Ideas towards Model Families for Multi-Criteria Decision Support: A COVID-19 Case Study

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Continued model-based decision support is associated with particular challenges, especially in long-term projects. Due to the regularly changing questions and the often changing understanding of the underlying system, the models used must be regularly re-evaluated, -modelled and -implemented with respect to changing modelling purpose, system boundaries, and mapped causalities. Usually, this leads to models with continuously growing complexity and volume. In this work, we aim to reevaluate the idea of the model family, dating back to the 1990s, and use it to promote this as a mindset in the creation of decision support frameworks in large research projects. The idea is to generally not develop and enhance a single standalone model, but to divide the research tasks into interacting smaller models which specifically correspond to the research question. This strategy comes with many advantages, which we explain using the example of a family of models for decision support in the COVID-19 crisis and corresponding case studies. We describe the individual models, explain their role within the family, and how they are used—individually and with each other.

CCS Concepts: • **Computing methodologies** → **Model development and analysis**; **Multiscale systems**; • **Applied computing** → **Health care information systems;**

Additional Key Words and Phrases: Model family, decision support framework, covid-19, sars-cov-2

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1 Introduction

Developing the right computer model for a specific purpose is crucial for good modelling practices, regardless of the area of application. This principle can be found in various modelling guidelines and tutorials [17, 41]. This pragmatism (compare Stachowiak, definition "model" [42]) refers only secondarily to the nature of the abstracted system but primarily to the questions to be answered about the system. It involves selecting the modelling method, database, in- and output, system variables, and resolution of the model. Especially, modelling in long-lasting decision support projects is challenging due to the constant need to modify the decision framework based on new tasks and information about the system.

The most straight forward solution to this problem is to *extend* or modify the one existing decision support model. This strategy is usually the quickest, but also the riskiest: If one retains or extends the model for too long one "may extrapolate beyond the region of fit" or "draw 33rd-order conclusions from a 1st-order model", both rendering the model *invalid* for the given purpose (we used the terminology of Golomb's famous "Do's and Don'ts of Mathematical Modelling" [24]). Moreover, if an existing model was extended beyond a certain complexity, it becomes *inflexible* due to long computation times and high number of model parameters. This causes problems related to *sensitivity, verification,* and *validation*. Finally, also model *documentation* and thus model *communication* becomes continuously more difficult.

To solve the problem, one can completely redevelop and *replace* the model for the new use case. This is costly but avoids problems with existing limitations. However, it requires developing, validating, and verifying a new model, as well as ensuring compatibility with the old one for the sake of *validity*, *credibility,* and *reproducibility* of the old results.

In this work, we advertise a different mindset for model development: instead of replacing an old model with a new one, the new model can be seen as an addition to an entire pool of models, henceforth referred to as a **model family (MF)**, a term which was, to the authors' knowledge, first introduced by P.K. Davis in the 1990s in a slightly different context [18, 19]. Hereby, we refer to a collection of different interacting models with different fields of applications, model boundaries, and resolutions. Instead of attempting to answer every decision-relevant question using the same model, the questions are distributed to the most suitable model(s) in the family. A comprehensive definition and related work will be given in the Methods section.

In general, relying on a framework with not only one but also multiple models is not uncommon, particularly when large complex systems are involved. An example focusing on urban modelling, the MARIUS framework, is found in [15]. Also, meteorological institutes usually found their work on a set of different models for different purposes, including models with high spatial resolution for short-term forecasts, models with lower resolution for long-term forecasts and even models for now-casting (compare [33]).

Between 2020 and 2023 a team of researchers from dwh GmbH and TU Wien provided decision support for Austrian policy makers and health care institutions on the subject of the SARS-COV-2 crisis. The team faced many challenges during these years, including a quickly growing knowledge base, a continuously evolving system and the constantly changing needs of the decision makers. To keep up with these changes, the team developed a family of seven different models in total. The four most relevant are discussed in detail in this work.

We will show the development and usage of the four decision support models in Austria and present case studies that illustrate the benefits of a MF versus a standalone model. Additionally, we will discuss the use of *Causal Loop Diagrams* to visualise and analyse the relationships and roles of the models within the family.

The aim of this work is to demonstrate the advantages and challenges of creating and utilising MFs. We want to encourage modellers working on complex issues like COVID-19 to prioritise developing a family of models instead of constantly improving a standalone model.

Methods

This chapter will describe our interpretation of the term *model family* and how we used the concept of CLDs to visualise the role of a model within its family. In addition, we will present the motivation and development of our COVID-19 MF, provide an introduction to each model, and provide an overview of their specifications, parameters, and implementation. Details can be found in the Appendix or previously published material.

General Model Family Concept

Based on the work in [18] and [19], we define an MF as a collection of different individual models which model different aspects of one large overall system. The models may have different

— modelling approaches,
— resolutions (spatial, temporal,...),
— modelling purposes,
— model boundaries,
— regions of validity, and
— time-frames of validity.

The last refers to the problem that the changing knowledge base of the overall system might render an existing model at least partially less valid due to novel information. By the term, *resolution*, we refer to temporal scale, spatial scale, process detail, object-related structure, and system structure, as specified in [19].

In any case, a family is well designed, if (a) any subsystem of the regarded overall system is covered by at least one model and (b) any two models differ by at least one of the aforementioned points. It is typically seen in context with its genesis and further development: Enhancement can take place by extending existing models, adding completely new ones which cover areas and questions previously not included, and also by dividing existing models into individual sub-models to enhance their flexibility.

To ensure that the family is well designed, it is highly relevant that modellers keep track of the *big picture* of the MF, that is which parts of the system are covered by which model, boundaries, inputs and outputs of the models in the family, how the models can interact and are/can be used together, and any other relevant information relevant for joint usage of the models such as calibration/parametrisation scheme or maturity level of the models. In [45], Zeigler proposed the term *Experimental Frame* for something very similar in 1984. The big picture distinguishes an MF from an arbitrary set of models, and a proper documentation of it ensures, that the MF will remain agile and synergetic. We will not specify how this documentation should be designed, but we will present a graphical approach based on CLDs, which might be helpful for this purpose.

We want to emphasise that an MF, in our understanding, does not rely on automated coupling of the models, neither interfaced, integrated, nor sequential (see [43]). This clearly distinguishes the concept from *multi-method modelling* [2], *co-simulation* [25], or *multi resolution modelling* [19], or *hybrid simulation* (different definitions, e.g., [12] and [36]). The idea of mega-modelling [3] from

the field of model-based software development can also clearly be distinguished for this reason: the method eventually leads to one executable source code in which the features of different models are combined. Moreover, the individual models in the family may follow different modelling purposes and goals. Therefore, they are not only versions of the same model with different resolution, which poses a difference to Davis' ideas of a *variable resolution-*, *multi resolution-* or *cross resolution model family* [18]. Strategically, the concept is also related to the interaction between a system entity structure and its model base [30]. However, unlike the MF, the elements of the model base are usually not independent simulation models and require the system entity structure (pruned entity structure, to be precise) in order to be put together into a functional simulation model.

Mapping Models with Causal Loop Diagram

The CLD concept was developed together with the modelling approach System Dynamics by. Forrester in the 1970s [22, 23]. The concept originally analyses causal relations and loops within a system to develop a System Dynamics model. The diagram uses nodes and directed edges to represent components and their relationships. Edges are labelled with signs indicating whether the causality acts reinforcing or balancing.

In our work, we put these diagrams in an entirely different context (e.g., Figure 1), namely to describe the model families big picture. Instead of using the diagram of the observed system to generate a model, we instead mark the system components and causal relations and loops covered by existing models, i.e., the models in our MF. For this use, we defined the following convention:

- Nodes representing system components which are not depicted in the model are coloured light-grey;
- Nodes representing modelled system components distinguished with respect to their role in the model: inputs are coloured green, state variables black, and outputs blue;
- Edges representing modelled causal relations are drawn in black, others are coloured light-grey.

