

Review Article

The Hidden AMR Gap: A Scoping Review and AI Framework for Detecting Under-Surveillance of Antimicrobial Resistance

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ABSTRACT

Background: Antimicrobial resistance (AMR) surveillance is essential for estimating resistance burden and guiding public-health responses, yet coverage remains uneven across geographic regions, populations, healthcare settings, and One Health domains. Low observed resistance may therefore reflect limited detection and reporting rather than genuinely low resistance.

Objectives: To map the nature and determinants of AMR under-surveillance, examine computational approaches for identifying surveillance blind spots, and develop an evidence-informed framework for AI-enabled detection of hidden AMR surveillance gaps.

Methods: PubMed and Dimensions were systematically searched for literature published from 2015–2026. Eligible studies addressed AMR surveillance coverage, capacity, representativeness, completeness, or computational approaches relevant to surveillance gaps. Study selection and synthesis followed JBI scoping-review methodology and PRISMA-ScR guidance.

Results: Twenty-two studies were included. Under-surveillance encompassed geographic and population underrepresentation, diagnostic and laboratory limitations, fragmented information systems, delayed reporting, weak genomic coverage, and incomplete One Health integration. Computational approaches included spatial and statistical modelling, machine learning, geographic information systems, genomic analytics, digital laboratory systems, and environmental surveillance. These approaches could identify or partially address surveillance incompleteness but remained constrained by data quality and representativeness. The synthesis informed a framework for detecting discordance between expected AMR risk and observed surveillance intensity.

Conclusions: AMR under-surveillance is a systems-level problem that can distort the apparent distribution of resistance. AI should complement microbiological surveillance by identifying uncertainty and prioritizing settings requiring strengthened surveillance.

Keywords: Antimicrobial Resistance; AMR Surveillance; Artificial Intelligence; Machine Learning; One Health; Surveillance Gaps; Global Health

Introduction

Antimicrobial resistance (AMR) is increasingly recognized not only as a therapeutic challenge but also as a surveillance challenge. Resistance estimates depend on the systems through which infections become observable, including healthcare access, specimen collection, microbiological testing, antimicrobial susceptibility testing (AST), data capture, analysis, and reporting. Consequently, the AMR burden documented by surveillance systems may represent only the fraction of resistance occurring where adequate diagnostic and reporting infrastructure exists. This creates a fundamental interpretive problem: low observed resistance may indicate genuinely low resistance, but it may also reflect limited capacity to detect it. [1]

Global AMR surveillance has expanded through national and international initiatives, including the World Health Organization Global Antimicrobial Resistance and Use Surveillance System (GLASS). Nevertheless, surveillance capacity remains heterogeneous across countries, healthcare settings, populations, pathogens, and One Health domains. Limited microbiology and AST capacity, dependence on tertiary-care facilities, fragmented reporting networks, inadequate laboratory informatics, unequal genomic sequencing capacity, and weak integration of human, animal, food, and environmental surveillance can systematically restrict what becomes visible. These limitations are particularly consequential where surveillance infrastructure is weakest, as settings with sparse observations may simultaneously carry substantial but poorly characterized resistance burdens. [2,17]

We conceptualize the discrepancy between observable resistance and resistance potentially missed because of insufficient surveillance as the **hidden AMR gap**. Under-surveillance therefore extends beyond missing data; it represents systematic insufficiency in surveillance coverage, intensity, representativeness, or analytical capacity that can distort the apparent geographic and epidemiological distribution of resistance. Identifying such blind spots requires attention not only to observed AMR prevalence but also to the surveillance processes that generate those observations.

In this review, AMR under-surveillance is defined as a broader systems-level condition in which surveillance processes insufficiently capture the occurrence, distribution, or determinants of antimicrobial resistance because of limitations in coverage, access, diagnostic capacity, representativeness, data systems, or analytical capability. Missing data refers more narrowly to absent,

incomplete, or unavailable observations within a surveillance dataset, whereas low surveillance intensity refers to limited frequency, volume, geographic reach, or population coverage of surveillance activities. Although missing data and low surveillance intensity may contribute to under-surveillance, they represent related but distinct components rather than equivalent concepts. Within this terminology, a surveillance deficit refers to measurable insufficiency in surveillance coverage or intensity that may contribute to under-surveillance, while a surveillance blind spot refers to a location, population, pathogen, sector, or time period in which available observations may inadequately represent the underlying AMR risk. Data uncertainty refers to uncertainty arising from incomplete, sparse, inconsistent, or otherwise limited surveillance information. The hidden AMR gap describes the broader discrepancy between observable resistance and resistance potentially missed because of these surveillance limitations.

Computational approaches offer an opportunity to interrogate this problem differently. Spatial and spatiotemporal modelling, predictive modelling, machine learning, anomaly detection, data fusion, missing-data methods, natural language processing, and genomic analytics can integrate heterogeneous information and potentially identify discordance between expected resistance patterns and observed surveillance signals. Rather than asking only whether artificial intelligence (AI) can predict antimicrobial resistance, a more consequential surveillance question is whether computational methods can identify **where AMR risk may be substantial but surveillance is insufficient to characterize it**. [18,19]

Existing literature has extensively examined AMR burden, surveillance systems, genomic prediction, One Health surveillance, and AI-assisted resistance prediction. However, these evidence streams remain fragmented, and comparatively little attention has been directed toward AMR under-surveillance itself as a measurable phenomenon or the computational identification of surveillance blind spots. This scoping review therefore maps evidence on the nature and determinants of AMR under-surveillance, examines computational approaches relevant to its detection, and integrates these findings into an evidence-informed conceptual framework for AI-enabled identification of potential surveillance blind spots contributing to the hidden AMR gap. [17–20]

Methods

Review Design and Reporting Framework

A scoping review design was adopted to accommodate heterogeneous evidence concerning AMR surveillance systems, surveillance limitations, laboratory and data capacity, One Health surveillance, and emerging computational approaches. The review was conducted in accordance with methodological guidance from the Joanna Briggs Institute (JBI) for scoping reviews and reported according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses Extension for Scoping Reviews (PRISMA-ScR). [3,4]

The review process comprised formulation of the research question, systematic literature searching, eligibility screening, data charting, descriptive mapping, thematic synthesis, and development of an evidence-informed conceptual framework.

Eligibility Criteria

Eligibility criteria were structured according to the Population/Problem–Concept–Context (PCC) framework.

Population/Problem: AMR and surveillance systems, networks, datasets, or processes used to detect, characterize, monitor, or report antimicrobial resistance.

Concept: Under-surveillance, including insufficient or unequal surveillance coverage, incomplete detection or reporting, limited laboratory or diagnostic capacity, geographic or population-level gaps, genomic surveillance gaps, data fragmentation, and other surveillance deficits that may contribute to potential surveillance blind spots, as well as computational approaches relevant to identifying or estimating such deficiencies.

Context: Human, animal, agricultural/food, environmental, and integrated One Health surveillance in any geographic setting.

Eligible sources included primary research, surveillance analyses, methodological studies, substantive systematic or narrative reviews, and relevant public-health evidence addressing AMR surveillance coverage, capacity, representativeness, completeness, or computational identification of surveillance limitations. Studies describing spatial or predictive modelling, machine learning, artificial intelligence, data integration, missing-data estimation, genomic analytics, or related computational approaches were eligible when they directly examined surveillance limitations or provided methodological approaches relevant to assessing surveillance completeness, representativeness, uncertainty, spatial heterogeneity, or data gaps. Computational studies focused solely on predicting antimicrobial resistance

phenotypes without relevance to surveillance limitations or observation gaps were excluded. Secondary reviews were included to capture synthesized evidence on broader surveillance patterns, methodological challenges, and conceptual developments relevant to AMR under-surveillance. To minimize potential duplication, review articles were not treated as independent replications of individual primary studies. Instead, primary studies and secondary reviews were charted according to their source type and interpreted according to their contribution to understanding surveillance gaps, determinants, and computational approaches. Where reviews summarized findings from overlapping primary studies, synthesis focused on recurring themes and methodological insights rather than cumulative study counts.

