BMC Research Notes

RESEARCH NOTE Open Access

Integrating patient metadata and pathogen genomic data: advancing pandemic preparedness with a multi-parametric simulator

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Abstract
Stakeholder training is essential for handling unexpected crises swiftly, safely, and effectively. Functional and tabletop exercises simulate potential public health crises using complex scenarios with realistic data. These scenarios are designed by integrating datasets that represent populations exposed to a pandemic pathogen, combining pathogen genomic data generated through high-throughput sequencing (HTS) together with patient epidemiological, clinical, and demographic information. However, data sharing between EU member states faces challenges due to disparities in data collection practices, standardisation, legal frameworks, privacy, security regulations, and resource allocation. In the Horizon 2020 PANDEM-2 project, we developed a multi-parametric training tool that links pathogen genomic data and metadata, enabling training managers to enhance datasets and customise scenarios for more accurate simulations. The tool is available as an R package: https://github.com/maous1/Pandem2simulator and as a Shiny application: https://uclouvain-ctma.Shinyapps.io/Multi-parametricSimulator/, facilitating rapid scenario simulations. A structured training procedure, complete with video tutorials and exercises, was shown to be effective and user-friendly during a training session with twenty PANDEM-2 participants. In conclusion, this tool enhances training for pandemics and public health crises preparedness by integrating complex pathogen genomic data and patient contextual metadata into training simulations. The increased realism of these scenarios significantly improves emergency responder readiness, regardless of the biological incident's nature, whether natural, accidental, or intentional.

Keywords Multi-parametric simulator, Pandemics, Natural, Accidental or intentional biological incident, Training, Preparedness, Response, Public health crisis, Functional exercise

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Introduction

The rapid, safe, and effective management of unusual crises, such as pandemics and accidental or intentional biological incidents, requires extensive training to develop the necessary expertise. Functional and tabletop exercises are regularly conducted to better prepare emergency responders and crisis managers for such scenarios [1, 2]. These simulations use a combination of realistic epidemiological, clinical, and biological data from affected populations to replicate complex public health crises [3]. To create meaningful functional and tabletop exercises, databases containing multiple variables that describe population groups exposed to simulated events – described as contextual metadata - are required.

To adequately prepare public health professionals for future pandemics or biological incidents, pathogen genomic data must be combined with patients' contextual metadata. High-throughput sequencing (HTS), also known as next-generation sequencing (NGS), has revolutionised the collection of pathogen genomic data by enabling the rapid sequencing of entire genomes during outbreaks [4, 5]. Since the onset of the COVID-19 pandemic, the availability of open-access genome databases has increased significantly, providing essential genomic features such as taxonomy, new mutations, drug resistance genes, and virulence factors [6, 7]. These genome insights are crucial for assessing the risk of pathogen spread, and must be integrated with patient metadata including as demographics, health histories, and disease outcomes, to gain a deeper understanding of the pathogen's lethality and transmission potential [8, 9].

If this integration were consistently possible in practice, it would greatly enhance the preparation of exercises for future pandemics. However, despite the increasing availability of genomic data, open access to this contextual metadata remains limited [10]. Data sharing and interconnection among EU member states face obstacles due to differences in data collection methods, standardisation practices, legal frameworks, privacy, and security regulations, as well as disparities in resources and infrastructure (Fig. 1) [11–13].

To address these challenges, the Horizon 2020 PANDEM-2 project developed a dedicated training platform to improve pandemic preparedness and response. As part of this initiative, our team designed an innovative multiparametric simulation tool that realistically links pathogen molecular data with patient contextual metadata [3, 14].

