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A Scoping Review of Artificial Intelligence and Machine Learning for Spatio-temporal Infectious Disease Forecasting

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Abstract

Infectious diseases spread across space and time, yet most artificial intelligence (AI) and machine learning (ML) models treat forecasting as a purely temporal problem. We conducted a scoping review of AI/ML methods for spatio-temporal infectious disease forecasting, searching five databases on 20th November 2025. We included 93 studies published between 2018 and 2026, spanning 14 infectious diseases. Recurrent neural networks (46%) and graph neural networks (39%) dominated, with hybrid mechanistic-ML models growing steadily after 2022. Over 30 distinct error metrics were used, with no shared benchmarks, making cross-study comparison infeasible. Uncertainty was quantified in only 19% of studies, external validation in 13%, and 71% did not share code openly. Forecasts were concentrated in middle- and high-income countries, and only one study conducted fairness analysis. Addressing these gaps in evaluation standardisation, transparency, and equity is essential for AI/ML forecasting to inform public health policy.

1 Introduction

Infectious diseases cause substantial morbidity and mortality [1], and can induce long-term sequelae such as post-COVID syndrome [2]. Their effects extend beyond health to the economy [3], education [4] and healthcare [5]. One analysis identified 3013 outbreaks globally between 1996 and 2023 [6], including SARS in 2003 [7], H1N1 influenza in 2009 [8], Zika in 2016 [9], COVID-19 in 2020 [10], and Mpox in 2022 [11]. COVID-19 illustrated this impact most starkly, with more than 700 million cases and 7 million deaths reported globally by November 25th, 2025 `https://www.who.int/news-room/fact-sheets/detail/coronavirus-disease-(covid-19)`). Forecasting infectious disease is therefore central to public-health decision making.

Forecasting is often treated as a purely temporal problem, yet infectious diseases propagate across space and time, with considerable spatial heterogeneity. In the UK, COVID-19 transmission via direct person-to-person contact [12] was shaped by socio-economic, demographic, pollution and mobility factors [13, 14]. Influenza and vector-borne diseases such as dengue and Zika show similar spatial heterogeneity, driven by socioeconomic factors, climate, mobility and for vector-borne diseases, environmental conditions favouring vector populations [14–17]. Despite this, traditional methods have largely relied on

time-series predictions alone [18]. Capturing spatio-temporal dynamics is essential to allocate resources and target interventions at the right time and place [19]. Transmission dynamics have traditionally been studied with mechanistic models such as the classical susceptible exposed infected recovered (SIR) model [20]. Other mechanistic models have been developed to incorporate spatial structure such as metapopulation models [21] and agent-based models [22].

The growing abundance of data has driven a shift towards artificial intelligence (AI) and machine learning (ML) [23]. These methods can capture complex, non-linear relationships and integrate diverse, multi-modal datasets [23], learning patterns by iteratively adjusting model parameters to minimise a loss function [24, 25]. Yet time series ML methods typically ignore spatial structure [26], and most studies forecast in either space or time rather than both simultaneously [27].

Several reviews have examined related topics. Shi and colleagues survey ML for spatio-temporal sequence forecasting across domains, but not specifically for infectious disease [28]. Lima and colleagues review temporal and spatio-temporal ML forecasting, but only for arboviruses [29]. Rodriguez and colleagues examine ML for epidemic forecasting more broadly, without focusing on spatio-temporal methods [30]. To our knowledge, no review synthesises spatio-temporal ML forecasting across multiple infectious diseases while also examining evaluation, uncertainty quantification, fairness, data access and interpretability. Given this fragmented and methodologically heterogeneous literature, a scoping review is the appropriate approach as the breadth of architectures, data sources and methods can be mapped.

By performing a scoping review of use of AI and ML in the field of spatio-temporal infectious disease forecasting we aim to map existing approaches to AI/ML architectures, data sources, evaluation methods, uncertainty quantification, and interpretability from the published literature. In doing so we aim to identify both successful and underused methods of forecasting, and identify areas which have not yet been well researched. This scoping review helps modellers select proven architectures, public health agencies appraise forecasting tools, and researchers identify new areas for investigation.

2 Methods

2.1 Protocol and Search Strategy

We conducted a scoping review on AI/ML methods for spatio-temporal infectious disease forecasting, following Arksey and O'Malley's framework [31] and PRISMA-ScR guidelines [32].

We searched five major databases - IEEE Xplore, Web of Science, Compendex, PubMed and Scopus on 20th November 2025, with no publication year restriction. Articles published online ahead of print

were included if available before the search date, regardless of print/issue year. The strategy combined four keyword groups (infectious disease, forecasting, spatio-temporal, AI/ML) using the Boolean operator "OR" for within groups and "AND" for between groups. Truncation (*) was used to capture word variants, e.g., "infectious disease*". The full search strategy is shown in Table 1. Additional records were identified through citation searching, hand searching and prior knowledge of the field. Two reviewers independently screened all records, resolving discrepancies by discussion.

Category	Search terms
Infectious disease	Infectious disease; Epidemic; Pandemic; COVID-19; Malaria; Dengue; Influenza; Virus; Bacteria; Tuberculosis; Zika; Chikungunya; HIV; Measles; Vector-borne disease; Respiratory infection
Forecasting	Forecast*; Predict*
Spatio-temporal	Spatio-temporal; Spatiotemporal
AI / Machine Learning	Machine learning; Deep learning; Artificial intelligence; Neural network*; Graph neural network*; Convolutional neural network*; Recurrent neural network*; Transformer*; Attention model; Support vector machine; Random forest

Table 1: Scoping review search terms

2.2 Definition of spatial employed in this scoping review

A study was classified as spatial only if it explicitly modelled geographic dependencies between locations. Operationally, a study met this criterion if it: (1) incorporated mobility data, (2) modelled spatial dependency between regions (e.g., via graphs) and (3) embedded explicit spatial structure in the model architecture (e.g., grid based partitioning or graph neural networks with nodes representing locations). Studies reporting results per region without explicitly modelling interactions between locations were not considered spatial; ambiguous cases were resolved by discussion.