COVID-19 Model Family Development

The COVID crisis is a perfect example for a highly complex, continuously evolving system with changing knowledge base and changing needs for decision support:

In early 2020, decision makers were primarily interested in scenario forecasts for the potential impact of the new virus on the population and the health care system. Due to the quick spread of the disease in spring 2020, the need for non pharmaceutical intervention modelling arose for policy making. Models had to be quickly adapted to new research on virus parameters, treatments, and vaccines. As immune escape variants emerged and vaccinations became widely available, models had to be extended to include population immunity. Finally, in mid-2022, decision makers required long-term analysis of the system to evaluate exit strategies.

These changes led to new modelling challenges, requiring changes to modelling purpose, boundaries, and causal relations. Table 1 in the Appendix provides a timeline of the changes and the team's modifications to their MF. We clearly see, that the ABEM played the most important role in the process, yet was not extended beyond a certain region of validity and usability. Instead, other models were added to supplement.

The first model in the family is a large-scale epidemiological agent-based model **(Agent-Based Epidemics Model, short ABEM)**. It was also the model of the family that was first developed and covers most components of the overall system. Therefore it is often taken as a reference. The second model **(Immunity Waning Model, short IWM)**, deals with the immunity of the population, the third model *(Hospitalisation Model, short HM)* depicts hospitalisations, and the fourth model

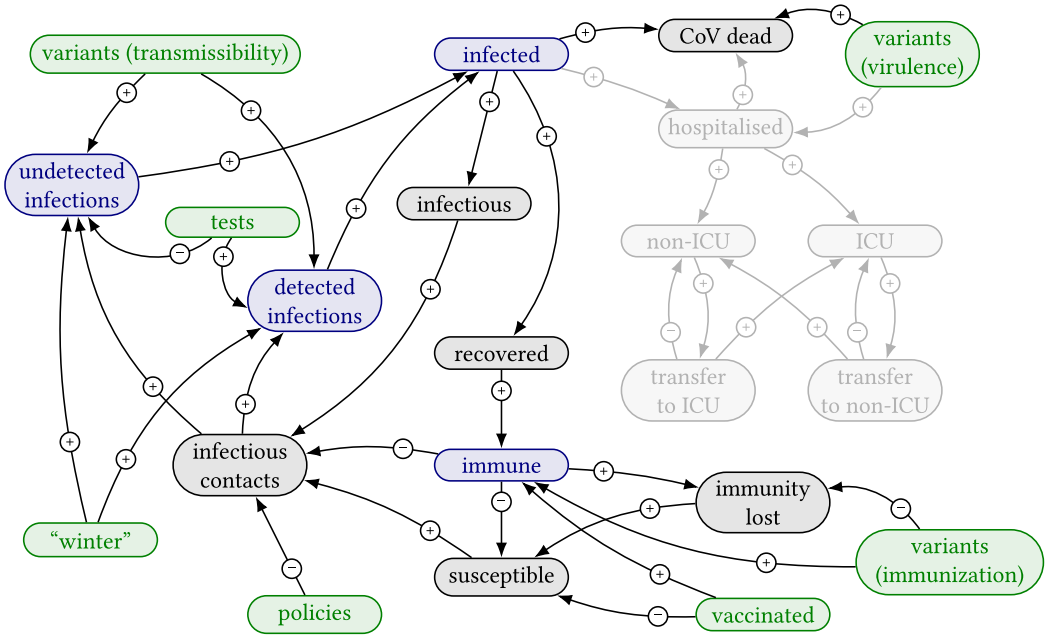

Fig. 1. Schematic Causal Loop Diagram of all elements regarded in the four models discussed in this work. The greyed out components are not regarded in the Agent-Based Epidemics Model. The components coloured in black represent the model states, the components coloured in green the model inputs and the components coloured in blue the model outputs.

(Age Structure Model, short ASM) solely regards the age-distribution of cases during an epidemic wave.

Agent-Based Epidemics Model

The Agent-Based Epidemics Model (henceforth ABEM) was the first and most complex member of the model family to be implemented. Adapted from an existing model to simulate the spread of influenza, it uses a population of agents and a contact network to model the spread of an infectious disease. As it reproduces the demographic of Austria and explicitly models *contact-locations* such as households, schools and work places, it has many fields of application:

— forecasting of infections (COVID Forecasting Consortium [11]);
— evaluation policies (tracing methods [7]);
— better understanding several aspects of the pandemic (undetected cases [39], immunity waning, and their impact on the herd immunity [6]);
— support for other logistical and strategic decisions (test logistics [44], vaccination program [9, 28], wastewater surveillance of virus variants [1]);
— source for synthetic epidemic data [38]

The model was also a cornerstone of many other commissioned modelling studies which were not published in peer reviewed journals (see https://www.dwh.at/en/projects/covid-19/ for details).

Figure 1 shows a schematic CLD of all elements and interactions regarded by the four models discussed in this work.

Short Model Description. The ABEM is an agent-based SEIR-model (susceptible–exposed–infectious–recovered, see [13]). Every inhabitant of the country is depicted as an agent with certain

sex, age and residence place (coordinate). According to regional and socio-demographic structure, agents are assigned contact locations (households, school classes, workplaces, care homes) where they are able to meet other agents. In case of a contact between susceptible and infectious agents, an infection occurs with a probability depending on many epidemiological factors, such as virus strain, seasonality, location, shedding, and adherence. Infected agents then follow a disease progression path including relevant events from infection to immunity loss: start of infectiousness, symptom onset, recovery or death, start of immunity to immunity loss. While interactions between agents are evaluated in discrete time steps of one day, the disease progression is simulated using a discrete event strategy.

The most comprehensive parts of the model are related to the implementation of policies including symptomatic/screening tests, quarantine, contact tracing, vaccinations, school/workplace closure, and increased awareness. Imported cases (tourism) and introduction of new variants are handled by random external infections.

Its original full model specification including parameter values was published in [7]. Since the model and its parametrisation is constantly updated to the newest information, its most recent version can be found on the homepage of dwh GmbH (https://www.dwh.at/en/projects/covid-19/, section "Technical documents, further information and resources").

Model Usage. For most usages, the model is calibrated to match the historical number of reported infections. This way, a population of agents is produced which matches the current Austrian population with regard to active or past infections and immunity. The model can than be computed into the future to make short or medium term forecasts or to analyse several scenarios which simulate varying strategies (e.g., different test concepts, lockdown strategies, vaccination programs, ...) or uncertain systemic events (introduction of new variants, immunity against new variants, ...).

Additionally, the simulated population can be used to analyse the past course of the pandemic with regard to the proportion of undetected cases or infection networks.

Parametrisation and Calibration. The model utilises an enormous number of over 30 different partially time-, partially location-, dependent model parameters. Values for these were taken from literature, surveillance data, census data, or were guessed by domain experts. Population data is mostly taken from the Austrian Bureau of Statistics, same holds true for data for contact locations. Contacts themselves are parametrised using data from the POLYMOD survey [35] and mobile phone data (origin-destination matrices). Disease and immunisation data is collected from literature and the national epidemiological surveillance system. Vaccination data is taken from aggregated exports of the Austrian electronic health record.

The ground truth for the calibration are reported confirmed cases which are matched with the outcomes of the symptomatic and screening tests in the model. The free variables of the calibration process are (mainly) parameters related to the efficiency of policies.

Implementation and Source Code. The model is implemented in JAVA based on our own agent-based simulation tool (**Agent-Based Template, ABT,** [21]). One simulation run for Austria with roughly 9 Mio agents requires about 30-40GB RAM and 15-30sec per simulation-day (i.e., 1.5-3h per simulation-year). Since the source code (a) is huge with more than 150 Java classes, (b) subject to constant updates, (c) partially uses parametrisation data subject to privacy, and (d) cannot be cleaned and prepared for the scientific community with feasible effort, it is not open access. It can be shared in scientific collaborations though.

