


3 DEPARTMENT: COMPUTER SIMULATIONS

4 **Formal Modeling and Simulation for SARS-**  
5 **CoV-2 Containment Scenarios in Catalonia**

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7 P. Fonseca I Casas , J. Garcia I Subirana, and V. García I Carrasco, *Universitat Politècnica de Catalunya, 08034,*  
8 *Barcelona, Spain*

9 X. Pi I Palomés, *Universitat Oberta de Catalunya, 08018, Barcelona, Spain*

10 Gabriel Wainer, *Carleton University, Ottawa, ON, K1S 5B6, Canada*

11 *We define interrelated models to simulate the spread of SARS-CoV-2 in Catalonia,*  
12 *which can be used to effectively build simulation applications and analyze the*  
13 *effects of nonpharmaceutical interventions. Due to the constant evolution of this*  
14 *pandemic, and the need to take a multidisciplinary approach, we use a formal*  
15 *specification to represent the model and to validate the model assumptions. We*  
16 *discuss the definition of the model using formal languages, and the Specification*  
17 *and Description Language to improve communication between stakeholders. We*  
18 *show formalization details, discuss implications in the validation process, and*  
19 *present how results obtained from the model of the pandemic in Catalonia can be*  
20 *used for decision-making.*

21 **B**uilding computer simulations to study complex  
22 systems hinges on collaboration in multidisciplinary  
23 teams including experts with diverse  
24 backgrounds. The models need to consider the assump-  
25 tions presented by the various specialists, which should  
26 be represented in the model to ensure that it reflects the  
27 system behavior accurately. During the pandemic of the  
28 disease caused by the SARS-CoV-2 virus, numerous simu-  
29 lation models were built and used to forecast the spread  
30 of the disease in different geographic regions. These mod-  
31 els were built using a variety of methods, including differ-  
32 ential equations, multiagent systems, Cellular Automata,  
33 and other alternatives. A common approach consists of  
34 using compartmental models, which have been available  
35 as early as 1930.<sup>1</sup> They divide the population under study  
36 into three main compartments: those including the popu-  
37 lation *Susceptible* to infection, those *Infected* and spread-  
38 ing the disease, and those *Removed* from the population  
39 under study (either because they are deceased or

recovered). Numerous improvements to these *SIR* mod- 40  
els have been considered, including the addition of new 41  
compartments leading to more realistic models. For 42  
instance, one can divide the *Removed* into two: *Deceased* 43  
and *Recovered*. One can also add an *Exposed* compart- 44  
ment, representing those that have been exposed to the 45  
disease (but do not spread the disease yet). 46

The changing situation of the COVID-19 pandemic 47  
made it important to be able to adapt the model as 48  
soon as new information about the disease became 49  
available. This changing situation also made it impor- 50  
tant to have models that could consider the influence 51  
of various nonpharmaceutical interventions (NPIs). 52  
And we needed to ensure that the simulation results 53  
were correlated with real-world data. Using a common 54  
language that all the experts involved in the process 55  
can understand, and ensuring the correctness of the 56  
assumptions made by the different experts is essential 57  
for the success of the effort. The team of experts can 58  
introduce errors when the model is built because of a 59  
misunderstanding of the system behavior, or because 60  
of errors introduced when implementing the computer 61  
programs that will execute the model. We improved 62  
such collaboration using formal models that provide 63  
an unambiguous common language for modeling, and 64

65 a concrete mechanism to generate correct simula-  
66 tions. Conducting proper validation is difficult because  
67 of the numerous changes to the information about the  
68 disease. We use a Model Comparison Validation and  
69 Verification technique, which uses different models to  
70 improve error detection, both on definition and imple-  
71 mentation: we define three models that represent the  
72 same system with different techniques to see if the  
73 results are similar, allowing the detection of errors. We  
74 combine three models that focus on different aspects  
75 of the model and can be used for cross validation  
76 between these models, increasing credibility of the  
77 forecast and simplifying error detection.

### 78 SD MODEL

79 The first model, seen in Figure 1(a) is a SEIRD<sup>4</sup> prototype  
80 defined using System Dynamics (SD) and focused on the  
81 analysis of the feasibility of the key assumptions used by  
82 the different experts. It is used to ensure that all main  
83 aspects are taken into consideration, for example, the  
84 composition of the population, the nature of the com-  
85 partments to be used on the model, and the initial para-  
86 metrizations for the SARS-CoV-2 spread. The evolution  
87 of an infected individual is Susceptible → Exposed →  
88 Infectious → Recovered or Dead. Each compartment  
89 represents a subset of the population in that specific  
90 state and the model of the pandemic evolves by transfer-  
91 ring individuals from one compartment to another. More  
92 advanced versions of the SD model include other scenar-  
93 ios, like confinements (built by adding a path from Sus-  
94 ceptible to Confined and allowing an analysis of the  
95 temporal evolution of the pandemic for each wave). This  
96 mode does not use real data, but it is used to analyze the  
97 preliminary model assumptions.

