

Guidelines for the Design of a Web Application Based on a 3D Visualization Model for the Prediction and Analysis of the Spread of Infectious Diseases

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Abstract: The prediction and visualization of infectious diseases are relevant for strengthening epidemiological surveillance and supporting decision-making in public health. This article proposes a set of eight guidelines for the design of a web application based on 3D visualization, aimed at the prediction and analysis of infectious diseases. The guidelines were formulated from an exploratory analysis of 30 scientific articles related to epidemiological dashboards, Web Geographic Information Systems (WebGIS), 3D visualization, and prediction models based on Long Short-Term Memory (LSTM), hybrid approaches, and environmental variables. These guidelines are organized into two categories: (i) guidelines for the design of 3D geospatial visualization, and (ii) guidelines for the integration of artificial intelligence models. An illustrative example is presented to show how these guidelines can be applied to the design of an application that allows users to select a disease, upload datasets, explore a 3D map, and visualize predictions through an interactive timeline. A preliminary evaluation involving 10 participants was conducted to explore user satisfaction with the prototype designed according to the proposed guidelines. The results suggest a positive initial perception of the application. This work provides an exploratory conceptual framework for the design of web-based tools for epidemiological monitoring and establishes a basis for future user validation and empirical studies.

1 INTRODUCTION

Infectious diseases, such as dengue, malaria, and COVID-19, represent a persistent challenge to public health and the economic stability of countries due to their high transmissibility and their impact on healthcare systems. These diseases can be transmitted through direct contact with infected individuals, indirect contact with contaminated surfaces, vector bites such as those from mosquitoes, as well as through contaminated food and water, thereby expanding the potential exposure scenarios for the population (MedlinePlus, n.d.). In Peru, the COVID-19 pandemic and recent dengue outbreaks have

highlighted limitations in epidemiological surveillance capacity, as well as the need for tools that integrate spatial and temporal information in an intuitive manner to enhance decision-making processes. (Médicos Sin Fronteras, 2021; Jacqueline, 2021).

The spread of infectious diseases is influenced by multiple factors, including climatological, demographic, environmental, and human mobility variables, all of which shape transmission dynamics. During colder seasons, respiratory infections tend to increase, whereas phenomena such as the Coastal El Niño create favorable conditions for the proliferation of the mosquito *Aedes aegypti*, the primary vector of

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dengue (Ministry of Health, n.d.; MINSA, 2025). In recent years, such conditions have been associated with the worst dengue epidemic recorded in the country, characterized by an unprecedented number of cases and an atypical expansion toward the central coast, where the population exhibits lower immunity to the disease (Daniel, 2023). These variations underscore the importance of developing tools that enable the simultaneous visualization of the spatial and temporal evolution of infections.

Various platforms have been developed to present epidemiological data, including the Situation Room of the Peruvian Ministry of Health (MINSA, 2024), geospatial dashboards, and predictive models based on time series or climatic variables. Although the Ministry of Health implements targeted preventive campaigns—such as recommendations to reduce dengue risk during high-mobility periods like Easter, promoting the use of protective clothing, repellents, and measures to eliminate mosquito breeding sites (Ministry of Health, 2025)—the literature indicates that current tools exhibit recurring limitations. These include fragmented interfaces, predominantly two-dimensional visualizations, limited integration between historical data and predictions, lack of standardization in visual representation, and insufficient clarity regarding which design elements facilitate the interpretation of disease spread.

This study proposes a set of eight guidelines to support the design of web applications based on 3D geospatial visualization for epidemiological analysis. Unlike studies focused on proposing a single predictive model, this work systematizes findings from the literature and synthesizes practical recommendations for integrating 3D maps, interactive markers, temporal sliders, predictive models (including LSTM, hybrid, and statistical approaches), and climatic and demographic variables within a unified application. These guidelines were formulated from a structured exploratory analysis of 30 scientific articles related to epidemiological dashboards, WebGIS systems, three-dimensional geospatial visualization, and predictive models applied to infectious diseases such as COVID-19 and dengue. Therefore, the guidelines should be understood as design recommendations derived from recurring patterns identified in the reviewed literature, rather than as definitive rules validated across all possible epidemiological visualization contexts. The guidelines are organized into two main groups: (i) guidelines for the design of three-dimensional geospatial visualization interfaces, and (ii) guidelines for the integration of epidemiological prediction models within the platform. An illustrative

example of a web application design incorporating guidelines G1 through G8 was developed. In addition, a preliminary evaluation was conducted with 10 participants from the healthcare sector, who interacted with the prototype by performing simulated tasks, including location selection, dataset upload, prediction generation, and temporal exploration. Upon completion, participants filled out a questionnaire based on the Moody and Lindland framework to assess Perceived Ease of Use (PEOU), Perceived Usefulness (PU), and Intention to Use (ITU). The results indicated a positive user perception.

