© DEC 2019 | IRE Journals | Volume 3 Issue 6 | ISSN: 2456-8880
DOI: https://doi.org/10.64388/IREV3I6-1723089

A Model for Improving Infection Detection Accuracy through Integrated Laboratory Information Systems

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Abstract- ***Infection detection depends on laboratory data that is usually scattered across analyser interfaces, standalone laboratory information systems, paper registers, medical records and notification channels that do not exchange information with one another. Detection is consequently slow, incomplete, and prone to both missed cases and false alarms. This paper develops a layered model, the Integrated Laboratory Information System for Infection Detection Accuracy (ILIS-IDA), which combines semantic standardisation of laboratory data, cross-source record linkage, and a hybrid analytic engine pairing deterministic case definitions with a supervised classifier whose disagreement with those definitions is treated as diagnostic information. Developed through design science research, the model spans six layers running from data acquisition through terminology binding, identity resolution, hybrid detection, alerting and governance, and is situated within work on diagnostic laboratory infrastructure, electronic laboratory reporting, automated surveillance of healthcare-associated infections, and health data protection. An accompanying evaluation framework measures diagnostic accuracy, timeliness, completeness and operational burden together, and is demonstrated on synthetic data. The central argument is that accuracy gains come less from any single algorithm than from the quality and integration of the pipeline that feeds it.***

Keywords: ***laboratory information system, infection detection, diagnostic accuracy, health information exchange, interoperability, electronic laboratory reporting, clinical decision support, disease surveillance.***

I. INTRODUCTION

Infectious disease continues to impose a heavy burden on health systems worldwide, and the speed with which an infection is detected largely determines how well it can be contained and treated. At the level of the individual patient, early and accurate identification of a pathogen shapes the choice of therapy, the timing of isolation, and the likelihood of survival. The evidence in sepsis is unusually direct: each additional hour to completion of the initial resuscitation bundle is associated with higher in-hospital mortality (Seymour et al., 2017), and the consensus redefinition of sepsis as life-threatening organ dysfunction due to dysregulated host response placed still greater weight on early recognition (Singer et al., 2016). At the population level, the same detection event is the trigger for outbreak investigation, contact tracing and public health response. Laboratory data is the evidentiary backbone of both processes, since culture results, molecular assays, serology, haematology profiles and biochemical markers are the signals from which clinicians and epidemiologists infer the presence of infection. (Aminu-Ibrahim, 2018; Ogbete, 2018; Peter, 2010; World Health Organization. (2019b). Molecular methods for antimicrobial resistance (AMR) diagnostics to enhance the Global Antimicrobial Resistance Surveillance System. WHO., 2019).

The capacity to generate those signals depends on physical and organisational infrastructure that is frequently overlooked in informatics research. Diagnostic laboratory infrastructure functions as a public health intervention in its own right, and the spatial planning, siting and lifecycle management of laboratories shape the accuracy, safety and throughput of the diagnostic process (Ogbete, Aminu-Ibrahim & Ambali, 2018). Regulatory-compliant design of molecular and pathology laboratories governs the

controlled environments on which assay validity depends (Ogbete, Aminu-Ibrahim & Ambali, 2019), and sustainable infrastructure models for emerging and resource-constrained health systems determine whether a laboratory can produce timely, reliable data at all (Aminu-Ibrahim, Ogbete & Ambali, 2018). Whether such facilities are delivered to specification and commissioned on time is in turn a question of capital project delivery in high-risk healthcare settings (Aminu-Ibrahim, Ogbete & Ambali, 2019). These infrastructural foundations matter because they determine the boundaries within which analytical quality can be defined and defended: consensus specifications for analytical performance presuppose an environment capable of sustaining them (Sandberg et al., 2015), guidance aimed at reducing interpretive diagnostic error in pathology and cytology presupposes a facility able to support the review processes it recommends (Nakhleh et al., 2016), and proposals to harness alternative data sources for antimicrobial resistance surveillance in low-resource settings are themselves a response to the infrastructural gaps described here (Ashley et al., 2019).

