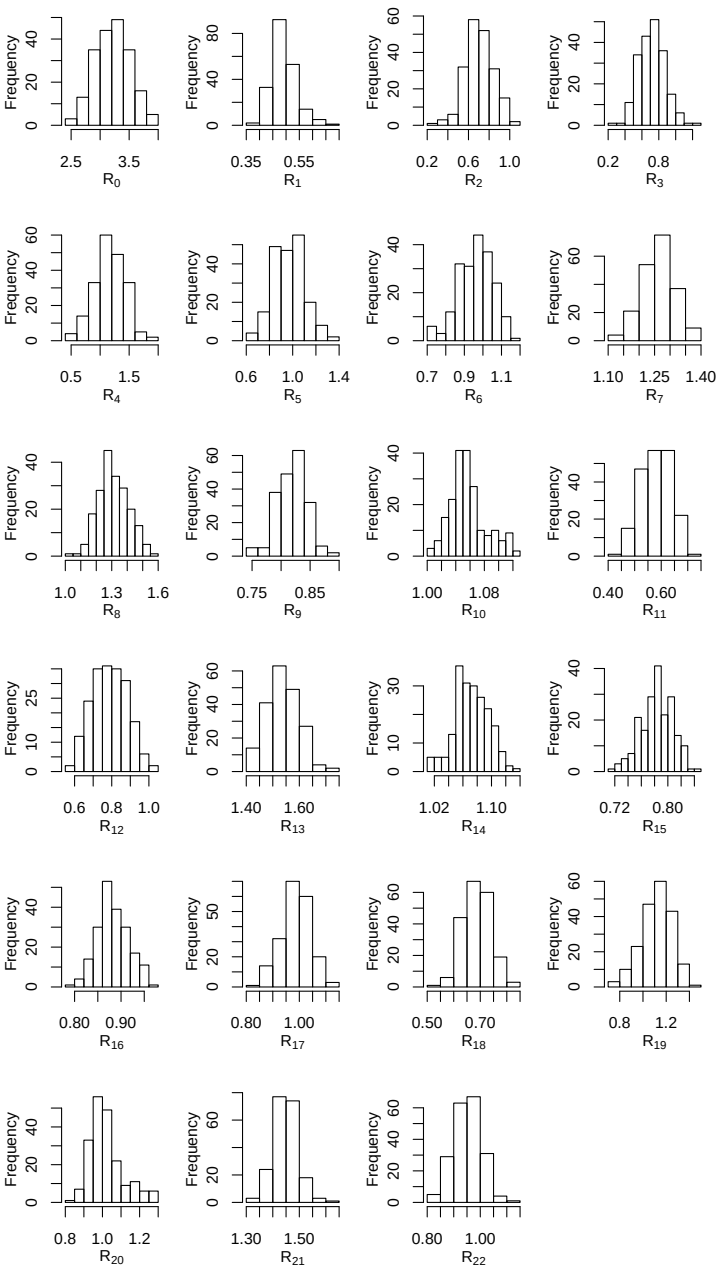


Figure 25: Estimated densities of the reproduction numbers. National model

Table 15: Assumptions

Assumptions	Mean	Distribution	Reference
Mobile Mobility Data			
Telenor coverage	48%		https://ekomstatistikken.nkom.no/
Data updated	August 29		
Data used in the predictions	August 27th	Fixed	Corrected to preserve population
Model parameters			
Exposed period ($1/\lambda_1$)	3 days	Exponential	Feretti et al 2020
Pre-symptomatic period ($1/\lambda_2$)	2 days	Exponential	Feretti et al 2020
Symptomatic infectious period ($1/\gamma$)	5 days	Exponential	Feretti et al 2020
Asymptomatic, infectious period ($1/\gamma$)	5 days	Exponential	Feretti et al 2020
Infectiousness asympt. (r_{I_a})	0.1	Fixed	Feretti et al 2020
Infectiousness presymp (r_{E_2})	1.25	Fixed	guided by Feretti et al 2020
Prob. asymptomatic infection (p_a)	0.4		Feretti et al 2020
Healthcare			
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	 0.1% 0.1% 0.5% 1.1% 1.4% 2.9% 5.8% 9.3% 22.3%	Fixed	Saljie et al 2020 corrected for: % of elderly living in elderly homes in Norway (last two age groups) and corrected for presence among positive tested since May 1.
Probability that an admission has been reported on Monday From Sunday From Saturday From Friday From Thursday	 32% 49% 68% 86%	Fixed	Estimated from "Beredskapsregistret BeredtC19"
Probability that an admission has been reported From one day before From two days before From three days before From four days before	 53% 77% 82% 91%	Fixed	Estimated from "Beredskapsregistret BeredtC19"
Probability that a positive laboratory test has been reported From one day before From two days before From three days before From four days before	 6.7% 59% 90% 97%	Fixed	Estimated from MSIS
Probability that a negative laboratory test has been reported From one day before From two days before From three days before From four days before	 16% 74% 92% 98%	Fixed	Estimated from MSIS