The remainder of this article is structured as follows. Section 2 presents related work on 3D visualization. Section 3 provides a detailed description of the eight proposed guidelines. Section 4 presents an illustrative example of the prototype developed based on these guidelines. Section 5 describes the preliminary validation. Finally, Section 6 outlines the conclusions and future research directions

2 STATE OF THE ART

This section reviews related work on the visualization, prediction, and analysis of infectious diseases in order to identify recurring design components, modeling strategies, and limitations of current systems. A structured exploratory literature review was conducted using academic databases such as Scopus and IEEE Xplore. The purpose of this review was not to provide a systematic or exhaustive mapping of the entire field, but to identify representative studies that could inform the formulation of design guidelines for web-based epidemiological visualization and prediction tools.

The search focused on studies published between 2020 and 2025, a period in which the development of epidemiological dashboards and predictive systems increased considerably due to the COVID-19 pandemic and the growing interest in data-driven public health surveillance. The following search string was used and adapted according to the syntax of each database: ("prediction" OR "forecasting") AND ("infectious disease" OR "epidemic") AND ("web platform" OR "data visualization" OR "dashboard" OR "3D visualization"). Additional combinations were used to capture studies related to recurrent neural networks, LSTM, BiLSTM, hybrid models, climatic variables and geospatial visualization.

The selection process was carried out in three stages. First, titles and abstracts were reviewed to identify studies related to infectious disease visualization, epidemiological dashboards, geospatial analysis, or predictive modelling. Second, the full text of potentially relevant studies was examined to verify whether they included real epidemiological, geospatial, climatic, or time-series data. Third, the selected studies were grouped according to their main contribution to the proposed guidelines. Inclusion criteria were as follows: (i) studies incorporating visual analysis or epidemiological prediction; (ii) studies using real geospatial or time-series data; and (iii) web-based systems aimed at the analysis or communication of epidemiological results. The exclusion criteria included: (i) studies lacking validation with real-world data; (ii) works not directly related to infectious diseases or visualization; and (iii) papers focused only on clinical diagnosis or biomedical image processing. The selected studies are grouped into three main categories: (i) epidemiological visualization applications; (ii) predictive systems based on external variables; and (iii) models based on time series or hybrid approaches.

After applying these criteria, 30 studies were selected for analysis. These studies were not intended to represent the complete body of literature on infectious disease prediction or visualization, but rather a representative exploratory sample of works relevant to the design of the proposed application. The selected studies were grouped into three categories: (i) epidemiological visualization applications; (ii) predictive systems based on external variables; and (iii) time series-based and hybrid prediction models. This grouping allowed the identification of recurring elements that later informed the proposed guidelines, such as geospatial map-based interfaces, interactive markers, temporal exploration controls, predictive models, external variables, and data-processing workflows. The reviewed studies are presented below.

2.1 3D and Geospatial Visualization Applications

Syafiq et al. (2021) developed an interactive dashboard to monitor and predict dengue cases in Pahang (Malaysia). The platform integrates geospatial visualization, weekly epidemiological data, and climatic variables through a statistical regression system. Its main contribution lies in the coherent integration of prediction, visualization, and dynamic map navigation. Kaya et al. (2023) proposed

an immersive virtual reality application to visualize COVID-19 data within an interactive 3D environment. The system employs three-dimensional volumes, multiple layers, and spatial navigation to examine distributions of cases, hospitalizations, and mortality. The results indicate that 3D immersion enhances depth perception and facilitates the detection of hidden trends. Mohd et al. (2022) implemented a web-based platform that applies the DBSCAN algorithm to cluster areas based on population density and COVID-19 vaccination levels. The system uses heat maps, interactive filters, and geographic layers to explore the distribution of vaccination centers and immunization coverage. This approach enables the identification of critical areas, prioritization of interventions, and optimization of healthcare resource allocation. Its main contribution lies in combining clustering techniques with visualization to support operational decision-making in public health. In conclusion, these studies indicate that visualization through 2D maps, 3D environments, or clustering-based techniques are useful for exploring spatiotemporal relationships, identifying high-risk areas, and communicating complex epidemiological information. The analyzed platforms show that direct interaction with maps, the use of geographic layers, and the visual representation of trends enable users to better interpret disease dynamics and respond accordingly. These findings are consistent with the design of a web application centered on geospatial exploration, where 3D visual encodings may be used to display predictions over the Peruvian territory (Syafiq et al., 2021; Kaya et al., 2023; Mohd et al., 2022).