Laboratory information systems (LIS) were introduced to manage the data these facilities generate. In their earliest form they were essentially electronic ledgers, replacing paper day books with digital records of specimen receipt, test allocation and result entry. Over successive generations they acquired instrument interfacing, quality control modules, billing integration and reporting functions, and accounts of what an ideal system should do now span the full analytical workflow rather than the clerical fringe of it (Sepulveda & Young, 2013). What most systems did not acquire, particularly in low and middle income settings, was the ability to exchange data meaningfully with the systems around them. A single hospital may run an LIS in the laboratory, a separate electronic medical record on the wards, a pharmacy system, an infection prevention and control register maintained in spreadsheets, and a notification workflow that still depends on a paper form carried to the district health office. Each holds a fragment of the picture that would allow an infection to be recognised, and none holds the whole. This fragmentation is not merely technical. Regional roadmaps for AMR surveillance participation depend on laboratories first being able to assemble a coherent record from these fragments (Seale et al., 2017); national programmes to strengthen laboratory quality management toward accreditation confront the same fragmented reporting directly, since a quality system cannot be audited across data it cannot see as a whole (Sisay et al., 2015); the wider public-sector literature on budget compliance and statutory reporting in Sub-Saharan Africa documents an analogous pattern of gaps and reform pathways for fragmented reporting outside the clinical setting (Dogbatsey & Ebhojie, 2018); and the governance risks of holding fragments of the same patient's data across disconnected systems are best modelled explicitly rather than assumed away (Mbonu et al., 2018).

This fragmentation has measurable consequences. Automated transmission of laboratory findings identifies substantially more notifiable cases, and identifies them earlier, than spontaneous paper-based reporting. A statewide comparison of electronic notifiable disease reporting against conventional methods found automated reporting both faster and more complete (Effler et al., 1999), work in a large health information exchange found that automated electronic laboratory reporting identified several times as many cases as the paper process and identified them roughly a week sooner (Overhage, Grannis & McDonald, 2008), and an evaluation across eight hospitals reported that electronic reports arrived a median of four days ahead of conventional reports, with completeness limited chiefly by the use of free text rather than coded values (Panackal et al., 2002). That last finding sets up the argument developed here: the bottleneck was not the transmission channel but the structure of the data being transmitted. The same conclusion is reached from the health system side, where scientific innovation is observed to fail to improve patient outcomes in the absence of effective delivery infrastructure (Ilodigwe & Adesemoye, 2019b). (Inal, 2018; Mbonu, 2018; Rehm, 2013; Adeyelu, 2018).

Efforts to improve detection have tended to fall into two camps, and each is incomplete on its own. The first focuses on connectivity. Electronic laboratory reporting projects and health information exchanges concentrate on moving results out of the laboratory and into the hands of clinicians and public health

authorities more quickly. These initiatives improve timeliness, but they inherit whatever quality problems exist in the source data. If organism names are entered as free text, if specimen types are recorded inconsistently, if patient identifiers differ between the LIS and the medical record, then faster transmission simply delivers ambiguous data sooner. Reviews of deployed electronic laboratory systems have documented exactly these problems of sensitivity, specificity and user interpretation, and have concluded that validation, standards and the preservation of human judgement are necessary alongside automation (M'ikanatha, Southwell & Lautenbach, 2003). (Yao, 2014; Use of WHONET-SaTScan system for simulated real-time detection of antimicrobial resistance clusters in a hospital in Italy, 2012).

The second camp focuses on algorithms. Machine learning models for early detection of sepsis and other infections report strong discrimination in retrospective data. A targeted real-time early warning score identified septic shock a median of many hours before onset (Henry et al., 2015); models trained on minimal electronic record variables outperformed conventional scoring systems under the current sepsis definitions (Desautels et al., 2016); interpretable models built on high-resolution physiological data achieved useful discrimination four to twelve hours ahead of clinical recognition (Nemati et al., 2018); and triage-time triggers derived from free-text and structured emergency department data have shown comparable promise (Horng et al., 2017). Multicentre validation across emergency, ward and intensive care settings has followed (Mao et al., 2018), and at least one randomised evaluation, a modest single-centre trial, has reported reductions in length of stay and in-hospital mortality after deployment of such an algorithm (Shimabukuro et al., 2017). Yet translation into routine practice remains slow. The recurring obstacles are false positive alerts and the alarm fatigue they produce (Ancker et al., 2017), limited interpretability, and dependence on data elements that are not reliably available at the moment a decision must be made.