Studies were excluded if they focused exclusively on treatment or antimicrobial stewardship without a surveillance component; predicted antimicrobial resistance without relevance to surveillance limitations; addressed infectious-disease surveillance or artificial intelligence without specific relevance to AMR; or consisted of editorials, commentaries, letters, conference abstracts, or other sources without sufficient empirical or methodological evidence.

Information Sources and Search Strategy

Systematic searches were conducted in PubMed and Dimensions on 30 August 2026. The search period was restricted to publications from 2015 to 2026 to capture contemporary developments in AMR surveillance, digital health infrastructure, genomic surveillance, and computational methods. PubMed was selected because of its extensive indexing of biomedical, clinical, microbiological, and public-health research relevant to AMR surveillance. Dimensions was selected to complement biomedical coverage with broader multidisciplinary indexing, including computational science, environmental research, policy-related evidence, and One Health literature. Together, these databases were considered appropriate for capturing both conventional surveillance evidence and emerging computational approaches relevant to identifying AMR surveillance gaps. Other databases, including Scopus, Web of Science, and Embase, were not searched and their omission may have resulted in the exclusion of potentially relevant studies.

The search strategy combined three conceptual domains: (1) antimicrobial resistance; (2) surveillance gaps, under-surveillance, limited surveillance capacity, under-reporting, and related terminology; and (3) computational approaches, including artificial

intelligence, machine learning, spatial and spatiotemporal modelling, predictive modelling, anomaly detection, data fusion, and missing-data approaches.

The initial PubMed search retrieved 420 records, of which 385 remained after restriction to the 2015–2026 publication period. The initial Dimensions search retrieved 686 records, with 591 remaining after application of the same publication-year criterion. No additional restrictions based on open-access status, species, sex, age, or subject category were applied.

The complete database-specific search strategies are provided in Supplementary Table S1 to support reproducibility.

Study Selection

Records retrieved from both databases were screened against the predefined eligibility criteria. Screening assessed whether each source contributed evidence concerning the existence, determinants, measurement, or computational identification of AMR under-surveillance. Studies addressing artificial intelligence or computational modelling were not included solely because they predicted antimicrobial resistance; they were required to contribute directly or methodologically to understanding surveillance coverage, missing observations, spatial or data heterogeneity, or potential surveillance blind spots. Title and abstract screening, followed by full-text assessment, was conducted independently by two reviewers using the predefined eligibility criteria. Any disagreements between reviewers were resolved through discussion and consensus. Where consensus could not be reached, a third reviewer was consulted to facilitate resolution. The screening process assessed each record according to its relevance to AMR surveillance coverage, surveillance limitations, data completeness, representativeness, or computational approaches relevant to identifying surveillance gaps.

The database searches identified 420 records in PubMed and 686 in Dimensions. Following restriction to publications from 2015–2026, 385 PubMed and 591 Dimensions records remained for screening. Screening against the predefined eligibility criteria resulted in 22 studies being included in the final synthesis, comprising 10 identified through PubMed and 12 through Dimensions.

Data Charting

A structured data-charting form was developed to systematically capture characteristics relevant to the review questions. Extracted variables included author and year, geographic setting, study design, surveillance domain, pathogen or resistance target, data source, type of surveillance limitation, laboratory or data-infrastructure constraints,

computational method where applicable, principal findings, and relevance to AMR under-surveillance. The data-charting process included classification of evidence sources as primary studies, secondary reviews, surveillance evaluations, modelling studies, or computational studies to support interpretation of heterogeneous evidence and reduce duplication during synthesis.

The characteristics of the included evidence are summarized in Table 1, the major surveillance gaps and their determinants in Table 2, and detailed study-level characteristics and computational contributions are provided in Supplementary Table S2.

Evidence Synthesis and Framework Development

Given the methodological and contextual heterogeneity of the included evidence, findings were synthesized descriptively and thematically rather than through meta-analysis. Studies were mapped across recurrent dimensions of under-surveillance, including geographic and population coverage, laboratory and diagnostic capacity, reporting and data infrastructure, genomic surveillance, and human–animal–environmental integration.

Thematic synthesis followed an iterative coding process. Extracted findings from included studies were first coded according to the reported mechanism of surveillance limitation, including gaps in geographic coverage, population representation, diagnostic access, laboratory capacity, data systems, One Health integration, and computational capability. Related codes were then compared and grouped into broader conceptual categories representing recurrent forms of AMR under-surveillance. Candidate themes were reviewed across the evidence base to identify consistency, overlap, and distinct mechanisms of under-observation. Final thematic domains and their definitions were refined through reviewer discussion and consensus.

The final taxonomy was therefore derived inductively from recurring patterns identified during evidence mapping rather than predefined categories imposed before study review. This process informed the identification of major surveillance-gap domains and their associated mechanisms of under-observation.

Computational evidence was mapped according to analytical approach, data requirements, surveillance function, and potential to reveal discordance between observed AMR signals and expected resistance patterns. These evidence streams were subsequently integrated to develop a conceptual framework in which surveillance intensity and contextual risk indicators complement observed AMR data to identify locations, populations, pathogens, or

One Health domains potentially affected by under-surveillance.

The translation from evidence synthesis to framework development followed a structured conceptual mapping process. Surveillance-gap domains identified during thematic synthesis were first linked to the types of information required to characterize incomplete observation, including AMR occurrence data, surveillance coverage indicators, laboratory capacity measures, genomic information, contextual risk factors, and One Health data streams. Computational approaches identified in the included literature were then mapped according to their potential analytical roles, including data integration, spatial assessment, uncertainty characterization, anomaly detection, and prioritization of surveillance needs. These evidence-to-function mappings informed the design of the proposed AI-enabled framework,

which represents an evidence-informed conceptual model rather than a validated operational system.

The resulting framework is presented in Figure 2 as an evidence-informed model for AI-enabled identification and prioritization of hidden AMR surveillance gaps.

Critical Appraisal

Formal critical appraisal was not undertaken because the primary purpose of this scoping review was to map the breadth, characteristics, and methodological diversity of evidence relating to AMR under-surveillance rather than to estimate a pooled effect or determine intervention effectiveness. Methodological limitations reported by individual studies were nevertheless charted and considered when interpreting the evidence and developing the conceptual framework.

Results

Study Selection and Evidence Base

The database searches identified 420 records in PubMed and 686 in Dimensions. Following application of the predefined publication-year restriction, 385 PubMed and 591 Dimensions records remained for screening. After screening against the predefined eligibility criteria, 22 studies were included in the final scoping review, comprising 10 identified through PubMed and 12 through Dimensions. The included evidence comprised primary surveillance studies, systematic and scoping reviews, surveillance-system evaluations, modelling studies, digital-health implementations, genomic analyses, and studies applying artificial intelligence (AI), machine learning (ML), geographic information systems (GIS), and related computational approaches to AMR surveillance.