2.2 Prediction Models Based on External Variables

Chen and Moraga (2025) compared ARIMA, Prophet, Random Forest, and LSTM models to predict dengue cases in Rio de Janeiro by incorporating temperature, humidity, and precipitation data. The results show that deep learning models, particularly LSTM, achieve higher accuracy when integrating exogenous variables that influence vector dynamics. Furthermore, the study suggests that the inclusion of climatic factors significantly reduces prediction error. Swathika et al. (2025) analyzed the impact of climate change on the transmission of dengue and malaria using a multivariate regression model driven by meteorological data. Their findings reveal that increases in temperature, humidity, and precipitation variability are directly associated with a higher epidemiological risk. The study not only

highlights the climate–health relationship but also suggests that models incorporating environmental variables can anticipate outbreak scenarios further in advance. Geeitha et al. (2023) presented a hybrid model combining Random Forest and fuzzy logic to manage uncertainty in epidemiological data. The system classifies regions according to risk levels using demographic, environmental, and epidemiological variables. This hybrid approach improves accuracy compared to traditional Random Forest models, particularly in environments with incomplete or noisy data. In conclusion, these studies agree that epidemiological models improve their performance when incorporating external variables such as climate, demographics, or mobility. These variables enhance the explanatory power of the models and enable more accurate outbreak prediction, particularly for diseases influenced by environmental factors. Although such approaches require high-quality data, the results indicate significant advantages over models that rely solely on historical case series. This supports the inclusion of external variables in the predictive architecture of the proposed web application to improve its accuracy (Chen & Moraga, 2025; Swathika et al., 2025; Geeitha et al., 2023).

2.3 Time Series–Based and Hybrid Prediction Models

Sharma et al. (2025) proposed the SW-LSTM model, which combines strong and weak memory components to simultaneously capture long-term patterns and local fluctuations in epidemiological time series. This approach significantly improves metrics such as RMSE and achieves a more accurate representation of abrupt infection peaks. Farooqui et al. (2025) developed a hybrid Transformer-VMD model that integrates attention mechanisms with signal decomposition. This approach stabilizes the time series prior to training and captures complex temporal dependencies. Liu et al. (2021) employed nonlinear autoregressive (NAR) neural networks to analyze COVID-19 trends and compared their performance with ARIMA, logistic regression, and SEIR models. The results indicate that the NAR model achieved errors below 3% and adapted better to nonlinearities in the data. In conclusion, these studies suggest that neural time series–based models, such as LSTM, NAR, and hybrid Transformer-VMD approaches, have shown competitive performance compared with traditional statistical methods in predicting outbreaks. Their ability to capture nonlinearities, noise, and multiscale patterns makes

them particularly suitable for diseases characterized by high temporal variability (Sharma et al., 2025; Farooqui et al., 2025; Liu et al., 2021).

3 DEFINITION OF GUIDELINES FOR APPLICATION DESIGN

This section presents a set of eight guidelines for the design of a web application based on a 3D visualization model for the prediction and analysis of infectious diseases in Peru. The guidelines were developed from the analysis of studies related to epidemiological dashboards, geospatial visualization systems, 3D environments, WebGIS platforms, and predictive models applied to COVID-19, dengue, and other infectious diseases. Each guideline addresses a relevant design or modeling aspect that may be considered when developing this type of application: (i) the central role of the 3D map as the main view; (ii) the use of interactive markers; (iii) the integration of historical data and predictions within the same visual environment; (iv) temporal control through a timeline; (v) the incorporation of Long Short-Term Memory (LSTM) and Bidirectional Long Short-Term Memory (BiLSTM) models for epidemiological time series; (vi) the use of hybrid models for increased robustness; (vii) the integration of external variables such as climate or mobility; and (viii) the establishment of an automated preprocessing and prediction pipeline. Each guideline is identified by the prefix “G” followed by a sequential number (G1, G2, G3, etc.). The proposed guidelines are presented below.

3.1 Guidelines for the Design of a 3D Visualization Web Application

G1. Use a geospatial map-based view with 3D visualization as an extension to support interpretation. The analyzed studies suggest that the interface of epidemiological applications benefits from being structured around a central geospatial view, from which users access the rest of the information. This guideline is derived from the following works: (i) Lipeng et al. (2020) developed a WebGIS-based simulation system for COVID-19 in which the map serves as the main screen, organizing navigation across regions, thematic layers, and time periods, suggesting that a central cartographic view facilitates the exploration of spatiotemporal patterns. (ii) Zhang et al. (2021) proposed a WebGIS-based COVID-19 simulation system where the web map

functions as the primary interface, allowing users to switch between different levels (national, regional, and local), with zoom and navigation controls guiding analysis toward critical areas. (iii) Macrohon and Jeng (2021) presented a real-time COVID-19 data repository for the Philippines, in which the interactive map acts as the entry point, providing access to tables, charts, and filters, reinforcing the idea that geographic visualization should be the core of the user experience.

