Situational awareness and forecasting for Norway

FHI COVID-19 modelling team

UPDATE NOTES-week 9 2021

Log of changes

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)[1]. 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.

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

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

– 15 May: **New parameters related to hospitalisation risk:** Our model requires the specification of the proportion of symptomatic and asymptomatic patients requiring hospitalisation. Previously we used estimates from Verity et al. (2020) based on Chinese data, adapted to the Norwegian demography and to the reduced mobility of elderly patients living in elderly homes, and calibrated to obtain a Infection Fatality Ratio (IFT) of roughly 0.3%. We adjust again the hospitalisation risk in our model based on Salje et al Science 13 May 2020[2], 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.

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

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

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

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

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

to determine sensible reproduction numbers. We compute the posterior probability of the time-varying reproduction number and plot the central 50% of this distribution to sketch the uncertainty. This band can be interpreted as the one which we predict to contain the daily reproduction number with 50% of posterior probability. We also compute the posterior probability that the reproduction number is above 1.

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

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

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

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

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

– 17 August: **New seeding data set** We change the source of the seeding data. Before, we used the first day with symptoms for every imported case. Now instead, we use the date of positive testing. The reason is that most imported cases might have been abroad when the symptoms appeared, while we are sure that they are in Norway on the day they test. The positive test data is also a more sure data point, compared to the first day with symptoms. This change makes a difference in March and April, as can be seen in the figure 22, where we show a comparison between the previous seeding (red) and the new one (black).

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

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

– 1 September: **Revised hospitalisation probabilities** We have changed the probability that an infected individual (symptomatic or asymptomatic) is hospitalised. In the last weeks it has become apparent that the age profile of the individuals who test positive does not follow the demography of the Norwegian population, with a much stronger representation of the age group between 20 and 29 years. Therefore we had to change our assumptions, namely that age of infected individuals was following the demographic age profile of the Norwegian population. Instead we learn the distribution of ages of the infected from the Norwegian data of who tested positive. We computed a correction factor for each age group, consisting of the ratio between the proportion tested of each group divided by the demographic proportion in the overall Norwegian population. We computed the percentage of each age group among all positive tests taken from May 1 until the last available data. For the age group 20-29 this percentage was on 1 September 26%, while in the general population, this age

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

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

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

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

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

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

– 12 October **Included reporting delay for hospital admissions:** We have implemented a reporting delay of new hospitalisations. We estimated it from all data since April using time from admissions to reporting in the Beredt-C19 registry. The reporting delay is implemented as a probability that an admission which happened on a certain day is actually reported with a delay of one to four days. We estimated these delay probabilities for the last four days from "today" and have different delay probabilities on Monday compared to the rest of the week, because the delay is more pronounced for admissions happening in the weekend. The probabilities are listed in Table 18, Assumptions.

–19 October **Using test data:** We include the test data in the calibration procedure of the changepoint model. Before, we have calibrated our model to hospital incidence only. In our simulations, we assume that the number of positively tested cases can be modelled as a binomial process of the simulated daily total incidence of symptomatic and asymptomatic cases, with a time-varying detection probability which we estimate.See in the model description above all details on the model we use for the detection probability and the way we actually perform the calibration. The estimated parameters of the detection probability are listed in Table 13.

–19 October **Included reporting delay for test data:** As for the hospitalisation data, we take into account the reporting delay of the test data for the last four days. Details are provided in the Model chapter of the report. The reporting delay probabilities are listed in Table 18, Assumptions.

–20 October **New figures for test data and detection probability** Figure 1b shows how our model follows the reported daily number of positive cases. In this figure we do not correct for the reporting delay in the last four days, so that the decay in the end is only due to such delay. Figure 4b is a daily varying estimate of the probability to detect a positive case. This is based on a logit model with intercept and total number of tests as covariate.

–27 October **Long term predictions use hospitalisation rates based only on demography.** When predicting the next 12 months, we assume a constant reproduction number distribution and a mobility matrix as today. For the first next three weeks we use hospitalisation rates, which utilise also the current age profile of positive cases. However, after the first three weeks, we use rates based on demography. This is because our compartmental model does not have age classes, and in the long term the number of immune per age class does matter. New projections include updated hospitalization parameters (see 12 October).

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

– 29 October: **New probabilities of being hospitalised when infected, per age group updated every month** We correct the hospitaliastion rates from Salje at al. 2020 based on the age profile of cases. We obtain a new estimate of the percentage of cases per age class every month. Since 1 May we use monthly age-structure corrections, see Table 16 and 17.

– 3 November: **Regional data are presented in this report.** This report combines the results of two models: the national and the regional models, which previously had each its own report. The two models are identical except for the following differences (1) the regional model uses county-specific hospitalisation incidence and county-specific test data, so for each fylke, while these data are aggregated together in the national model; (2) each county has its own reproduction numbers in the regional model, while there is only a national reproduction number in the national model; the changepoints of the national model and of the regional model are placed in different days. The results of the national model are not a simple average or aggregation of the results of the regional model, because they use different data. The national results should be used when analysing the pandemics nationally, while the regional results should be used when specifically looking to the different counties. The estimates and predictions of the regional model are more uncertain than the ones of the national model, because there are more parameters to estimate and there are less data in each county. We cannot have too many change points in the regional model, because in each county there are less data (for example many days without any hospitalisation).