Immunity Waning Model

Due to the long course of the pandemic and the emergence of new virus variants, research on immunity and in particular immunity waning became more and more relevant. Since the number

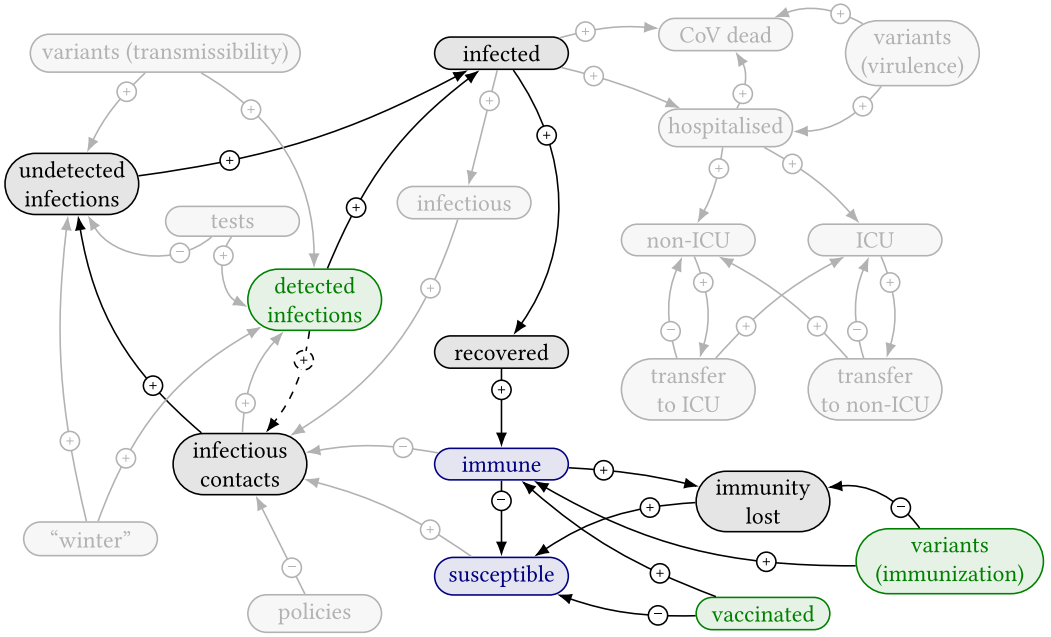

Fig. 2. Schematic Causal Loop Diagram of all elements regarded in the four models discussed in this work. The greyed out components are not regarded in the Immunity Waning Model. The components coloured in black represent the model states, the components coloured in green the model inputs and the components coloured in blue the model outputs. The dashed arrow indicates a causal link which is implemented inversely in the model.

of immunised persons has massive implications on the progress on epidemic waves, estimates for this quantity became an important variable of interest. Although the ABEM is fully capable of giving estimates for this number (e.g., see [6] and[40]) long computation times limit its capabilities to experiment with different waning distributions. The **Immunity Waning Model (IWM)** was developed to overcome this problem. Focusing only on the past and current situation, the model does not include classic epidemiological mechanisms like infections, but treats them as inputs. This leads to much smaller computation times and improved capabilities for parameter studies.

Short Model Description. The IWM itself is conceptualised based on the idea that the immunisation level against a certain virus variant is solely dependent on past infections and vaccinations.

As displayed in Figure 2, the model uses this historical data as input and creates *immunisation-events,* which are then distributed among the entities. To get a correct picture of the overall immunity, the officially confirmed infection numbers are not sufficient because not all actual infections are getting detected, e.g., due to a lack of symptoms. To solve this problem model applies an estimate for the detection rate (taken from literature with corresponding studies) to compute an estimate for the overall infection count from the detected infections. This is indicated by the dashed arrow in Figure 2. Undetected infections are furthermore treated and distributed analogously to the detected ones. The distribution process is deliberately kept very simple: the events are distributed randomly among the subset of eligible entities, regardless of age, gender, or other personal properties. An entity is considered eligible for an infection-based immunisation-event if they are not already labelled as *immune* and they may be assigned a first/second/third/... vaccination-based immunisation-event if they have already received no/one/two/... shots with sufficient time between the shots.

Once an entity has been assigned an immunisation-event, they gain immunit—in specific immunity against infection by an observed SARS-COV-2 variant—with a given probability. In case the entity has been labelled as immune, an *immunity-loss* event is scheduled after a certain amount of time drawn randomly from a previously defined distribution.

In order to evaluate "immunity" against, e.g., a severe disease progression (hospitalisation), a second *immune* state is introduced for which different distributions are used.

A detailed model specification is found in the supplemental material, Section 1.

Model Usage. The models' usage can be split into four areas. First, the model can be used to estimate the current and past immunisation level against infection. This can be valuable to get an idea of the immunisation level necessary for natural peaks of disease waves. Second, the model can be used to estimate the future dynamics of the current immunisation level without regarding any future infections or vaccinations. Third, the model can be applied to forecasts of case-numbers and/or vaccination numbers generated by other models to estimate the immunisation level during an upcoming epidemic wave (see Case Study 3). Finally, the model can also be used for communication purposes showing differences between immunity against infection and "immunity"[1] against hospitalisation.

Parametrisation and Calibration. Besides input timelines of vaccinations and daily new reported cases the model is parameterised with various assumptions about the immunisation process, in specific using distributions and distribution parameters for immunity waning. So far, we estimated the parameters by fitting survival curves to published data about vaccine effectiveness controlled for the time since vaccination. Besides, the model requires a feasible assumption for the case-detection rate. All other model parameters have a smaller impact on the immunisation level and can be estimated easier.

Implementation and Source Code. The model was implemented in Python3. The source code to the model implemented in Python3 including a base-parametrisation is found in https://github.com/dwhGmbH/covid19_model_family.

Hospitalisation Model

Hospital and **intensive care unit (ICU)** bed occupancy drove Austria's COVID policies in the first two years of the pandemic. Overcrowded hospitals posed as the key argument for policies like quarantine regulations, mandatory face-mask wearing, school closures, and lockdown. To advise decision-makers, we needed to provide projections for these variables.

Initially, hospitalisations were integrated into the ABEM, but its complexity and long run times made it difficult to calibrate. So, we created a separate, simpler stock-flow model called the **Hospitalisation Model (HM)**.

This model was developed by the Gesundheit Österreich GmbH in cooperation with the members of the Austrian COVID Forecasting Consortium and uses real and/or predicted reported case numbers as input and provides estimates for the occupancy. It was introduced in [11] and has since been modified. Here, we introduce a more flexible and generic version of the model, which is better suited for long-term analysis. See Figure 3 for a causal map of the model.

Short Model Description. The model makes use of the time-series of daily new confirmed cases and maps it onto a time series for the hospital occupancy. It uses a scalar hospitalisation rate and two duration distributions which state (a) how much time passes between positive test

[1]In this case, this should be interpreted as the additional level of protection against severe disease gained through infection or vaccination, compared to a fully naive individual.

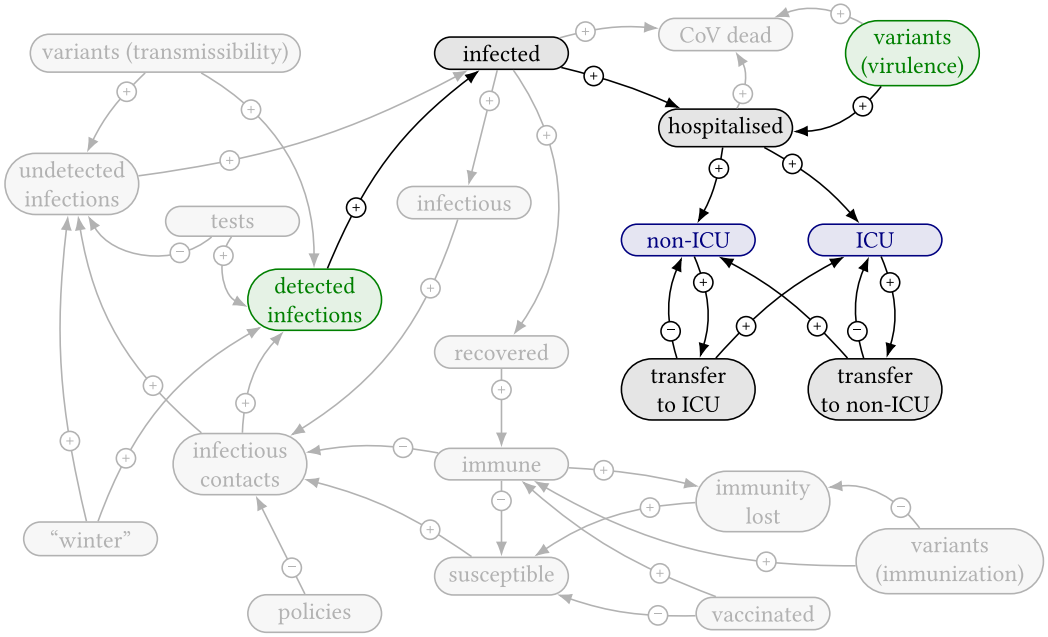

Fig. 3. Schematic Causal Loop Diagram of all elements regarded in the four models discussed in this work. The greyed out components are not regarded in the Hospitalisation Model. The components coloured in black represent the model states, the components coloured in green the model inputs and the components coloured in blue the model outputs.