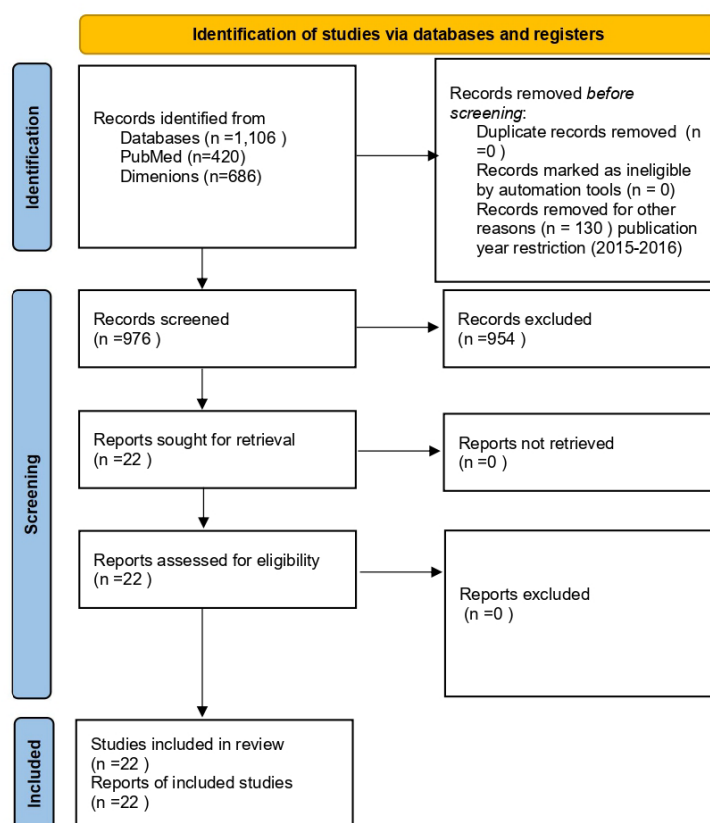
The evidence base spanned sub-Saharan Africa, South and Southeast Asia, the Eastern Mediterranean Region, and global datasets, with individual studies examining settings including Nigeria, Somalia, Rwanda, Ethiopia, India, Kenya, Tanzania, Burkina Faso, the Democratic Republic of the Congo, Cambodia, Thailand, Vietnam, and South Africa. Surveillance depth varied substantially across and within settings, particularly in laboratory capacity, sampling intensity, data availability, and longitudinal coverage. [26,27]

Across the 22 included studies, surveillance gaps were distributed across multiple overlapping domains. Geographic under-surveillance was addressed in 10 studies, laboratory and diagnostic limitations in 9 studies, One Health and sectoral surveillance gaps in 9 studies, data/informatics and reporting limitations in 8 studies, genomic surveillance

limitations in 5 studies, and computational or digital approaches relevant to surveillance-gap assessment in 12 studies. Temporal or reporting-continuity limitations were specifically identified in 3 studies. Because several studies addressed more than one dimension of under-surveillance, these frequencies represent thematic coverage across the evidence base rather than mutually exclusive study categories.

Human clinical surveillance predominated, although veterinary, food-chain, environmental, wastewater, and integrated One Health surveillance were also represented. Pathogen-specific studies included *Escherichia coli*, *Salmonella* spp., *Salmonella Typhi*, *Neisseria gonorrhoeae*, and methicillin-resistant *Staphylococcus aureus* (MRSA), while other studies examined resistance patterns or resistomes across multiple bacterial taxa. [21–24,26,27]

PRISMA 2020 flow diagram for new systematic reviews which included searches of databases and registers only



Source: Page MJ, et al. BMJ 2021;372:n71. doi: 10.1136/bmj.n71.

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Figure 1. PRISMA 2020 flow diagram showing the identification, screening, eligibility assessment, and inclusion of studies in the scoping review. Adapted from Page et al. (2021) under the CC BY 4.0 licence. [25]

Table 1. Characteristics of the included evidence

Characteristic	Evidence represented in the review
Included studies	22
Databases contributing included studies	PubMed (n=10); Dimensions (n=12)
Major geographic focus	Global; sub-Saharan Africa; West and East Africa; South and Southeast Asia; Eastern Mediterranean Region; LMICs
Surveillance domains	Human clinical, veterinary, food-chain, environmental/wastewater, genomic, and integrated One Health
Major study approaches	Primary surveillance studies; retrospective laboratory analyses; surveillance-system evaluations; systematic/scoping reviews; modelling studies; AI/ML studies; GIS and digital-platform studies
Major surveillance technologies and approaches	AST; LIS/LIMS; WHONET-compatible systems; WGS; metagenomics; GIS; wastewater/environmental surveillance; statistical modelling; ML/AI
Recurring surveillance gaps	Geographic underrepresentation; diagnostic under-ascertainment; laboratory constraints; sampling bias; fragmented data systems; poor interoperability; delayed reporting; weak One Health integration
Computational/digital responses	Predictive modelling; machine learning; GIS mapping; digital LIS/LIMS; genomic analysis; wastewater surveillance; data integration; automated resistance interpretation

Abbreviations: AI, artificial intelligence; AMR, antimicrobial resistance; AST, antimicrobial susceptibility testing; GIS, geographic information system; LIS/LIMS, laboratory information system/laboratory information management system; LMIC, low- and middle-income country; ML, machine learning; WGS, whole-genome sequencing.

Under-Surveillance Was Multidimensional Rather Than Synonymous with Missing Data

Across the included evidence, AMR under-surveillance emerged not simply as an absence of observations but as a multidimensional failure of surveillance coverage and representativeness. Five recurrent forms were identified: geographic, population and healthcare-access, diagnostic and laboratory, sectoral or One Health, and temporal and data-system under-surveillance. [1,8,20,22,23,26,27]

These five initial dimensions represented broad thematic categories derived from the evidence mapping process. During further synthesis, some categories were subdivided to better capture distinct mechanisms through which surveillance information may be lost. Specifically, diagnostic limitations and laboratory-capacity limitations were separated because failure to access appropriate testing differs conceptually from limitations in the ability to perform and interpret testing. Similarly, data-system limitations and temporal limitations were separated because incomplete data capture and delayed reporting represent different stages of the surveillance pathway. The resulting seven-domain taxonomy therefore represents a refinement of the initial thematic structure rather than a separate or contradictory classification.

This distinction was particularly evident in global burden estimation. A global systematic analysis of bacterial AMR incorporated 471 million individual records or isolates across 204 countries and territories, yet statistical modelling was still required to estimate AMR burden in locations without direct data. Serious data gaps remained in many low-income settings, highlighting the need for expanded microbiology laboratory capacity and data-collection systems. [1]

These findings indicate that absence of reported resistance cannot reliably be interpreted as absence of resistance. Observed AMR instead reflects both the underlying resistance burden and the surveillance processes through which it becomes detectable, including healthcare access, diagnostic testing, specimen collection, laboratory capacity, reporting infrastructure, and inclusion within surveillance networks.

Geographic Underrepresentation Created Systematic Blind Spots

Geographic inequity was among the clearest surveillance gaps identified across the evidence. This occurred at both global and regional levels, with low-resource settings frequently contributing

comparatively sparse primary surveillance data despite substantial estimated AMR burden. [1,5,26,27]

GIS analysis of the ATLAS dataset illustrated this imbalance. Only 13 of 55 African countries were represented, and longitudinal coverage was inconsistent even among participating countries. Nigeria, for example, had data for 2013–2014 and 2018–2021, whereas the United Kingdom had continuous data from 2004 to 2021. Of more than 800,000 isolates represented in the dataset, approximately 22,000 originated from Africa. [5]

Geographic imbalance was also evident within multicountry evidence. A scoping review of *Neisseria gonorrhoeae* surveillance across Cambodia, Thailand, Vietnam, and South Africa identified 29 eligible studies, of which 83% originated from South Africa and none from Cambodia. Only four studies contained antimicrobial susceptibility data, demonstrating that apparent regional coverage can conceal substantial differences in the depth of usable resistance information. [6]

Collectively, these findings demonstrate spatial heterogeneity in AMR surveillance at multiple levels, from continental and national representation to the depth and continuity of surveillance within individual settings.