– 3 November: **Long term scenarios get new fixed reproduction numbers.** In the scenario runs with fixed reproduction numbers we now use three, all higher than the currently estimated reproduction number.

– 3 November: **Importations from abroad also seeded in short term predictions.** From this week, we include also importation of cases for the first three weeks into the future, by repeating the importation four, three and two weeks ago. We do not use the most recent week, as this might be subject to a reporting delay. These importations are also amplified with the stochastic amplification factor.

– 3 November: **Check for change point in amplification factor** Currently our model has a unique amplification factor for the whole epidemic. This is a random variable, with a mean which we estimate from all the data. We start to check regularly (we hope every month) if a change point in the amplification factor is needed. We have tested now that a change point in the amplification factor on 1 August does not appear to be needed, and is therefore not included.

– 10 November: **Number of imported cases subtracted from number of positive cases, daily, before calibration.** In our model we calibrate parameters by comparing the simulated number of positive cases generated by our SEIR model with the actual reported numbers of laboratory-confirmed cases. We seed with all the known imported cases in our model. Because the imported cases are not produced by our infection model (but by a competing model abroad), we subtract the daily number of known imported cases from the total number of daily positive cases, before calibration.

– 17 November: **Updated estimates of reporting delay for positive cases.** We estimated the delay in reporting of positive lab tests in MSIS using the data of the last 20 days and found the following new values:

6.7%, 59%, 90%, 97% for the last four days. We will not list future changes which will happen regularly.

– 25 November: **Updated estimated hospitalisation parameters.** All the hospitalization parameters have been updated and current values are reported in the table at the end of the report and in the diagram (figures 28 and 29). We re-estimated all the parameters with data since August 1st. In addition, we updated the weights of the hospitalization probabilities (also updated on table 17) using the age profile of the cases.

– 25 November: **SMC now uses also test data.** From today we use also test data to estimate all parameters in the SMC model. We use the same approach as in the changepoint model, namely we estimate the probability that an infected individual is detected positive by a laboratory test. We use the same logistic regression with an intercept and the total number of daily performed tests as covariate. In the SMC we calibrate the parameters at daily level, so we have a likelihood of daily number of positive test cases, while in the changepoint model we calibrate using a weekly moving average. In the SMC, like in the changepoint model, we can trust the estimates of the reproduction number until about a week before the last day with data, because there are about 5 days between infection and appearance of symptoms and about 2 days of reporting delay. The SMC figure is still a weekly smoothed version of the daily estimated reproduction number. The SMC currently uses test data only from 1 August, because the test data before are more heterogeneous. This can be seen in the SMC figure, where the credibility interval is more narrow from that day on, as more data are then available. The SMC used, in the test data model: $\pi_0 = 2.2374084357$ and $\pi_1 = 0.0001640311$, estimated by first running only on hospital data, thus obtaining an estimate of the number of infected individuals (symptomatic and asymptomatic), which is then used to fit the logistic regression to the test data. Later we will try to estimate them together with all other parameters, in order to estimate the uncertainty better. The uncertainty can be a little too small now.

– 1 December: **SMC now esimates effective reproduction numbers.** From today we estimate the daily effective reproduction number which is the reproduction number (based on the betas in the compartmental model) times the estimates of the proportion susceptibles.

– 1 December: **Hospital re-admissions are excluded from the calibration data.** Some patients are admitted to hospital then discharged and then readmitted, sometimes multiple times. It is only the first admission which informs us about the time this patient has been likely infected. Therefore we have now excluded from the hospitalisation data that we use for calibration all readmissions. This is about 5% of the total number of admission, and the difference on the estimated parameters is very small.

– 7 December **Effective reproduction numbers.** From today we multiply the calibrated reproduction numbers (given by the estimated β) by the estimated median proportion of susceptible in the corresponding period (when the reproduction number is active, between changepoints). This is called the effective reproduction number and is of key interest. As the proportion susceptible is very close to 1, this does not make much difference compared to the reproduction number which assumes everybody is susceptible. This will change when vaccination will start.

– 7 December **Data from Norsk Pandemiregister.** From today, we use data only from Norsk Pandemiregister, because of their better quality and completeness. The number of cases is different from what we used in the past.

– 7 December **Excluding imported cases from the hospitalisation data used in calibration.** From today, we exclude the cases imported from abroad from the hospital incidence used for calibration. We do this as these imported cases are not informative about the transmissibility within Norway, as these cases were infected abroad. This affects our results, so that the estimated transmissibility becomes lower. Hence, we estimate a lower total number of cumulative infections, and thus also a higher detection probability for the positive tests. When we predict the number of new hospitalisations

and the prevalence of hospitalisation, we have to add back the patients who have been infected abroad, as they occupy a bed irrespective of the origin of their infection. The amplified individuals (representing undetected importations) if hospitalised in our simulations, are also added to the predicted numbers of hospitalisations. We currently use the same probabilities to send cases to hospitals, irrespective of them being imported or not. We will check if the age profile in the imported cases is different from the non-imported ones, and in this case update the probabilities accordingly.

