Long-term scenarios for the number of new hospitalizations during the Belgian COVID-19 epidemic

RESTORE consortium
Report version 7.0

Steven Abrams[1,2], Jan M. Baetens[3], Jenna Vergeynst[3,4], Tijs W. Alleman[4], Ingmar Nopens[4], Kurt Barbé[10], Fred Vermolen[5], Nicolas Franco[1,6], Sébastien Clesse[7], Lander Willem[8], Christel Faes[1], Geert Molenberghs[1,9], Philippe Beutels[8], Niel Hens[1,8]

[1] Data Science Institute, I-BioStat, UHasselt, Hasselt, Belgium

[2] Global Health Institute, Department of Epidemiology and Social Medicine, University of Antwerp, Antwerp, Belgium

[3] KERMIT, Department of Data Analysis and Mathematical Modelling, University of Ghent, Ghent, Belgium

[4] BIOMATH, Department of Data Analysis and Mathematical Modelling, University of Ghent, Ghent, Belgium

[5] Computational Mathematics (CMAT), UHasselt, Hasselt, Belgium

[6] Namur Institute for Complex Systems, University of Namur, Namur, Belgium

[7] Service de Physique Théorique, Université Libre de Bruxelles (ULB), Brussels, Belgium

[8] Centre for Health Economic Research and Modelling Infectious Diseases, Vaccine and Infectious Disease Institute, University of Antwerp, Antwerp, Belgium

[9] I-BioStat, KU Leuven, Leuven, Belgium

[10] Biostatistics and medical informatics (BISI), Vrije Universiteit Brussel, Belgium

www.covid-en-wetenschap.be/restore

February 23, 2020

Summary

- This report describes the possible impact of the 501Y.V1 variant and vaccination for Belgium and illustrates the importance of epidemic control in the period to come.
- Due to its larger transmission potential, the 501Y.V1 variant is expected to completely take over the old variants by mid-March. Due to large uncertainty on the transmission characteristics exerted by the 501Y.V1 variant, we explore increases in transmission of 30 %, 50 % and 70 %. The variant might cause, if the current transmission dynamics are sustained, a challenge but not an insurmountable problem for epidemic control.
- Lifting measures can, in spite of the ongoing vaccination campaign, still lead to a third wave. However, postponing deconfinement allows the vaccination campaign to offset the increased transmission risk and associated disease burden. It is therefore essential to release influential measures to reduce transmission rather later than sooner.
- Vaccination and seasonality (currently not modelled) are expected to have a positive impact on the incidence of new hospitalisations in the coming period. However, recent evidence from the UK indicated that the 501Y.V1 variant is associated with a higher per-case probability of severe and lethal disease. This latter aspect has been ignored in the simulations in this document.
- Our results are consistent with results obtained in UK, NL and CH (cfr: Recover and EpiPose consortium meeting reports).

Introduction

After an initial outbreak of *Severe Acute Respiratory Syndrome coronavirus 2* (SARS-CoV-2) in early 2020 in Wuhan, China, the epidemic has evolved into a global pandemic. The prevention of COVID-19 outbreaks has been depending on the successful implementation of non-pharmaceutical interventions, such as social distancing, testing, contact tracing and quarantine. Recently, vaccines have become available and enable many new deconfinement strategies, which can be evaluated via data-driven models to assist in the policy making process. Within this RESTORE consortium, multiple mathematical models have been applied to perform scenario analyses tailored to the Belgian setting, for example, the stochastic compartmental model of Abrams et al. (2020), the deterministic metapopulation model of Alleman et al. (2020), the deterministic compartmental model, explicitly accounting for the nursing home population, by Franco (2020), the individual-based model by Clesse (2020) and a time-series model by Barbe, Blotwijk, and Cools (2020).

All these models have been independently created for the same purpose: to understand and study the spread of SARS-CoV-2 in Belgium. However, modeling the transmission of an infectious disease implies a detailed investigation and understanding of human behaviour, which is not trivial to translate into a set of mathematical equations. As a consequence, each of the mathematical models relies on different assumptions and modelling techniques. By combining the different scenario analyses into an ensemble, we investigate structural model uncertainty. This is standard practise when it comes to model-based decision support, e.g. the Intergovernmental Panel on Climate Change (IPCC) considers the outcomes of more than 10 different models for supporting its reports on climate change (Gerstengarbe et al. 2015). Moreover, an ensemble can be used to mutually validate the projections over time. This report contains different long-term scenarios for the spread of SARS-CoV-2 in Belgium with the purpose of informing upcoming mitigation/relaxation policies.

Methods

Long-term forecasting models

All models used in this report (SIMID, UGent and UNamur) are compartmental models and capture the dynamics of the epidemic by dividing the population into different compartments. By default, it contains susceptible (S), infectious (I) and removed (R) compartments, which is called an SIR model (Kermack and McKendrick 1927). The models used here differ in the way the compartments are further subdivided to capture the details of COVID-19 disease dynamics, making each model subject to different assumptions (Table 2). The models are based on disease mechanics, hence called mechanistic models, and are well-fit to study long-term scenarios. Since the spread of SARS-CoV-2 is mainly driven by social contact behaviour, data on social contact behaviour at different locations, e.g., home, school, workplace, public transport and during leisure activities are used to translate government policies into tangible scenarios (Willem et al. 2012; Willem et al., 2020b).

For this report (version 7.0) in which the effect of the 501Y.V1 variant is explored, the ULB and VUB models have not been included. More details on the specific properties, assumptions and limitations of each model can be found in the Supplementary materials.

The 501Y.V1 variant

The scenarios in this consider the introduction of a new variant of concern (VOC), i.e. 501Y.V1 or VOC-202012/01 (lineage B.1.1.7), in the Belgian population from January 1, 2020 onward. The most recent data indicate that this VOC is more transmissible than the original strain, with an increase varying between 30% and 70% compared to the original strain (hereafter referred to as wild-type strain) (Wenseleers 2021). To account for the uncertainty with regard to the increase in transmission potential and to show the impact thereof, we have used either a 30%, 50% or 70% increase in transmissibility as compared to the wild-type strain in the studied scenarios.

Other new VOCs such as the 501Y.V2 or 501Y.V3 variants, are not accounted for, since their prevalence in Belgium at this time is low and their transmissibility is uncertain. Although some preliminary evidence suggests that the probability of hospitalization and death is higher for 501Y.V1, the models currently do not account for this increase (Nicholas G. Davies et al. 2021; Horby et al. 2021).

Vaccination campaign

All scenarios account for the national vaccination campaign in place. Since age-specific data on the administered vaccinations are not available yet and there is no official communication on the planned number of doses, we used a hypothetical vaccination scheme to reach full population coverage by the end of the summer as published by Fluit, Segers, and Serrure (2021) in *de Tijd* (see Table 1 and Figure 1).