and hospitalisation and (b) how long persons stay in the hospital. The model can be regarded as a deterministic difference equation model involving discrete convolutions with the duration distributions:

$$\text{admissions}_{(i \to i+k)} = \text{cases}_i \cdot \text{rate} \cdot (\text{distribution admissions})_k \tag{1}$$

$$\text{admissions}_i = \sum_{k=1}^{i} \text{admissions}_{(k \to i)} \tag{2}$$

$$\text{releases}_{(i \to i+k)} = \text{admissions}_i \cdot (\text{distribution releases})_k \tag{3}$$

$$\text{releases}_i = \sum_{k=1}^{i} \text{releases}_{(k \to i)} \tag{4}$$

$$\text{occupancy}_{i+1} = \sum_{k=1}^{i} \text{admissions}_k - \text{releases}_k . \tag{5}$$

A detailed model specification is found in the supplemental material, Section 2.

Model Usage. As a deterministic difference equation model, it can be executed highly efficient. In the typical case, the model is used on a concatenated input time-series consisting of reported daily new SARS-CoV-2 cases and a case forecast for a specific federal-state or the country as a whole. It then produces forecasts for the occupancy of both normal beds and ICU beds. For long-term forecasts, we usually vary the base hospitalisation rate by including additional assumptions

for immunity or virulence dynamics using a second input time-series. This makes the result more feasible and provides a better picture of the uncertainty of the result.

Parametrisation and Calibration. The model is calibrated using historic data of new confirmed daily cases and hospital occupancy. Usually, the most recent 120 days are regarded, where the first 100 days are used as a transient phase and the latter 20 as calibration window (see, supplemental material Section 2, for a more detailed description of the calibration process). Note that flattening is usually not necessary, since the performed convolutions by the model provide a rather smooth solution anyway.

When writing the two duration distributions as functions of the scalar moments of the distribution, standard algorithms like Nelder-Mead simplex can be used as a calibration method.

Implementation and Source Code. The model is implemented in Python using vector operations. The packages *Numpy* and *Scipy* provide routines to make this highly efficient. Finally, the Nelder-Mead simplex implementation from the *Scipy's optimize* package is used to find the optimal parameter set. Full calibration and subsequent simulation only take a few seconds on a standard notebook. Consequently, also hyper-parameter studies, e.g., for different shapes of distributions or different calibration time-frames are possible. The source code to the model including sample input data is found in https://github.com/dwhGmbH/covid19_model_family.

Age Structure Model

The age structure of infected individuals, split by vaccination status, is a crucial input for the HM. For short-term forecasts, the current distribution can be extrapolated. However, this strategy is not viable for medium- or long-term scenario simulations.

Although the ABEM can be used to evaluate disease waves with respect to age structure, it is challenging to calibrate the model for the current age distribution of cases. This is because, like most other SEIR-type models, simulations cannot be simply started at an arbitrary point in time (see [8]). Since many events from the past impact the dynamics of the near future, simulations always have to be started from the very beginning of the pandemic.

To overcome this problem, the **Age Structure Model (ASM)** was developed. By neglecting the "exposed"-state of an infected person and limiting the model structure to a SIR-type, the model became "memoryless" in the sense that it can be initialised with observed data (active cases, vaccinated cases, etc.). While the model's epidemiological accuracy for forecasting case numbers may suffer from this simplification, the dynamics of the age structure of the cases is well predicted. We refer to Figure 4 for a causal map of the model, analogous to Figure 1.

Short Model Description. Motivated by a work of McKendrick [32], which he published the year before his groundbreaking publication about the concept of **susceptible—infectious—recovered (SIR)** modelling together with Kermack [29], we decided to develop an epidemic compartment model wherein age is a second continuous variable next to time. For example, the compartment of susceptible individuals $S = S(a, t)$ is analysed as a function of time t and age a. This way, the approach essentially becomes a **partial differential equation (PDE)**. A key feature of the model is a contact kernel which decides about contact between infectious persons with age a_1 with susceptible persons with age a_2. Models following this strategy are well known and their properties are well analysed (see [4], [27], and [20]). Our approach founds on a classic SIR model published in [27] and was extended by a second disease path to depict vaccinations and vaccine effectiveness. For more information the reader is referred to the detailed model specification in the supplemental material, Section 3.

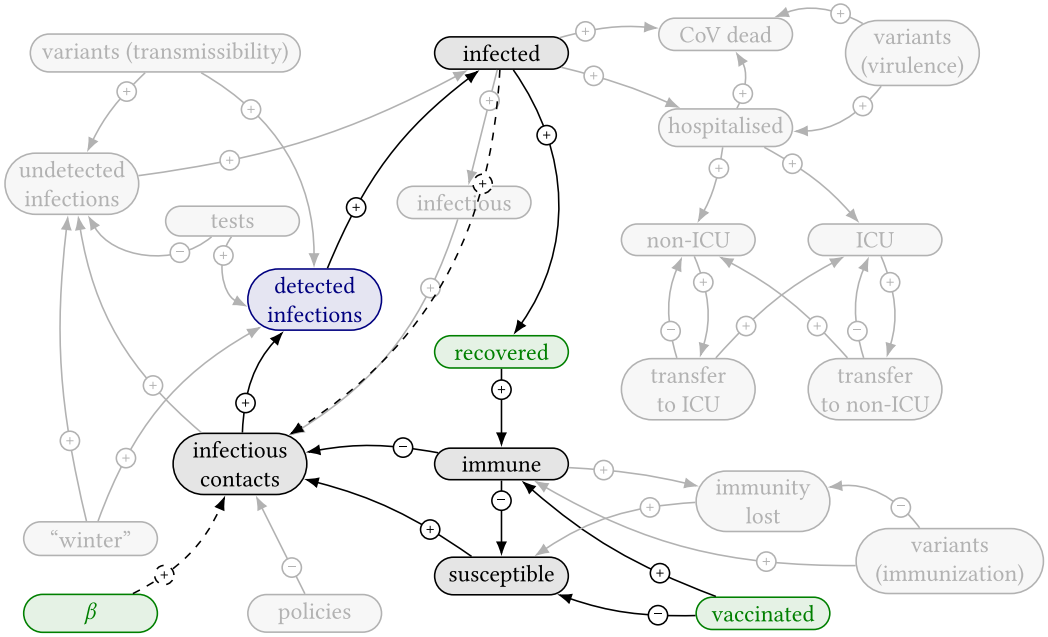

Fig. 4. Schematic Causal Loop Diagram of all elements regarded in the four models discussed in this work. The greyed out components are not regarded in the Age Structure Model. The components coloured in black represent the model states, the components coloured in green the model inputs and the components coloured in blue the model outputs.

Model Usage. Although the ASM itself is an epidemiological model, its main purpose is not forecasting of disease numbers. For this purpose the contact process, the disease path and the immunisation process are too much simplified. It is purely used to investigate the dynamics of the age-distribution of infected persons. An age-dependent contact kernel and age-dependent information on previous infections and vaccinations are used as model input. Usually the model is then calibrated to a given disease progression over the course of an epidemic wave to provide information about the current age-distribution among the infected cases. Hence, the detected infections pose both input via the overall number as calibration reference, as well as variable of interest via their age structure.