Comparable geographic and sectoral imbalances were identified across Southeast Asia. A systematic review and meta-analysis of 137 observational studies on Enterobacterales found evidence concentrated in Thailand and Vietnam, with sparse representation from Laos and Myanmar and no eligible studies from Brunei. Only one study incorporated all four One Health sectors, highlighting simultaneous geographic and ecological gaps in regional AMR surveillance [29].

Diagnostic and Laboratory Capacity Determined What Resistance Became Visible

A second dominant theme was the dependence of surveillance visibility on diagnostic and laboratory infrastructure. Under-surveillance frequently occurred upstream of surveillance databases because infections were not sampled, cultured, identified, or subjected to antimicrobial susceptibility testing [28].

This was demonstrated in a multicentre analysis from Nigeria involving 84,548 culture results from 26,630 patients across 25 public laboratories. Stool samples accounted for only 3% of specimens despite the study's focus on *Salmonella*. Limited stool collection, poor laboratory-data integration, inadequate species

resolution, inconsistent laboratory performance, and absence of integrated One Health surveillance were identified as factors potentially limiting accurate characterization of *Salmonella* and associated resistance patterns. [7]

Similar deficiencies were identified in gonococcal surveillance across Cambodia, Thailand, Vietnam, and South Africa, where limited phenotypic susceptibility testing constrained comprehensive resistance monitoring. Gaps in extragenital sampling were also identified as a potential source of under-ascertainment in specific populations. [6]

Together, these findings demonstrate that diagnostic and laboratory capacity functions as a surveillance gatekeeper: infections occurring outside diagnostic reach are less likely to be represented in national or global AMR surveillance datasets.

Surveillance Systems Were Vulnerable to Selection and Representativeness Bias

Even where microbiological data were available, they were not necessarily representative of the populations to which resistance estimates were subsequently generalized.

Evaluation of GLASS implementation in the WHO Eastern Mediterranean Region identified substantial between-country variation in representativeness, completeness, and data quality. Differences in laboratory record keeping and information systems complicated reporting, while patient-selection procedures and limitations in quality assurance potentially affected surveillance sensitivity. [8]

Much of the submitted surveillance data also originated from nosocomial infections or patients who had previously received antibiotics. Such sampling may preferentially capture populations with greater likelihood of resistant infection and consequently inflate resistance estimates when extrapolated to the broader community. Representativeness was further influenced by the geographic distribution of surveillance sites, inclusion of public and private healthcare facilities, healthcare-seeking behaviour, and completeness of medical records. [8]

These findings demonstrate that surveillance incompleteness and selection bias can coexist: resistance may be under-observed across poorly sampled populations or locations while appearing disproportionately high among selected populations that enter surveillance systems. Surveillance representativeness therefore depends not only on data volume but also on who, where, and what enters the surveillance denominator.

One Health Surveillance Remained Structurally Fragmented

A substantial cross-study gap involved incomplete integration of human, animal, food, and environmental AMR surveillance. [11,12,22,23]

Veterinary surveillance was particularly constrained. Assessment of veterinary laboratories in India identified lack of dedicated AMR-surveillance funding, absence of standardized AST guidelines, shortages of reference strains and quality-assurance resources, and limited mechanisms for data sharing. [9]

Similarly, investigation of slaughterhouse-associated AMR surveillance in western Kenya identified limitations in funding, personnel, infrastructure, and laboratory capacity. Participants reported an absence of surveillance capable of detecting resistant pathogens within some slaughterhouse settings. [10]

Food-chain surveillance showed comparable fragmentation, characterized by uneven geographic coverage, voluntary participation, weak veterinary laboratory infrastructure, and limited representation of LMICs. Recurring deficiencies included non-standardized sampling, lack of integrated human–animal–environmental databases, inadequate monitoring of emerging resistance mechanisms, and insufficient coordination between public-health and veterinary authorities. [11]

Environmental surveillance represented an additional blind spot. Evidence from Tanzania, Burkina Faso, and the Democratic Republic of the Congo indicated that wastewater and environmental AMR surveillance remained limited and predominantly project-based. Such approaches nevertheless provide complementary population-level signals that are less dependent on healthcare access and individual diagnostic testing than conventional clinical surveillance. [12]

Fragmented Information Systems Converted Laboratory Capacity Into Data Loss

An additional surveillance failure occurred after microbiological testing had been performed: incomplete capture, standardization, transmission, and integration of laboratory results.

Laboratory informatics was repeatedly identified as an under-resourced component of AMR surveillance. Deficiencies in laboratory information management systems can prevent improvements in microbiological capacity from translating into comprehensive surveillance, particularly where systems for capturing, collating, standardizing, and transmitting laboratory data remain fragmented. [20]

The magnitude of this information loss was illustrated by evidence from Rwanda. Baseline assessment identified capture of only 60% of culture observations and 25% of AST data, alongside non-

standardized AST panels and limited capacity to generate cumulative antibiograms. WHONET and other surveillance platforms also operated separately from routine clinical workflows, limiting integration of laboratory information into real-time clinical and surveillance processes. [13]

Across the wider evidence, heterogeneous laboratory information systems, incompatible file formats, inconsistent organism and antimicrobial nomenclature, variable AST methodologies, and missing variables further constrained interoperability. [13,20]

Collectively, these findings demonstrate that resistance information can be lost from the surveillance pathway even after microbiological testing has occurred, creating a distinct post-analytical form of under-surveillance.

Reporting Delays Reduced the Temporal Sensitivity of Surveillance

Under-surveillance also had a temporal dimension. Annual or irregular reporting cycles reduced the timeliness with which emerging resistance patterns could be detected and translated into surveillance action.

Within the Eastern Mediterranean GLASS evaluation, annual reporting constrained local feedback loops and delayed the availability of information for decision-making. Delays in reporting and dissemination occurred at both local and international levels, limiting the capacity of surveillance systems to provide timely evidence for intervention. [8]

Surveillance gaps were therefore not exclusively geographic or population-based. Settings formally participating in surveillance could remain temporally under-observed when substantial delays occurred between data generation, reporting, and availability for public-health action.

Computational Approaches Addressed Different Forms of Incomplete Observation

A second major body of evidence concerned computational and digital approaches that addressed different components of incomplete surveillance observation. These approaches did not directly detect hidden AMR surveillance gaps in most included studies; rather, they contributed methodological capabilities relevant to surveillance-gap assessment, including estimation in data-sparse settings, identification of spatial heterogeneity, integration of heterogeneous datasets, improvement of data completeness, and characterization of uncertainty. These approaches clustered into statistical and spatial modelling, artificial intelligence and machine learning (AI/ML), GIS and spatial analytics, genomic and bioinformatic surveillance, digital laboratory

infrastructure, and environmental surveillance. [5,14-16,18,19,21,22,24]

Therefore, the computational evidence identified in this review should be interpreted as supporting capabilities rather than direct demonstrations of AI-based surveillance-gap detection. Existing applications primarily addressed resistance prediction, burden estimation, spatial characterization, data harmonization, and improvement of surveillance completeness. The proposed AI-enabled framework extends these capabilities conceptually by integrating them toward identification of potential mismatches between AMR risk and surveillance intensity, but this application requires empirical development and validation.