Two borderline cases exemplify this ambiguity. Kavouras and colleagues trained models across multiple countries simultaneously, capturing some cross-country signal but no explicit inter-regional relationships were modelled [33]. Additionally, Mills and colleagues used a Besag-York-Mollié Bayesian model for retrospective spatial analysis of dengue but treated provinces as independent units during forecasting [34]. Neither met our definition of spatial.

2.3 Eligibility criteria

We included peer-reviewed journal articles and conference papers using AI/ML methods to forecast human infectious disease transmission spatio-temporally regardless of transmission mechanism, with eligible outcomes of cases, anomalies, deaths or hospitalisations.

We excluded studies that forecast disease spatially or temporally in isolation, did not model spatial relationships (as defined in section 2.2), used statistical-only or mechanistic-only models without any AI/ML component, forecast vector or animal infections without human infection, did not forecast disease, lacked an accessible full text in English, or evaluated models as part of a forecasting competition.

2.4 Data extraction and analysis

We used a Microsoft Excel template to capture bibliographic details (authors, title, year, journal, country of study), disease, spatial and temporal granularity, model architecture, data, evaluation metrics and interpretable or explainable AI techniques, performed independently per article and then compared. Data were analysed in Python, with plots generated using Matplotlib. The code for the analysis is available at https://github.com/ai4ci/scoping-review-figures.

2.5 AI statement

During the preparation of this work, the authors used Claude (Opus 4.8) to improve the readability and language of the text. The authors reviewed and edited the output as needed and take full responsibility for the content of the published article.

3 Results

3.1 Study Selection and Metadata From Papers

The search retrieved 709 studies from five databases: Scopus (n=251), Web of Science (n = 178), Compendex (n=124), PubMed (n=99) and IEEE Xplore (n = 57). After removing 359 duplicates, 350 records were screened by title and abstract after which 219 were excluded because they did not fit the assessment criteria. Of the 131 left, four reports could not be retrieved. The remaining 127 were assessed at the full text level and 79 of these met inclusion criteria. A further 14 studies were identified through citation searching, hand searching, and field knowledge, giving 93 included studies. The selection process is summarised in the PRISMA flowchart (fig. 1) [35].

Reasons for exclusion at full-text stage are detailed in the PRISMA flowchart (fig. 1), with absence of explicit spatial structure or mobility data the most common (n=19).

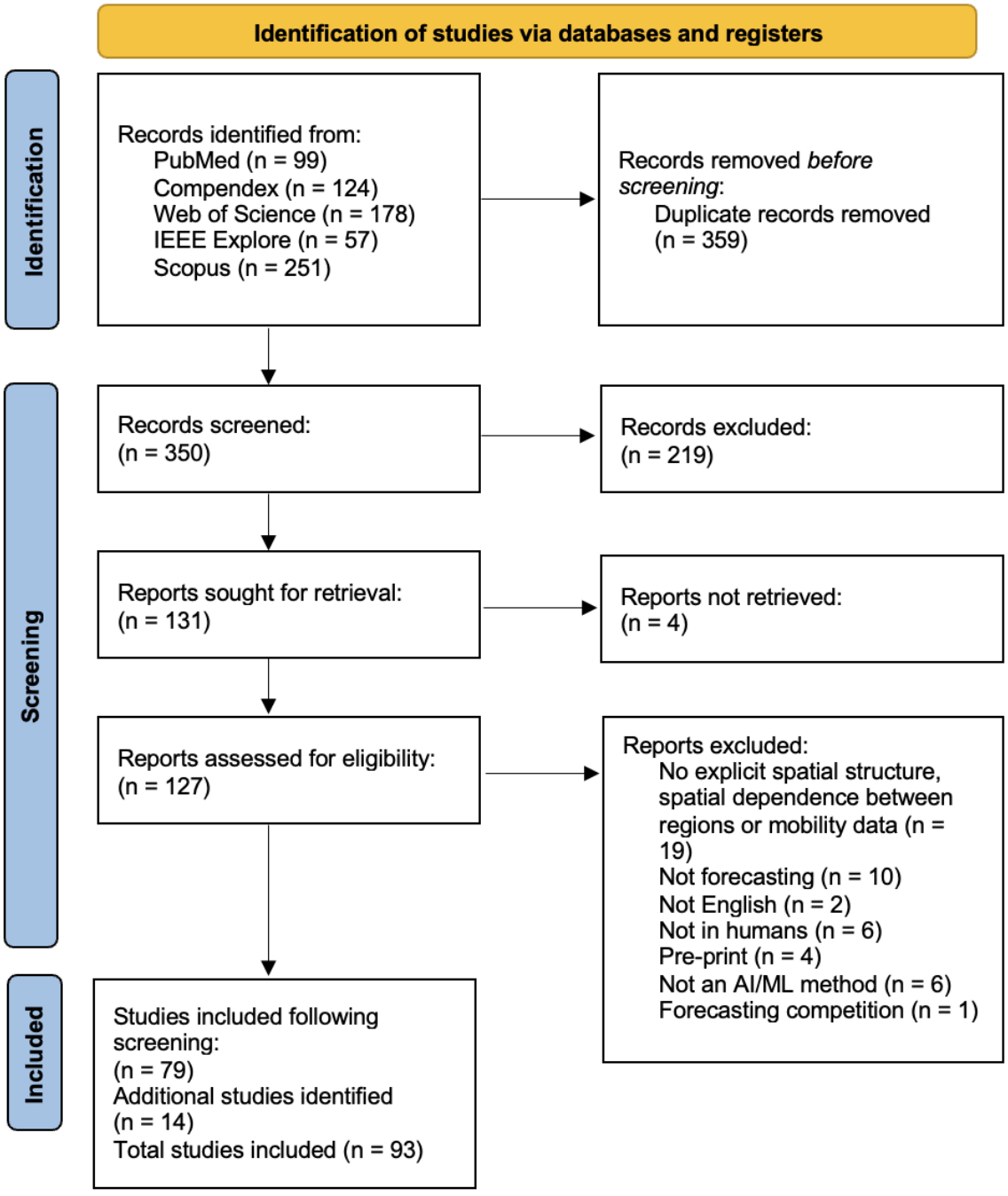


Figure 1: PRISMA flowchart detailing the search strategy, screening process and article selection.