In conclusion, it is recommended to design the application around a geospatial map-based interface that allows users to explore epidemiological information by territory. In this proposal, 3D visualization is considered an optional extension of the geospatial interface, particularly useful when representing magnitude, density, or temporal variation through visual encodings such as extruded columns, elevated surfaces, or volumetric markers. Other interaction elements, such as disease selection, dataset selection, temporal filters, and external variable layers, should be organized around the map to support a coherent workflow. This design facilitates the integration of historical values, contextual variables, and prediction outputs within a single geospatial scene, while avoiding the assumption that 3D visualization is always required in every epidemiological dashboard.

G2. Include interactive markers to display information upon user interaction. The reviewed studies show that interactive elements are useful strategies for presenting detailed information without overloading the overall map view. This guideline is derived from the following works: (i) Mohd et al. (2022) developed an application that visualizes vaccination rates and immunization centers in Malaysia using markers and spatial clustering (DBSCAN); when interacting with each point, detailed information about the center is displayed, enabling the identification of coverage gaps without saturating the map with persistent labels. (ii) Sharma and Walker (2021) proposed a tool that combines COVID-19 and crime data, where each region is represented by markers that, when selected, display combined health and safety indicators, reporting that contextual pop-ups enhance the interpretation of multiple variables. (iii) Abouzahir et al. (2024) introduced a dynamic dashboard for malaria that integrates markers associated with monitoring stations, risk hotspots, and administrative units; these markers display epidemiological and climatic data upon user interaction, thereby avoiding information overload on the screen.

In conclusion, it is recommended to include interactive elements for each district, where information is displayed only when the user clicks on or hovers over the marker. Each marker should trigger a pop-up panel containing district-level data (historical cases, weekly predictions, and date), maintaining a clean and readable 3D map. This approach helps reduce visual clutter and supports focused interpretation, especially when the application presents multiple layers of epidemiological and environmental information.

G3. Represent historical data and predictions directly on the map. The analyzed studies suggest that integrating both historical data and predictions within the same geospatial view enhances the understanding of disease spread dynamics. This guideline is derived from the following works: (i) Syafiq et al. (2021) developed a Dengue Dashboard for Pahang that displays both observed incidence and values forecasted by statistical models directly on the map, enabling visual comparison of past and future trends by district. (ii) Meng et al. (2022) presented a visualization platform for COVID-19 mortality and vaccination in the United States, using choropleth maps and geospatial representations to show the evolution of indicators over time, highlighting the usefulness of combining data from different periods within a unified visual framework. (iii) Kaya et al. (2023) evaluated an immersive 3D environment for COVID-19 data in which bars and volumetric representations over the map depict cumulative cases and temporal variations, facilitating the identification of peaks and regional patterns.

In conclusion, it is recommended to represent both historical values and model-based predictions directly within the geospatial visualization, while clearly differentiating observed and estimated data. This differentiation may be achieved through visual encodings such as color, height, opacity, line style, or separate layers. In addition, because predictions in public health contexts may influence decision-making, the interface should communicate uncertainty whenever possible. This approach allows users to interpret predictions as estimates subject to uncertainty rather than as exact future values.

G4. Integrate an interactive timeline to explore temporal evolution on the map. The reviewed studies indicate that temporal controls, such as interactive timelines, are used in epidemiological visualization to support the exploration of changes over weeks or months. This guideline is derived from the following works: (i) Ionescu and Enescu (2020) presented a web application for visualizing COVID-19 data in Romania that uses an interactive timeline;

by moving the cursor across different dates, the map and associated indicators are updated, allowing users to track the progression of the outbreak. (ii) Talavia et al. (2021) developed a COVID-19 Tracker for India, where users can select specific dates and observe how case numbers and pandemic intensity evolve across the territory, showing that temporal controls enhance the exploration of extended time series. (iii) Maskey et al. (2021) implemented a tool to explore mobility data during the pandemic, combining maps with a timeline; as users navigate through the timeline, changes in mobility patterns are visualized, which helps relate mobility trends to variations in infection rates.

In conclusion, it is recommended to integrate an interactive timeline when the application requires the exploration of temporal evolution. The timeline may allow users to navigate through epidemiological weeks, months, or selected date ranges, dynamically updating the values displayed on the map. However, the timeline should be considered one possible mechanism for temporal exploration rather than the only valid option. Depending on the target users and analysis tasks, it may be complemented with alternative temporal representations such as date selectors, animation controls, small multiple maps, trend charts, or comparison panels. This approach supports a clearer and more flexible analysis of the evolution of infectious diseases across the territory.