Statistical and Spatial Modelling

The global AMR burden analysis used predictive statistical models to estimate burden in locations without direct observations, demonstrating the application of model-based inference to surveillance-sparse settings. [1]

Similarly, global antibiotic-consumption surveillance integrated household surveys and data from WHO, IQVIA, and ESAC-Net within Bayesian geostatistical models to estimate consumption across 204 countries over 19 years. This demonstrated how heterogeneous data sources can be integrated to characterize patterns where direct measurements are incomplete. [14]

Artificial Intelligence and Machine Learning

The Somalia pilot provided the clearest direct application of AI to AMR surveillance in a low-resource setting. A Random Forest model using five routinely available variables—age, sex, organism, ward, and specimen source—achieved 91.4% sensitivity for identifying multidrug resistance. However, overall discrimination was modest (AUC 0.607; specificity 12.5%; MCC 0.06), indicating substantial limitations despite high sensitivity. [15]

Broader evidence identified random forests, gradient boosting, and deep neural networks as approaches for forecasting resistance trends, identifying potential hotspots, and integrating electronic health records, laboratory results, and genomic data. Many reported applications, however, remained retrospective or proof-of-concept and were dependent on the geographic coverage, temporal completeness, and quality of available data. [18,19]

Machine learning was also applied at the global scale by integrating bacterial genomes, resistance phenotypes, socioeconomic indicators, antimicrobial consumption, climate, and health data to forecast resistance traits to 2050. This demonstrated the potential of multimodal modelling to characterize

resistance trajectories beyond those apparent from conventional isolate surveillance alone. [16]

GIS and Digital Mapping

GIS-based approaches enabled the geographic distribution of surveillance data and gaps to be visualized directly. Interactive dashboards integrating more than 860,000 ATLAS observations from 83 countries revealed substantial geographic disparities in data availability, particularly across Africa, while facilitating spatial exploration of large AMR datasets. [5]

Digital Laboratory Surveillance

The Rwanda laboratory information system intervention addressed surveillance incompleteness by improving the capture and integration of data generated during routine microbiological testing. The system incorporated CLSI/EUCAST rules, automated AST interpretation, AWaRe-based cascade reporting, and WHONET-compatible export, with a centralized architecture designed to support standardized surveillance and expansion from individual facilities to broader networks. [13]

Genomic and Environmental Surveillance

Whole-genome sequencing, metagenomics, and environmental monitoring extended surveillance beyond conventional clinical isolate-based approaches. Across the One Health evidence, genomic, environmental, and wastewater surveillance were identified as complementary approaches for detecting resistance signals across human, animal, and environmental compartments. Digital One Health approaches further combined genomic information, GIS, machine learning, and environmental data to characterize resistance patterns, hotspots, and potential transmission pathways. [21-24]

Technology Did Not Eliminate the Surveillance Denominator Problem

Despite technological advances, the included evidence consistently demonstrated that computational and digital approaches remained dependent on the

availability, quality, and representativeness of their underlying data.

AI/ML models were constrained by the geographic and temporal coverage of training data, while GIS approaches could identify spatial gaps without generating observations where surveillance had not occurred. Genomic surveillance provided high-resolution resistance information but remained dependent on specimen acquisition, sequencing capacity, and genomic representation. Environmental surveillance broadened observational coverage but remained limited by methodological heterogeneity and incomplete standardization. [18,19,22,24]

Similar limitations were evident in integrated One Health surveillance. The One Health resistome literature identified frequent convenience sampling, cross-sectional study designs, isolate-focused surveillance, and limited spatially co-located or temporally synchronized sampling across human, animal, and environmental compartments. [22]

Collectively, the evidence indicates that computational and digital technologies can identify, characterize, or partially compensate for specific dimensions of surveillance incompleteness, but they do not eliminate the underlying limitations of incomplete or unrepresentative observation.

An Integrated Taxonomy of the Hidden AMR Surveillance Gap

Synthesis across the 22 included studies generated a seven-domain taxonomy of AMR under-surveillance (Table 2). This taxonomy was developed as a refinement of the five broad thematic dimensions identified during initial evidence mapping. The refinement separated conceptually distinct mechanisms of under-observation, including the distinction between diagnostic gaps and laboratory-capacity gaps, as well as between data/informatics gaps and temporal gaps. These domains represent interacting points across the surveillance pathway at which resistance may become incompletely observed, characterized, captured, or reported.

Table 2. Taxonomy of AMR under-surveillance identified across the included evidence

Surveillance gap	Mechanism producing under-observation	Examples identified in the evidence	Potential computational/digital response
Geographic gap	Countries, regions, or facilities contribute little or no surveillance data	Sparse African representation; absent or discontinuous national data [5]	GIS gap mapping; spatial modelling; Bayesian/geostatistical estimation
Population/access gap	Populations have limited access to healthcare or diagnostic testing	Community cases and poorly served populations incompletely represented	Wastewater surveillance; community sampling; multimodal population modelling

Diagnostic gap	Appropriate specimens are not collected or tested	Stool under-sampling; limited gonococcal AST; inadequate phenotypic testing [7]	Diagnostic decision support; targeted surveillance; strengthened testing pathways
Laboratory-capacity gap	AST, quality assurance, reagents, reference strains, sequencing, or workforce capacity is limited	Veterinary and resource-constrained laboratory limitations	Digital AST systems; automated interpretation; genomic surveillance where feasible
Data/informatics gap	Results are generated but incompletely captured, standardized, linked, or transmitted	Low AST capture; incompatible LIMS; fragmented databases [13]	Interoperable LIS/LIMS; WHONET integration; automated data harmonization
One Health/sectoral gap	Human surveillance predominates while animal, food, and environmental compartments remain poorly integrated	Weak veterinary, slaughterhouse, food-chain, and environmental monitoring	Integrated databases; WGS/metagenomics; wastewater surveillance; data fusion
Temporal gap	Reporting delays or discontinuities limit timely detection of changing resistance patterns	Annual reporting; inconsistent longitudinal datasets	Timely digital reporting; anomaly detection; early-warning models

Proposed AI Framework for Detecting AMR Under-Surveillance

The evidence supported a conceptual distinction between AMR prediction and surveillance-gap detection. Existing computational applications predominantly focus on predicting resistance phenotypes or genes, mapping geographic patterns, or forecasting future resistance. The evidence mapped in this review suggests an additional analytical target: identifying where the observed surveillance record may inadequately represent the underlying AMR risk. The framework therefore represents an evidence-informed synthesis of identified surveillance limitations and available analytical capabilities rather than a direct implementation of any single AI system described in the included literature. Accordingly, the framework should be interpreted as a proposed analytical pathway rather than evidence that AI systems currently detect surveillance blind spots in routine AMR surveillance practice.

The proposed framework comprises four analytical layers. First, a surveillance-observation layer captures available AST results, specimen volumes, reporting sites, pathogen distributions, and longitudinal completeness. Second, a contextual-risk layer integrates indicators such as antimicrobial consumption, healthcare access, laboratory capacity, socioeconomic conditions, animal production, and environmental signals. Third, a gap-detection layer applies spatial modelling, anomaly detection, machine learning, and missing-data analysis to identify discordance between expected AMR risk and observed

surveillance intensity. Finally, a prioritization layer translates these discrepancies into geographically and sectorally explicit priorities for strengthened surveillance.