Included studies were published between 2018 and 2026, with a surge in publications since the COVID-19 pandemic and most papers being published in 2022 (22.5%) (Figure 3). 14 infectious diseases were included in the review, with COVID-19 dominating, followed by influenza, and Dengue.

Several studies forecast more than one disease [36–42].

Geographically, most studies forecast disease in high- and middle-income countries including the USA (36 papers) [27, 38, 40, 42–74], Italy (11 papers) [44, 72, 75–83], Japan (10 papers) [38, 42, 47, 59, 71, 84–88], China (9 papers) [85, 89–96], the UK (9 papers) [41, 55, 69, 78, 79, 83, 94, 97, 98], Spain (8 papers) [42, 78, 79, 81, 83, 99–101] and Brazil (6 papers) [39, 96, 102–105]. As multiple studies forecast disease across multiple countries, these counts reflect country-level study contexts rather than unique publications.

Disease was also forecast in Iran [106], the Republic of Türkiye [107, 108], Portugal [109], Sri Lanka [1, 110], India [36, 111, 112], Taiwan [113, 114], Germany [81, 91, 115], New Zealand [116], Hungary [41, 117, 118], France [78, 79, 83, 94], Sweden [119], Indonesia [120, 121], Australia [42, 94], the Netherlands [94, 122] and Peru [102] (Table 2. fig. 2). A small number of studies used unspecified [37], synthetic [123], or global settings [52, 62, 124]. One study covered 37 European nations [38]. Notably, only one study forecast disease in Africa [125], indicating a geographic gap. Overall there was an over-representation of higher income countries.

Country	Papers
USA	36
Italy	11
Japan	10
China	9
Spain	8
Brazil	6
UK	9
France	4
India	3
Germany	3
Hungary	3
Sri Lanka	2
Taiwan	2
Indonesia	2
Australia	2
The Netherlands	2
Türkiye	2
Iran	1
Peru	1
Portugal	1
Sierra Leone	1
Sweden	1
New Zealand	1

Table 2: Country disease was forecast in in the included papers

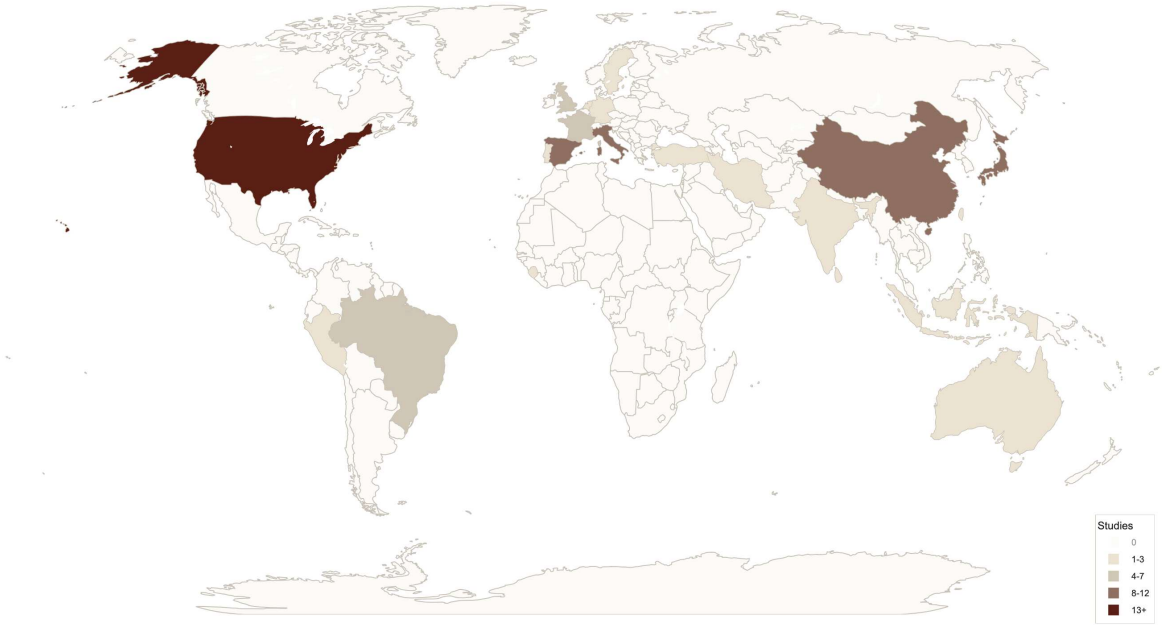


Figure 2: Global distribution of study locations in the reviewed spatio-temporal infectious-disease modelling literature. Shading shows the number of included papers mentioning each country or region, grouped into five frequency bands.

The included studies spanned a broad range of disciplinary venues, including computer science, artificial intelligence, theoretical and computational biology, epidemiology, public health and data science, reflecting the interdisciplinary nature of this field.

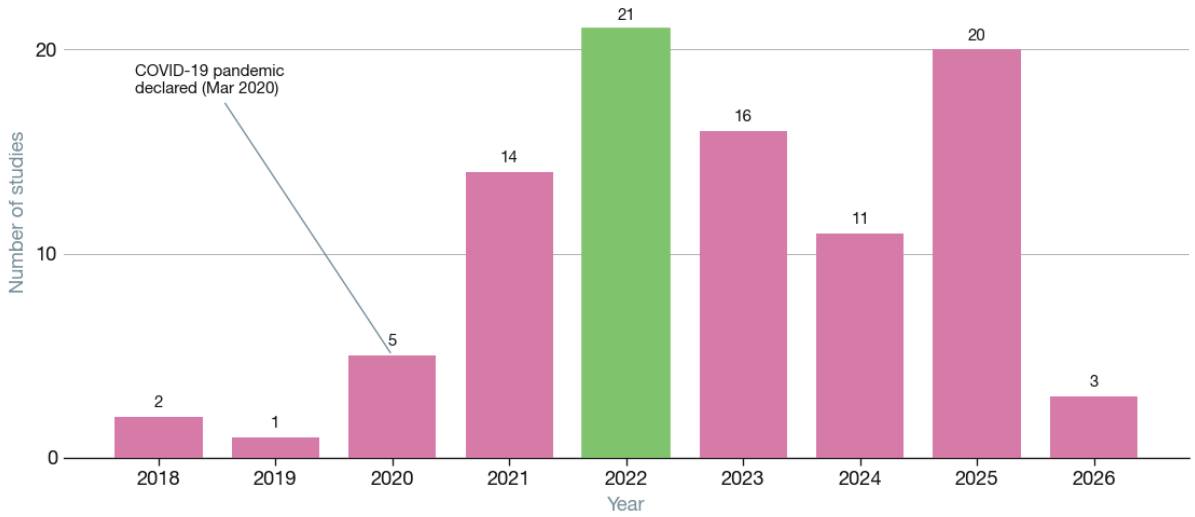


Figure 3: Year of publication of included studies.