3.2 Guidelines for the Integration of AI-Based Prediction Models

G5. Use Long Short-Term Memory (LSTM) and Bidirectional Long Short-Term Memory (BiLSTM) models to capture temporal dependencies in epidemiological time series. The reviewed studies indicate that LSTM networks and their variants have been widely used for modeling epidemiological time series due to their ability to capture nonlinear trends, seasonal patterns, and abrupt peaks associated with outbreaks. These architectures have shown competitive performance in several infectious disease forecasting studies, particularly when compared with traditional statistical models under specific datasets and forecasting horizons. (i) Chimmula et al. (2020) applied an LSTM model to forecast COVID-19 transmission in Canada, suggesting that the network more accurately follows rapid changes in the epidemic curve and achieves lower errors compared to classical methods. (ii) Tomar et al. (2020) developed an LSTM-based model and its variants to predict COVID-19 cases in India, reporting

significant reductions in metrics such as RMSE and MAE compared to purely statistical approaches. (iii) Iqbal et al. (2021) proposed an LSTM-based system for predicting the number of COVID-19 patients, showing that the architecture effectively captures complex temporal fluctuations without requiring strict assumptions of linearity or stationarity.

In conclusion, this guideline recommends that the temporal prediction module of the application should be based on LSTM or BiLSTM models trained on historical case series. At the model level, it is recommended to explicitly define a prediction window (e.g., 8 to 16 epidemiological weeks), a short-term forecasting horizon (1 to 4 weeks), and a set of input variables that can be extended with external factors. At the backend level, the system should expose a prediction service that receives the historical range and forecasting horizon as parameters, encapsulating the complexity of preprocessing and the recurrent model. Finally, at the frontend level, the interface should provide a dedicated panel where users can configure these parameters in a guided manner (e.g., location selection, historical period, and forecasting horizon) and visualize the transition between observed data and projected values directly on the 3D map, clearly distinguishing both types of information through colors or layer styles.

G6. Implement hybrid approaches that combine statistical models and deep learning techniques. Hybrid models can combine the theoretical structure of epidemiological or statistical models with the capacity of neural networks to learn nonlinear patterns, resulting in more robust and stable forecasts. (i) Ma et al. (2024) presented an enhanced compartmental model combined with an RNN, in which an SEIR-like structure is coupled with a recurrent network that adjusts discrepancies between theoretical dynamics and observed data, reducing prediction error. (ii) Dolker et al. (2023) developed a hybrid CNN–LSTM model to predict infectious diseases, simultaneously capturing spatial and temporal features and reporting significant improvements over purely recurrent models. (iii) Farooqui et al. (2025) proposed a deep optimization approach based on a hybrid deep learning model to predict the spread of emerging diseases, improving prediction stability in complex scenarios.

In conclusion, this guideline recommends hybrid modeling strategies in addition to a core deep learning model such as BiLSTM. At the model level, this may involve integrating outputs from multiple machine learning models (e.g., combining BiLSTM with XGBoost or Random Forest) or coupling BiLSTM

with traditional epidemiological or time series models such as SEIR, SARIMA, or others, allowing each component to contribute a different perspective on the phenomenon. At the backend level, this recommendation translates into the ability to orchestrate multiple prediction engines and fuse their outputs before delivering results to the frontend. At the interface level, the application should provide clear mechanisms for comparing approaches (e.g., selecting “BiLSTM only” versus “hybrid model” or visualizing multiple overlapping curves on the map and timeline), enabling users to assess the impact of combining models without requiring detailed knowledge of their internal implementations.

G7. Integrate external variables such as climate, mobility, and demographic factors into prediction models. The reviewed studies suggest that incorporating external variables can improve the explanatory and predictive capacity of epidemiological models by capturing factors that directly influence disease transmission and outbreak dynamics. This guideline is derived from the following works: (i) Dubey et al. (2025) analyzed infectious disease surveillance supported by artificial intelligence techniques and suggested that the inclusion of demographic, surveillance, and behavioral data enables earlier identification of risk scenarios and improves early outbreak detection. (ii) Guo et al. (2024) presented an XGBoost–LSTM predictive framework driven by traffic data, showing that vehicular mobility correlates with increases in transmission, providing key information to anticipate epidemic peaks in highly connected areas. (iii) Swathika et al. (2025) studied the impact of climate change on disease spread using predictive models, suggesting that variables such as temperature, humidity, and precipitation explain a significant portion of variability in climate-sensitive diseases.