As an illustrative application, consider a district reporting few resistant infections but also characterized by low specimen-testing volume, limited AST capacity, few reporting laboratories, and irregular data submission. The surveillance-observation layer would identify the sparse microbiological and reporting record, while the contextual-risk layer could incorporate indicators such as antimicrobial consumption, healthcare access, population characteristics, livestock production, or environmental AMR signals. The gap-detection layer would assess whether the low observed resistance signal is discordant with the contextual risk profile and surveillance intensity. If substantial discordance and uncertainty were identified, the prioritization layer could classify the district as a candidate surveillance blind spot and direct attention toward additional specimen collection, laboratory strengthening, environmental sampling, or other targeted surveillance activities. This scenario is illustrative rather than a validated application of the framework.

The framework therefore shifts the computational question from “**Where is AMR high?**” to “**Where is AMR risk high but our capacity to observe it disproportionately low?**”

The included literature provides individual components of this architecture—including predictive burden modelling, GIS mapping, AI-based resistance

prediction, digital laboratory systems, genomic surveillance, and environmental monitoring—but no single approach identified within the reviewed evidence integrated these components into a dedicated system for detecting AMR surveillance blind spots. This unresolved intersection represents the principal computational and surveillance gap identified by the review.

Characteristics and Contributions of Individual Studies

The 22 included studies were heterogeneous in geographic setting, surveillance domain, study design, data source, and analytical approach (Supplementary Table S2). This heterogeneity reflected different points of failure across the AMR surveillance pathway. Laboratory-based studies primarily identified limitations in specimen collection, antimicrobial susceptibility testing, laboratory capacity, and data capture; surveillance-system evaluations highlighted deficiencies in representativeness, completeness, timeliness, and interoperability; One Health studies identified gaps across animal, food-chain, and environmental surveillance; and computational studies demonstrated approaches for spatial mapping, model-based estimation, genomic analysis, data integration, and resistance forecasting where direct surveillance was incomplete.

Cross-Study Convergence of Surveillance Blind Spots

Despite methodological heterogeneity, the evidence converged around surveillance failures occurring across the AMR information pathway, from entry into diagnostic systems through laboratory characterization to data capture, transmission, and reporting. These failures could be organized into three broad layers of under-observation.

The first was pre-analytical under-observation, in which infections did not adequately enter the surveillance pathway because of limited healthcare access, insufficient or inappropriate specimen collection, restricted diagnostic access, or omission of animal and environmental compartments. The Nigerian *Salmonella* analysis illustrated this mechanism, with substantial stool under-sampling limiting surveillance before susceptibility testing could occur. Environmental and wastewater surveillance provided complementary population-level approaches that were less dependent on individual healthcare access and diagnostic testing. [7,12]

The second was analytical under-observation, arising from limitations in organism identification, AST, genomic characterization, quality assurance, laboratory resources, or methodological standardization. Veterinary laboratory evidence from

India identified deficiencies in standardized AST procedures, reference strains, and quality-assurance resources, while gonococcal surveillance demonstrated that detection of infection did not consistently translate into phenotypic resistance characterization. [6,9]

The third was post-analytical under-observation, in which laboratory information was generated but incompletely captured, standardized, integrated, transmitted, or reported. This was evident in Rwanda, where only 25% of AST data were captured at baseline, and across resource-limited laboratory settings in which data-management and informatics capacity remained under-resourced. [13,20]

Together, these findings indicate that surveillance completeness cannot be inferred from isolate counts or numbers of reporting sites alone because under-observation may occur at multiple stages of the surveillance pathway.

AMR Burden and Surveillance Intensity Were Frequently Misaligned

A recurring pattern across the evidence was a mismatch between epidemiological need and observational capacity. The global AMR burden analysis estimated particularly high attributable mortality in western sub-Saharan Africa while simultaneously identifying substantial primary-data gaps in low-income settings. Geographic underrepresentation was independently evident in the ATLAS-based GIS analysis, where African countries and isolates constituted a small proportion of overall surveillance coverage and longitudinal data were frequently discontinuous. [1]

Comparable limitations occurred at regional and national levels. Settings characterized by constrained diagnostic capacity, fragmented laboratory networks, or incomplete surveillance infrastructure frequently had less representative direct AMR data. Within the WHO Eastern Mediterranean Region, variation in laboratory infrastructure, surveillance coverage, and information systems affected the completeness and representativeness of reported data. [8]

These findings identify surveillance intensity as an important dimension in the interpretation of observed AMR: sparse reporting may reflect limited observational capacity and therefore cannot, by itself, be interpreted as evidence of low resistance.

Evidence for a Surveillance Paradox

The synthesis identified a surveillance paradox in which different forms of surveillance bias could operate simultaneously. Insufficient geographic, population, or diagnostic coverage could underestimate the distribution of AMR, while selective sampling of hospitalized, previously treated, or

otherwise higher-risk patients could produce resistance estimates that were disproportionately high relative to broader populations.

This pattern was evident in the GLASS evaluation, where surveillance data frequently originated from nosocomial infections or patients with previous antibiotic exposure. Consequently, observed resistance estimates were influenced not only by the underlying resistance burden but also by the populations entering surveillance. [8]

These findings demonstrate that increasing data volume alone does not ensure representative surveillance. The composition and coverage of the surveillance denominator remain critical to the interpretation of resistance estimates.

The One Health Surveillance Deficit

AMR surveillance remained disproportionately concentrated in human clinical settings despite evidence spanning human, animal, food, and environmental compartments. Veterinary surveillance limitations were documented in India, while slaughterhouse surveillance in western Kenya was constrained by limitations in laboratory capacity, staffing, funding, and infrastructure. Food-chain evidence similarly demonstrated uneven geographic coverage, weak veterinary surveillance infrastructure, and limited cross-sector integration. [9–12,29]

Environmental surveillance was less routinely institutionalized. Evidence from Tanzania, Burkina Faso, and the Democratic Republic of the Congo indicated that wastewater and environmental surveillance remained predominantly project-based rather than consistently embedded within national surveillance systems. [12]

Collectively, the evidence demonstrates that AMR under-surveillance is not only geographically incomplete but also ecologically and sectorally incomplete, with animal, food-chain, and environmental compartments less consistently represented within integrated surveillance systems.

From Retrospective Reporting to Predictive Surveillance

The computational evidence indicated a transition from approaches primarily describing observed resistance toward methods capable of forecasting resistance patterns, identifying anomalous signals, and estimating risk where direct observations were incomplete. [5,14-16,18,19,21,22]

This transition was evident across several methodological classes. Global burden models generated estimates for locations without direct observations; Bayesian geostatistical models reconstructed antibiotic-consumption patterns across data-sparse settings; GIS approaches visualized

geographic gaps in surveillance; AI models predicted multidrug resistance using routinely available clinical variables; and multimodal machine-learning approaches integrated genomic, socioeconomic, antimicrobial-consumption, climate, and health data to forecast resistance trajectories. [1,5,14-16]

The maturity of these approaches nevertheless varied substantially. Some applications remained retrospective or proof-of-concept, while performance and external validation were inconsistent. The evidence therefore demonstrates expanding computational capacity to complement conventional AMR surveillance through forecasting, spatial analysis, data integration, and methods potentially relevant to surveillance-gap assessment.

Derivation of a Surveillance Blind-Spot Detection Framework

Integration of the mapped evidence suggests that AMR under-surveillance can be conceptualized as a discordance between expected AMR risk and observed surveillance intensity. Within the proposed framework, a location, population, pathogen, or One Health compartment may represent a candidate surveillance blind spot when three conditions converge

1. Underlying AMR risk is plausibly elevated, based on epidemiological, antimicrobial-use, socioeconomic, healthcare, genomic, environmental, or ecological indicators;
2. Direct surveillance intensity is disproportionately low, reflected by limited sampling, reporting facilities, AST results, genomic sequences, reporting periods, or population coverage; and
3. Substantial uncertainty remains regarding whether the low observed resistance signal reflects genuinely low resistance or insufficient observation.