3.2 Model Architectures

We characterised each study at two levels. First, we recorded every architectural family, grouping them into eight categories: graph neural network (GNN), recurrent neural network (RNN), including long short-term memory (LSTM) and gated recurrent unit (GRU) variants, convolutional neural network (CNN), transformer, hybrid mechanistic-ML models (models combining a physics-based model with ML), probabilistic/Bayesian model, classical machine learning (not based on neural networks e.g., random forest, XGBoost, support vector machine, naive Bayes, symbolic regression) and "other" for approaches fitting none of these (generative adversarial networks, radial basis function networks, pseudo-grouping adversarial learning, and a multilayer perceptron). Categories were not strictly orthogonal, as studies often combined components (e.g., spatial and temporal). Second, we recorded two cross-cutting design properties independent of architectural family: ensembling and probabilistic output, keeping the distinction between a model's architecture and its output type clear.

AI/ML forecasting models in this field are predominantly modular, combining a small set of recurrent and graph-based building blocks rather than relying on any single architecture. RNNs were the most frequently employed family (used in 43 studies; 46%), followed by GNNs (used in 36 studies; 39%), CNNs (used in 20 studies; 22%), transformers (used in 9 studies; 10%), probabilistic/Bayesian models (used in 8 studies; 9%), classical machine-learning models (used in 16 studies; 17%), and "other" 4% (Figure 4).

Hybrid mechanistic/ML models, combining domain knowledge, often via differential equations, with ML, were absent before 2022 and grew steadily thereafter (3 studies in 2022, 3 in 2023, 4 in 2024, and 7 in 2025), suggesting growing interest in integrating domain knowledge with AI for epidemic forecasting.

Ensembles were less common, used in 7 studies (8%) [40, 52, 61, 102, 103, 116, 119]. Transformers adoption remained limited, despite established strengths in multi-modal integration [126] and modelling long-range dependencies [127].

Across included studies, methods have converged on a set of recurrent and graph-based building blocks, increasingly augmented with mechanistic structure. Notably, no included study used transfer learning or foundation-model approaches [128], potentially limiting rapid deployment against novel pathogens.

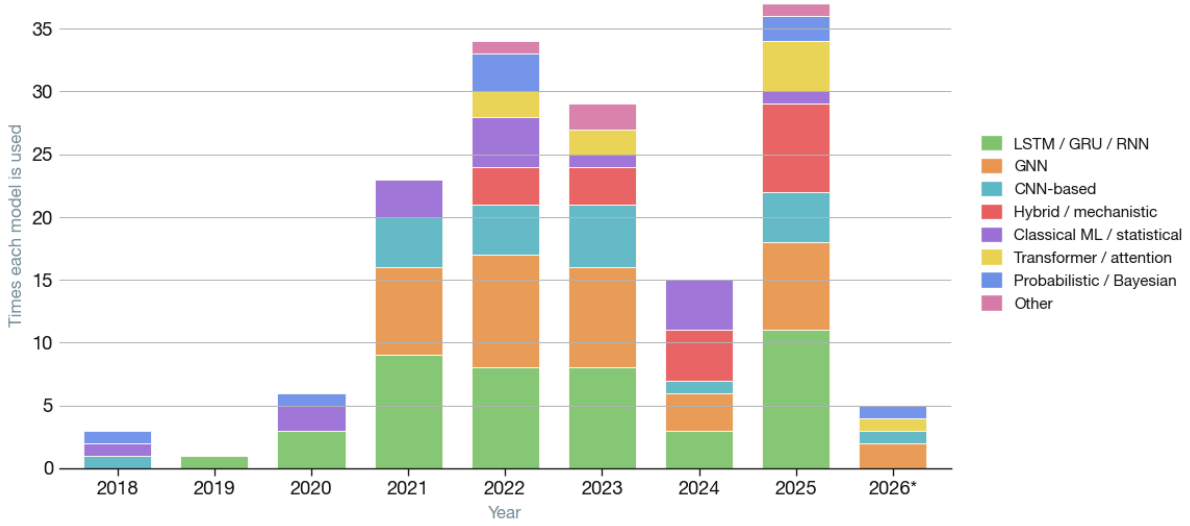


Figure 4: Model architectures employed in the included studies. LSTM = long short-term memory model, GRU = gated recurrent unit, RNN = recurrent neural network, GNN = graph neural network CNN = convolutional neural network. Categories are not mutually exclusive, as some studies used more than one model. The search was conducted in November 2025 so 2026 reflects incomplete-year coverage.

3.3 Data and Model Co-variates

Across included studies, model covariates spanned six domains - epidemiological (case counts, variants, vaccination), mobility (movement data, social connectivity), environmental (climate, pollution, satellite, remote sensing images, geographic co-ordinates), socio-demographic, policy (interventions, mask wearing), and clinical (hospital and medical claims data) (Figure 5). Case data were used in all but one study (92; 99%), typically from national government reporting systems, with temporal granularity varying by disease - daily for COVID-19, weekly for influenza, monthly for dengue. The exception used synthetic data [123].

Beyond case data, the most common covariates were human mobility (45 studies; 48%), socio-demographic variables (34 studies; 37%), climate (20 studies; 22%), and hospitalisation or medical-claims data (14; 15%). Spatial connectivity was used in 12 studies (13%). Passive surveillance (e.g., website search or social media data) was used in three studies (3%) [45, 68, 104]. Other sources saw similarly limited uptake, including vaccination status (4 studies; 4%), satellite data (4 studies; 4%), pollution (3 studies; 3%), and remote-sensing imagery (3 studies; 3%).