In conclusion, this guideline recommends that the application design should support the incorporation and visualization of complementary variables influencing epidemiological behavior. These variables may be included as additional features in LSTM/BiLSTM or hybrid models alongside historical case data, enabling the backend to process enriched datasets (e.g., cases + precipitation + temperature + mobility indicators) and feed them into the prediction engine. At the 3D visualization layer, the interface should provide controls to enable or disable thematic layers (e.g., climate, mobility, population density) on the map, as well as panels or timeline-linked charts that display the evolution of these variables over the same period as the predictions. This approach allows users to explore

how projections change when external variables are considered, without modifying the internal configuration of the model, following a contextual analysis workflow: select a district, activate external variables, and observe their influence on risk interpretation

G8. Design the application to support a continuous update workflow between data, predictive models, and 3D visualization. The reviewed studies indicate that epidemiological analysis platforms may benefit from workflows in which data acquisition, model updating, and visualization operate as connected processes rather than as isolated components. (i) Vettrithangam et al. (2025) analyzed the use of advanced machine learning techniques for COVID-19 predictive modeling and emphasized the need for iterative data update cycles. (ii) Zhao et al. (2022) described a COVID-19 data crawling and visualization system based on big data, where the architecture is structured into data collection, processing, and presentation layers, enabling automatic updates of visualizations as new data becomes available. (iii) Wang et al. (2022) examined the experiences of software engineering teams developing COVID-19 dashboards during a public health crisis and highlighted the importance of designing clear data update workflows from the outset, including mechanisms for data refresh.

In conclusion, this guideline recommends that the application should function as a continuous pipeline connecting data sources, predictive models, and 3D visualization. At the backend level, this involves implementing periodic data update processes (e.g., ingestion of new epidemiological reports or climate time series), services for retraining or updating models when new data is available, and prediction endpoints that consistently operate with the most recent model artifacts (e.g., trained models and scalers). At the frontend level, each relevant user action (such as changing the disease, dataset, district, or cutoff date) should automatically trigger this workflow: data retrieval, model execution, and subsequent updating of the 3D map and timeline. The interface should also include process indicators (e.g., loading messages, brief animations, or “updating data” states) to make this cycle visible and convey that the displayed predictions reflect the most up-to-date information available.

Although the guidelines are presented separately, three cross-cutting considerations should be addressed throughout the application design: uncertainty communication, accessibility, and explainability. Since epidemiological predictions are

estimates rather than exact future values, the interface should communicate uncertainty through prediction ranges, confidence intervals, error indicators, or visual cues such as opacity and warning labels. Accessibility should be supported through readable labels, sufficient contrast, color-blind-friendly palettes, keyboard navigation, and alternative textual representations. Finally, prediction outputs should include simple explainability mechanisms, such as relevant input variables, historical trends, model performance metrics, or comparisons between observed and predicted values. These considerations are particularly important in public health contexts, where visualizations may influence interpretation and decision-making.

Table 1: Summary of the eight proposed guidelines.

Category	Guideline	Details
Guidelines for the design of the 3D visualization web application	G1	Geospatial map-based interface with 3D visualization as a supporting extension.
	G2	Interactive elements to display information on demand and reduce visual overload.
	G3	Joint representation of historical data, predictions, and uncertainty.
	G4	Temporal exploration through an interactive timeline or alternative temporal controls.
Guidelines for the integration of AI-based prediction models	G5	LSTM and BiLSTM models for temporal dependencies in epidemiological series.
	G6	Hybrid models combining deep learning and statistical approaches.
	G7	External variables such as climate, mobility, and demographic factors.
	G8	Update workflow for data loading, preprocessing, prediction, and visualization.

4 ILLUSTRATIVE EXAMPLES

This section presents a web application illustrating how guidelines G1–G8 can be integrated into the design of a geospatial and 3D visualization platform for the analysis and prediction of infectious diseases in Peru. The prototype demonstrates a user interaction workflow, including disease type selection, dataset upload, 3D geospatial exploration, and temporal navigation through an interactive timeline.

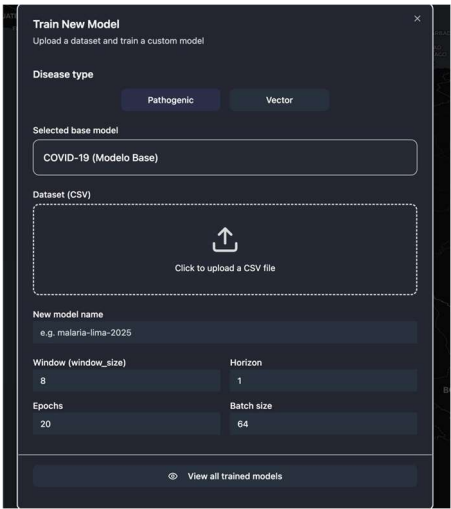


Figure 1: Initial Prediction Configuration Screen

Figure 1 shows the initial configuration interface where the user selects the type of disease to be analyzed, such as vector-borne or pathogen-based diseases, and the data source, either through an internal dataset or CSV upload. Guideline G1 is reflected as part of the configuration stage preceding the 3D map within a workflow centered on geospatial exploration. This stage supports Guideline G7 by allowing the incorporation of enriched datasets with external variables, such as climate, mobility, or demographic factors. It also supports Guideline G8 by connecting the data input stage with the preprocessing and prediction workflow.