### 98 PYTHON MODEL

99 The second model, built using Python, uses the SD  
100 model structure and optimizes and fits the observed  
101 data using a simulated annealing algorithm<sup>2,a</sup>. The  
102 objective is to obtain the parameters needed for the  
103 third model. The optimization model uses the observed  
104 cases as an input and tries to find a curve that fits with  
105 these observations (the mean of seven days). This  
106 model has the objective of studying the evolution of  
107 cases in Catalonia to define a basic transmission rate to  
108 be used in the SDL model. We estimate several param-  
109 eters for the spreading of the virus, including the effective  
110 reproductive number  $R_t$ , which is used to measure the  
111 likely transmission of the disease.  $R_t$  represents the

average number of secondary infections produced by a  
single infection (if  $R_t > 1$ , the number of cases will  
increase, and if  $R_t < 1$ , the number of cases will decrease).  
NPIs (e.g., reducing the mobility of the population, or  
mandating the use of a mask) affect the value of  $R_t$ . Our  
model estimates the Transmission Rate  $\beta$  (which is  
equivalent to  $R_t$ , calculated as  $\beta = R_t \gamma$  with recovery  
rate  $\gamma$ ).  $\beta$  is calculated using observed data that is input-  
ted to our Python model, optimizing and fitting the  
observed data. We can find the trend of the observed  
cases, and when the trend changes (for instance,  
because of new interventions like vaccines), we can  
compute a new  $\beta$  value.

At this point, with the main assumptions made and  
the key parameters calculated, we build a third model  
that includes all the needed assumptions for decision  
making and that is able to provide a forecast based on  
historical data and expert knowledge.

### SDL MODEL

The last model is built using Specification and Descrip-  
tion Language (SDL),<sup>2</sup> which provides a formal and  
unambiguous mechanism to describe real-world sys-  
tems.<sup>3</sup> The SDL model allows us to add detailed assump-  
tions and behaviors when NPIs are applied or new  
knowledge about the virus spread is available. Our team  
developed a variety of versions of the SDL, each of which  
includes the assumptions or the interventions applied at  
the time of the analysis. To validate this third model, we  
compared the daily new cases forecast with a dataset  
that contains the daily new cases in Catalonia.<sup>b</sup>

SDL is a graphical object-oriented language with  
unambiguous formal semantics, standardized by the  
International Telecommunication Union. SDL uses  
four hierarchical building blocks: 1) SYSTEM, 2) BLOCK,  
3) PROCESS, and 4) PROCEDURES. The SYSTEM and  
BLOCK diagrams represent the model's structure,  
using a hierarchical decomposition. PROCESS and  
PROCEDURES define the model's behavior. BLOCK  
and PROCESS are AGENTS that establish the commu-  
nication, sending SIGNALS through CHANNELS.  
SIGNALS function as a trigger, generating the execu-  
tion of a set of actions in a PROCESS. To represent  
time, all SIGNALS own a delay parameter and are  
sorted by delay and priority in the input queue of every  
input channel. SYSTEM is the topmost diagram in any  
SDL model, representing the main elements of the  
structure of the model.

Figure 1(b) shows the model used to forecast the  
second pandemic wave in Catalonia. The diagram

<sup>a</sup>Find the Python model in the CodeOcean service at the fol-  
lowing URL: <https://doi.org/10.24433/CO.9635632.v1>

<sup>b</sup>[http://governobert.gencat.cat/en/dades\\_obertes/](http://governobert.gencat.cat/en/dades_obertes/)