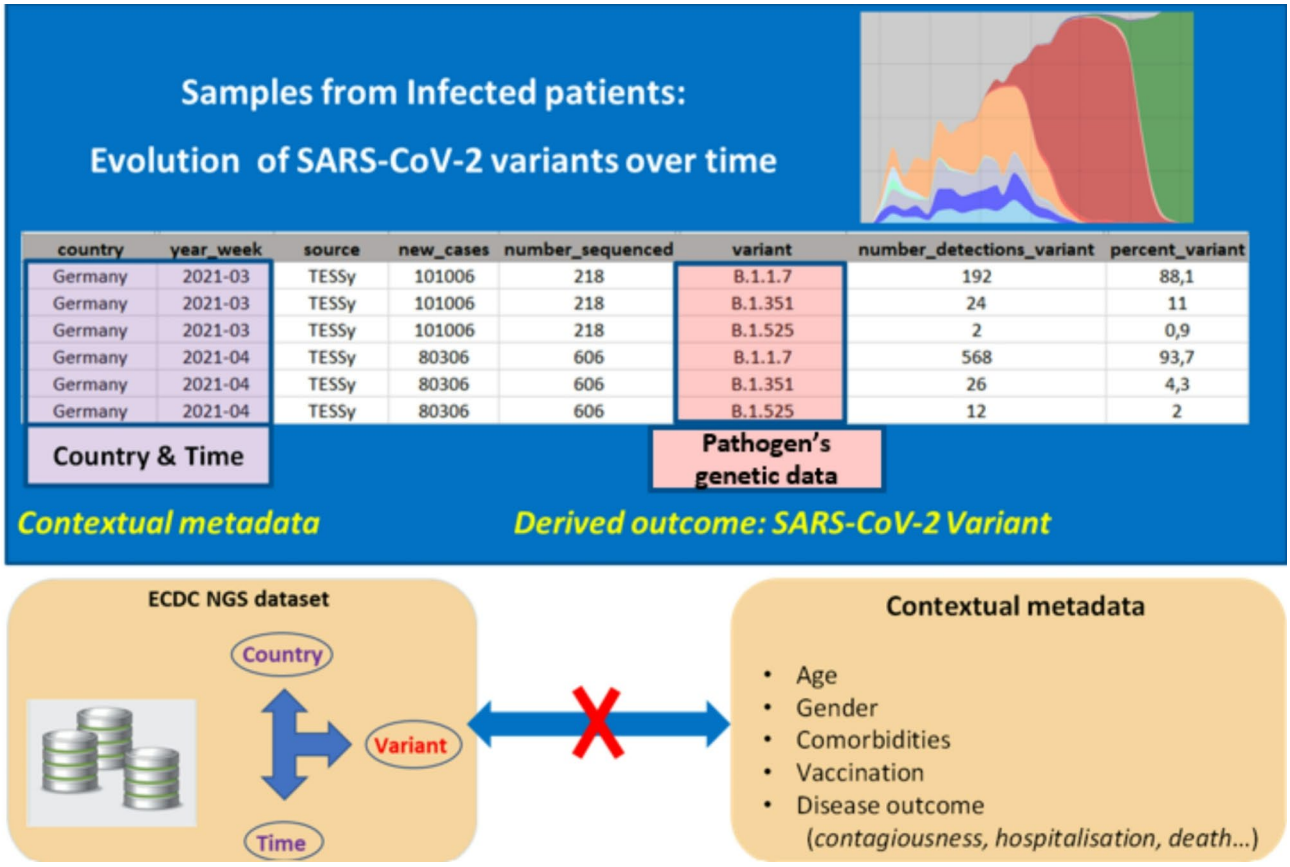

Fig. 1 Illustration of the missing link between contextual metadata and molecular data from pathogens. The figure shows weekly time series of pathogen data provided by the TESSy dataset. (source ECDC [15]) to monitor the evolution of SARS-CoV-2 variants in one EU Member State.

By combining pathogen genomic data with patient contextual metadata, this tool allows trainees to work on realistic training scenario that simulate disease transmission, evolution, and impact on various populations based on specific genomic features. When incorporated into training exercises, these integrated databases not only better prepare trainees for real-time monitoring and rapid response to emerging pathogen variants but also enhance their ability to track pathogen spread and inform targeted public health interventions.

This simulator enables training managers and trainees to enrich existing datasets by adding new variables through data-driven or random simulations. It also allows users to adjust the proportion of specific variables based on scenario requirements and objectives, helping to achieve desired outcomes. Built using an R package and accessible via a Shiny application, the tool enhances accessibility and usability.

The purpose of this paper is to present the simulator, providing an overview of its features and demonstrating the applications and training procedures developed during the PANDEM-2 project.

Materials and methods

Our multiparameter simulation tool enables the user to adjust an existing initial dataset corresponding to the scenario-driven evolution of the number of cases during a specified period.

Accordingly, the initial dataset should include at least two variables: (i) the time expressed in a pre-defined format (e.g., YY-MM-DD) and (ii) the incidence expressed as an integer. It is worth noting that this incidence can correspond to the number of new cases or of new hospitalizations at any given time.

Aside from these two mandatory columns, the initial dataset can also include additional variables (e.g., localisation [country name or region], vaccination status).