We note that the vaccination scheme published on January 16th, 2021 is subject for discussion. The SIMID model slightly deviates from the scheme up to February 11th by including the reported uptake by Sciensano, which is little less compared to the uptake described above. None of the models can identify professional functions nor co-morbidity's, hence the vaccination of health care personnel, general practitioners and individuals with underlying medical conditions is incorporated by the vaccination of a fraction of the working age population (20-65). Therefore, the goal and additional advantage of prioritising these groups in avoiding deaths and virus spread among

the most vulnerable people, is not captured by the models. Moreover, in the current absence of consensus in the literature on the effect of vaccination on transmission, we implemented an "all-or-nothing" vaccination model implying that a certain percentage of vaccinated individuals is fully protected against infection. As such, we do not account for the possibility that vaccinated people can acquire protection against severe disease and/or hospitalization but still transmit the virus (i.e. a leaky vaccine model).

For simplicity, the models assume that vaccinated people are fully protected one month after their first vaccination. Despite the reported differences in vaccine efficacy observed during for the vaccines that are currently licensed (Pfizer/Moderna/Astra Zeneca), we assumed a fixed effective coverage of 70%.

Months	**Doses/day**	**Population**
January 2021	31.765	Residents and personnel of nursing homes and care personnel in hospitals
February 2021	45.897	General practitioners
March-April 2021	128.499	65+ age group and individuals with underlying medical conditions
May-August 2021	78.358	People involved in essential sectors and the general 18+ population

Table 1: Targeted vaccination strategy to reach full population coverage by August 2021 (Fluit, Segers, and Serrure 2021).

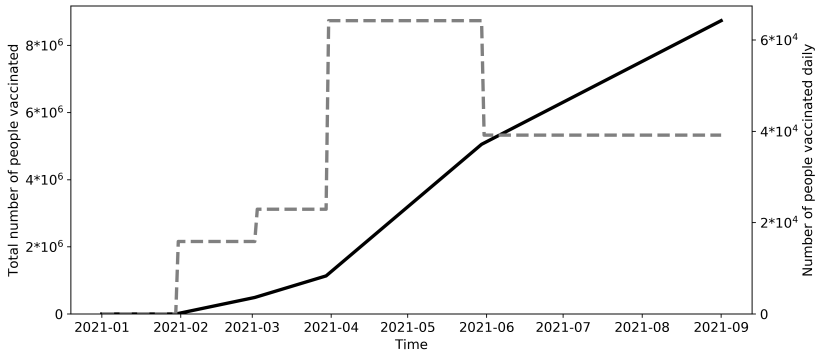

Figure 1: Total number of individuals vaccinated with a 1st dose (black line) and daily number of available 1st doses (grey dashed line) over time according to the implemented vaccination strategy.

Scenarios

We calibrated the models with Belgian incidence data until February 1, 2021. In all scenarios, schools are closed from February 15th-21th, 2021, and from April 5th-18th, 2021.

Scenario 1 Extrapolation of current social contact behaviour.

Scenario 2 Contact behaviour similar to September 2020, starting on March 1st, 2021.

Scenario 3 Contact behaviour similar to September 2020, starting on April 1st, 2021.

Scenario 4 Contact behaviour similar to September 2020, starting on May 1st, 2021.

Each scenario assumes that the targeted vaccination scheme is followed with an effective coverage of 70%. For each scenario's, we include 3 options regarding the VOC:

a) Assuming 30% more transmissibility of the 501Y.V1 variant.

b) Assuming 50% more transmissibility of the 501Y.V1 variant.

c) Assuming 70% more transmissibility of the 501Y.V1 variant.

Results

Extrapolation of the current situation (Scenario 1)

Figure 2 shows the combined impact of the 501Y.V1 variant and the vaccination campaign under the assumption that the transmission potential of the 501Y.V1 variant is 30 %, 50 % or 70 % more compared to the wild-type. In the best case (30 % increase), the ongoing vaccination campaign alleviates the increase in transmission potential, with the hospitalisations admissions reaching the threshold of 75 new hospitalizations between March 9th, 2021 and May 14th, 2021. In Report 6.1 it was stated that we would reach the 75 new hospitalizations threshold between January 10th and March 11th, though these estimations did not account for the emergence of the 501Y.V1 variant.

In spite of the ongoing vaccination campaign, but without (voluntary) behavioural changes, a 70 % increase in transmission potential of the VOC may lead to a situation where the Belgian maximum ICU bed capacity is reached (SIMID), slightly surpassed (UGent) or largely surpassed (UNamur) (see Figure 4). In the intermediate scenario of a 50 % increase, a third COVID-19 wave occurs, albeit not as large as the second COVID-19 wave of October-November 2020. Overall, the 501Y.V1 variant will most likely not cause capacity issues for the Belgian health care system if we maintain the current social contact dynamics.

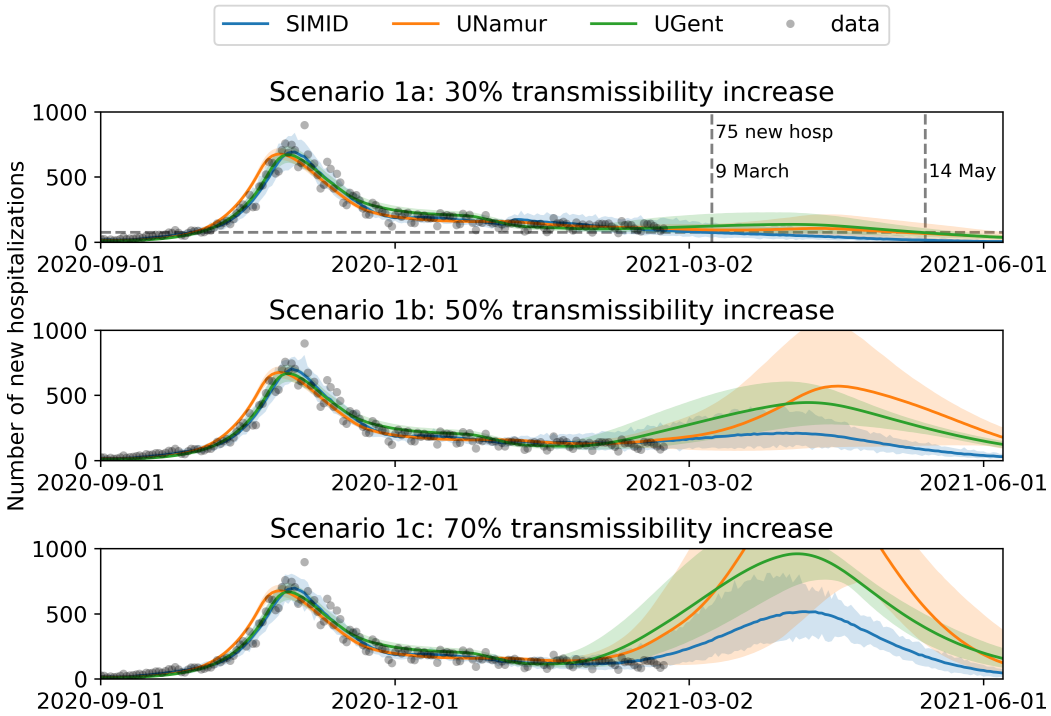

Figure 2: Model trajectories for the number of new hospitalizations under an extrapolation of the current contact behaviour: mean with 95% confidence interval. Models calibrated on February 1, 2020; new data shown up to February 15th, 2020.