The space between these two camps is where this paper is situated. Detection accuracy is a property of the whole pipeline, not of the transmission layer alone or the analytic layer alone, and it is therefore treated here as an end-to-end design problem in which data acquisition, semantic standardisation, identity resolution, analysis and alerting are specified as a single system, with governance, security and workforce capability handled as design constraints rather than afterthoughts. The paper develops a layered model, the Integrated Laboratory Information System for Infection Detection Accuracy (ILIS-IDA), specified across six layers; it defines a hybrid detection engine in which deterministic case definitions and a probabilistic classifier are evaluated in parallel and their disagreement is treated as diagnostic information rather than as noise; and it proposes an evaluation framework that measures diagnostic accuracy, timeliness, completeness and operational burden together rather than reporting discrimination in isolation. In drawing together two literatures that have largely developed apart, health information exchange and computational clinical decision support, the account also incorporates work on diagnostic infrastructure, health system delivery and data protection governance that has rarely been brought to bear on detection accuracy.

Two boundaries should be stated at the outset. The model is specified at the architectural and algorithmic level rather than tied to a particular commercial LIS product, assuming only that laboratory results can be exported in some machine-readable form. And the evaluation reported in Sections 3.15-3.18 uses synthetic data generated for demonstration, so its figures illustrate the measurement approach rather than establishing clinical performance; prospective validation remains necessary. Procurement, licensing and financing questions lie outside the analysis, although the paper notes where they constrain design choices, drawing on work on health financing mechanisms in emerging markets where relevant (Ilodigwe & Adesemoye, 2019a).

The remainder of the paper is organised as follows. Section 2 reviews related work. Section 3 presents the model's development and evaluation: it sets out the methods, including requirements, data categories and evaluation measures (Sections 3.1-3.4), specifies the model layer by layer (Sections 3.5-3.11), discusses implementation under resource constraints (Sections 3.12-3.14), and presents the illustrative evaluation

(Sections 3.15-3.18). Section 4 discusses the findings and their limitations, and concludes.

II. RELATED WORK

2.1. Laboratory Information Systems and the Pre-analytical Phase

The laboratory information system emerged in the 1970s as a specialised transaction processing application with narrow functions: register a specimen, assign an accession number, record a result, print a report. Successive generations added bidirectional instrument interfacing, which removed manual transcription from the analyser to the record and eliminated a significant source of error, followed by quality control, turnaround time monitoring, and reagent management. Comprehensive accounts of what a modern system should provide extend well beyond these clerical functions to encompass rules-based result handling, decision support and integration with the wider record (Sepulveda & Young, 2013).

The functional maturity of the LIS was not, however, matched by architectural openness. Many systems store results in proprietary schemas with limited export capability, and where export exists it often takes the form of a flat file or a printed report rather than a structured, coded message. This design was rational when the laboratory was conceived as a service producing documents for human readers. It becomes an obstacle once laboratory data is expected to feed automated detection or algorithmic screening of the kind demonstrated in computational diagnostic work on medical images (Ejofodomi et al., 2014).

A parallel literature locates a large share of diagnostic error outside the analytical phase entirely. Systematic examination of errors in a stat laboratory found that the majority arose in the pre-analytical and post-analytical phases rather than during analysis (Plebani & Carraro, 1997), a finding subsequently generalised in arguing that the relevant unit of concern is error in laboratory medicine rather than error in the laboratory (Plebani, 2006). Specimen collection, labelling, transport interval and receipt therefore fall within the scope of any system intended to improve detection accuracy, and are treated in Section 3.6 as first-class data rather than as background conditions.