This initial dataset can be modified by the user through two distinct operations: (i) adding a new variable and (ii) modifying a relative risk characterising the association between two selected variables. These two operations can be used multiple times in order to add multiple distinct variables and/or modifying multiple distinct relative risks. The following steps are described in detail:

Methodological steps

Step 1: addition of a new variable

The multi-parametric tool can be used to enrich the initial dataset (which represents the evolution of the number of infected cases) in two ways: A data-driven simulation or a random simulation.

(a) *Data-driven simulation* (Fig. 2): This method uses a KNN (K-Nearest Neighbours)-based supervised classification method. The user must provide a second (named learning) dataset that has a variable (named X) that is also present in the initial dataset, as well as an additional variable (named Y) that will be added to the initial dataset. The KNN method learns the relationship between X and Y in the learning dataset and then predicts realistic values for this Y variable in the training dataset based on the values of the X variable.

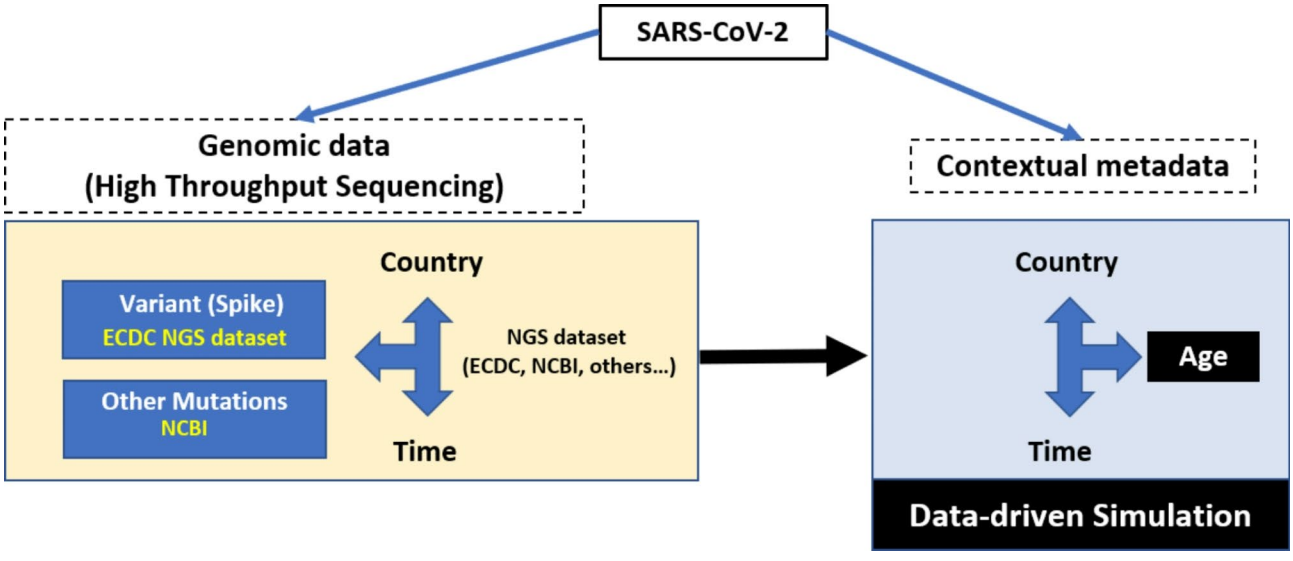

Fig. 2 Data-Driven Integration of an Additional Variable into the Simulation Dataset. *Note* Data-driven are employed to introduce an additional variable into the initial dataset using the multi-parametric simulation tool

This straightforward method can be viewed as a means of connecting databases that were previously unconnected but share a common variable (for instance, time).

(b) *Random simulation* (Fig. 3): This is useful if the user wants to add another additional variable but does not have a learning database (as in data-driven simulation). The user can enter the name of the new categorical variable (for instance, vaccination status) as well as each of its levels (unvaccinated, first and second dose of vaccination). The user can then choose the desired appropriate proportion of each level.