Parametrisation and Calibration. Age-dependent surveillance data about previous infections and vaccinations are evaluated to provide feasible initial conditions. One of the most valuable features of the model is that it is well capable of being initialised by data with different age resolutions. This is guaranteed by a **kernel density estimation (KDE)** performed on top of the datasets. This KDE is required anyway to make the initial curves differentiable. The age-dependent contact kernel is the key parameter of the model. Thanks to fantastic studies like POLYMOD [35] or COMIX [14], in which contact-records from thousands of volunteers were collected over different time periods in different countries, lots of data is available on this subject.

The calibration to a specific disease progression is done by varying the parameters of the time dependent infectiousness parameter function β which can be interpreted as a summary of policies, seasonality and infectiousness of the virus (variant). In principle there is no limitation on where the calibration reference comes from. Typically, either historic data from previous disease waves or forecasts from other more accurate models such as the ABEM are used. Calibration is performed with an iterative bisection method.

Implementation and Source Code. Due to its great numerical properties, the model is developed in MATLAB. To solve the PDE a standard Method of Lines approach is chosen with a Numerical Differential Formula time-integrator (MATLAB's ode15s solver [31]). The integral parts on the right-hand side of the differential equation are solved using the trapezoid-method. The source code of the model can be found in https://github.com/dwhGmbH/covid19_model_family.

Results

This work emphasizes the benefits of using an MF, and therefore our interpretation of a result differs from classical modelling and simulation studies. We will not delve into specific simulation outcomes, but rather focus on how the result was generated and used in decision support. Four case studies will illustrate how the models created value in decision making, and representative model outcomes will be presented to demonstrate this value. For the result figures displayed in this work, open data interfaces of the **Austrian Ministry of Health and the Austrian Agency for Health and Food Safety GmbH (AGES)** were used to gather the parametrization/input data for daily new confirmed cases, variant distribution, vaccination rates and hospital occupancy.

Case Study 1: Combined usage of the ABEM and the HM. In April 2020, about a month after the first detected case of SARS-COV-2 in Austria, the COVID Forecasting Consortium of the Ministry of Health was established. By 2023, the consortium produced and published more than 150 short-term forecasts of SARS-CoV-2 case numbers and COVID-19 hospital bed occupancy (see https://datenplattform-covid.goeg.at/prognosen). Forecast generation involved three modelling groups each producing a case number forecast using an epidemiological model. The TU Wien used the ABEM, while the other two groups used macroscopic modelling approaches. These forecasts of detected infections were then harmonised into an ensemble forecast which was used as input for a common occupancy model producing the final forecast for the hospital occupancy. The HM highlighted in this work and described in detail in Section 2 in the supplemental material is a simplified version of this pavement model.

The splitting of the forecasting process into caseload and pavement forecasting should prove to be one of the cornerstones of the consortium's success. The strategy helps validate, verify, and compare the epidemiological models, some of which are highly complex. It simplifies and accelerates scenario calculations by allowing for uncertainties and different assumptions in both forecast sections. Finally, it is also flexible, fail-safe, and the results are easily reproducible.

Figure 5 provides an example of forecasts generated by combining the two models. They were produced on 2022-05-16 to estimate the potential burden on the hospitals resulting from the emergence of the new variant $BA_{4/5}$. Assumptions about the higher infectivity and immune escape of the variant were handled by the ABEM which thus produced different forecasts for the case numbers. Further assumptions on the virulence were included in the HM which thus generated different forecast for the hospital occupancy for each of the result scenario of the ABEM. These forecasts provided an early image of the possible range of hospital occupancy. As soon as better information for properties of the new variant was available in the literature, the range of the results could be narrowed down.

Case Study 2: Combined usage of the ASM and epidemiological models. In August 2021, the Austrian COVID Forecasting Consortium (see [11]) was tasked to summarise findings and scenario based forecasts for the upcoming Delta wave, with a focus on ICU occupancy. Therefore, scenario-based forecasts for reported cases were developed and the HM was applied to translate cases to occupancy. Although this strategy has been well applicable for the prior disease waves, vaccinated persons needed to be factored into the computations now—about 56%, primarily elderly, have received at least two vaccination doses by September 2021 [26]. Vaccinated persons were already

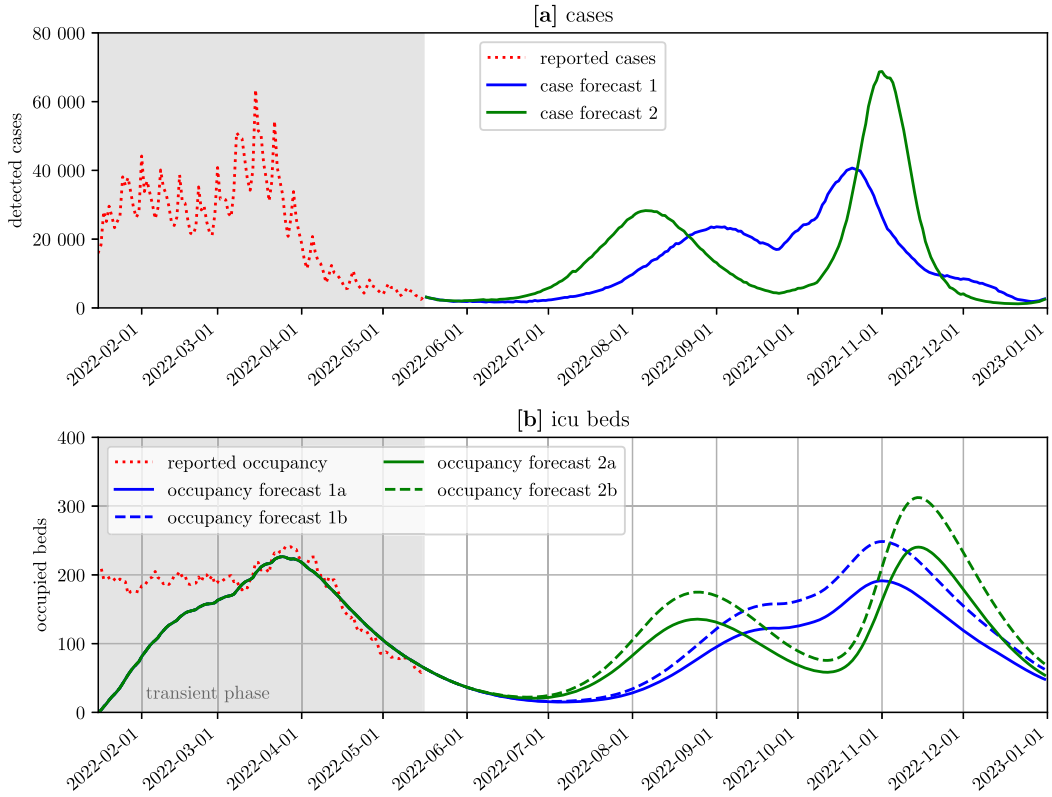

Fig. 5. Combining different case forecast scenarios from the ABEM [a] with different assumptions for virulence (equal and 30% increased) of the a new variant in the HM [b].

known to have a reduced infection, but even lower hospitalisation and ICU risk. In order to quantify this advantage, estimates were needed how the case population would be split into age and vaccination groups.

Therefore, the ASM was applied in addition to the ABEM. First, a medium-range forecast for the Delta wave was generated with the ABEM. Then, the ASM was initialised to the current population distribution with respect to vaccinated, recovered and infected persons. Finally, the ASM was calibrated to match the case number forecast generated by the ABEM. This was done by using a step-function $\beta(a,t) := \hat{\beta}(a) \sum_{i=0}^{6} 1_{[7i,7i+7)}(t)\beta_i$ for the transmissibility, and by fitting the seven scalar parameters $\beta_0, \ldots, \beta_6$ (we refer to the model specification for details). The results of the ASM provided a proper insight into the expected age distribution of overall, vaccinated and non-vaccinated cases in the upcoming wave and are shown in Figure 6.