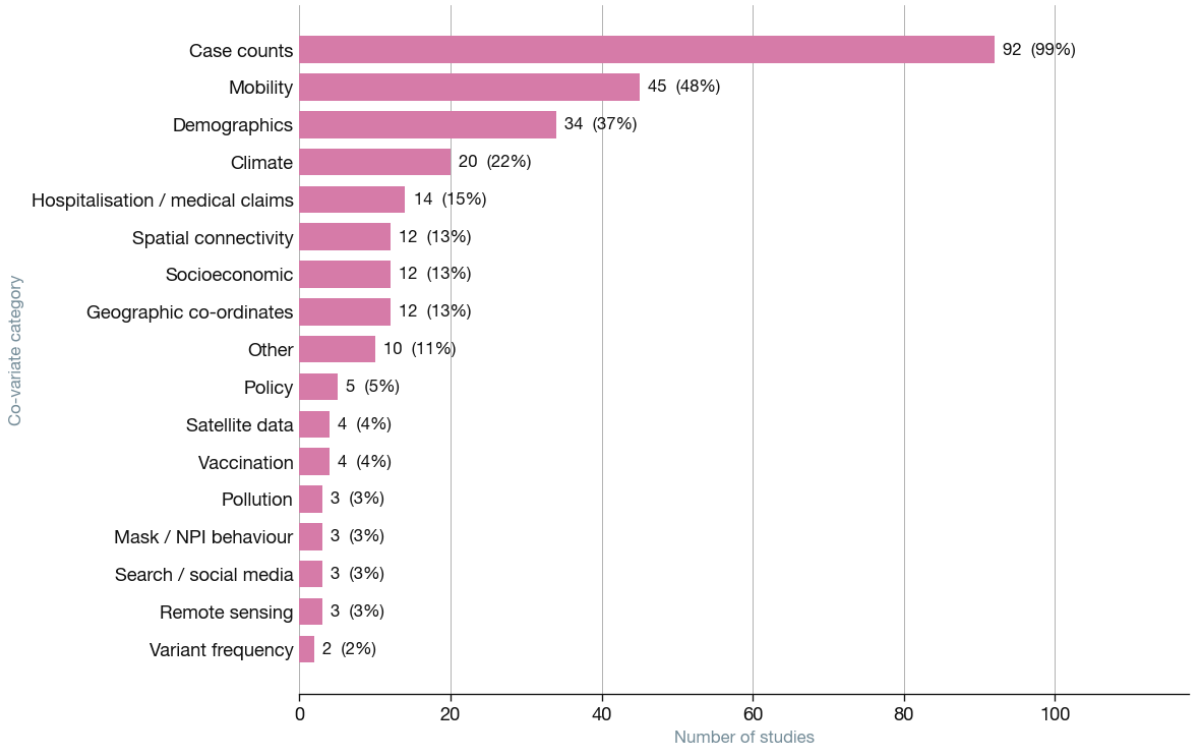


Figure 5: Main co-variates included in models.

3.4 Space and Time

Forecast horizons varied considerably, from short-term predictions (1-14 days) to multi-year forecasts. We classified each study by its longest horizon into three bands: one week or less, one to four weeks, and more than four weeks. Eleven studies (12%) did not report a horizon. Of the 82 remaining studies, 25 (30%) forecast one week or less, 30 (37%) forecast one to four weeks, and 27 (33%) forecast more than four weeks ahead. Overall, 67% of studies reporting a horizon forecast one month or less, indicating a focus on short- to medium-term rather than longer-range forecasting, likely reflecting the decline in predictive performance as horizons lengthen.

Spatial scales were similarly heterogeneous. Most studies used predefined administrative units (countries, states, counties, prefectures), with fewer using health-care specific units or gridded representations. Where multiple scales were reported, the finest was used for classification. By forecasting granularity, studies were overwhelmingly subnational (87/93; 94%), followed by national (5; 5%) and regional (1; 1%); none forecast at a single global resolution. This partly reflects our inclusion criteria, which required modelling of dependencies between locations and therefore favoured fine-grained units, but may also be consistent with the value of localised predictions for targeted interventions.

3.5 Evaluation

Forecast evaluation assesses how closely predictions align with observed outcomes. Most included studies used pointwise accuracy metrics, and reported more than one. Over 30 unique error metrics were used. Root mean squared error (RMSE) was the most common (56 studies; 60%), followed by mean absolute error (MAE; 46; 49%) and mean absolute percentage error (MAPE; 26; 28%) (fig. 6). RMSE and MAPE are unsigned and so cannot indicate over- or underestimation [30]. The diversity of error metrics made a quantitative comparison of model performance infeasible.

Probabilistic forecasting, where a model outputs a distribution over possible outcomes rather than a single output [129], was less frequently applied. Only 18 studies (19%) reported uncertainty intervals, despite uncertainty quantification being persistently identified as vital for model development for policy [130, 131]. External validation on data from different regions or time periods was performed in 12 studies (13%) and cross-validation in 10 (11%), leaving most models assessed only on data resembling their training set, a recognised limitation of prediction models [132]. Sensitivity analyses were not consistently conducted with only 12 papers (13%) reporting the results of a sensitivity analysis. Most studies compared their model against baselines, though these varied widely, and no standard set has been established.

Taken together, the large number of evaluation metrics and the limited use of uncertainty quantification, external validation, and sensitivity analysis show a need for greater standardisation in how spatio-temporal forecasting models are evaluated.