2.2. Electronic Laboratory Reporting and Its Limits

Electronic laboratory reporting (ELR) is the automated transmission of reportable laboratory findings from clinical laboratory systems to public health authorities. Its rationale was articulated clearly at the outset: conventional reporting relying on paper delivered by mail is slow and incomplete, and electronic reporting should be more timely and more complete (Jernigan, 2001). Evaluations have largely confirmed this. Statewide electronic reporting from clinical laboratories proved both more rapid and more complete than conventional notification (Effler et al., 1999), automated reporting was at least as complete as conventional reporting in multi-hospital studies (Panackal et al., 2002), and comparisons within health information exchanges found large gains in case ascertainment and lead time (Overhage, Grannis & McDonald, 2008).

The literature is equally clear about the limits. Panackal and colleagues attributed the great majority of cases missed by electronic reporting to the use of free text in the source system, which locates the problem in data representation rather than transmission. M'ikanatha and colleagues, reviewing five implementations, identified problems with transmission reliability, sensitivity, specificity and user interpretation, and argued for backup transmission methods, systematic validation, adherence to standards, and retention of human judgement in the loop. Wurtz and Cameron (2005) set out what an effective ELR pipeline requires: extraction logic capable of recognising reportable results within the laboratory system, controlled vocabularies such as LOINC for observations and SNOMED for organisms and findings, and a messaging syntax such as HL7 to carry the content.

Taken together, this work supports a specific conclusion. Connectivity without semantics yields fast but ambiguous data. The controlled vocabulary layer is not an optional refinement; it is the precondition for automated detection to work at all.

2.3. Interoperability Standards and Controlled Vocabularies

Three standards families are directly relevant to the model proposed here.

HL7 v2 and HL7 FHIR. HL7 version 2 messaging remains the workhorse of laboratory result transmission in most hospital environments, with the ORU^R01 message type carrying observation results. Its flexibility is also its weakness, since optional fields and local extensions produce implementations that are nominally conformant but practically incompatible. HL7 FHIR, built on resource-oriented principles and web APIs, addresses this with tighter resource definitions and explicit profiling (Bender & Sartipi, 2013), and its Observation, DiagnosticReport, Specimen and Patient resources map naturally onto laboratory workflow. Application platforms layered over these resources demonstrate that substitutable clinical software can be built against a standard interface rather than against a particular vendor's schema (Mandel et al., 2016).

LOINC. Logical Observation Identifiers Names and Codes provides universal identifiers for laboratory observations, distinguishing what was measured, on what specimen, by what method, and in what units (McDonald et al., 2003). Binding local test codes to LOINC is what allows a blood culture result from one laboratory to be recognised as the same kind of observation as a blood culture result from another.

SNOMED CT. SNOMED Clinical Terms supplies coded concepts for organisms, clinical findings, specimen types and procedures. Its hierarchical structure is particularly valuable for detection logic, because a rule written against a parent concept such as Enterobacteriaceae will automatically capture subsumed organisms without needing enumeration. The general requirements such a vocabulary must satisfy, including formal definitions, explicit hierarchies, non-redundancy and controlled evolution over time, were set out well before their adoption in laboratory settings became widespread (Cimino, 1998).

A fourth standard set concerns antimicrobial susceptibility. Interpretive criteria published by CLSI and EUCAST determine whether a minimum inhibitory concentration is reported as susceptible, intermediate or resistant, and inconsistency in applying these criteria across laboratories undermines any attempt to detect resistance patterns computationally.

2.4. Diagnostic Infrastructure as a Precondition for Detection Accuracy

An informatics model that ignores the physical and organisational substrate of the laboratory will overstate what software can deliver. Spatial planning strategies have been linked directly to diagnostic accuracy, safety and clinical throughput, on the argument that layout determines specimen handling paths, cross-contamination risk and the queueing behaviour of the bench (Ogbete, Aminu-Ibrahim & Ambali, 2018). Regulatory-compliant design systems for molecular and pathology laboratories address the controlled environments on which molecular assay validity depends, including containment, airflow and separation of pre-amplification and post-amplification work (Ogbete, Aminu-Ibrahim & Ambali, 2019). Sustainable infrastructure models developed for emerging and resource-constrained health systems address the prior question of whether such facilities can be built and operated at all under the relevant financial and utility constraints (Aminu-Ibrahim, Ogbete & Ambali, 2018), and capital project delivery models for high-risk healthcare infrastructure address whether they are completed to specification and commissioned on schedule (Aminu-Ibrahim, Ogbete & Ambali, 2019).