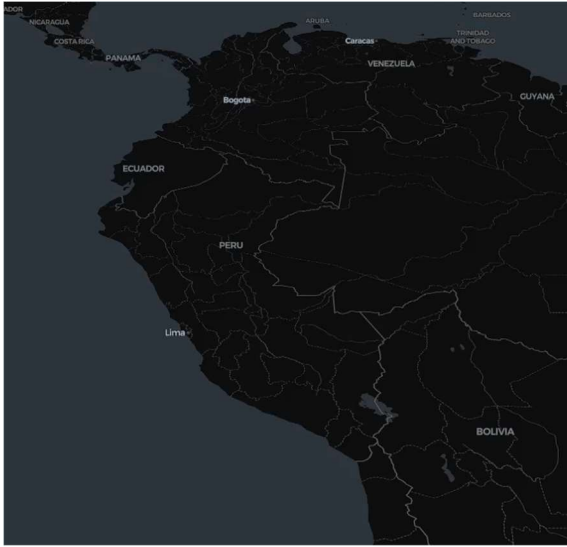


Figure 2: 3D Geospatial Visualization of Peru

Figure 2 shows the geospatial visualization of the Peruvian territory, which acts as the central interface of the prototype. This view implements Guideline G1 by organizing the user workflow around a map-based interface with 3D visual encodings. Users can select departments, provinces, or districts to access historical values and prediction outputs. Guideline G2 is reflected through selectable regions and contextual panels that display information on demand, while Guideline G3 is applied by representing historical data and model-based predictions within the same geospatial environment.

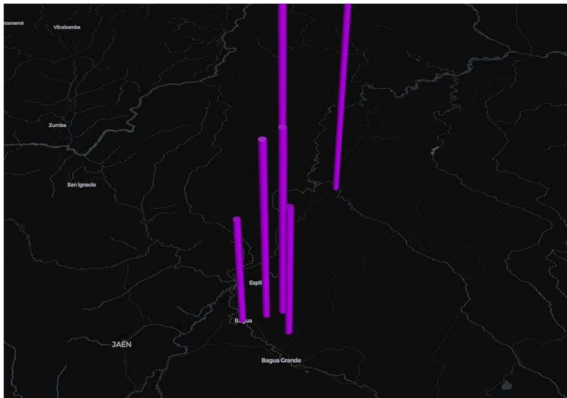


Figure 3: Visualization of Predictions on the 3D Map.

Figure 3 shows how the application displays predictions generated by the model directly on the 3D map using vertical bars and visual encodings that indicate magnitude and risk levels. Guideline G3 is implemented by combining historical information with predictive results within a single view and by

differentiating observed and estimated values. In addition, the design may include uncertainty indicators, such as prediction ranges, error metrics, or confidence-related visual cues, to help users interpret the outputs as estimates rather than exact future values. Guidelines G5 and G6 are also applied, as the predictions are produced by LSTM/BiLSTM or hybrid models, while explainability elements may be incorporated through complementary panels showing historical trends, relevant variables, or model performance metrics.

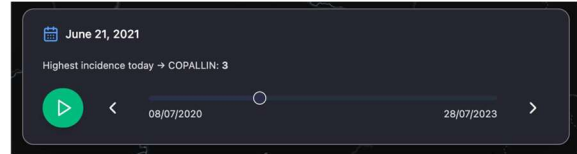


Figure 4: Interactive Timeline for Temporal Evolution

Figure 4 shows the timeline module, which allows users to navigate through epidemiological weeks or selected date ranges and dynamically update the values displayed on the map over time. This view implements Guideline G4, which recommends incorporating an interactive timeline to facilitate temporal analysis, and is also related to Guideline G3, as both historical and projected data are updated in real time as the user adjusts the selected period. Finally, Guideline G8 is reflected in the automatic updating of data and predictions, integrated within the system's visual refresh pipeline. In summary, the illustrative example shows one possible implementation of Guidelines G1–G8 in a web-based epidemiological visualization prototype. The example should not be interpreted as the only possible design solution, but as a practical application of the proposed recommendations in the Peruvian context.