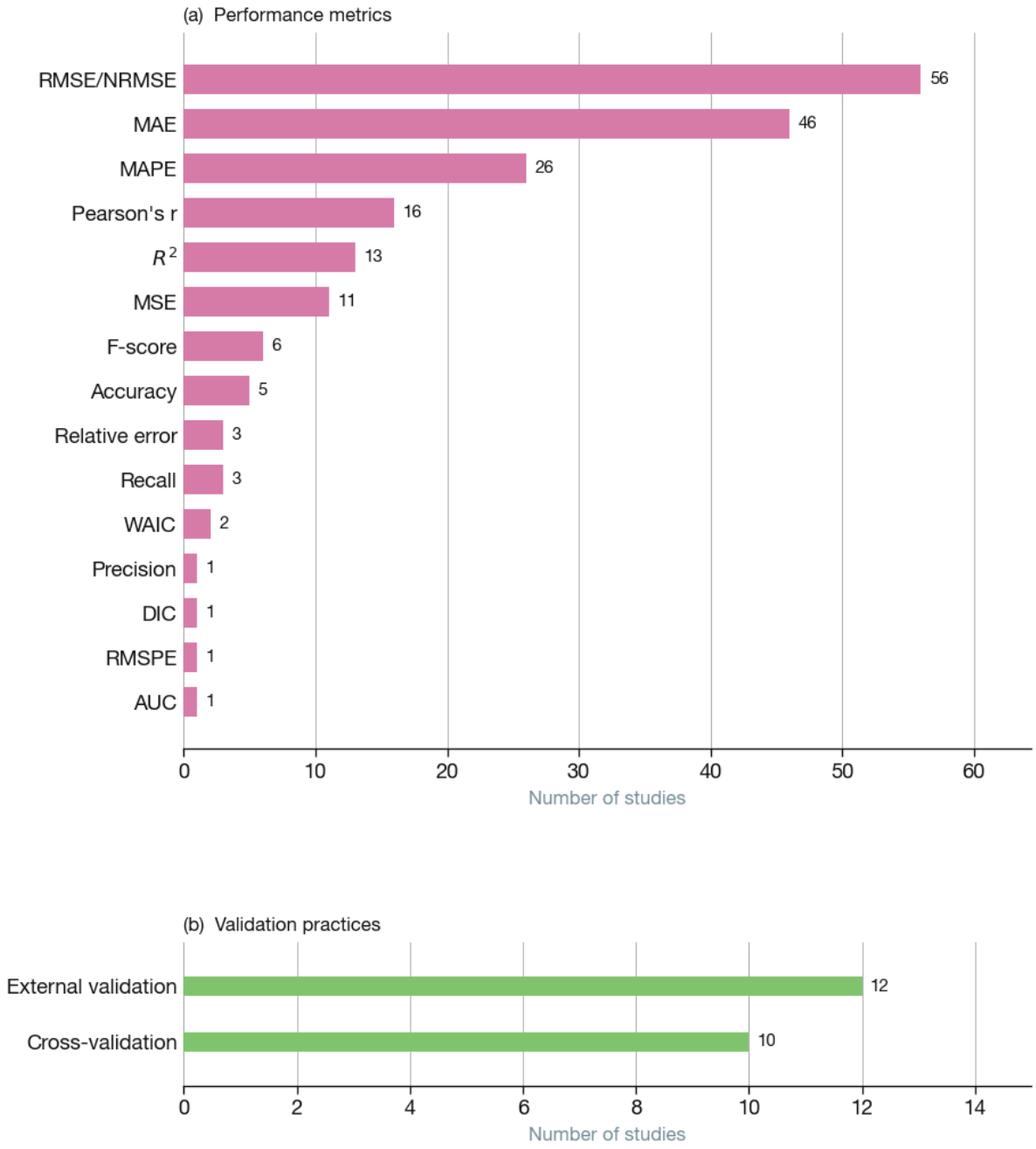


Figure 6: Evaluation metrics and validation processes reported across included studies. (a) Frequency of selected performance metrics reported across included studies. (b) Validation practices reported across included studies. RMSE = root mean squared error, NRMSE = normalised root mean squared error, MAE = mean absolute error, MAPE = mean absolute percentage error, MSE = mean squared error, WAIC = Watanabe–Akaike information criterion, RMSPE = root mean squared percentage error, DIC = deviance information criterion, AUC = area under the curve.

3.6 Uncertainty Quantification

Of the 18 studies (19%) that reported uncertainty intervals, methods were highly heterogenous, spanning six families: Bayesian, distributional, ensemble-based, approximate Bayesian, distribution-free, and

resampling-based.

Bayesian approaches (5 studies) represent uncertainty through probability distributions over parameters and predictions, and included Bayesian spatial Poisson regression [99], Bayesian model averaging [103], Gaussian processes [108], Bayesian generalised linear models [61], and probabilistic neural networks [76]. Distributional approaches (6 studies) directly estimated predictive distributions via quantile regression [27, 66, 102], distributional regression [115], explicit probability-distribution outputs [109], and Gaussian mixture models [48]. Ensemble-based approaches (4 studies) derived uncertainty from multiple models, including random forest ensembles [102], deep learning ensembles [27], ensemble standard errors [115], and repeated GNN training [91]. Approximate Bayesian methods (3 studies), specifically Monte Carlo dropout, estimated uncertainty in neural network predictions [52, 68, 86]. Distribution-free uncertainty was obtained via conformal prediction [85, 105], and one study estimated uncertainty by resampling via cross-validation [80]. Some studies used more than one method, so family counts sum to 21 across the 18 studies that quantified uncertainty. No single method was used by more than six studies, reflecting the absence of a standardised approach to uncertainty quantification.

3.7 Explainability

AI/ML models are often regarded as ”black boxes”, a key barrier to adoption in public health decision-making. A range of explainable AI (XAI) techniques have been developed to address this, offering insight into how models generate predictions [133]. Ablation was the most frequently reported technique (28 studies; 30%), identifying which components or data sources most influence predictions by systematically removing them, however, ablation primarily informs the modeller rather than providing explanations post model development. Post-hoc explanation methods aimed at interpretability were rarer. SHapley Additive exPlanations (SHAP), which quantify the contribution of input features to predictions [134], were reported in only 6 studies (7%). This limited and largely development-oriented use of XAI techniques suggests that explainability of models remains a challenge.

3.8 Fairness analysis and bias

Infectious diseases affect populations differently, with well-documented disparities by socioeconomics [135] and ethnicity [136]. We defined fairness analysis as assessing whether a model performs inequitably for individuals/groups with sensitive attributes [137]. Only one included study conducted such analysis [117]. No other studies examined whether predictive performance varied across populations. Forecasting models therefore risk under-performing for subpopulations and reinforcing existing health inequalities

[138], a gap previously identified in epidemiology more broadly [139].