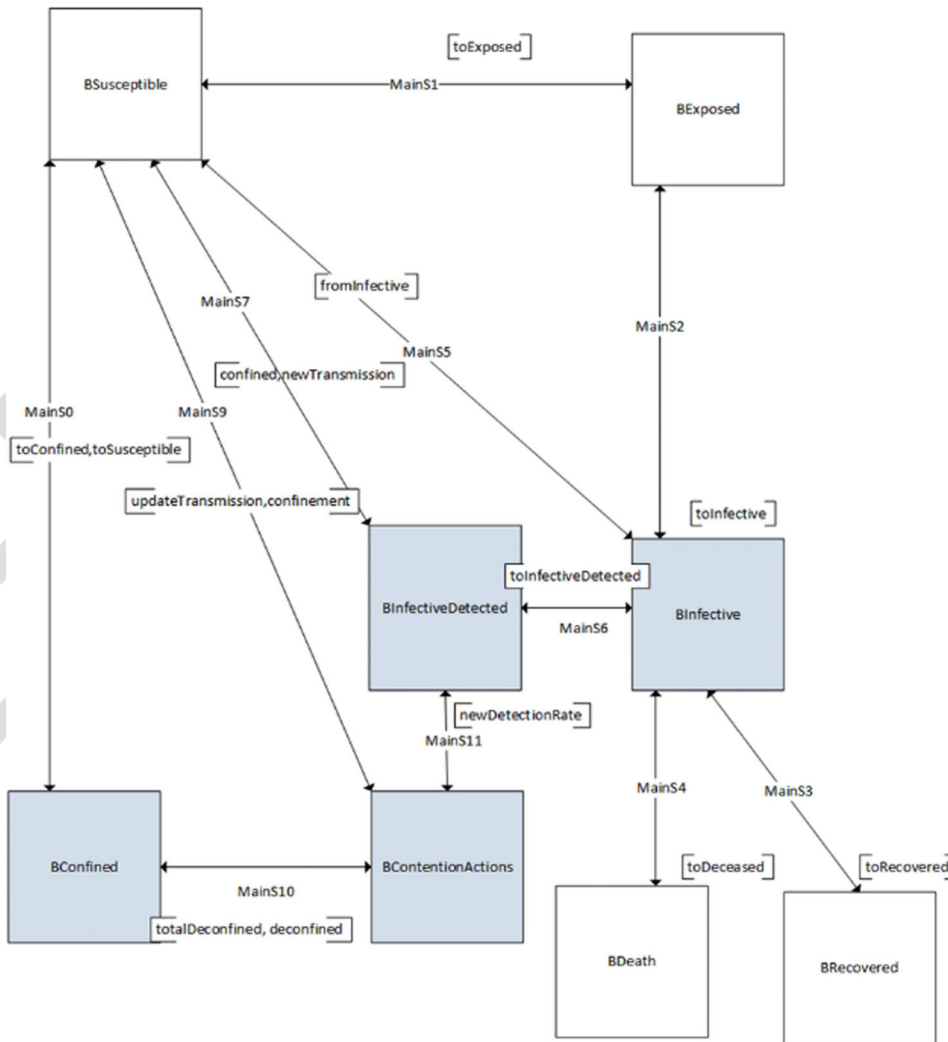
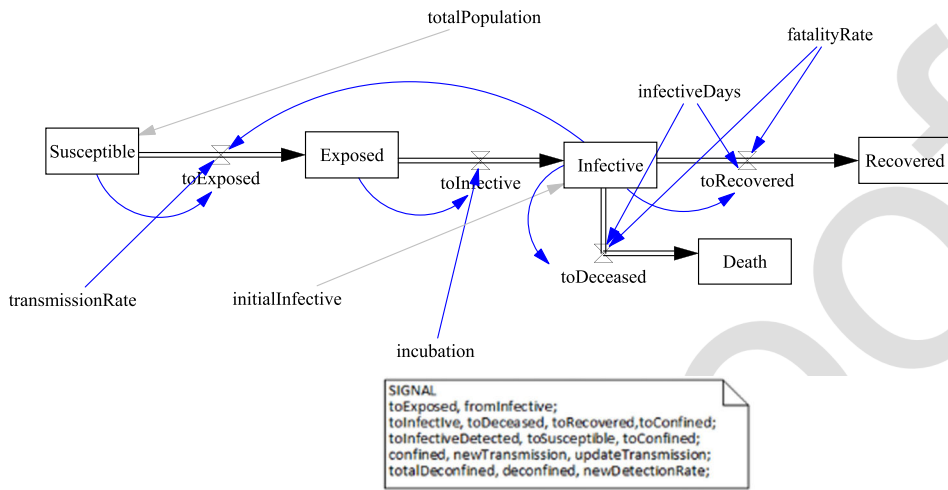
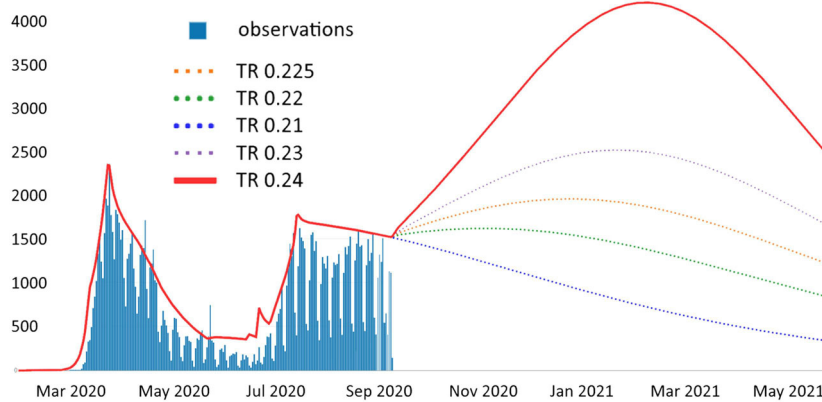