Model results (correctly) showed that the Delta wave shifted the active cases towards younger age cohorts, a result of older age groups being prioritised in the vaccination program, leaving many children insufficiently vaccinated by autumn 2021. The age distribution of vaccinated and non-vaccinated cases (lower two plots in Figure 6) illustrate this problem. This stood in contrast to previous waves, which were initialised with younger cohorts and shifted towards the older ones during the upswing of case numbers. (see Figure 7). Up to the current date, the Delta wave was the only one showing this very profile.

Results had important implications for the expected hospitalisation rates. Despite the majority of cases being non-vaccinated, their relatively young age profile indicated a low hospitalisation risk,

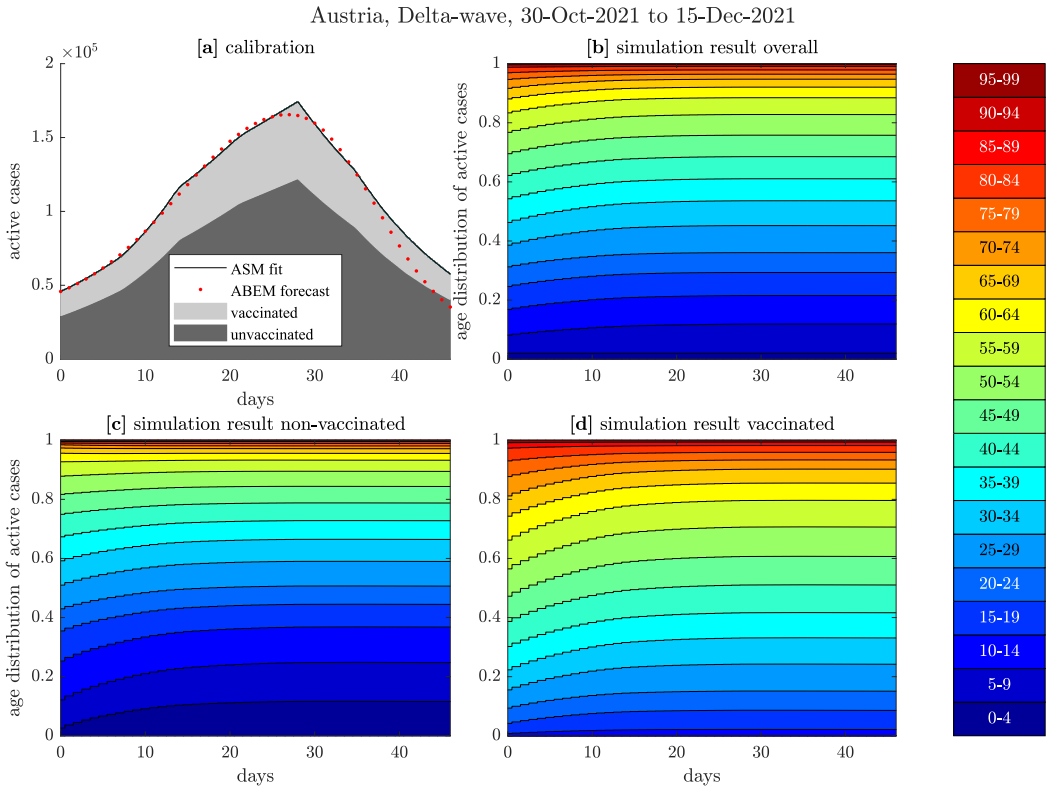

Fig. 6. Result of the ASM when fitted to a forecast from the ABEM between 30-Oct-2021 to 15-Dec-2021 (Delta wave). Part [a] shows reference data, the fitted simulation result and the split between vaccinated and unvaccinated cases. Part [b] shows age distributions of all active cases. Parts [c] and [d] show the age distribution of active cases separately for people with and without vaccination.

with hospitalisation rates less than half the size of rates in a fully non-vaccinated population. Limits for critical ICU occupancy (33%) were increased from about 2,400 to 5,100 daily new confirmed cases in the steady state. Results were published on the homepage of the Austrian Ministry of Health, see [16].

Case Study 3: Combined usage of ABEM and IWM.. Since March 2021, when Austria had already observed two epidemic waves and the vaccine started to become widely available, the IWM was used in combination with case data from the official reporting system to generate monthly estimates for the level of immunity against certain targets, typically infection with a specific variant or severe disease progression. Results help to get an image of the current pandemic risk and were published monthly on http://www.dexhelpp.at/en/immunization_level.

An example of this model application is shown in Figure 8. Case data up to May 16th, 2022 (part [a]) has been fed into the IWM to estimate the time dynamics of the immunity level of the population against severe disease progression (part [b]). The historical case data has then been extended with a forecast for the future dynamics of the new variant Omicron BA.4/5 generated using the ABEM (grey area in part [a]). Applying the IWM on the joint time-series of case data and forecast, a prognosis for the immunity level was made, seen in the grey area of part [b] of the figure.

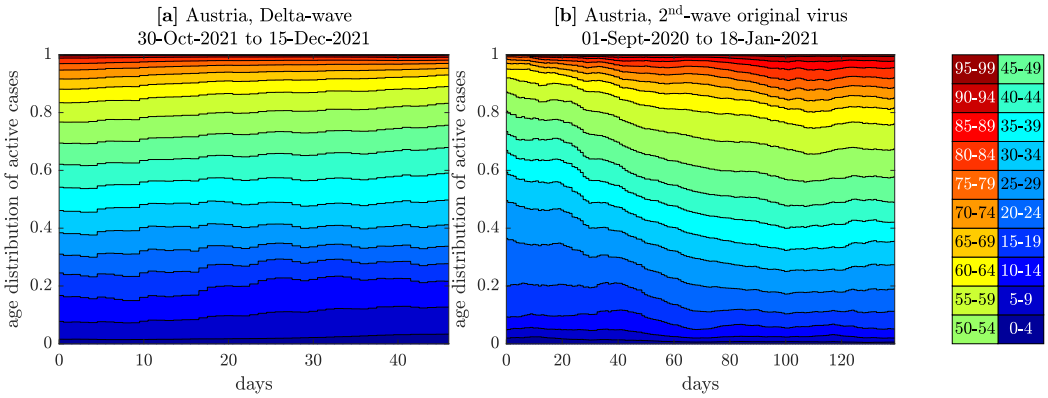

Fig. 7. Comparison of the reported age distribution of active cases between the a in autumn 2021 [a] and a wave in autumn 2020 [b]. Because mainly older people were vaccinated, the 2021 delta-wave showed clearly different age dynamics than the other waves.

These results provided valuable insights to the decision makers since they gave a proper image of possible but also impossible long-term strategies to overcome the COVID-19 crisis. For details and interpretation of the specific results we refer to https://www.dwh.at/en/news/covid-19-scenario-simulations-for-summer-autumn-winter-2022/.

Case Study 4: Joint usage of the ABEM, IWM and the HM. In the course of the scenario calculations on the future dynamics of infections driven by Omikron.BA.4/5 (see Case Study 3 and [16], respectively), the potential impact on the utilisation of Austrian hospitals was also evaluated. For this purpose, both the case number scenarios of ABEM and the corresponding immunity levels from IWM were used as input to the HM. The latter idea is based on the basic assumption that the hospitalisation rate is directly proportional to the proportion of the risk group among those infected. Defining the risk group as the proportion of those susceptible to infection who are not protected against a severe disease progression, this ratio can be calculated from the corresponding result curves of the IWM: Let PS denote being protected against severe disease and PI against infection, then

$$\text{hospitalisationrate} \propto P(\neg PS|\neg PI) = \frac{P(\neg(PS \vee PI))}{P(\neg PI)} \underbrace{=}_{PI \Rightarrow PS} \frac{P(\neg PS)}{P(\neg PI)} = \frac{1 - P(PS)}{1 - P(PI)}. \tag{6}$$

Figure 9 shows one result from this study. Section [a] visualises the dynamics of the different levels of protection. The effect on the HM results can be seen in sections [b] when comparing the blue and yellow curves: fast decreasing protection against infection in the prognosis period increases the relative protection of susceptibles against severe progression and correspondingly decreases the overall hospitalisation rate.