This conceptualization extends conventional missing-data analysis by treating surveillance insufficiency itself as an analytical target. Candidate indicators derived from the reviewed evidence are summarized in Table 3.

Table 3. Candidate indicators for an AI-based AMR Surveillance Blind-Spot Score

Dimension	Candidate indicators	Potential interpretation
Observed surveillance intensity	Isolates per population; AST tests per 1,000 patients; number of reporting laboratories; reporting months/years; specimen diversity	Extent to which the population or setting is directly observed
Laboratory capacity	Microbiology laboratories per population; culture availability; AST capacity; quality assurance; sequencing availability	Capacity to detect and characterize resistant infections
Healthcare access	Facility density; diagnostic access; healthcare utilization; rurality; financial barriers to care	Likelihood that infections enter clinical surveillance
Data completeness	Missing AST fields; missing demographic variables; incomplete organism identification; delayed data submission	Extent to which generated information is retained within the surveillance pathway
AMR risk context	Antimicrobial consumption; stewardship indicators; infection incidence; prior MDR prevalence	Contextual evidence potentially associated with resistance risk
Population vulnerability	Conflict or displacement; socioeconomic deprivation; population density; relevant population-level health indicators	Conditions potentially associated with elevated burden or reduced surveillance access
One Health exposure	Livestock density; food-production activity; slaughterhouse activity; wastewater signals; environmental ARG abundance	Potential resistance signals or reservoirs outside conventional clinical surveillance
Geographic continuity	Distance to sentinel sites; neighbouring resistance patterns; spatial clustering	Potential geographic discontinuities or unsampled areas
Temporal continuity	Reporting gaps; time since last submission; abrupt reductions in testing	Potential temporal deterioration in surveillance coverage
Genomic representation	Genomes sequenced relative to isolates or population; lineage diversity; resistance-gene coverage	Extent to which circulating lineages and resistance mechanisms are genomically represented

The framework proposes a **Surveillance Blind-Spot Score (SBSS)** as a conceptual prioritization measure rather than a validated predictive score. The SBSS is intended to summarize potential discordance between contextual AMR risk, surveillance intensity, and uncertainty in available observations:

SBSS = f(predicted AMR risk, surveillance deficit, data uncertainty, system capacity)

This formulation represents a conceptual structure for future model development and does not imply an established mathematical relationship or validated weighting scheme.

Operational development of the SBSS would require empirical definition and validation of the variables contributing to each component. Predicted AMR risk could incorporate indicators such as observed resistance trends, antimicrobial consumption patterns, pathogen distribution, epidemiological characteristics, socioeconomic conditions, and environmental or One Health risk factors. Surveillance deficit could include measures of testing volume, isolate availability, geographic coverage, reporting frequency, laboratory availability, and population representativeness. Data uncertainty could be

characterized using indicators such as missingness patterns, variability between data sources, temporal inconsistency, incomplete metadata, and model uncertainty. System capacity could incorporate laboratory infrastructure, diagnostic availability, workforce capacity, data connectivity, quality-assurance systems, and participation in surveillance networks.

Importantly, uncertainty would not be interpreted solely as a statistical limitation to be minimized; persistent uncertainty may itself indicate insufficient observation and therefore contribute to the identification of potential surveillance blind spots. Future SBSS development would require calibration against representative longitudinal datasets and evaluation of whether score-based prioritization improves detection and strengthening of surveillance gaps. Future SBSS development should derive and calibrate variable weights empirically using representative datasets, with expert-informed weighting considered where data are limited. In the absence of an established reference standard for AMR surveillance blind spots, validation could compare SBSS-identified priorities with evidence from

intensified surveillance, expanded microbiological testing, laboratory assessments, or genomic and environmental sampling. External validation should assess performance using independent geographic, temporal, and One Health datasets.

A high SBSS would not indicate confirmed high resistance prevalence. Rather, it would identify settings in which elevated contextual risk coincides with insufficient observation and substantial uncertainty,

thereby prioritizing them for strengthened microbiological, genomic, environmental, or One Health surveillance.

The SBSS is therefore proposed as an evidence-informed conceptual construct rather than a validated predictive model. Its weighting, calibration, thresholds, and external validity would require evaluation using representative, longitudinal, and multisectoral surveillance datasets before operational application.

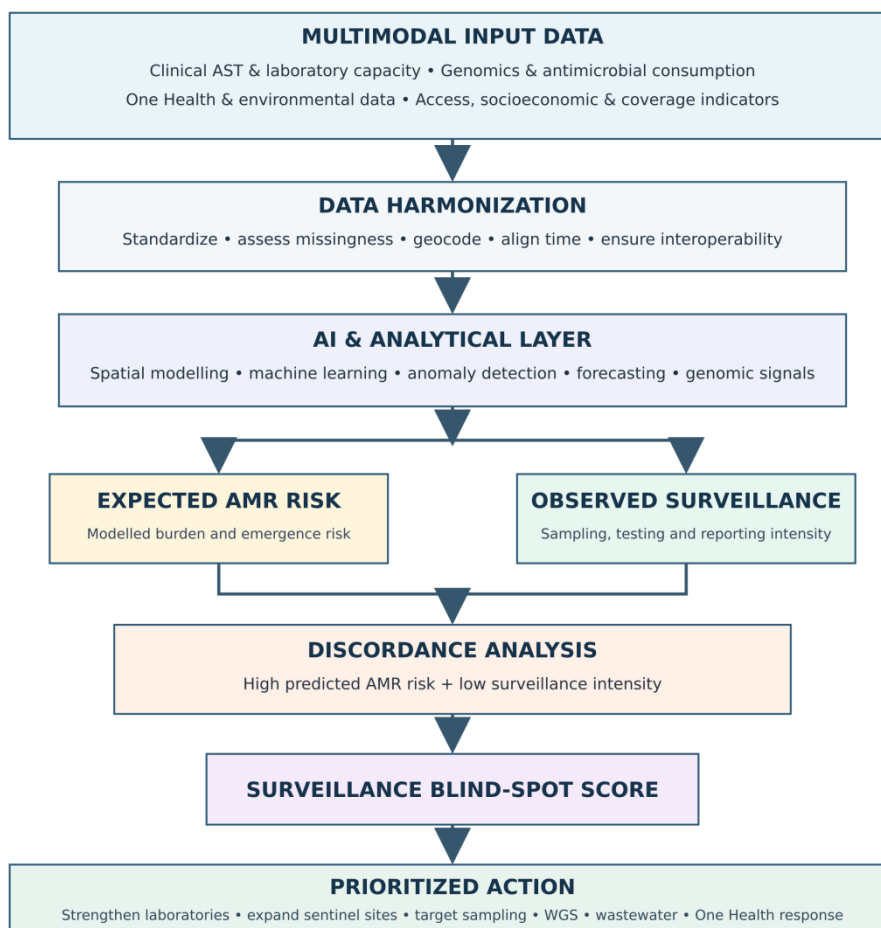


Figure 2. Proposed artificial-intelligence framework for detecting hidden antimicrobial-resistance surveillance gaps.

Multimodal clinical, laboratory, genomic, environmental, One Health, socioeconomic and health-system data are harmonized and analysed using complementary computational methods. Expected AMR risk is compared with observed surveillance intensity to identify discordance. Areas with high predicted risk but limited surveillance receive elevated blind-spot scores and are prioritized for targeted sampling, laboratory strengthening and enhanced surveillance. The framework is intended to augment, rather than replace, microbiological surveillance.