FIGURE 1. Model diagrams: on top, SD SEIRD model; bottom: SDL model SYSTEM diagram.



**FIGURE 2.** Forecast for new infections: red line, SDL model. Other scenarios with different hypotheses.

161 represents the SDL model SYSTEM diagram equivalent  
 162 to the SD model defined earlier. On both diagrams, the  
 163 squares represent the different compartments of the  
 164 SEIRD model (BLOCKS in the SDL model, and by Levels  
 165 for the SD model). We compare the outboth models'  
 166 outputs for validation: the SD model provides an approx-  
 167 imation to the pandemic's evolution, while the SDL  
 168 model provides more detail, allowing us to understand  
 169 the effects of the NPIs.

170 If needed, more BLOCKS can be added in the SDL  
 171 model to include new behavior (for instance, vaccinated  
 172 individuals, deceased, and other categories). These new  
 173 BLOCKS of the SDL model are 1) *BConfinement*, repre-  
 174 senting the population in confinement that cannot  
 175 become exposed; 2) *BInfectiveDetected*, the proportion  
 176 of infected individuals detected, assuming that detec-  
 177 tion improves over time; 3) *BContainmentActions* con-  
 178 trols the NPI actions taken by the authorities to prevent  
 179 the spread of SARS-CoV-2.

180 The SDL model also includes a cellular automaton  
 181 (CA)<sup>5</sup> in which each cell represents the spread of  
 182 SARS-CoV-2 over each of Catalonia's Health Regions.  
 183 This allows validating the model's assumptions by com-  
 184 paring the results with the data for each health region.

## 185 MODEL IMPLEMENTATION AND 186 CALIBRATION

187 To implement the SDL models, we use SDLPS,<sup>c</sup> a com-  
 188 puter software that can execute SDL and DEVS models.

189 To obtain accurate results, the models should fine-  
 190 tune the simulation parameters, including the  $\beta$  parameter  
 191 discussed earlier, to better predict the spread of the virus.  
 192 To forecast the value of  $\beta$  during the second wave at the  
 193 start of the school year in Fall 2020, we used common

194 patterns found in other countries that started the school  
 195 year earlier, such as South Korea (August 25, 2020) and  
 196 Israel (September 1, 2020). Using the real-world data from  
 197 those countries, we applied the Python optimization model  
 198 to identify those data points where the  $\beta$  value changed.  
 199 These were correlated with each of the NPIs put in place.

200 The simulation with the model of the second wave on  
 201 Catalonia began on January 29, 2020. With the rise in  
 202 cases, on the March 15, 2020, a lockdown was applied  
 203 (except for essential workers). Air space was closed on  
 204 the March 23. When the situation improved on the April  
 205 13, the workers of the industrial sector returned to work.  
 206 On the April 20, the government provided basic masks to  
 207 its citizens. In the following months, the restrictions were  
 208 gradually lifted, until July 2020. At this point, we calculated  
 209 a new  $\beta$  to represent a change in the spread of the virus  
 210 using the analysis done on the data from Israel and used  
 211 the cumulative incidence in Catalonia and Israel. We also  
 212 considered that the numbers observed during the summer  
 213 would increase due to a higher level of activity and  
 214 contact, and that they would not be smaller than the  
 215 numbers obtained during the lockdown. Other param-  
 216 eters were the detection rate and the asymptomatic popu-  
 217 lation.<sup>6</sup> Figure 2 shows the forecast for new cases  
 218 predicted using different scenarios.