5 EARLY VALIDATION

This section describes an early validation conducted to obtain preliminary feedback on the applicability of the proposed guidelines in the design of a 3D geospatial visualization web application for epidemiological analysis. For this purpose, a high-fidelity prototype was developed implementing Guidelines G1 to G8. The prototype incorporated core functionalities such as disease type selection, dataset upload, 3D geospatial visualization, prediction display, and temporal exploration through an interactive timeline. The validation was conducted with 10 healthcare professionals from Lima. Each participant interacted with the prototype through a

guided demonstration that included the main application views: disease type selection, dataset upload, 3D visualization of the Peruvian territory, and temporal exploration using the timeline. Participants performed simulated tasks such as selecting a region, uploading a dataset, generating predictions, and examining the temporal evolution of cases across epidemiological weeks. After the interaction, participants completed a satisfaction questionnaire based on the framework proposed by Moody (2003) and Lindland et al. (1994), aimed at measuring three constructs: Perceived Ease of Use (PEOU), Perceived Usefulness (PU), and Intention to Use (ITU), using a five-point Likert scale (1 = strongly disagree, 5 = strongly agree). For this preliminary analysis, responses were grouped by construct and summarized using descriptive percentages in order to identify the general tendency of user perception.

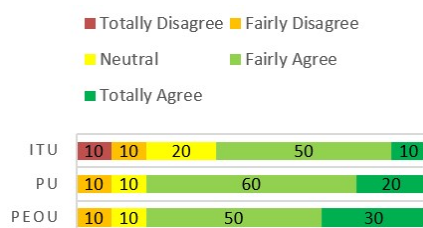


Figure 5: Satisfaction results.

Figure 5 shows the distribution of responses from the satisfaction questionnaire for the three evaluated constructs: Perceived Ease of Use (PEOU), Perceived Usefulness (PU), and Intention to Use (ITU). The results suggest a predominance of positive responses. For PEOU, approximately 80% of participants selected “Agree” or “Strongly agree,” indicating that the interface was perceived as understandable and intuitive. For PU, around 80% reported that the tool could be useful for analyzing epidemiological trends. For ITU, about 60% selected positive responses, suggesting a moderate initial intention to use the application in its final version.

However, these findings should be interpreted as preliminary feedback rather than generalizable evidence of effectiveness. The sample size was limited to 10 participants from the healthcare sector, which restricts the possibility of drawing broader conclusions about usability, satisfaction, or adoption in broader clinical and public health contexts. Therefore, this early validation provides initial support for the applicability of the proposed guidelines, while highlighting the need for future studies with larger and more diverse samples, task-based usability metrics, and comparative evaluations.

6 CONCLUSIONS

This study proposed a set of eight exploratory design guidelines for the development of a web application based on geospatial and 3D visualization for the prediction and analysis of infectious diseases in Peru. Based on a structured exploratory analysis of 30 studies on epidemiological dashboards, Web Geographic Information Systems (WebGIS), 3D visualization, and predictive models, the guidelines were organized into two groups: visualization-oriented recommendations and Artificial Intelligence (AI)-oriented recommendations. The visualization-oriented guidelines address the use of a geospatial map-based interface, interactive elements for on-demand information, the representation of historical data and predictions, and temporal exploration mechanisms. The AI-oriented guidelines address the use of Long Short-Term Memory (LSTM) and Bidirectional Long Short-Term Memory (BiLSTM) models, hybrid modeling strategies, external variables, and update workflows connecting data, models, and visualization. The illustrative example showed one possible implementation of the proposed guidelines in a prototype that includes disease and dataset selection, a geospatial visualization of the Peruvian territory with 3D visual encodings, prediction visualization, and temporal exploration through an interactive timeline. The prototype also illustrates how complementary design considerations, such as uncertainty communication, accessibility, and explainability, can be incorporated to support the interpretation of epidemiological predictions in public health contexts. A preliminary evaluation with 10 participants from the healthcare sector suggested positive initial perceptions regarding perceived ease of use, perceived usefulness, and intention to use. However, due to the limited sample size, these results should be interpreted as exploratory feedback rather than generalizable evidence of effectiveness. In addition, since the literature review was structured but exploratory, the selected studies should not be interpreted as an exhaustive representation of the entire field. Future work should include a more extensive validation with larger and more diverse groups of healthcare professionals, epidemiologists, and public health decision-makers. Further studies should evaluate task completion time, interpretation errors, accessibility, uncertainty communication, and the explainability of prediction outputs. In addition, future research may compare applications designed with and without the proposed guidelines to assess their effect on user performance, comprehension, and decision-support capabilities.

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