This facility-level literature sits within a longer continental effort to strengthen laboratory systems as such, and the illustrative gains reported in Table 4 depend on that broader effort as much as on any single facility. National strategic planning has been identified as a precondition for laboratory system strengthening in resource-poor settings generally, not only within individual facilities (Nkengasong et al., 2009), and the case that laboratory systems and services have been chronically neglected relative to their contribution to health outcomes has been made explicitly at the level of global health policy (Nkengasong et al., 2010). The regional accreditation process subsequently developed for the WHO African region operationalised this argument, giving laboratories a stepwise route to demonstrable quality improvement rather than treating infrastructure investment and quality management as separate problems (Gershy-Damet et al., 2010). The present model's dependence on adequate infrastructure, discussed further in Section 3.13, should be read against this history: it is a further

response to a gap that strategic planning, policy attention and accreditation have each addressed only partially.

Two further strands of the built environment literature bear on the same question. Environmental control is not incidental to assay validity, and analysis of how climatic variables constrain building envelope design in humid regions describes the physical problem that laboratory air handling has to solve (Nwafor, Uduokhai, Ifechukwu, Stephen & Aransi, 2018), while work on thermodynamic efficiency and control strategies in air conditioning addresses how stable internal conditions are maintained at acceptable running cost (Sunday, Omoegun, Essien & Oluokun, 2019). Material selection determines whether that envelope can be built and maintained locally, and quantitative evaluation of locally sourced building materials speaks directly to the affordability of laboratory construction outside major centres (Nwafor, Uduokhai, Ifechukwu, Stephen & Aransi, 2019c). Delivery efficiency in public infrastructure programmes governs whether the resulting facilities appear at all (Nwafor, Uduokhai, Ifechukwu, Stephen & Aransi, 2019b), and procurement practice determines what they cost and how reliably they are equipped (Okonkwo, Ogunwole & Okeke, 2018a). Reagent and consumable availability is the operational counterpart, since a laboratory that cannot run a test produces no data at all, and models linking inventory availability to plant uptime formalise that dependency in an adjacent industrial setting (Okonkwo, Ogunwole & Okeke, 2018b).

The relevance to the present model is direct. Terminology binding, identity resolution and analytic detection all presuppose that specimens are collected correctly, transported within acceptable intervals, and analysed in an environment that does not itself introduce error. Where infrastructure is deficient, the data quality flags described in Section 3.7 will fire frequently, and the appropriate response is capital and process investment rather than algorithmic adjustment.

2.5. Automated Surveillance and Computational Detection

Approaches to detecting infection from routine data fall into three families.

Rule-based case definitions. These encode published surveillance definitions directly, for instance the criteria for a laboratory-confirmed bloodstream infection or the SIRS criteria historically used for sepsis screening. Their strengths are transparency, auditability and alignment with reporting requirements. Their weakness is rigidity: they perform poorly where data is missing, and they cannot weight evidence, so a patient meeting three criteria weakly is treated identically to one meeting three criteria strongly. Automated surveillance of healthcare-associated infections built on such definitions has nonetheless been shown to reduce the labour of manual chart review substantially while improving reproducibility, since the algorithm applies the same criteria to every record (Klompas & Yokoe, 2009). Reviews of the state of the art report that most operational systems are semi-automated, using algorithms to exclude the clear negatives and referring a reduced set for manual confirmation (Sips, Bonten & van Mourik, 2017), and that surveillance design must be reconsidered rather than merely digitised once automation and reporting mandates are both in play (van Mourik et al., 2018). External validation of one such model for drain-related meningitis demonstrated both the feasibility of transfer between institutions and the need for local updating before use (van Mourik et al., 2012).

Statistical aberration detection. Methods such as cumulative sum control charts, exponentially weighted moving averages and space-time scan statistics detect departures from expected counts. These are well suited to outbreak detection at the aggregate level but say nothing about whether a given individual is infected.