Supplementary analysis: EpiEstim estimation of reproduction number based on laboratory-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 combination of hospitalisation data and test data used in the main analysis are likely a less biased information source for the number of real infections, but since testing-criteria have remained constant over a long period of time, we also expect that using confirmed cases can give a reasonable estimate of the reproduction number in this phase of the epidemic. In this approach we do not take into account changes in the number of tests, for example during holidays, so the results in these periods are likely to under-estimate the reproduction number when the holiday starts and overestimate it when the holiday ends and the number of tests return to it's normal level.

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 4 days nationally and 7 days regionally, see figure 26. 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.

Table 16: Estimated reproduction numbers 7 days ago

Location	Reff
National	0.9(0.87 - 0.93)
Oslo	0.91(0.87 - 0.94)
Rogaland	0.68(0.59 - 0.77)
Møre og Romsdal	0.86(0.74 - 0.97)
Nordland	0.86(0.69 - 1.04)
Viken	0.97(0.94 - 1.01)
Innlandet	0.75(0.65 - 0.86)
Vestfold og Telemark	1.08(0.96 - 1.2)
Agder	0.74(0.65 - 0.83)
Vestland	0.72(0.65 - 0.81)
Trøndelag	0.83(0.76 - 0.9)
Troms og Finnmark	1.04(0.87 - 1.23)

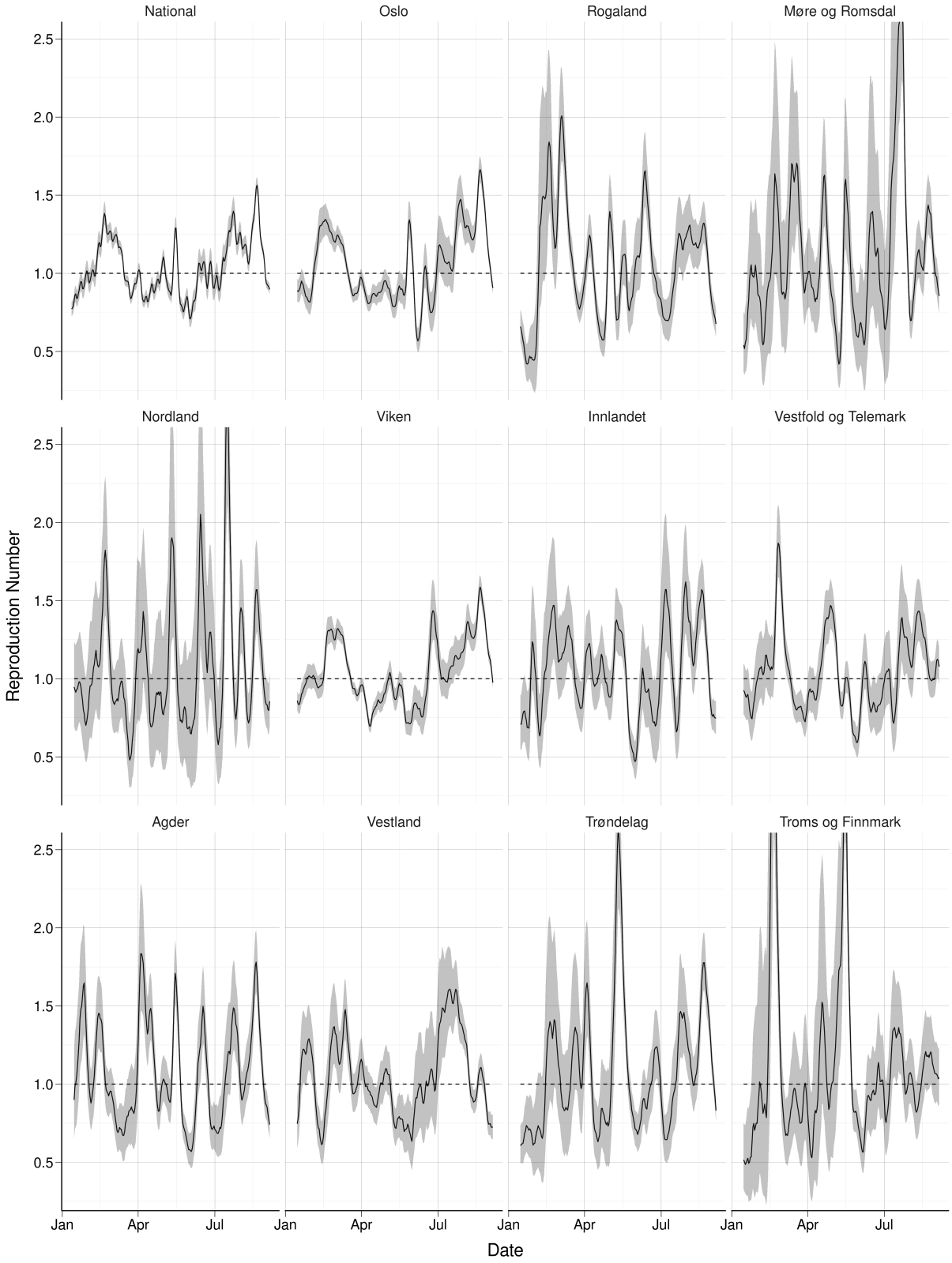


Figure 26: Reproduction number estimated using the R package EpiEstim.