3.9 Data access, code availability and federated learning

Access to data and code varied across studies, with implications for reproducibility, transparency, and model deployment. Most studies used publicly available surveillance data from health agencies. Mobility data in particular were frequently subject to access restrictions. Only 27 studies (29%) provided open-source code, limiting the ability of others to reproduce results or use models in new settings. Software reporting was similarly limited despite the range of tools being used (Python, R, MATLAB, QGIS, ArcGIS, and Stata). Python was the most common software, used in 49 studies. 30 studies did not report the software used.

One approach to tackle data access is federated learning, a distributed method where models are trained locally and only parameters are shared, keeping the data in place, protecting privacy [140, 141]. It has been proposed for using sensitive data, enabling model development without direct data sharing. However, no included study used federated learning, consistent with its limited uptake in infectious disease forecasting more widely [142]. Privacy preserving methods thus remain largely unexplored in spatio-temporal infectious disease forecasting, despite their potential to ease the access constraints noted above and to support cross-institutional collaborations.

4 Discussion

This scoping review synthesised 93 studies published between 2018 and 2026 on AI/ML approaches to spatio-temporal infectious disease forecasting. Three cross cutting themes emerged. (1) Numerous AI/ML architectures are employed, yet standardised benchmarks for datasets and model evaluation are not used. (2) Models are often not built to be trusted or reproduced, lacking uncertainty quantification, validation and interpretability methods. (3) Issues remain in making models equitable, with very few papers produced in low income countries and fairness analysis being almost absent.

RNNs were the most commonly used (43 papers), effective for sequential data as they can learn temporal patterns and long-term dependencies in data [143]. Various strategies added spatial structure to RNNs, for example, mobility covariates [26, 27, 53, 58, 101] or convolutional recurrent hybrids [44, 75, 76, 100]. GNNs were the second most commonly used architecture (36 studies), especially suited spatio-temporal forecasting, modelling dependencies between regions explicitly while allowing each node's contribution to be quantified, increasing interpretability [144]. Approaches used to extend

GNNs to forecast spatio-temporally varied. Earlier models used case counts as node features [83]; hybrid models combined a graph component, with a temporal component such as a LSTM; and more recent models have used attention mechanisms and dynamic graphs, in which adjacency relationships or edge weights are updated over time [144].

Hybrid mechanistic ML models, combining domain knowledge, with machine learning, have grown. For example, physics informed neural networks (PINNs) [145] and epidemiology-aware AI models which extend models such as RNNs and GNNs [146]. A review of 245 studies found hybrid approaches suited to address many epidemiological challenges [146], with particular promise with sparse and noisy data and in early outbreak response [146]. Future work should develop these models further and establish when they outperform purely AI/ML or purely mechanistic alternatives.

Few studies used transformer based architectures [127], despite their strengths in integrating multi-modal data, handling complex non-linear relationships [126], and capturing long-range dependencies [147]. Developing transformer-based models for multi-modal integration is a promising direction for future work. Table 3 summarises the trade-offs of each architectural family observed in the included studies.

This methodological convergence is not matched by convergence in evaluation. Included studies used over 30 distinct error metrics, most often RMSE (56 studies; 60%) and MAE (46; 49%) with no shared baselines or benchmark datasets used, making performance infeasible to compare across studies. Both dominant metrics are also unsigned, making it unclear whether errors stem from models under or over predicting [30]. Standardised evaluation, as in the CDC FluSight challenge `https://www.cdc.gov/flu-forecasting/evaluation/2024-2025-report.html`), would make comparing the accuracy of models possible. Recent benchmarking efforts have begun to address this gap. EpiCastBench provides 40 datasets spanning eight diseases and 27 regions with evaluation on 15 models [148]. SpatialEpiBench extends this to spatio-temporal settings, evaluating 11 datasets on 11 spatial forecasting methods [149]. Future work should prioritise using shared datasets and evaluation methods, enabling robust comparison of models.

For a forecast to inform public health, it must be not only accurate but validated, interpretable and reproducible. Across these, current models fall short. Uncertainty was only quantified in 18 of the included studies, despite being regarded as essential for policy [130], where reported, methods were highly heterogeneous, with no approach used by more than 6 studies. Validation was similarly sparse, with external validation in 12 studies (13%) and cross-validation in 10 (11%), leaving most models assessed only on data resembling their training set, a serious limitation given that models trained on

Architecture	Strengths	Limitations	Data needs	How used in included studies
GNN	Explicitly models dependencies between regions; graph structure maps naturally onto spatial networks	Requires defining an adjacency matrix; performance sensitive to graph construction choices; prone to overfitting; challenges with generalising to new pathogens or populations	Multi-region case data; mobility or connectivity matrix	COVID-19 and Influenza spread across counties and prefectures
RNN / LSTM / GRU	Captures temporal patterns and long-range dependencies in data	Spatial structure must be added externally, e.g., via mobility covariates, convolutional layers or GNNs	Time series case data	Short-term forecasting at subnational level
CNN	Captures local spatial correlations; don't need to specify which regions interact; computationally lightweight relative to graph-based approaches	Assumes spatial regularity; ignores network topology	Gridded or raster spatial data	Primarily used as a spatial component within overall architectures
Transformer	Suited for multi-modal data integration; good at capturing long-range dependencies	Requires large volumes of data; attention scales quadratically with the token length	Large multi-feature datasets	Rarely used; mostly COVID-19 studies
Hybrid mechanistic-ML	Incorporates domain knowledge; performs better in sparse data and early outbreak settings	More complex to build and validate than purely data-driven models	Can perform with limited case data when domain knowledge encoded	Increasingly used post-2022; applied across multiple pathogens
Probabilistic / Bayesian	Produces uncertainty estimates natively	Computationally expensive; harder to scale to large spatial networks	Case data; prior knowledge of transmission parameters	Small number of studies; used where uncertainty quantification was prioritised
Classical ML	Interpretable; low data requirements; fast to train	Limited capacity to model temporal or spatial structure directly	Tabular covariates; does not require sequential data	Primarily used as baseline comparisons

Table 3: Architectural trade-offs observed across included studies. Entries reflect patterns reported in the included literature rather than formal benchmarking.

particular regions or outbreak phases transfer poorly to new contexts [150]. Interpretability was also limited. Post-hoc explanation through SHAP appeared in just 6 studies (7%), and although ablation was more common (28; 30%), it informs the modeller about component importance rather than providing the interpretable explanations needed for policy use [134]. Finally, reproducibility was constrained by limited code sharing. 66 studies (71%) did not provide an open repository, making methods challenging to reproduce and scrutinise, preventing external verification of performance [151]. Taken together, these gaps show development of increasingly capable models that remain difficult to trust, validate or reproduce. Data access is another issue. Proprietary datasets were common, with mobility data in particular often inaccessible.