Notes: (A) The upper part of the figure represents the data-driven simulation, as illustrated and commented on in Fig. 2, in this simulation "Age" is used as a data-driven simulated parameter alongside structured metadata such as country and time for modelling outcomes based on available open-access data. (B) The lower part corresponds to random simulation, applicable when broader genomic factors - such as single nucleotide variations (SNVs), insertions and deletions (indels), virulence, and multidrug resistance - are incorporated in a scenario where a learning database is unavailable. This simulation also integrates non-genomic factors, such as disease outcomes (e.g., vaccine efficacy or new drug therapies) and comorbidities for risk modelling. Plain and dashed arrows: Plain arrows (solid black) represent direct data flow from genomic data (variants, mutations) to the data-driven simulation model, emphasizing the use of structured metadata (e.g., country, time, age) for predictive modelling; dashed arrows (red) represent indirect or complementary associations where data from genomic sources may influence random simulations; These arrows highlight the inclusion of disease outcomes and comorbidities for risk modelling, particularly when open-access metadata are insufficient or missing, requiring supplementary randomisation for a more comprehensive risk profile.

All these parameters can be used individually or in combination to simulate complex FX scenarios.

When no existing database is available, the tool supports random simulation. Users can define a new categorical variable (e.g., vaccination status), specify its levels (e.g., unvaccinated, first dose, second dose), and assign proportions for each level as needed.

Step 2: modifying a relative risk

In addition to enriching an initial dataset by adding new variables, the multivariate simulation tool also enables users to adjust the proportions of levels of variables within specific groups of patients based on pre-specified

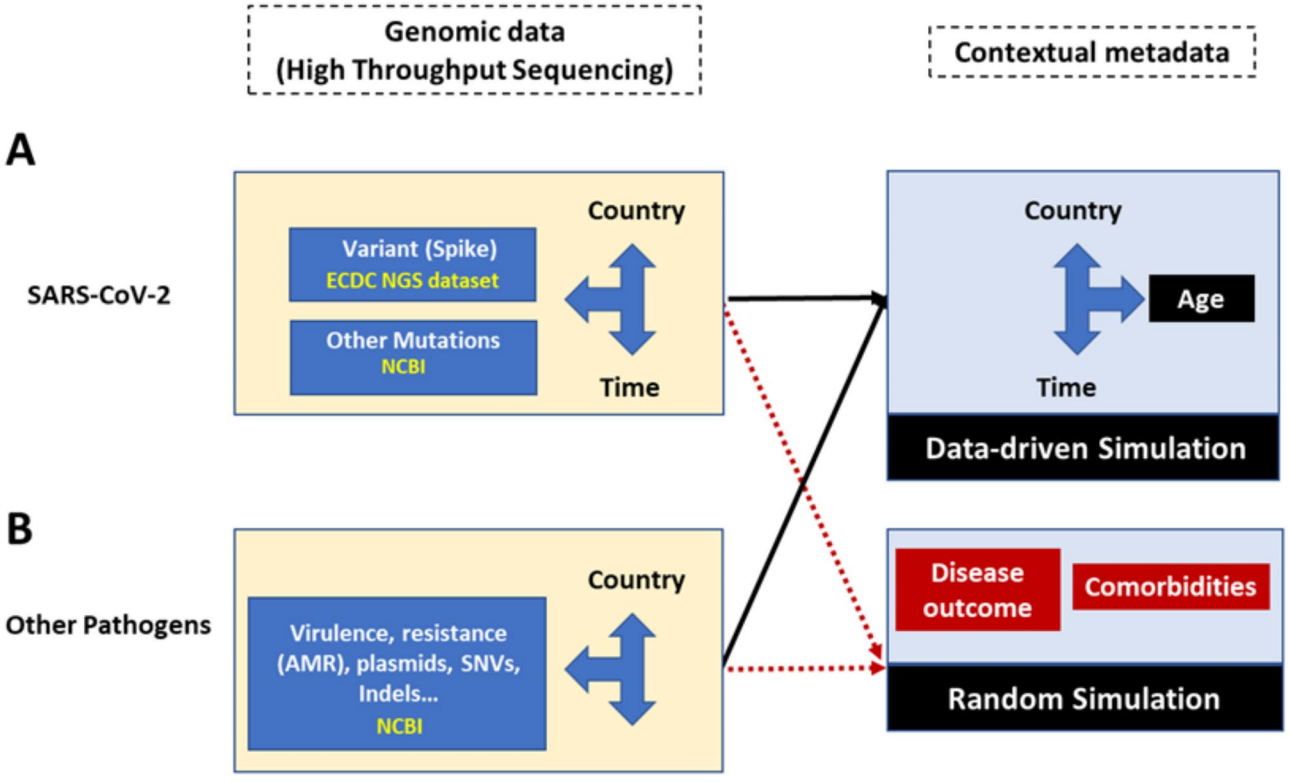

Fig. 3 Application of Data-Driven and Random Simulations: Integrating Direct and Indirect Links for SARS-CoV-2 and other Pathogens Risk Modelling

levels of other variables. Such adjustments can be made to meet the requirements and objectives of various scenarios. The «enrichment» function T is used to achieve the desired result. Users can adjust the relative risk (RR) to a desired level, enhancing the tool's flexibility for creating diverse scenarios during epidemic training sessions. It is worth noting that, when the RR is modified, proportions of the levels of each variable are maintained.