Deconfinement strategies (Scenarios 2-4)

An increase in social mixing, and as such transmission, from March 1st onward similar to the dynamics we estimated for September 2020 (Scenarios 2a and 2c), leads to a third COVID-19 wave which could overload hospitals' capacities. Only for one model and in the most optimistic case of a 30 % transmissibility, this is not the case. In addition, the sooner social contacts increase, the faster the new strain can become dominant. A relaxation with contact behaviour similar to September 2020 from May 1st onward (Scenarios 4a and 4c) leads to a more controllable situation, even if the transmissibility of the 501Y.V1 variant is high. Releasing measures later allows the vaccination campaign to anticipate more on the increase in transmission. For the hospital admissions and load, it is better to release measures rather later than sooner.

Hospital incidence

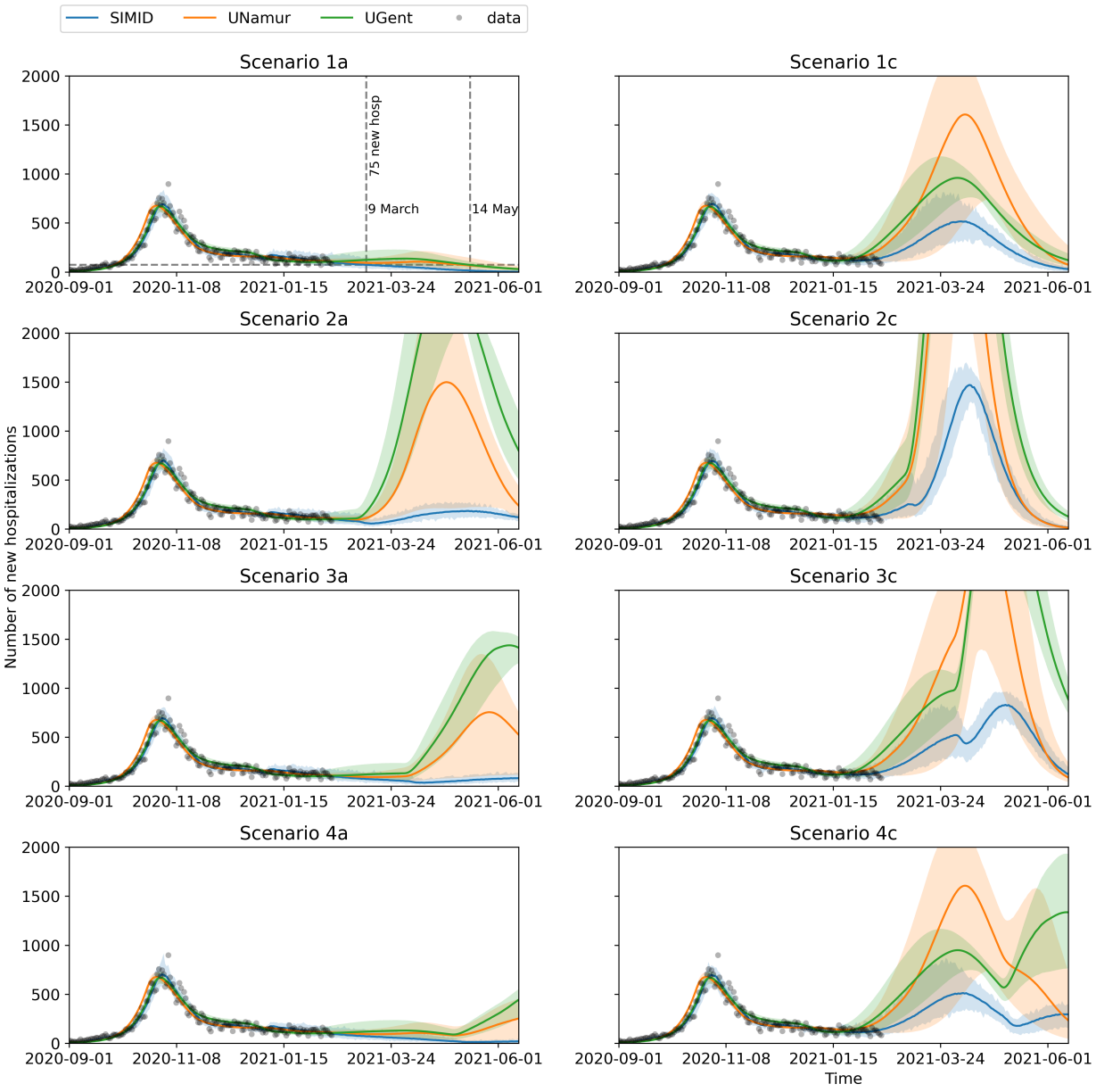

Figure 3: Model trajectories for the number of new hospitalizations for the different scenarios: mean value with 95% confidence interval. Models were calibrated on February 1, 2020 and new data are shown up to February 15th, 2020.