– 14 December **Including imported cases in predictions of hosptalisation.** As opposed to last week, we include the imported cases from abroad in the hospital predictions, even though they are not used for calibration. This is done because even though they are not informative about transmissibility in Norway, they occupy hospital capacity.

– 14 December **Hospitalisation parameters based on Norsk Pandemiregister.** As we transitioned to using hospitalisation data from Norsk Pandemiregister last week, we have now updated the estimates of all hospitalisation parameters based on this data.

– 5 January 2021 **Convergence difficulty of the regional model.** We continue to have difficulties in convergence of the sequential ABC regional model. It takes now 48 hours to run about 65 rounds, and for many counties we do not see convergence yet. This is not so unexpected, because of the very large number of parameters (many changepoints for each fylke). We are working with several options to speed up convergence.

– 7 January 2021 **Imported cases in predictions.** This is something that we have been doing for a long time, but we might not have documented it here. Therefore this happens now: When we simulate the next three weeks, we introduce the same imported cases that happened 4, 3 and 2 weeks ago. with the same amplification. When we do longer predictions we do not include any new importation.

- 10 January 2021 **New algorithm for the sequential ABC for the regional model.** In order to improve convergence in a limited time (about 2 days), we split the data in two, estimate separately the parameters in the first part with a long run; then take over the last parameters and the simulated compartments into the second estimation, where we estimate the parameters until today. This second run has less parameters and can be run to convergence in 2 days. We are preparing a technical note on this method, and are still testing its actual implementation.

- 1 February 2021 **New regional hospitalisation rates for the regional model.** Since 1 September we have been using the percentage of cases per age class, to correct the hospitalisation rates. Now we compute these correction coefficients separately for each region (fylke), because the age profile of cases can be different in the various regions.

- 1 February 2021 **The SEIR model is now moved from the municipality scale to the regional scale.** Since the convergence of the regional model is so slow, and we must produce results within 48 hours, we have decided to abandon the municipality scale, in favour of a fylke-wise scale. This means that now every fylke has its various compartments, instead than the municipalities. The Telenor mobility matrices are added up to fylke level. This speeds up each single simulation. We will still be able to produce predictions at municipality level, as this is useful in some contexts (HSØ for example).

24 February 2021 **Calibrating Oslo and Viken separately.** We obtain very broad credibility intervals for the reproduction numbers for all fylker, excluded Oslo and Viken. We do not know if this is because (1) the data we have for those fylker do not carry enough information about the parameter, or (2) because the model is such that time-consecutive reproduction numbers are negatively correlated, and therefore difficult to estimate well, or (3) because the test and hospitalisation data in these fylker are non consistent and therefore the estimation is uncertain or (4) because the convergence of the regional model is so slow, and we have not converged yet. We have now tested with calibrating separately Oslo and Viken and all other fylker together. In this way we ask the sequential ABC

to improve the estimation of the reproduction number of those fylker from one round to the next. Before, it might not be so important that the estimates of those rep number would improve, because Viken and Oslo have most data and it is enough to just improve fro them. We run this separate calibration for the regional model in the pre and post-split runs.

24 February 2021 **Stop estimating internal test parameters in the regional model.** Since the convergence of the regional model is so slow, the parameters π_0, π_1 and the delay d are now sampled from the posterior distribution estimated by the last national model, instead than estimate them ex-novo in the regional model.

– 8 March 2021 **New algorithm for the regional model.** In order to get better estimates of the effective reproduction numbers for each county, we now proceed as follows: We run as before the full model until a split point. Currently it is 4 January. This pre-split run is on data that do not include the last 5-6 days, so that it can be run for several days until Monday morning, when we start the post-split run using the most recent data. The pre-split run is in fact also divided into two, to again rely on longer runs of the first part of the history of the epidemic and focus on the most recent part of the epidemic (though pre split 4 Jan) when running typically from Thursday morning to Monday morning. The post-split run assumes one change point per county (so two reproduction numbers per county need to be estimated). We run a full model, with different rep numbers (betas) per county, and where the calibration error is such that every round of the sequential ABC improves by 20% the fit of Oslo and Viken, and by 20% the fit of all other counties together. This last component of the calibration error does therefore not require that every county sees its beta improve. To improve this situation, we run also 9 additional and separate models, each focusing on the 9 counties (not Viken and Oslo, which are always well calibrated): here we have a beta for that county and for all other ten counties we assume the same beta. This run requires the calibration to improve 20% for the county in focus. After these separate runs, we perform one additional run with all counties having their own betas, but using the results from the focused runs as priors for the betas for all counties. This final run has the purpose to correct for dependencies between the betas if the various counties. This final run is run for only a few rounds.

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