We developed our multi-parameter simulation tool using the R package, which is available at https://github.com/maous1/Pandem2simulator. We practised functional programming with the purrr package [16]. To enhance user-friendliness and ensure widespread accessibility, we also created a Shiny application, which can be accessed at: https://uclouvain-ctma.Shinyapps.io/MultiparametricSimulator/.

Training session to teach non-expert trainees how to use the multi-parametric tool

As part of H2020 project PANDEM-2, which aims to develop a pandemic preparedness training platform, we conducted a training session on February 1, 2023. This session involved 20 participants from the PANDEM-2 project, including first responders, epidemiologists, public health experts, analysts, software developers, supply chain managers, and disaster management professionals. During the 30-minute training session, the trainees learnt how to use the multi-parametric tool. This was followed by a hands-on training activity in which they were tasked to create datasets for the following pandemic scenarios:

- New SARS-CoV-2 variant of concern (VOC) spreading rapidly in young people: trainees were asked to create a realistic dataset for a FX (Functional exercise) that tracked the evolution of the number of infected cases caused by this new Sars-CoV-2 VOC.
- Highly virulent and resistant bacteria which spreads mainly in immunocompromised people and/or those above the age of 65: trainees were asked to generate a dataset for a FX based on the evolution of the number of infected cases.
- Influenza H1N1 virus with a risk of hospitalisation depending on vaccination status and age group: trainees were tasked with generating a dataset for a FX that reflected the evolution of the number of infected cases.

A questionnaire-based evaluation of the multiparametric simulator was conducted with trainees after their training session to assess the tool's effectiveness in generating data and facilitating functional exercises (supplementary file 1: Questionnaire S1). The questionnaire focused on the clarity of training explanations concerning variable generation methods, data enrichment concepts, and dataset visualisation. It also examined the tool's ability to modify and visualise datasets and gathered feedback on usability improvements. Finally, suggestions for tool development, layout refinement, and content enhancement were solicited to fully capture the assessment's scope.

Use of the multi-parametric tool in a functional exercise (FX)

In the context of crisis management and preparedness, a FX is a type of simulation or drill that tests and improves the capabilities and coordination of stakeholders involved in responding to a major crisis or emergency. The goal of FX is to simulate a realistic crisis scenario, allowing participants to practise their roles, responsibilities, and decision-making processes in a safe environment [17], and to evaluate their responses.

On March 15–16, 2023, the multi-parametric tool was used to simulate an influenza pandemic caused by the transmission of a novel viral strain from birds to humans. The FX evaluated the response strategies implemented by two interacting Public Health Emergency Operation Centres from the national public health agencies of neighbouring countries (Germany and the Netherlands) and assessed their preparedness levels.

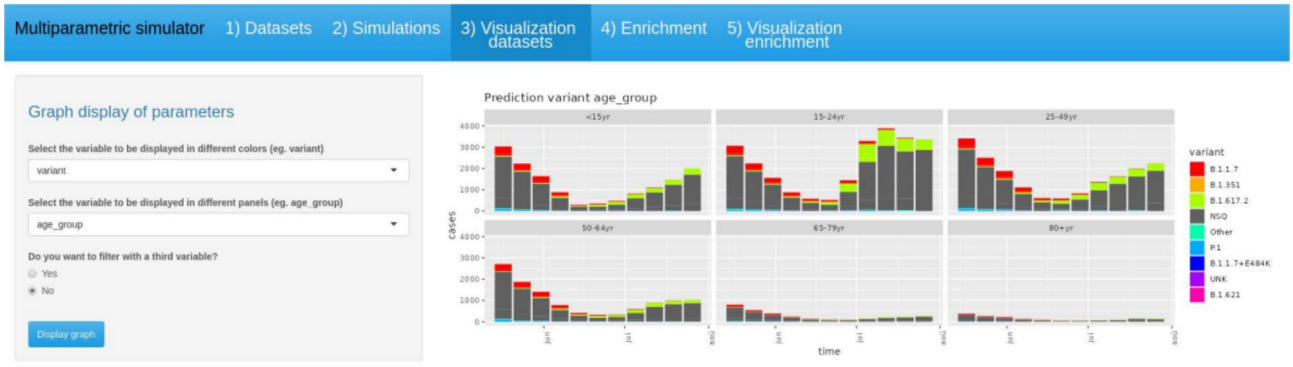

Fig. 4 Screenshots of the Third Tab in the Multi-Parametric Simulator Shiny Application