Hospital load

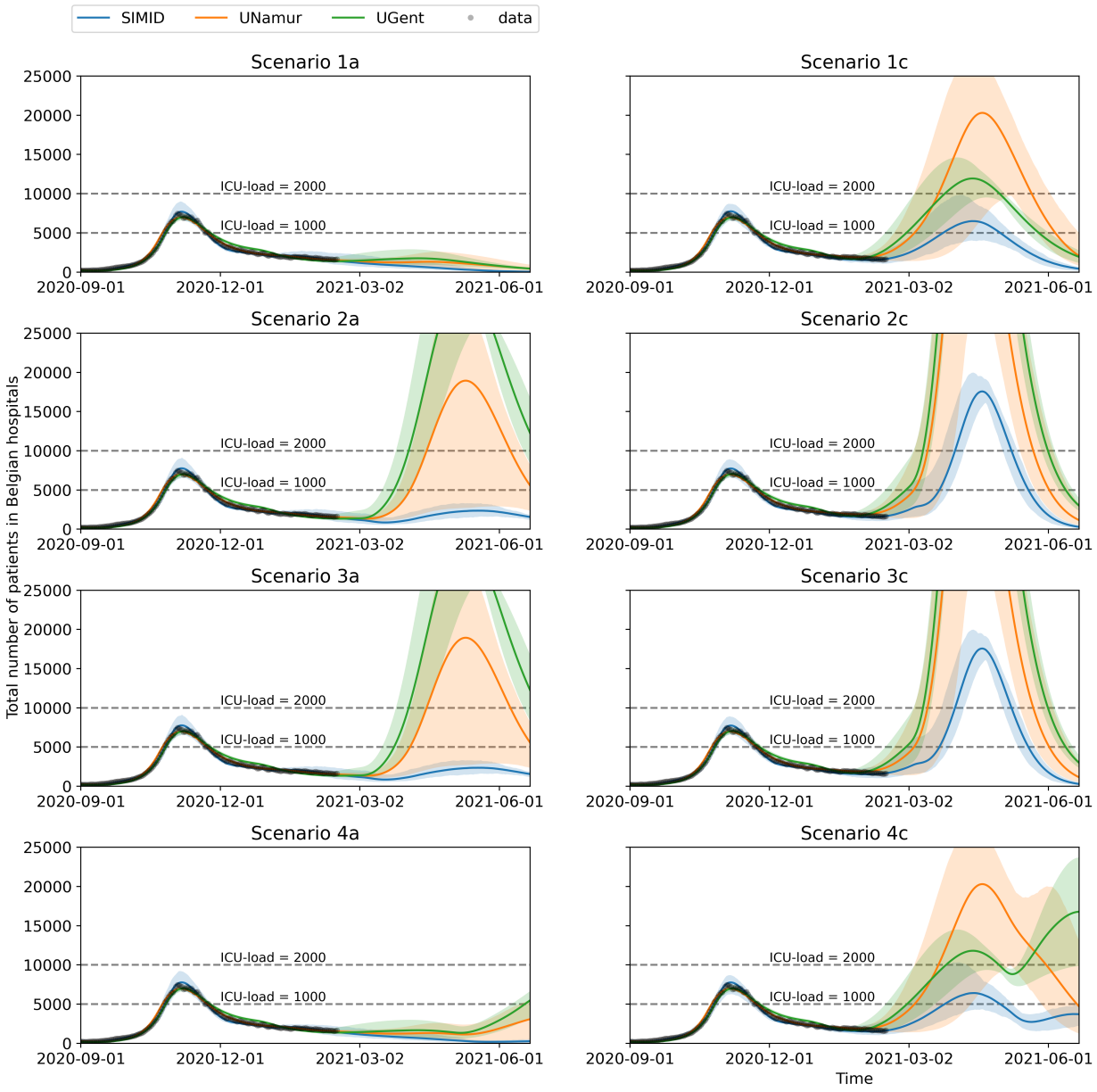

Figure 4: Model trajectories for the hospital load: mean value with 95% confidence interval. The dashed lines indicate the number of available ICU beds for COVID-19 patients (1000: normal capacity and 2000: increased capacity).

Limitations

There are several limitations for the models used in this report,

- The different scenarios are expressed in terms of changes in social contact behaviour. These are used as proxies for changes in transmissibility, which result from the combination of social distancing and hygienic measures taken at different locations, e.g., at home, at work and at school.
- Scenarios should not to be interpreted as predictions, since we are not able to discern the most plausible scenario given the unpredictable nature of adjusted social behaviour, future measures, the appearance of new strains and uncertainties with regard to vaccine efficacy and supply.
- The models do not consider the spatial structure of the population. Although at Ghent University, a spatially explicit model is nearing completion.
- We do not account for seasonality nor cross-immunity, although these effects might influence the transmission dynamics.
- The effects of contact tracing, testing and self-isolation are incorporated indirectly within the estimated transmission potential within the population over time.
- We do not account for other VOCs than the 501Y.V1 variant although the 501Y.V2 variant and the 501Y.V3 variant have been detected in Belgium by February 2021. Preliminary evidence suggests the 501Y.V2 variant has roughly the same transmissibility as the 501Y.V1 variant, meaning the results should be sufficiently robust as this variant becomes more prevalent.
- The models do not accommodate for VOC-specific hospitalization probabilities and mortality rates. This could lead to an underestimation of the impact of the VOC on the number of new hospitalizations as preliminary evidence suggests the disease burden may be higher (Nicholas G. Davies et al. 2021; Horby et al. 2021).
- Vaccine protection is included as a step-function representing an all-or-nothing immunity one month after the first dose. We do not account for an incremental build-up of immunity, nor a differential protection for severity of disease instead of infection. The effective coverage equals 70 % for all results shown in this report. Differences in effectiveness between different vaccines have not been addressed.
- The vaccination strategy implemented in the scenarios is based on an optimal vaccine scheme to reach full coverage by August 2021. In the future, there might be a significant difference between the assumed vaccination strategy and the actual one, which will be addressed in future reports.
- The advantage of prioritising vulnerable people and care personnel is underestimated in all models, since only age-specific vaccination effects are captured.

Acknowledgements

The authors gratefully acknowledge the support by Prof. dr. Heidi Theeten, Prof. dr. Pierre Van Damme and dr. Sereina Herzog with regard to the serial serological survey data through personal communication on the matter.

NH acknowledges financial support by the ERC TransMID (682540) project. NH, CF and PB acknowledge support from the Horizon 2020 Epipose (101003688) project. JB, SA, LW and NH gratefully acknowledge support from the Research Foundation Flanders (RESTORE project – G0G2920N and postdoctoral fellowship 1234620N). JB, TA and JV acknowledge the financial support they received from the UGent Special Research Fund and the VZW 100 km Dodentocht Kadee through the organisation of the 100 km COVID-Challenge.

References

Abrams, Steven, James Wambua, Eva Santermans, Lander Willem, Elise Kuylen, Pietro Coletti, Pieter Libin, et al. 2020. "Modeling the early phase of the Belgian COVID-19 epidemic using a stochastic compartmental model and studying its implied future trajectories." medRxiv, https://doi.org/10.1101/2020.06.29.20142851.

Alleman, Tijs W., Jenna Vergeynst, Elena Torfs, Daniel Illana Gonzalez, Ingmar Nopens, and Jan M. Baetens. 2020. "A deterministic, age-stratified, extended SEIRD model for assessing the effect of non-pharmaceutical interventions on SARS-CoV-2 spread in Belgium." medRxiv, https://doi.org/10.1101/2020.07.17.20156034.

Barbe, Kurt, Susanne Blotwijk, and Wilfried Cools. 2020. Data-driven epidemiological model to monitor the sustainability of hospital care. Technical report ICDS300420. Vrije Universiteit Brussel.

Davies, Nicholas G, Petra Klepac, Yang Liu, Kiesha Prem, Mark Jit, Carl A B Pearson, Billy J Quilty, et al. 2020. "Age-dependent effects in the transmission and control of COVID-19 epidemics." Nature Medicine, ISSN: 1546-170X. https://doi.org/10.1038/s41591-020-0962-9. https://doi.org/10.1038/s41591-020-0962-9.

Davies, Nicholas G., Christopher I. Jarvis, W. John Edmunds, Nicholas P. Jewell, Karla Diaz-Ordaz, and Ruth H. Keogh. 2021. "Increased hazard of death in community-tested cases of SARS-CoV-2 Variant of Concern 202012/01." medRxiv, https://doi.org/10.1101/2021.02.01.21250959. https://www.medrxiv.org/content/early/2021/02/03/2021.02.01.21250959.

Eberhart, R., and J. Kennedy. 1995. "A new optimizer using particle swarm theory." In MHS'95. Proceedings of the Sixth International Symposium on Micro Machine and Human Science, 39–43.

Faes, Christel, Steven Abrams, Dominique Van Beckhoven, Geert Meyfroidt, Erika Vlieghe, and Niel Hens. 2020. "Time between symptom onset, hospitalisation and recovery or death: Statistical analysis of belgian COVID-19 patients" [in eng]. International Journal of Environmental Research and Public Health 17, no. 20 (October): 1–18. ISSN: 16604601. https://doi.org/10.3390/ijerph17207560.

Fluit, Andries, Thomas Segers, and Ben Serrure. 2021. "De steile klim naar de verlossing." de Tijd (January). Accessed February 16, 2021. %5Curl%7Bhttps://www.tijd.be/dossiers/coronavirus/de-steile-klim-naar-de-verlossing/10277780.html%7D.

Foreman-Mackey, Daniel. 2016. "corner.py: Scatterplot matrices in Python." The Journal of Open Source Software 1, no. 2 (June): 24. https://doi.org/10.21105/joss.00024. https://doi.org/10.21105/joss.00024.