The evidence base is skewed towards high income settings. Only one study forecast in Africa [125]. Fairness analysis was almost absent, conducted in only one study [117], leaving the risk of inequitable performance for under-represented populations largely unexamined [152]. Future work should extend forecasting to under-represented regions and incorporate stratified fairness analysis by attributes such as ethnicity and socioeconomic deprivation [153], to develop models that perform equitably for the whole population.

Several priorities follow from these gaps. Although the COVID-19 pandemic substantially increased data availability [154], integration of novel data sources remained limited. Most studies relied on case data with sources such as satellite, pollution, variant, and demographic data each used in under 5% of studies, despite the value of demographic covariates for forecasting deaths and hospitalisations [155]. Because every data source carries its own biases, and surveillance data are frequently noisy, inconsistent, and subject to reporting delays [156, 157], combining data sources may help distinguish genuine epidemic signals from artefact. Future models should therefore prioritise multi-modal data integration across, for example, mobility, wastewater and genomic data [23, 128].

Where real data are scarce, synthetic data could provide training data for models [128]. Large-scale ABMs such as JUNE [158] and Covasim [159], alongside stochastic compartmental [160] and metapopulation models [21], can generate data that are validated against observed data. Generative methods such as generative adversarial networks and variational autoencoders could augment limited datasets [161] and large language models could handle data inconsistencies [162].

Federated learning provides an opportunity for data sharing across institutions without revealing sensitive information [140, 141]. None of the included studies adopted it, a notable gap given issues with data access previously identified in this review.

Strengthening surveillance infrastructure is equally important. Wastewater monitoring is a promising

emerging source, enabling high-resolution pathogen surveillance that could fill spatial gaps, though its coverage can be sparse, such as in the early COVID-19 pandemic [163], so it is important these data are used in combination with other co-variates. Establishing such systems will require sustained cross country collaboration [164].

Behavioural and feedback data, which shape transmission yet are largely absent from current models [165], are a further opportunity. Studies proposed game-theoretic or agent-based models linking policy and mobility responses [43], or counterfactual forecasting to assess interventions [46, 62, 68].

Few studies addressed operational use, only 3 papers discussed application as an early warning system, and none addressed real-time deployment. Yet such forecasting is valuable for telling decision-makers when and where to target interventions [19]. This points to a persistent gap between methodological development and real-world decision making.

Most models only forecast one disease. Future research should focus on developing models which generalise to multiple infectious diseases, including fine tuning to generalise to new, unseen outbreaks [128].

This scoping review has several limitations. The included literature was limited to English language, full-text articles, which may introduce language and publication bias. Preprints were excluded to ensure all included studies had undergone peer review, however this may be particularly consequential given the field's rapid evolution. The heterogeneity of included studies may have complicated comparison of study designs and findings. Classifying studies as spatial required subjective judgement, as the boundary between spatial and non-spatial modelling approaches was not always clear. Borderline cases were resolved through discussions, however, some papers capturing some geographic signal may have been excluded. As a scoping review, the quality of included studies was not appraised.

AI/ML for spatio-temporal infectious disease forecasting has grown rapidly, driven by big data and the COVID-19 pandemic. This scoping review synthesised 93 studies published between 2018 and 2026, spanning 14 infectious diseases, and found that recurrent and graph neural networks dominate the landscape, with hybrid mechanistic-ML models growing in prominence since 2022.

Despite the convergence in methodology, critical gaps remain. Over 30 distinct error metrics and the absence of shared benchmark datasets make cross-study comparison challenging. Uncertainty quantification remains rare (19% of included studies), and external validation (13% of included studies) and open code sharing (29%) are similarly limited. Forecasting remains concentrated in middle- and high-income countries, with fairness analysis conducted in only one study.

For spatio-temporal AI/ML forecasting to meaningfully inform public health policy, three priorities

must be addressed. (1) adoption of shared benchmarks and evaluation standards, (2) consistent reporting of uncertainty, interpretability, and external validation, (3) extension of methods to under-represented regions with rigorous fairness analysis. Without these advances, increasingly sophisticated models risk remaining difficult to compare, trust, or deploy equitably.

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6 Author contributions

AP, LD, and ZL conceptualised the study. AP led the literature search, screening, and data extraction, and wrote the original draft. ZL contributed to the literature search, screening, and data extraction. AP and ZL directly accessed, processed, and verified the underlying data reported in the manuscript. LD provided project administration, supervision, and funding acquisition. MZ and RC contributed to writing – review and editing. All authors reviewed, edited, and approved the final manuscript.

7 Competing interests

L.D. reports grant funding from the National Institute for Health and Care Research (NIHR) as a co-applicant on the Health Protection Research Focus Award in Vaccines at the University of Bristol; was an investigator on a study funded under a collaborative agreement by Pfizer Inc., which has concluded and is unrelated to this article; reports grant funding from EPSRC as a co-applicant on the UQ4Covid project (EP/V055515/1); and is an unpaid member of the NIHR Better Methods Better Research funding committee. M.Z. reports grant funding from the University of Oxford, the University of Bristol, and an NCCR Automation fellowship, and consulting fees from Yale University, all unrelated to this manuscript. A.P., Z.L., and R.C. declare no competing interests.

8 Data Availability

The data underlying this review (bibliographic details, disease, spatial and temporal granularity, model architecture, data sources, evaluation metrics, and explainability techniques extracted from included studies) are available at `https://github.com/ai4ci/scoping-review-figures`.

9 Code Availability

The code used to analyse the extracted data and generate the figures in this article is available at `https://github.com/ai4ci/scoping-review-figures`.

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