Results

Shiny application overview

The Shiny application comprises 5 tabs, each dedicated to a different stage in the process. The first tab focuses on importing the initial dataset import (Fig. 4). In the second tab the user can easily add new variables to the dataset. The third tab allows the user to visualise the dataset according to three specific variables. The time, the first variable, is consistently displayed on the x-axis. Meanwhile, the levels of the second variable are shown in separate panels, while the levels of the third variable are differentiated by different colours. In the fourth tab, the user can modify the RR, which is then displayed in the fifth tab.

Training session

The training session, which included 20 participants, demonstrated the user-friendliness and accessibility of the multi-parametric Shiny application. The evaluation provided by the trainees confirms that the concise video presentation of the tool and the subsequent creation of three distinct scenarios resulted in a thorough understanding of its functionalities (Table 1).

This successful training session demonstrates that the simulator can be effectively used by a variety of stakeholders, including public health practitioners, researchers, and policymakers.

The initial datasets for these scenarios, along with solutions on how to modify them using the tool (supplementary file 2: Dataset), and a video explaining the tool's main functionalities are available as supplementary materials (supplementary file 3: Video).

Use of the multi-parametric tool in a H2020 PANDEM-2 functional exercise (FX)

The FX organisers provided an initial dataset that tracked the evolution of case numbers over time, which served as the basis for the simulation. The multi-parametric tool was applied using the R package available on GitHub (https://github.com/maous1/Pandem2simulator), producing numeric and graphic representations of case numbers over time, with a typical execution time of approximately 90 s, highlighting its computational efficiency. To further enhance the realism of the simulation, a new variable was introduced into the dataset representing the emergence of a variant (Fig. 5). This variable contained two levels, corresponding to the previous strain (referred to in the FX as Alpha) and a new strain (referred to in the FX as Gamma), emerging in December according to the timeline of the pandemic scenario (Fig. 4). The Gamma variant in the FX was inspired by the historical evolution of the Delta variant of COVID-19, aligning the dynamics of the simulated variant with observed epidemiological trends during the emergence of a new variant.

Table 1 Overview of the training session participants' evaluations

Aspect	Appreciation (1–10 scale) - Averaged from 10 feedback
Clarity of presentation*	7.6
User-friendliness (easy to operate, straightforward to handle)	7.1
Usefulness of the tool for creating a functional exercise-targeted dataset	7.9
Understanding by the user of the range of functionalities	7.6

*Well organised menus, intelligible display design, universal symbols, clean visualisation, understandable terminology

Discussion

Considering that integration of HTS-driven pathogen genomic database and patient contextual metadata is not yet a reality, having a tool that can simulate this combination in a realistic manner is essential for enhancing training exercises and tabletop simulations. Genomic insights are increasingly vital for assessing the risk of pathogen spread and must be combined with patient metadata, such as health histories and disease outcomes, to prepare public health stakeholders for rapid and adaptive responses. These responses include real-time monitoring, addressing unusual changes in pandemic dynamics, and effectively communicating with the population—particularly vulnerable groups. Furthermore, this integration supports the implementation of targeted diagnostic and monitoring strategies for pathogens and cases, as well as the development of focused public health interventions, such as antiviral treatments and vaccination strategies.

The development and implementation of the multi-parametric simulation tool presented in this study represents a significant step forward in improving training procedures for pandemic preparedness and response. Its versatility makes it suitable for training emergency responders and crisis managers to handle various public health crises whether naturally occurring, accidental, or intentional.

A key strength of the tool is its ability to enrich existing datasets and generate new variables through data-driven or random simulations, providing useful insights and practical applications across various crisis scenarios, including tabletop and functional exercises [11]. The capacity to connect previously unconnected databases greatly improves the realism of training simulations, which is essential for effective learning.