Franco, Nicolas. 2020. "Covid-19 Belgium: Extended SEIR-QD model with nursing homes and long-term scenarios-based forecasts." medRxiv, https://doi.org/10.1101/2020.09.07.20190108.

Ganyani, Tapiwa, Cécile Kremer, Dongxuan Chen, Andrea Torneri, Christel Faes, Jacco Wallinga, and Niel Hens. 2020. "Estimating the generation interval for coronavirus disease (COVID-19) based on symptom onset data, March 2020." Euro surveillance 25, no. 17 (April). ISSN: 1560-7917 (Electronic). https://doi.org/10.2807/1560-7917.ES.2020.25.17.2000257.

Gerstengarbe, Friedrich-Wilhelm, Peter Hoffmann, Hermann Österle, and Peter Christian Werner. 2015. "Ensemble simulations for the RCP8.5-Scenario." Meteorologische Zeitschrift 24, no. 2 (April): 147–156. https://doi.org/10.1127/metz/2014/0523.

Goodman, Jonathan, and Jonathan Weare. 2010. "Ensemble samplers with affine invariance." Communications in Applied Mathematics and Computational Science 5, no. 1 (January): 65–80. https://doi.org/10.2140/camcos.2010.5.65.

Google. 2020. "Community mobility reports." https://www.google.com/covid19/mobility/.

Gudbjartsson, Daniel F., Agnar Helgason, Hakon Jonsson, Olafur T. Magnusson, Pall Melsted, Gudmundur L. Norddahl, Jona Saemundsdottir, et al. 2020. "Spread of SARS-CoV-2 in the Icelandic Population." New England Journal of Medicine 382 (24): 2302–2315. https://doi.org/10.1056/NEJMoa2006100.

Herzog, Sereina, Jessie De Bie, Steven Abrams, Ine Wouters, Esra Ekinci, Lisbeth Patteet, Astrid Coppens, et al. 2020. "Seroprevalence of IgG antibodies against SARS coronavirus 2 in Belgium – a serial prospective cross-sectional nationwide study of residual samples." medRxiv, https://doi.org/10.1101/2020.06.08.20125179.

Horby, Peter, Catherine Huntley, Nick Davies, John Edmunds, Neil Ferguson, Graham Medley, and Calum Semple. 2021. NERVTAG. %5Curl%7Bhttps://app.box.com/s/3lkcbxepqixkg4mv640dpvvg978ixjtf/file/768458300892%7D.

Kermack, W. O., and A. G. McKendrick. 1927. "A Contribution to the Mathematical Theory of Epidemics." Proceedings of the Royal Society of London, Series A 115:700–721.

Sciensano. 2020. "COVID-19: Datasets." https://epistat.wiv-isp.be/covid/.

Wei, Wycliffe E., Zongbin Li, Calvin J. Chiew, Sarah E. Yong, Matthias P. Toh, and Vernon J. Lee. 2020. "Presymptomatic Transmission of SARS-CoV-2 — Singapore, January 23–March 16, 2020." Morbidity and Mortality Weekly Report 69:411–415. https://doi.org/http://dx.doi.org/10.15585/mmwr.mm6914e1.

Wenseleers, Tom. 2021. newcovid_belgium. https://github.com/tomwenseleers/newcovid_belgium.

Willem, Lander, Thang Van Hoang, Sebastian Funk, Pietro Coletti, Philippe Beutels, and Niel Hens. 2020b. "SOCRATES: An online tool leveraging a social contact data sharing initiative to assess mitigation strategies for COVID-19." BMC Research Notes 1 (13): 293. https://doi.org/10.1186/s13104-020-05136-9.

Willem, Lander, Kim Van Kerckhove, Dennis L Chao, Niel Hens, and Philippe Beutels. 2012. "A nice day for an infection? Weather conditions and social contact patterns relevant to influenza transmission" [in eng]. PloS one 7 (11): e48695–e48695. ISSN: 1932-6203. https://doi.org/10.1371/journal.pone.0048695.

Table 2: Main properties, assumptions and limitations of each model. The complete model descriptions can be found in the supplementary materials.

	SIMID (Abrams et al. 2020)	UGent (Alleman et al. 2020)
model type	stochastic, extended SEIRD	deterministic, extended SEIRD
	nation-level	nation-level
	SDEs (exponentially distributed rates)	ODEs
	mechanistic	mechanistic
properties	age-stratified	age-stratified
	asymptomatic cases	asymptomatic cases
	pre-symptomatic infectiousness	pre-symptomatic infectiousness
	no re-susceptibility	no re-susceptibility
	no re-importations	no re-importations
assumptions	asymptomatic individuals 50% less infectious	asymptomatic individuals not infectious
	age-dependent probability of being asymptomatic & developing severe symptoms	age-dependent probability of being asymptomatic & developing severe symptoms
	deaths in hospitals only	deaths in hospitals only
	distinction between ICU and non-ICU care	distinction between ICU and non-ICU care, recovery stay after ICU
	UNamur (Franco 2020)	VUB (Barbe, Blotwijk, and Cools 2020)
model type	deterministic, extended SEIQRD	deterministic, extended SIR
	nation-level	nation-level
	ODEs	ODEs
	mechanistic	moving window calibration (gray box)
properties	age-stratified	non-age-stratified
	asymptomatic cases	no asymptomatic cases
	pre-symptomatic infectiousness	no pre-symptomatic infectiousness
	no re-susceptibility	no re-susceptibility
	re-importations from travellers	no re-importations
assumptions	estimated infectiousness per severity	homogeneous hospitalization probability
	age-dependent probability of being asymptomatic & developing severe symptoms	age-dependent probability of being asymptomatic & developing severe symptoms
	separated deaths from nursing homes and hospital	deaths in hospitals only
	ULB (Clesse 2020)	
model type	stochastic, extended SEIQRD	
	nation-level	
	individual-based model	
	mechanistic	
properties	non-age-stratified	
	no asymptomatic cases	
	no pre-symptomatic infectiousness	
	no re-susceptibility	
	no re-importations	
	no vaccination	
assumptions	accounts for transmission in households	
	temperature correlation for infectiousness	
	short and long-term hospitalizations	
	shorter stays at hospitals in summer	

Supplementary materials

Model comparison

Of the five models, four models (Abrams, Alleman, UNamur and Barbé) assume homogeneous mixing of the entire population. As a non-spatial individual-based model, Clesse is the only exception. Currently, two patch models are under development. These allow to simulate the disease at a smaller spatial resolution (municipalities) and account for the effects of work & leisure mobility. Of the five models, four models (Abrams, Alleman, Franco and Clesse) extended the classical SIRD model structure to an extension of a SEIRD model structure. The addition of an exposed (E) compartment accounts for individuals being infected with the virus who are not yet infectious (latent). The infectious (I) compartment is split to account for the effects of pre-symptomatic, symptomatic and fully asymptomatic transmission, as these have been shown to be important in the spread of SARS-CoV-2 (Ganyani et al. 2020; Gudbjartsson et al. 2020). Opposed is the model of (Barbe, Blotwijk, and Cools 2020), which uses SIRD dynamics. The models of Abrams, Alleman and Franco split every compartment into age layers to account for different COVID-19 severity in individuals of different ages, as COVID-19 shows remarkably higher incidences in older individuals (Faes et al. 2020). These models then differ subtly in the hospital dynamics and assumptions made. Some of the key differences are: Abrams et al. (2020) and Alleman et al. (2020) assume deaths only arise in hospitals, while Franco (2020) accounts for nursing home deaths. Alleman et al. (2020) assume mildly symptomatic individuals self-quarantine while Abrams et al. (2020) and Franco (2020) assume these individuals are still infectious to some degree. The model of Franco (2020) does not explicitly account for intensive care while the models of Abrams et al. (2020) and Alleman et al. (2020) do. Four models use a mechanistic approach (Abrams, Alleman, Franco and Clesse) while one model (Barbé) uses a data-driven approach. A detailed overview of the key differences is provided in Table 2. In what follows, each model is discussed separately in more detail.