Supervised machine learning. Models trained on routinely collected clinical and laboratory data have been applied extensively to sepsis and infection prediction, and the six studies introduced in Section 1 repay closer examination for how they were validated rather than only for what they found. Henry et al. (2015) and Desautels et al. (2016) each report discrimination on data held out from the same retrospective cohort used for development, so temporal generalisation is assumed rather than demonstrated. Nemati et al. (2018) is more explicit about this limitation, and its four-to-twelve-hour lead

time is reported against a held-out later period rather than a held-out sample, which is a stronger but still retrospective design. Horng et al. (2017) evaluates in a separate emergency department triage setting, which addresses transportability across sites but not prospective deployment, and Mao et al. (2018) extends multicentre validation across emergency, ward and intensive care settings on the same retrospective basis. Only Shimabukuro et al. (2017), in a modest single-centre randomised trial, reports outcomes from an algorithm actually running prospectively in care, associating deployment with reductions in length of stay and in-hospital mortality. The distance between the first five studies' retrospective discrimination and the last study's prospective, single-site outcome evidence is the gap the evaluation in Sections 3.15-3.18 is designed to acknowledge rather than close: the illustrative results in Table 4 report structural gains under synthetic conditions, and prospective validation of the kind only Shimabukuro et al. (2017) among these six studies attempted remains the necessary next step. The availability of large de-identified critical care datasets has been an important enabler of the retrospective work in particular (Johnson et al., 2016). Detection from routinely collected operational data is not unique to clinical medicine, and the same structural problems appear wherever a signal must be extracted from records generated for another purpose. Predictive compliance monitoring applied to aviation consumer complaint data illustrates the detection of systemic risk from an incidental data stream (Adeyelu, 2018), while predictive maintenance and condition monitoring in critical power infrastructure demonstrate continuous inference from sensor histories under the same constraints of noise and missingness that clinical time series present (Adaramola, Fadero & Gideon, 2018). Reliability engineering and failure analysis supply the vocabulary in which such systems are assessed, including the distinction between a fault, its manifestation and its detection (Gideon, Adaramola & Fadero, 2019). The industrial safety literature offers a closer analogy still: near-miss and hazard observation data are the operational equivalent of a rule-negative but suspicious case, and their systematic utilisation depends on whether the reporting pathway is trusted and low-friction (Arumosoye & Obriki, 2019; Obriki & Arumosoye, 2018). Spatial and temporal clustering methods developed for contaminant migration in data-limited settings address the same aggregate detection problem as outbreak surveillance, with comparable constraints on data density (Azeez & Badmus, 2018; Lamidi & Olamide, 2018). Work on data-driven executive decision systems addresses the presentation layer on which all of these depend, since an inference that is not delivered in a form matched to the decision is not acted upon (Lawal & Oduleye, 2019b).

Against this, deployment experience is mixed, and the gap between retrospective discrimination and operational usefulness is attributed largely to alert burden, interpretability and data availability rather than to modelling technique. Alert fatigue is empirically well documented: the probability that a clinician accepts a given alert declines with workload, with case complexity, and with the number of times the same alert has been seen before (Ancker et al., 2017). A detection system that improves sensitivity while degrading the precision of its alerts may therefore reduce, rather than increase, the number of infections acted upon in time.

2.6. Data Protection, Security and Governance

Integration multiplies the value of health data and simultaneously multiplies its exposure. Conceptual work on legal and ethical risk modelling in enterprise data protection governance sets out how obligations arising from statute, professional duty and contract can be represented as modelled risks rather than as a compliance checklist appended after the system is designed (Mbonu et al., 2018). Comparative analysis of data protection regulation across jurisdictions, together with secure implementation strategies for cloud-hosted systems, is directly relevant where a clinical integration platform spans sites, vendors or national borders (Mbonu et al., 2019a). Operationally, enterprise log analytics and automated incident response architectures describe the monitoring substrate on which auditability depends, since a system that cannot reconstruct who accessed what, and when, cannot support either clinical accountability or breach investigation (Mbonu et al., 2019b).