The FX conducted as part of the H2020 PANDEM-2 project further validated the effectiveness and adaptability of the simulation tool. It successfully simulated the progression of cases during an influenza pandemic

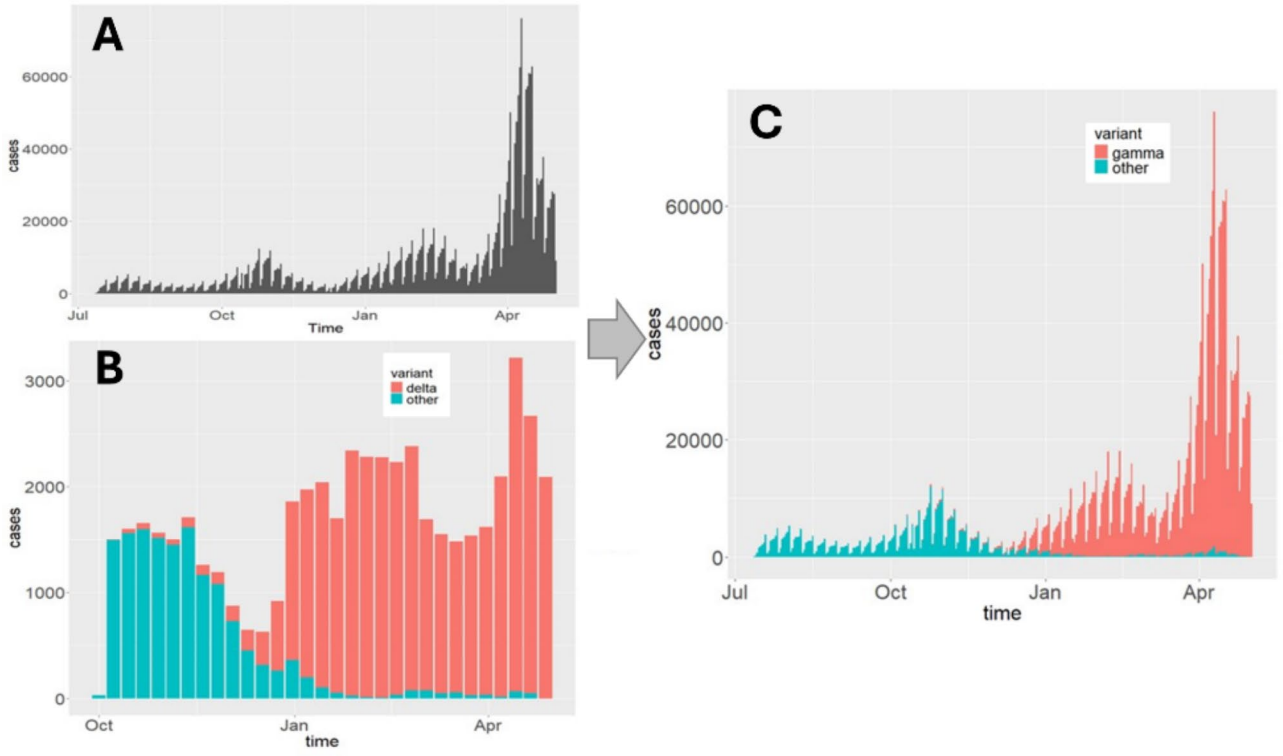

Fig. 5 Application of the Multi-Parametric Tool in a Simulated Pandemic Scenario. *Note* Data-driven are employed to introduce an additional variable into the initial dataset using the multi-parametric simulation tool

and the emergence of a new strain on a predefined date within the scenario. This demonstration highlighted its applicability to a range of infectious agents and scenario-driven genetic evolution models, including the emergence of new strains or variants.

The simulation tool also proved valuable for evaluating response strategies of two interacting Public Health Emergency Operation Centres and their preparedness levels. The flexibility and multi-parametric capabilities of the Shiny application made it a key resource for FX, helping public health professionals enhance their crisis management skills.

User-friendliness was another highlighted benefit during the training session, as confirmed by positive feedback from 20 participants. The combination of a brief video presentation and a hands-on training session allowed trainees to explore provided databases and generate scenario-specific data, leading to a comprehensive understanding of the tool's functionalities and applications.

The integration of the simulation tool with the R programming language as part of the Pandem2simulator package, underscores its potential for broader and adoption within the scientific community.

Certain limitations must be acknowledged. Although, the tool generates rich datasets, they remain fictional and cannot fully replace real-world data. A key challenge persists in the collection and integration of real patient metadata related with pathogen genomic data into properly structured databases. To facilitate data sharing between countries and institutions, future efforts should address privacy, regulatory and standardisation concerns, as well as improve data management policies [18].