SIMID (UHasselt/UAntwerp) (Abrams et al. 2020)

We use a stochastic discrete age-structured compartmental model (Abrams et al. 2020) calibrated on high-level hospitalization data (Sciensano 2020), serial serological survey data (Herzog et al. 2020) and Belgian mortality data (Sciensano 2020). More specifically, the stochastic model predicts (stochastic realisations of) the daily number of new hospitalizations per age group (i.e., 10 year age groups). The modeling approach depends on assumptions with regard to the transmission process which inevitably implies an underestimation of the level of uncertainty. As the model-based long-term predictions rely on changes in social contact behaviour following the exit strategy initiated May 4, 2020, we present such predictions under various scenarios which aim at giving some insights in the future course of the epidemic without being able to assign a probability to each scenario related to the likelihood of a given scenario to become reality. We do account for the current resurgence of COVID-19 in the selection and presentation of plausible scenarios. In this model we are not explicitly accounting for re-importation of the pathogen in the population

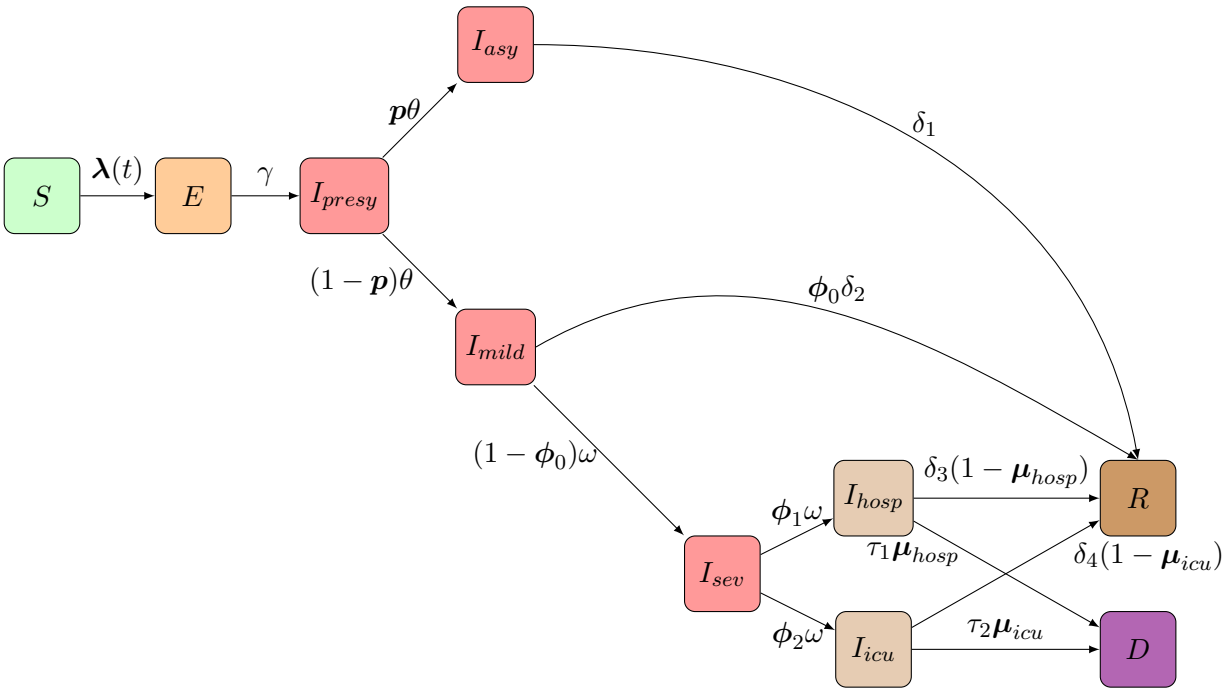

Figure 5: Schematic overview of the flows of individuals in the compartmental model: Following SARS-CoV-2/COVID-19 infection susceptible individuals (S) move to an exposed state (E) and after a latent period individuals further progress to a pre-symptomatic state (I_{presym}) in which they can infect others. Consequently, individuals stay either completely symptom-free (I_{asym}) or develop mild symptoms (I_{mild}). Asymptomatic individuals will recover over time. Upon having mild symptoms, persons either recover (R) or require hospitalization (going from I_{sev} to I_{hosp} or I_{icu}) prior to recovery (R) or death (D).

UGent (Alleman et al. 2020)

We extend the classical SEIRD model to incorporate more expert knowledge on SARS-CoV-2 (Alleman et al. 2020). The model accounts for pre-symptomatic and asymptomatic transmission, as these have been shown to be important contributors to SARS-CoV-2 spread (Ganyani et al. 2020; Wei et al. 2020; Gudbjartsson et al. 2020). Furthermore, the susceptibility to SARS-CoV-2, the severity of the disease and the susceptibility to an asymptomatic infection depend on the age of the individual (Nicholas G Davies et al. 2020). Our model takes hospitals explicitly in account and distinguishes between regular hospital wards (Cohort) and intensive care units (ICUs). Our model further accounts for a recovery stay of 6 days in Cohort after an ICU stay. From the pooled dataset of two Ghent (Belgium) hospitals, we computed the mortalities, length-of-stays in both hospital wards and the probability of needing intensive care. A flowchart of the model and its compartments is available in Figure 6.

We used age-stratified social contact rates from a study which has been made available using the Socrates tool (Willem et al., 2020b) to model age-specific social mixing. These social contact data are available at home, in the workplace, in schools, on public transport, during leisure activities and during other activities. The *Community mobility data* from Google (2020) are used as the primary weights for the contributions of work (G_{work}), transport ($G_{\text{transport}}$), recreation ($G_{\text{retail \& recreation}}$) and other contacts ($G_{\text{supermarkets}}$). Next, an effectiveness parameter Ω is introduced for home interactions, school interactions, work interactions and for the combination of transport, leisure and other interactions. These effectiveness parameters scale the relative contributions of each interaction matrix under lockdown measures and must be inferred from hospitalization data (Sciensano 2020) under varying social policies. All the above results in the following linear combination of interaction matrices to model social policies,

$$\begin{aligned}\boldsymbol{N}_{\text{c, total}}(t) = \Omega_{\text{home}}\boldsymbol{N}_{\text{c, home}} + \Omega_{\text{schools}}H_{\text{schools}}(t)\boldsymbol{N}_{\text{c, schools}} + \Omega_{\text{work}}G_{\text{work}}(t)\boldsymbol{N}_{\text{c, work}} + \\ \Omega_{\text{rest}}\Big[G_{\text{transport}}(t)\boldsymbol{N}_{\text{c, transport}} + G_{\text{retail \& recreation}}(t)\boldsymbol{N}_{\text{c, leisure}} + G_{\text{supermarkets}}(t)\boldsymbol{N}_{\text{c, others}}\Big],\end{aligned} \tag{1}$$