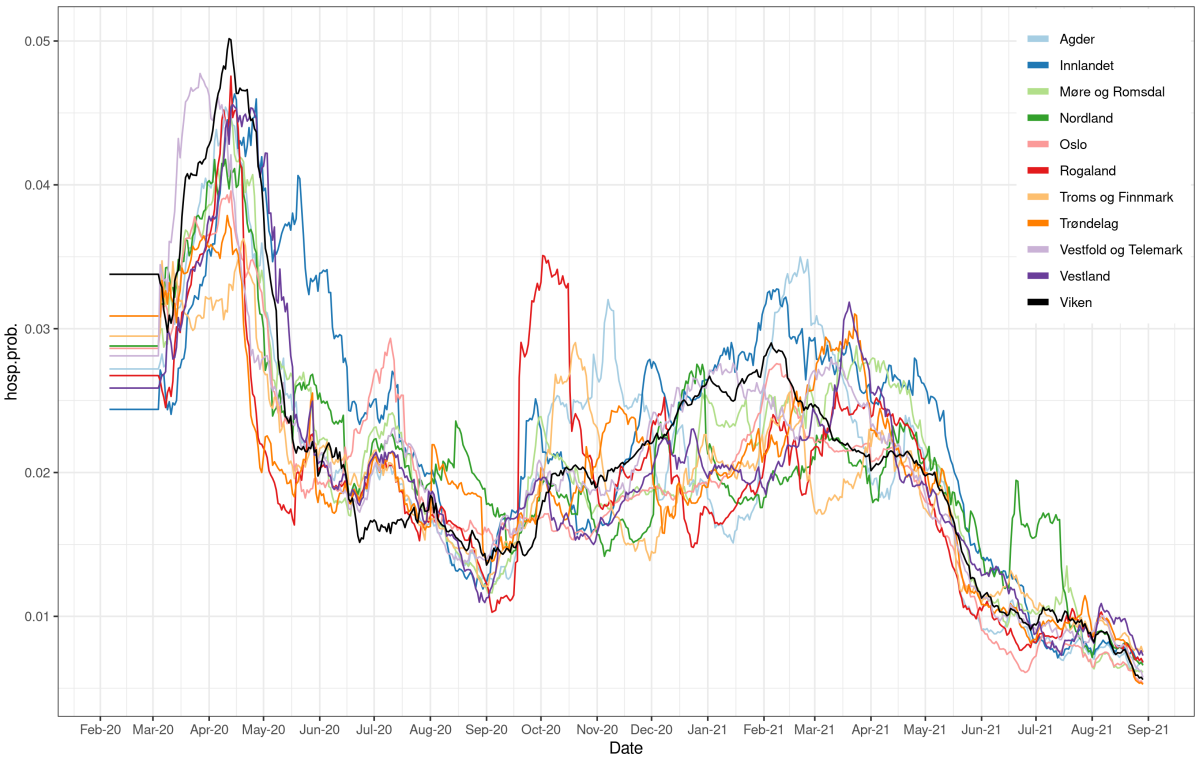


Figure 27: Regional hospitalization probabilities

FHI COVID-19 modelling team:

- **Birgitte Freiesleben de Blasio** - Department of Method Development and Analytics. Norwegian Institute of Public Health and Oslo Centre for Biostatistics and Epidemiology, University of Oslo.
- **Francesco Di Ruscio** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Gunnar Øyvind Isaksson Rø** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Solveig Engebretsen** - Norsk Regnesentral.
- **Arnoldo Frigessi** - Oslo Centre for Biostatistics and Epidemiology, University of Oslo and Oslo University Hospital.
- **Alfonso Diz-Lois Palomares** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Magnus Nygård Osnes** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Anja Bråthen Kristoffersen** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Kenth Engø-Monsen** - Telenor Research.
- **Louis Yat Hin Chan** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Jonas Christoffer Lindstrøm** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Richard White** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Gry Marysol Grøneng** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Chi Zhang** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Jørgen Eriksson Midtbø** - Department of Method Development and Analytics. Norwegian Institute of Public Health.
- **Geir Storvik** - Department of Mathematics. University of Oslo.