To further enhance the tool's impact, regular updates to both functionalities and user interface would improve usability and relevance. Despite these limitations, the learning experience provided by the simulator significantly contributes to strengthening health emergency preparedness and response training, empowering key personnel to manage pandemic responses effectively.

The tool's further development could expand its applications beyond pandemics to other crises, such as CBRNe (Chemical, Biological, Radiological, Nuclear, and Explosive) events. This would involve training for first responders' safety, effective communication with exposed individuals and at-risk populations, and the implementation of protective measures.

Another application of the simulation tool would be the incorporation of patient genomic data, focusing genetic predispositions to severe disease outcomes. Integrating this third layer of data (i.e., pathogen genomics, patient metadata, and host genetics) would allow for a more comprehensive simulation of individual and population risks during pandemics, further improving the capacity

for personalized crisis modelling and targeted public health interventions.

While other pandemic simulation tools have been reported [19–22], they often focus on specific aspects such as viral genealogy [19], healthcare resource allocation [20], and COVID-19 symptomatic case projections [22]. The multi-parametric tool presented here stands out due its ability to simulate a wide range of crisis scenarios and its adaptability, making it a valuable asset for pandemic preparedness training and broader public health crisis management.

In conclusion, integrating pathogen genomic data with patient contextual metadata in training simulations enables the replication of complex public health crises, significantly enhancing pandemic preparedness. The multi-parametric simulation tool developed in the H2020 PANDEM-2 project offers a powerful and versatile resource for public health officials, policymakers, and practitioners to prepare for various crisis situations. By bridging the gap between pathogen genomic data and patient epidemiological, clinical, and biological metadata, the tool represents a major step forward in pandemic preparedness training.

Abbreviations

CBRNe	Chemical, Biological, Radiological, Nuclear, and Explosive
ECDC	European Centre for Disease Prevention and Control
EU	European Union
FX	Functional exercise
HTS	High-throughput sequencing
KNN	K-Nearest Neighbours
NGS	Next-generation sequencing
RR	Relative risk
VOC	Variant of concern

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13104-025-07207-1.

Supplementary Material 1

Supplementary Material 2 (Dataset)

Supplementary Material 3

Acknowledgements

We express our sincere gratitude to the entire H2020 PANDEM-2 technological team for their invaluable contributions to the development and implementation of the integrated dashboard featuring the multi-parametric simulator. Specifically, we would like to extend our appreciation to the following individuals for their dedicated efforts: C. Tighe, O; Zayed, C. Green, A. Ortiz, J. Albert, H. Chen (University of Galway, Ireland); G. Pacurar, B. Bucura, M. Enache (Clarisoft, Bucarest, Romania); C. Houareau (Robert Koch-Institut, Berlin, Germany); B. Kaluza, S. Römer (Fraunhofer, Munchen, Germany); L. Ngongalah (Trilateral Research LTD, London, United Kingdom).

Author contributions

Conceptualisation, J.A., A.S., F.O. and J-L.G.; Methodology, J.A., MB., J.H, F.O., A.S. and J-L.G.; Validation, J.A., MB. and J-L.G.; Formal Analysis, J.A., M.B., F.O.; Investigation, J.A., MB. and J-L.G.; Resources, J-L.G.; Data Curation, J.A., M.B., J.H. and F.O.; Writing – Original Draft Preparation, M.B., J.A., and J-L.G.; Writing – Review & Editing, J.A., F.O., M.C. and J-L.G.; Visualisation, J.A. and J-L.G.; Supervision, J-L.G.C.; Project Administration, J-L.G.; Funding Acquisition, J-L.G. and M.C.

Funding

The project received funding from the European Union's Horizon 2020 Research and Innovation programme under the Grant Agreement No. 883285. The material presented and views expressed here are the responsibility of the author(s) only. The EU Commission takes no responsibility for any use made of the information set out.

Data availability

The applications presented in this study are open access. The link is provided in the manuscript.

Declarations

Ethics approval and consent to participate

As part of this training, we used open-source data from the ECDC database, in accordance with the EU Open Data Directive and the ECDC open data policy. This approach avoids ethical issues relating to confidentiality and consent, while aligning our research with the principles of data transparency and re-use promoted by the ECDC. This approach also promotes the reproducibility of the research and maximises the public health and scientific impact of the data used.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

Received: 16 September 2024 / Accepted: 27 March 2025
Published online: 15 April 2025

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