The model takes into account the effect of *social inertia* when lockdown measures are taken. In reality, lockdown restrictions represent a large change in behaviour which is gradual and cannot be modeled using a step-wise change of the social interaction matrix $\boldsymbol{N_c}$. In our model, we use a delayed ramp to model compliance,

$$\boldsymbol{N_c} = \boldsymbol{N}_{\text{c, old}} + f^k(\boldsymbol{N}_{\text{c, new}} - \boldsymbol{N}_{\text{c, old}}) \tag{2}$$

where,

$$f^k = \begin{cases} 0.0, & \text{if } k \leq \tau \\ \frac{k}{l} - \frac{\tau}{l}, & \text{if } \tau < k \leq \tau + l \\ 1.0, & \text{otherwise} \end{cases}$$

where τ is the number of days before measures start having an effect and l is the number of additional days after the time delay until full compliance is reached. k denotes the number of days since a change in social policy. The nine model parameters (transmission rate, $R_0(\beta, \omega, d_a)$; compliance model, l and τ; and the four effectiveness parameters) were calibrated to the daily Belgian hospitalizations between September 1st, 2020 and Februrary 1st, 2021. First a *particle swarm optimization* (Eberhart and Kennedy 1995) is performed to find the global minimum of the Poisson objective function. Next, the optimal parameter set is used as a starting point for the red-blue Markov-Chain Monte-Carlo method proposed by Goodman and Weare (2010). The chain is run until the length exceeds 50 times the integrated autocorrelation time. Subsequently, the

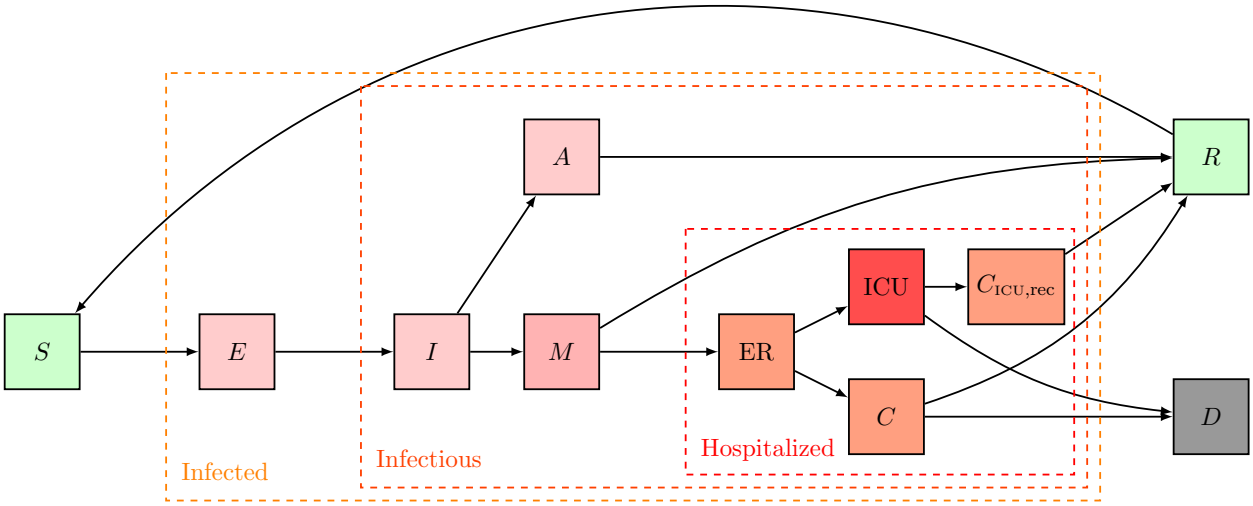

Figure 6: Extended SEIRD dynamics used in this study. Nodes represent model states, edges denote transfers.

chain is thinned and the cornerplots (Foreman-Mackey 2016) are examined to analyse correlations between model parameters and unidentifiability issues. All calibrated parameters were identifiable.

UNamur (Franco 2020)

The model initially developed at UNamur (Franco 2020) is a continuous age-structured compartmental model based on differential equations, calibrated on public Sciensano data on hospitalization, mortality and serology from blood donors.

The Belgian population is divided into 8 compartments in order to take account of the different possible stages of the disease as well as the separation between asymptomatic and symptomatic people with a different infectiousness. Each compartment is divided into 5 age classes with different characteristics concerning the behaviour and evolution of the disease. A schematic view of the structure of the model is presented in Figure 7. The transmission of the coronavirus between all classes is computed using social contact data at different places (home, work, school, leisure) (Willem et al. 2012; Willem et al., 2020b). Except social contact data, all of the 70 parameters of the model are estimated using a Monte Carlo method, hence there is no assumption coming from others studies. Nursing homes are modelled as isolated entities in order to take account of the different spread timing of the coronavirus compared to the general population. Specific parameters for the situation in nursing homes take account of a variable hospitalisation policy based on hospitals load as well as a probability that deaths coming directly from nursing homes are related to the covid-19. There is a specific estimation of potential reimportations coming from travellers during the holiday period. The model is mainly calibrated using hospitalisations and deaths using both incidence and prevalence data (depending on which one is the more appropriate for the considered data) coming from Sciensano's public raw data (Sciensano 2020). The model specifically accounts for the under-reporting in new hospitalizations due to transfers of patients from a non-COVID unit as well as improvement of care methods at the hospital since the first wave. Additional constraints on seroprevalence are coming from Sciensano's serological studies on blood donors as reported in Sciensano epidemiological reports. The only positive PCR tests which are taken into consideration are those coming from nursing homes from an overall test campaign in April-May.

All the technical details as well as estimated parameters can be found in (Franco 2020).