This observation was one of many that was valuable to decision makers from this analysis. The prospect of hospital loads again reaching similar high ranges in the winter of 2022 than in 2021 also provided added value to planning.

2 Discussion

In the present work, we described development, specification and usage of four entirely different models describing one part of a large system. Each model comes with different modelling purpose, input, output and limitations due to its view and model boundaries. The four presented case studies

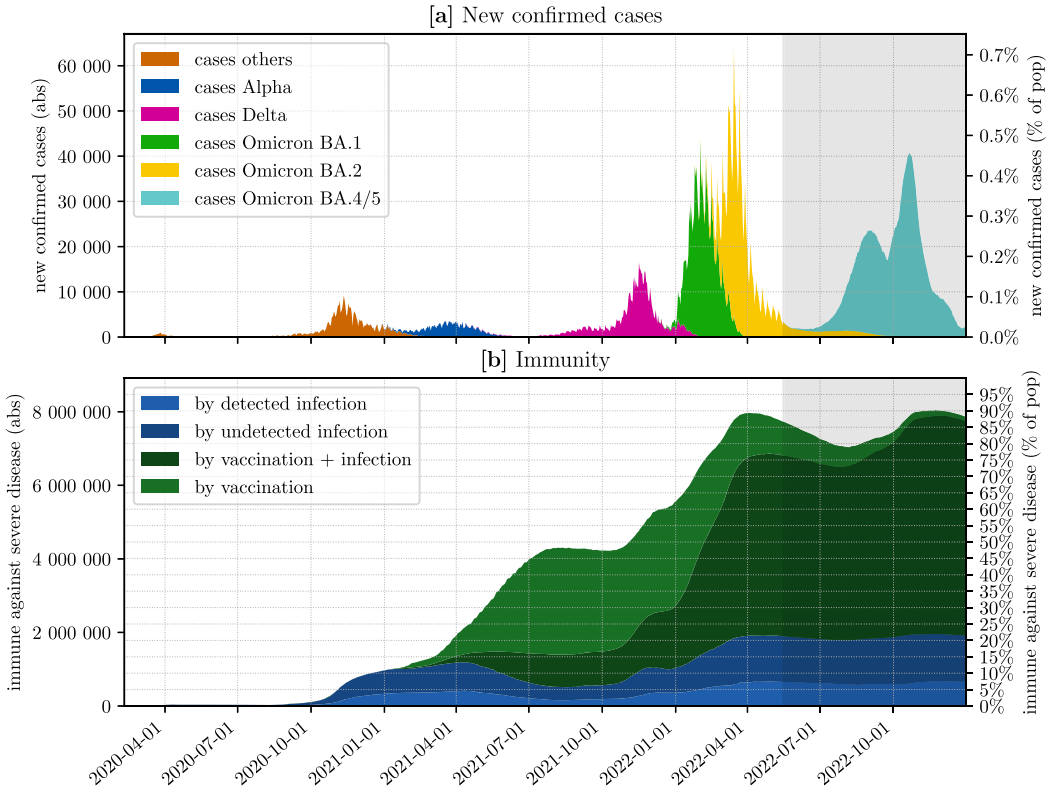

Fig. 8. Combined usage of IWM and ABEM. The variant specific case numbers [a] are fed into the IWM to estimate the level of immunity [b] against severe disease progression (i.e., hospitalisation). Combined with a case number forecast from the ABEM (grey area), a forecast for the immunity level can be made. The shown forecast was based on data until May 16th, 2022.

are not only examples for the successful joint use of the models, they also highlight the **advantages** of the MF in contrast to one large, complex stand-alone model:

Model Resolution and Validity. Each model in the MF is itself stand-alone and can be customised accordingly in the choice of the modelling method and model resolution to fit the problem. For example, ABEM and IWM are each microscopic, HM and ASM are considered to be macroscopic. Also, ABEM and IWM differ greatly in the level of detail of individuals and scalability. The adequate choice of the modelling strategy and resolution are not only basic requirements of general good modelling practices, but are also in advantage to the large stand-alone model, where the resolution of the whole model is fixed by the resolution of the component which requires the highest resolution. This circumstance is often problematic, as demonstrated in Case Study 2. Due to its high resolution and high sensitivity the ABEM is not well suited for simulating age shift in infection waves. However, in the MF it can be supported by the much lower resolution ASM.

Computation time and parametrisation efforts. Because (a) from the MF only those models are used, which are necessary for the respective problem, and (b) the resolution of the individual models is usually lower than the one of the stand-alone model, the computational effort for experiments in the MF is usually lower. The same is true for the parametrisation effort and the potential sources of error. This advantage was exploited in Case Study 3: Even though in principle all scenarios could

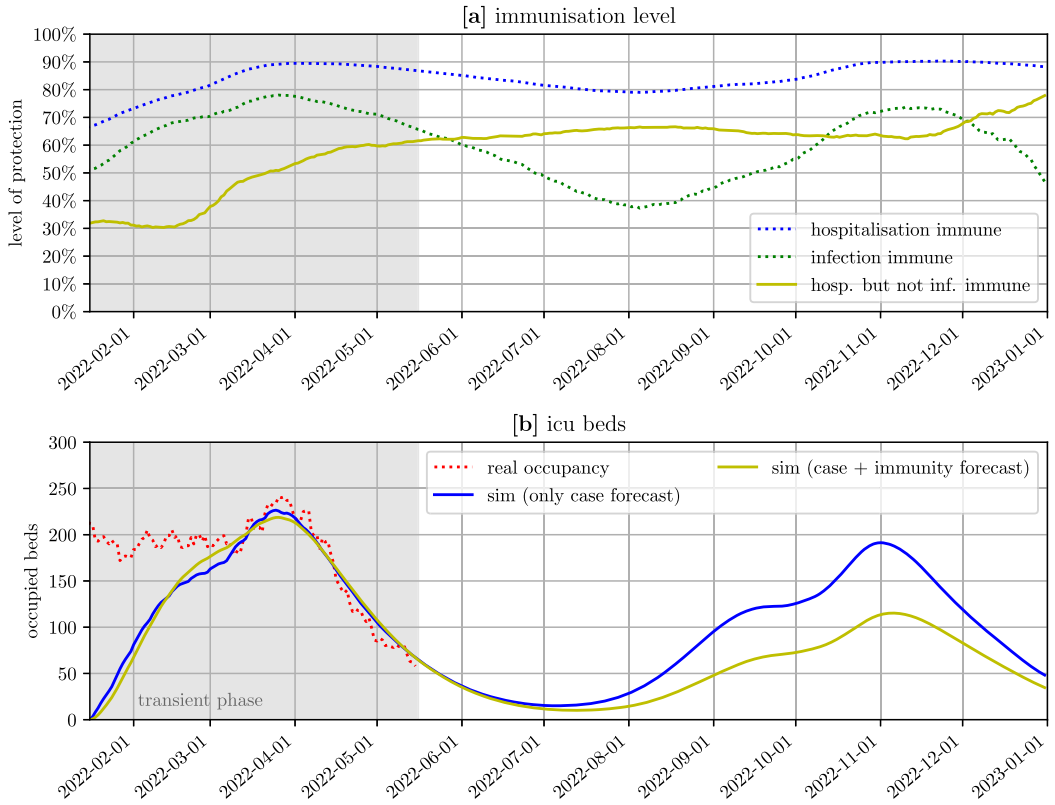

Fig. 9. Comparison of hospital forecast with and without regarding the immunisation level against severe disease. Part [a] shows the dynamics of the different levels of protection estimated with the IWM. The dotted lines represent the probability to be immune against infection and severe disease progression (hospitalisation) respectively. The yellow line shows the conditional probability to be protected against severe disease if one is not protected against infection. Part [b] shows the effect of either neglecting or including this conditional immunisation as additional input to the HM.

have been computed with ABEM alone, the sequential use of ABEM and IWM greatly reduced the computational effort, the error-sensitivity and the effort for parametrisation.