219 The forecasting model uses past data to adjust the  
 220 parameters to calculate the evolution curve of new cases.  
 221 In the figure, the most likely situation is shown in red,  
 222 along with other scenarios that represent less likely situa-  
 223 tions. This analysis of different options allows managers  
 224 to understand the future evolution of the pandemic and  
 225 make informed decisions. The red line in the figure shows  
 226 the forecast most accepted by the domain experts con-  
 227 sidering all model assumptions and hypotheses. The simu-  
 228 lation generates alternatives to help decision-makers  
 229 when considering different NPIs (as well as errors in the  
 230 experimental hypotheses). If during the evolution of the

<sup>c</sup><https://sdpls.com/>



231 pandemic new available data modifies previous empirical  
 232 results, the pandemic will evolve differently. The different  
 233 trend lines shown on the figure can be useful to predict  
 234 how to act in those cases. This can be used by domain  
 235 experts in decision-making.

236 We built a dashboard<sup>d</sup> including Key Performance  
 237 Indicators (KPIs) and the model forecast, which is con-  
 238 tinuously validated against real data (using a Continu-  
 239 ous Solution validation approach). When the model  
 240 gives invalid results (i.e., we detect a divergence be-  
 241 tween the model's forecast and real data time series), we  
 242 reevaluate the hypotheses and recalibrate the model.  
 243 This provides valuable information to understand the  
 244 latest changes in the pandemic's evolution. This hap-  
 245 pens often since new NPIs are applied throughout the  
 246 pandemic.

## 247 CONCLUSION

248 The definition of models and rapid prototyping is espe-  
 249 cially important to study the spread of diseases like  
 250 COVID-19, caused by SARS-CoV-2. Simulation models  
 251 allow building *what-if* scenarios to compare future possi-  
 252 ble trends of the pandemic evolution based on the past  
 253 epidemics data. We showed how to build advanced mod-  
 254 els to improve the process, by building more than one  
 255 formal model of the system under study (in our examples  
 256 above, three related models) that allow continuous verifi-  
 257 cation and validation of the model when new data from  
 258 the system under study become available. The first  
 259 model (using SD) allows us to understand the validity of  
 260 the initial assumptions and the nature of the spread of  
 261 the disease; a second model (in Python) allows studying  
 262 the temporal behavior of the phenomenon and to esti-  
 263 mate the parameters of the model. The third model (built  
 264 in SDL) is used to understand the influence of NPIs on  
 265 the population and perform the forecast. The combina-  
 266 tion of the three models provides a solid mechanism to  
 267 validate the quality of the models and help make deci-  
 268 sions and study the influence of NPIs. The use of formal  
 269 modeling methods to represent the system improves  
 270 communication with experts and analysis of the hypoth-  
 271 eses while providing a mechanism for monitoring and  
 272 continuous validation, improving decision making.

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<sup>d</sup><http://pand.sdpls.com>

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**P. FONSECA I CASAS** is a professor at Polytechnic University of Catalonia (UPC), in the field of simulation, data processing, operations research, and statistics. Since 2017, he is a member of the committee 4.0 of the engineering industry in Catalonia. Contact him at [pau@fib.upc.edu](mailto:pau@fib.upc.edu).

**J. GARCIA I SUBIRANA** is a professor at Polytechnic University of Catalonia (UPC) and Universitat de Barcelona, in the Statistics and Operations Research Department, with nearly 10 years of experience in projects related to modeling and simulation projects. Contact him at [joan.garcia-subirana@upc.edu](mailto:joan.garcia-subirana@upc.edu)

**V. GARCÍA I CARRASCO** received the master's degree in computer and applied physics. He participates in simulation and modeling projects in Polyhedra Tech, a startup of Inlab FIB, and a TECNIO center of the Polytechnic University of Catalonia. Contact him at [victor.garcia@polyhedra.tech](mailto:victor.garcia@polyhedra.tech).

**X. PI I PALOMÉS** teaches in the Master on Industry 4.0 at UPC, as well as Open University of Catalonia. He received the M.Sc. degree in industrial engineering from Polytechnic University of Catalonia (UPC). Contact him at [xpi@engineers.net](mailto:xpi@engineers.net).

**GABRIEL WAINER** is a professor with the Department of Systems and Computer Engineering, Carleton University, Ottawa, ON, Canada. He is a fellow of SCS, the Society for Modeling and Simulation International. Contact him at [gwainer@sce.carleton.ca](mailto:gwainer@sce.carleton.ca).