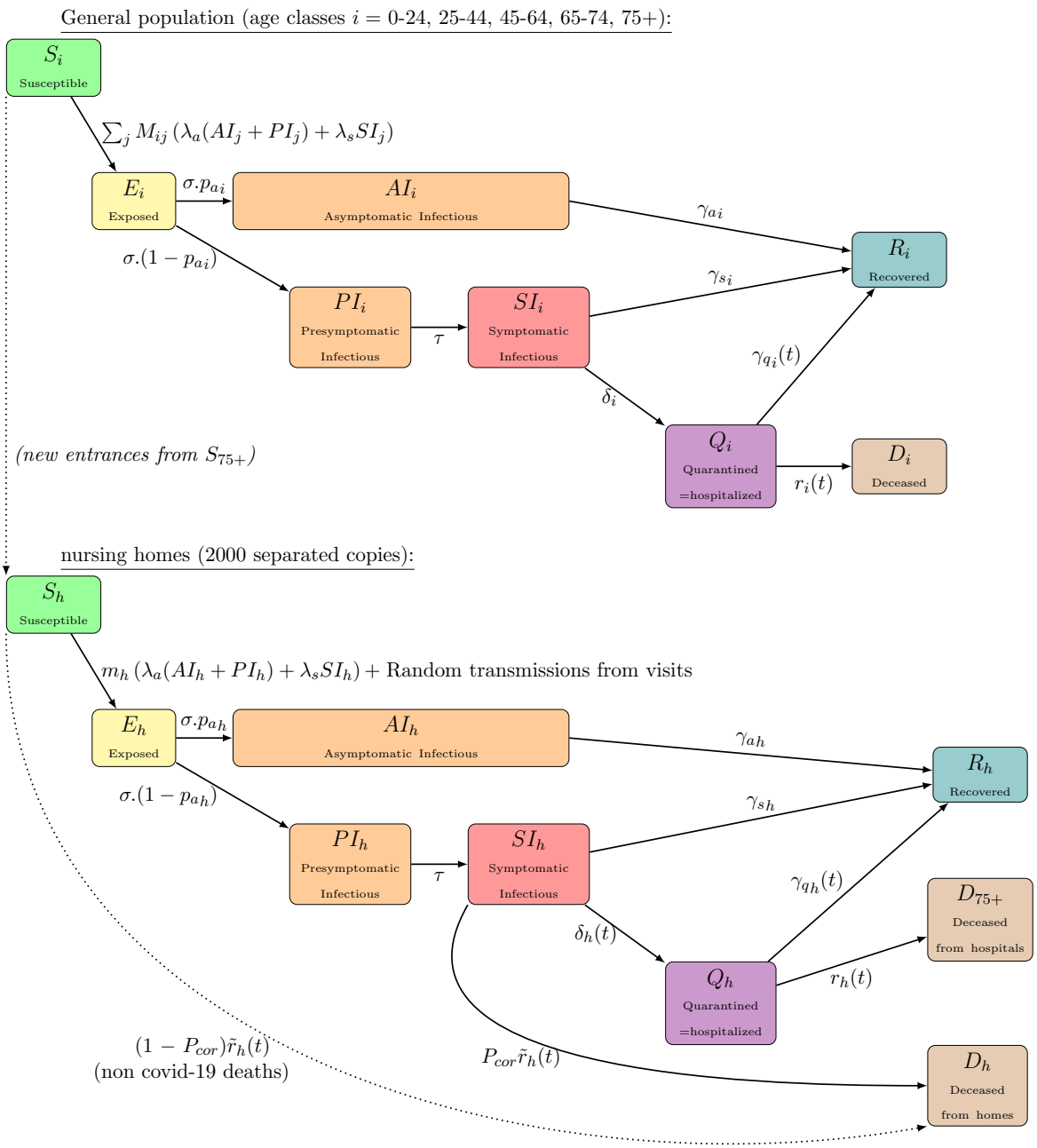

Figure 7: Schematic view of the UNamur compartmental model.

VUB (Barbe, Blotwijk, and Cools 2020)

This analysis applies a time series approach wherein the log-number of events $\log(X_t)$ (with X_t the number of events of interest) is assumed to follow a first order auto-regressive process with a piecewise linear drift driven by a Gaussian cyclo-stationary process. The cyclo-stationarity is a priori set to a weekly periodicity to account for the weekend effect. The model choice is derived from a linearisation of the standard SEIR-model equations. The analysis uses the publicly available national data daily distributed by Sciensano. Forecasts are obtained by transforming the time series parameters to the parameters of the SEIR model equations proceeded by solving the SEIR differential equations numerically through a standard Runge-Kutta 4/5 numerical scheme. Currently the model applies 23 parameters and 7 knot points.

The model is data-driven which serves as a prediction model with limited possibility of scenario simulations. The uncertainty analysis relies on the assumed Gaussian cyclo-stationary noise process. The weekend-effect is modelled non-parametrically by analysis of the periodogram of the model residuals w.r.t $\log(X_t)$. The Fourier coefficient corresponding to a weekly periodicity is used in the residual's spectral density.

ULB (Clesse, 2020)

This individual-based SEIQRD model is calibrated on the daily number of hospitalizations. The model is *not* aged-structured but it implements optional effects such as intra-familial contamination, week-end fluctuations, two populations with different contact behaviours, and a possible correlation between the reproduction number and the averaged daily temperature. Eleven periods, limited by ten time knots, are considered according to the evolution of measures taken by Belgian authorities, and one reproduction number is associated to each of them. Stochasticity is included on the duration of the infecting period as well as on the time between infection and hospitalization. The effect of Christmas and/or New year parties is implemented through an effective one-day variation of the reproduction number corresponding to product of the averaged number of additional contacts, the probability of transmission, and the fraction of the involved population.

A total of 13 calibrated parameters are considered. The parameter means, best-fits and uncertainties are reconstructed through a Markov-Chain-Monte-Carlo method based on the Metroplolis-Hastings algorithm, using the public `MontePython` code. Details on the model and parameter assumptions (fixed, varying...) are available on demand.

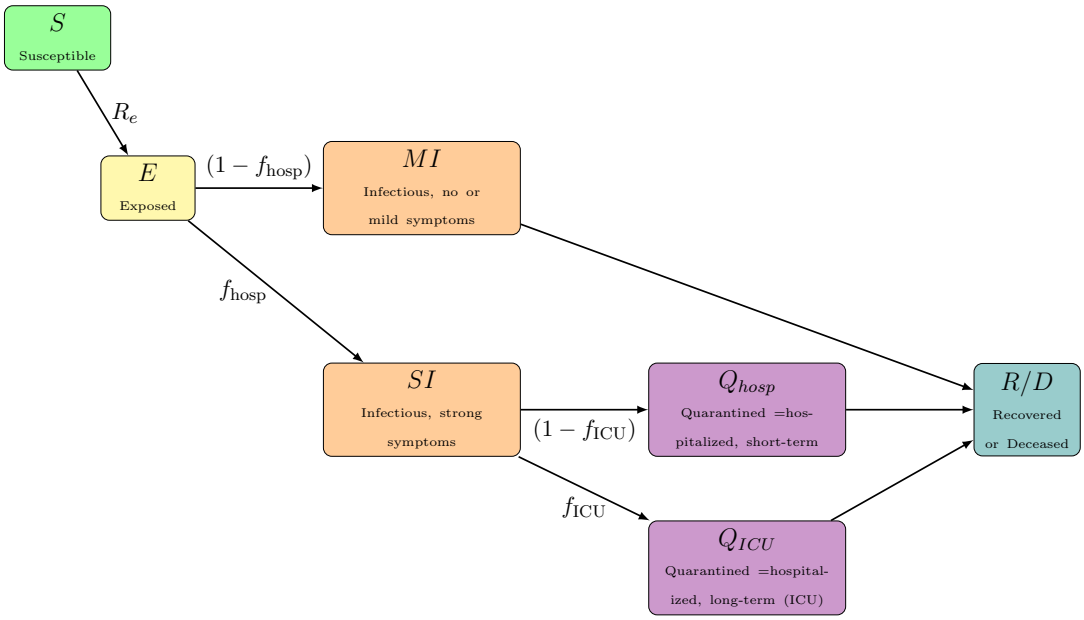

Figure 8: Schematic view of the ULB compartmental model. Each compartment is doubled in order to allow the analysis of two populations with different contact behaviours.