Flexibility. The interfaces between the models, i.e., input and output, offer many possibilities for manual or automated intervention in the process. This makes the models essentially modules, which can be used even beyond the boundaries of the research institution. Case Study 1 demonstrates this on the example of the ensemble forecast, which is used as input to the pavement model.

Validation and Verification. Each of the models in the family can be independently validated and verified. Model uncertainties and parameter sensitivities can be determined individually. Accordingly, experiments based on the linkage of the models are as valid and correct as the individual models. The uncertainty of the result can be derived from the uncertainties of the individual models. To perform an appropriate model analysis for a large stand-alone model, each component of the model would have to be analysed with the same care as the corresponding model of the MF. However, this would become much more costly with the longer computation time and higher parametrisation effort of the stand-alone model. As additional bonus, the overlap regions of the individual models can be used for cross-model validation (see [37]).

Clearly, the MF also needs to be validated in the big-picture. Even apart from its value in collaborative work, the usage of (modified) CLDs has proven useful for representing and validating the big picture of the MF. First, superimposing the diagrams provides a complete picture of the processes mapped in the family. One can see overlapping areas, which can be used for cross-validation, input-output relationships between the models, which would allow sequential simulation, and poorly covered areas, which indicate weaknesses in the MF and can serve as motivation to create new models. The diagram of a single model immediately shows neglected causal relationships and broken causal loops, which can be useful for validation.

Communication. Good communication of models and model results is one of the cornerstones in successful model-based decision support: if they are not comprehensible to the decision makers and domain experts, they lose credibility and face validation is not possible. In this matter, the MF concept can be helpful as well: In contrast to the stand-alone model, the family provides a clear structure on how the model and the model results can be communicated. Using separate documentations and results from the individual models, involved persons face and comprehend the models one at a time which is easier to digest for the decision makers and helps the domain experts to focus on their specific area of expertise for face validation.

Efficient creation and use. The MF is also advantageous from a project management (PM) perspective. Implementation, maintenance, extension, analysis, execution, etc. can be distributed (and passed on) much better to several persons or project teams. Thus progress can be made much more efficient. In the contrast, splitting simulation experiments on multiple models requires a whole and well understood picture of strengths, weaknesses, in-, output and boundaries of the individual models. In our applications, we found the CLDs helpful to get a quick overview and proper assignment of the given tasks to the right model(s).

Undoubtedly, the MF also comes with **challenges and problems** which are primarily found on the PM perspective as well. The concept of the MF requires PM to be thought of in at least two layers: the model itself and the big picture that connects the models. While the lower layers involves the usual challenges in modelling, the upper layer is where decisions have to be made as to whether, when and which models are developed and how they are connected. Even if this approach is basically very compatible with modern agile software development (e.g., Scrum), it means unavoidable overheads that may not be affordable for smaller research groups or individual modellers. We will discuss three of these overheads in more detail:

First of all, *joint usage* of the models could potentially suffer from bottlenecks. Efficient joint development was before stated as one of the benefits of the strategy, since responsibilities can be shared. However, this advantage can quickly become a disadvantage, in case the models can ultimately only be operated by the respective responsible persons. Hence, for every simulation results which is based on the interaction of models, all those responsible for the models are always required to operate them and each of them becomes a potential bottleneck for the application process. Of course, this can be prevented if knowledge about how to operate each of the models is shared within the team. This is a challenge that increases with the heterogeneity of the models (modeling approach, programming language, etc.).

Moreover, the additional *development time* that has to be invested in the adaptation of existing and the development and validation of new models of the MF, as well as in the documentation and administration of the big picture is likely the most obvious overhead. With sufficiently foresighted PM, this overhead can be reduced, but never completely avoided. The workflow for the development of the presented COVID-19 MF was certainly not optimal: Most models were motivated by strong time pressure due to policy making involvement and by failures: as soon as one of the models did not perform sufficiently well for a specific problem, model parts were extracted, a new model was developed and was added to the MF. Although this eventually led to a flexible

MF (which even saved time in the long run, due to the increased stability and smaller run-times of less complex models), a more foresighted approach is clearly beneficial. Namely, as soon as the modelling process of a large system is started, modellers should already ask themselves where and how the system can be broken up in parts in order to develop the different models in parallel (see, https://www.dwh.at/en/news/ecdc-rahmenvertrag/ for a more recent project in which we decided for a strategy with more foresight). Note, that the involved systemic split must allow to create individual models which can be evaluated, verified and validated separately.

This directly leads to the limitation, that this work *cannot give any guidance on how a MF is or should be developed.* Every project is different and comes with unique features, challenges and problems that need to be overcome. However, independent of how the family is developed—slowly and over time, motivated by the need for change, or in a more foresighted approach – we argue that the process can be highly successful if the big picture, i.e., the overall system and the interaction of the models, is omnipresent, documented and continuously updated.

Summarising, we clearly recommend modellers working on decision support in large and complex systems to invest overhead time for the development of model families instead of one large, complex stand-alone model. Maintaining two or more models in parallel causes overheads, but pays off in the long run. In this approach, it does not matter, whether a MF was planned right from the start or existing models are split as soon as they become too large and complex. A CLD of the overall system, exended by additional features like in and output of the models, is a useful tool to keep track of the big picture and to find out which links can be neglected or which feedback loops can be broken without causing additional model errors.

With this case study, however, we are just at the beginning of (re)defining the concept of the MF and exploring its potential and dangers. We are currently gathering new experience from three other large projects in which the model family concept is being used, and international exchange is also being promoted in order to incorporate the experience of other modelling groups. Finally, also the CLD-based visualisation strategy leaves space for improvement to increase the information content of the picture, e.g., by including different temporal or spatial resolutions.

Acknowledgments

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A Appendix

A.1 Model Family Development Timeline

Table 1. Changing Tasks and Knowledge Base as well as Genesis of the Model Family

date	changed knowledge base	new tasks	developments
Jan 2020	SARS-CoV-2 was detected in Europe	Decision makers required an estimate of the threat	First version of ABEM was developed from a population (GEPOC [10]) and influenza model [34].
Feb 2020	SARS-CoV-2 started spreading in Austria	Decision makers needed lockdown policy estimates	The policy module of ABEM was developed.
Apr 2020	A common agreement upon the parameters of COVID-19 and SARS-CoV-2 emerged	The need for a coordinated forecast arises among decision makers	The Austrian COVID-19 Forecasting Consortium was founded. The ensemble forecast strategy was established and A common hospital model was developed [11].
Jul 2020		Policies of the first wave needed to be reevaluated	ABEM was extended to cover additional policies, e.g., contact tracing [7]. A detailed differential equation model was developed for cross-model validation of the ABEM.
Dec 2020	Vaccines were announced	Vaccine prioritsation was discussed.	ABEM was extended to include vaccinations and prioritisation scenarios were calculated [9, 28]. A vaccine supply model was developed for Austria.
Jan 2021	Variants with evolutionary advantage were detected (Alpha).		ABEM was extended for multiple variants. A macro model was developed to analyse the takeover of a new variant and its evolutionary advantage [5].
Jun 2021	The first reinfections were detected. Immunity waning was confirmed.		ABEM was extended from a SIR to SIRS.
Jul 2021		Scenarios for evaluation of the current immunity level of the population of Austria were required	ABEM was deemed too computationally expensive for a problem that didn't require its epidemiological core features. Thus, the IWM was developed as a faster alternative and for cross-model validation.
Sep 2021	Inhomogeneous vaccination rates affect the age-shift in epidemic waves	A forecast of the age-shift in the upcoming Delta wave was needed	The ABEM could not depict the age shift in previous waves. The ASM was developed.
Nov 2021	Hospitalisation rates dropped and feedback of hospitalised persons became negligible.		The hospitalisation module was removed from the ABEM.
May 2022		A scenario based outlook for Autumn 2022 was requested by the policymakers.	The more flexible HM was developed based on the original model from Gesundheit Österreich GmbH. The model was applied using forecasts from ABEM and the IWM.

Grey parts describe vital members of the model family as well, yet we decided not to describe them in the context of this work.

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