Overall Synthesis

Across the included evidence, AMR under-surveillance reflected failures across the surveillance

pathway, including where and from whom specimens were collected, diagnostic and laboratory capacity, representation of One Health compartments, data capture and interoperability, and reporting timeliness. Under-surveillance therefore emerged as a systems-level property rather than simply an absence of records.

Computational and digital approaches addressed different components of this problem. Laboratory information systems reduced post-analytical data loss; genomic approaches increased surveillance resolution; wastewater and environmental surveillance expanded observational coverage; GIS exposed spatial gaps; statistical models characterized patterns in data-sparse settings; and AI/ML enabled

integration of heterogeneous surveillance and contextual signals.

However, the evidence did not support treating algorithmic prediction as a substitute for missing microbiological observations. Instead, the synthesis

supports a complementary role for computational approaches in characterizing uncertainty, identifying discordance between expected AMR risk and observed surveillance intensity, and prioritizing settings in which additional surveillance may be most informative.

Discussion

Principal Findings

This scoping review identifies AMR under-surveillance as a multidimensional systems problem extending beyond simple data scarcity. Across the included evidence, geographic exclusion, restricted diagnostic and laboratory capacity, selective sampling, fragmented information systems, delayed reporting, limited genomic representation, and incomplete One Health integration collectively shaped what resistance became observable. The apparent geography of AMR therefore reflects not only the distribution of resistance but also the distribution of surveillance capacity.

A central implication is that absence of surveillance evidence cannot be interpreted as evidence of low resistance. Global burden estimation has required model-based inference where direct observations are sparse or unavailable, demonstrating the distinction between AMR burden and surveillance visibility. This review extends that distinction through the concept of the hidden AMR gap: the uncertainty created when resistance risk and the capacity to observe it are systematically misaligned. [1,2]

Importantly, this gap can emerge across the surveillance pathway. Limited healthcare access and specimen collection restrict entry into surveillance; inadequate microbiological testing and AST constrain resistance characterization; and fragmented informatics can prevent generated laboratory evidence from becoming usable surveillance data. Surveillance strengthening must therefore extend beyond laboratory expansion to the entire pathway connecting case detection, microbiological characterization, data capture, interoperability, and reporting. [7,13,20]

The synthesis further reveals a surveillance paradox. Limited coverage may underestimate the geographic or population distribution of resistance, while selective sampling of hospitalized, previously treated, or otherwise higher-risk populations may simultaneously produce disproportionately high resistance estimates among those observed. The resulting challenge is therefore not simply insufficient data volume but biased observability—systematic differences in who, where, and what enters the surveillance denominator. [8]

These findings provide the rationale for shifting computational surveillance from resistance prediction alone toward surveillance-gap detection.

The proposed Surveillance Blind-Spot Score (SBSS) operationalizes this concept by considering expected AMR risk alongside surveillance deficit, uncertainty, and system capacity. A high SBSS would not constitute evidence that resistance is definitively high; rather, it would identify settings in which the mismatch between contextual risk and observational capacity warrants intensified surveillance. The framework should therefore be understood as an evidence-informed prioritization concept requiring empirical development and external validation before operational use.

The Surveillance Paradox: Low Resistance or Low Observability?

The distinction between low resistance and low observability has important implications for the interpretation of AMR surveillance. Conventional resistance estimates are conditional on infections passing through multiple observational filters, including healthcare access, specimen collection, microbiological testing, AST, data capture, and reporting. Surveillance intensity therefore influences not only how much resistance is detected but also the populations, pathogens, and settings represented in available datasets. [2,8,20]

This problem is particularly consequential where diagnostic and surveillance infrastructure is uneven. Evidence from Nigeria demonstrated how specimen under-sampling and variable laboratory capacity can alter the apparent distribution of *Salmonella*, while evidence from Southeast Asia showed substantial geographic and sectoral concentration of AMR data. Such patterns indicate that surveillance scarcity is structured rather than random and may systematically affect the epidemiological picture derived from available observations. [7]

Surveillance datasets should therefore not be assumed to provide a neutral representation of underlying AMR epidemiology. Data-rich settings may appear disproportionately prominent because resistance is more observable, whereas poorly monitored populations and ecological compartments may remain underrepresented. Conversely, selective sampling of higher-risk clinical populations can produce disproportionately high resistance estimates among those observed. Interpretation of geographic differences in AMR should therefore consider

surveillance intensity and representativeness alongside reported resistance prevalence. [5,8]

This reframes missingness from a statistical limitation into a potentially informative epidemiological signal. Where surveillance is sparse, why it is sparse, and whether that sparsity coincides with contextual indicators of elevated AMR risk become analytical questions in their own right. This provides the conceptual bridge from conventional resistance prediction toward computational identification of surveillance blind spots.

Limitations

This review has several limitations. The search was restricted to PubMed and Dimensions and did not include grey literature or additional bibliographic databases such as Scopus, Web of Science, or Embase. Although PubMed and Dimensions were selected to capture biomedical, multidisciplinary, and computational AMR surveillance literature, omission of other databases may have resulted in the exclusion of potentially relevant evidence, particularly from disciplines or sources not fully represented in these databases. No formal critical appraisal was undertaken, consistent with the review's primary aim of mapping the breadth and characteristics of the evidence rather than estimating intervention effects; consequently, the

methodological quality of individual studies was not used to weight the synthesis. The included evidence was also heterogeneous in design, geographic coverage, surveillance domain, and analytical approach, limiting direct comparison across studies.

The review protocol was not prospectively registered or published before initiation of the review. This represents a limitation in methodological transparency, as potential protocol modifications cannot be independently assessed. However, the review was guided by predefined eligibility criteria, a structured search strategy, systematic screening procedures, and standardized data-charting methods, and was conducted in accordance with JBI scoping review methodology and PRISMA-ScR reporting guidance. The applicability of the proposed AI framework would also depend on the availability, quality, representativeness, and interoperability of surveillance data across geographic, clinical, and One Health settings. Data limitations or systematic underrepresentation could affect model performance and the reliability of identified surveillance priorities.

Finally, the proposed Surveillance Blind-Spot Score is an evidence-informed conceptual construct and requires empirical calibration and external validation before operational application.

Conclusion

Global AMR surveillance is constrained not only by the distribution of resistance but also by where and how effectively resistance can be observed. This scoping review demonstrates that under-surveillance can arise across the surveillance pathway, including healthcare access, specimen collection, laboratory capacity, data integration, reporting, genomic representation, and One Health coordination. Consequently, low observed resistance cannot automatically be interpreted as low AMR burden where surveillance is limited or systematically unrepresentative. [1,2,20,22]

Addressing this hidden AMR gap requires moving beyond surveillance systems that primarily describe detected resistance toward approaches capable of identifying where observation itself is inadequate. The proposed AI-enabled framework provides a conceptual basis for this shift by evaluating discordance between expected AMR risk and observed surveillance

intensity. Rather than using AI to generate potentially misleading resistance estimates in data-poor settings, computational approaches could help characterize uncertainty and prioritize where additional sampling, laboratory strengthening, genomic surveillance, environmental monitoring, or integrated One Health surveillance is most needed.

Future research should progress from framework development to pilot testing of the proposed SBSS in selected surveillance settings, followed by empirical calibration of its indicators and weighting, external validation using independent representative and longitudinal datasets, and evaluation of its integration into existing national and One Health AMR surveillance systems. Such implementation should assess whether the framework improves identification and prioritization of surveillance blind spots without substituting modelled risk for microbiological evidence.

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