Integration also has a platform dimension. Scalable and secure cloud architectures for enterprise messaging describe the transport substrate over which laboratory results move between systems (Ahmed & Odejobi, 2018a), and extract, transform and load

design patterns describe how heterogeneous source records are reconciled into a common representation, which is the engineering problem Layer 2 of the proposed model solves in a clinical vocabulary (Badmus, Dosunmu & Ozowara, 2019a). Governance frameworks for platform management in regulated healthcare environments address the configuration control and change management that a clinical integration platform requires once it is live (Badmus, Dosunmu & Ozowara, 2019b), and continuous integration and deployment practice supplies the release discipline by which changes reach production without unreviewed drift (Badmus, Dosunmu & Ozowara, 2018).

Access control is the other half of the problem. Secure identity and access management for distributed and federated systems addresses the case where several institutions share an analytic platform without merging their administrative domains (Oshoba, Hammed & Odejobi, 2019), and directory service design and assessment describe how those controls are implemented and audited in practice (Ladapo, Jooda, Dosunmu & Abolaji, 2019; Ladapo, Dosunmu, Jooda & Abolaji, 2018). Insider threat modelling is directly pertinent to clinical records, where the greatest exposure is often authorised access misused rather than perimeter compromise (Akeju et al., 2018). Security audit and enterprise risk assessment frameworks provide the periodic assurance function (Dosunmu & Ogundele, 2019), risk-based cybersecurity assurance connects that assurance to availability rather than confidentiality alone, which matters for a system that must keep detecting during disruption (Fadayomi et al., 2019), and technology-enabled internal audit models describe how such checks are made routine rather than occasional (Akomolafe & Agu, 2018).

These concerns are not peripheral to detection accuracy. An audit trail is what makes a historical detection reproducible, and reproducibility is what allows a disputed alert to be examined rather than argued about. Access control determines whether the identity resolution described in Section 3.8 can be performed and reviewed safely. And the lawful basis for processing determines whether the training data required by Section 3.9 can be assembled at all.

2.7. Issues Left Unresolved

Five issues recur across the work reviewed above and shape the model described in Section 3 (Sections 3.4-3.11); Issue Four in particular maps to the evaluation framework in Section 3.4 rather than to the layer specification in Sections 3.5-3.11.

First, semantic fragmentation. Free text and local codes defeat automated detection, yet terminology binding is treated in most implementations as a downstream mapping exercise rather than as a designed layer with its own quality measures (Panackal et al., 2002; McDonald et al., 2003).

Second, identity fragmentation. A patient's laboratory record, clinical record and prior results are frequently not linkable, so the analytic engine sees isolated results rather than trajectories, and the temporal features that carry most of the predictive signal in sepsis models cannot be constructed (Nemati et al., 2018).

Third, reliance on a single detection method. Systems adopt either rules or learned models. Rules are auditable but insensitive; learned models are sensitive but opaque and prone to false alarms. Semi-automated surveillance combines them only in the weak sense of triage, using the algorithm to reduce manual workload rather than treating disagreement between methods as informative (Sips, Bonten & van Mourik, 2017).

Fourth, narrow measurement. Evaluation typically reports sensitivity, specificity and area under the receiver operating characteristic curve on retrospective data, without accounting for timeliness, completeness of capture, or the operational cost of false positives, despite evidence that alert acceptance falls sharply as alert volume rises (Ancker et al., 2017). Fifth, governance treated as an afterthought. Security, privacy, auditability and validation are typically retrofitted, despite the argument that they are better represented as modelled design constraints from the outset (Mbonu et al., 2018).

III. MODEL DEVELOPMENT AND EVALUATION

3.1. Approach

The study adopts a design science research approach, appropriate where the intended contribution is an

© DEC 2019 | IRE Journals | Volume 3 Issue 6 | ISSN: 2456-8880
DOI: https://doi.org/10.64388/IREV3I6-1723089

artefact rather than an explanation of an existing phenomenon, and where the artefact is evaluated against the requirements of the problem environment as well as against the existing knowledge base (Hevner et al., 2004). The process followed comprises six activities: problem identification, definition of objectives for a solution, design and development, demonstration, evaluation and communication (Peffers et al., 2007). Sections 1 and 2 discharge the first two activities, Sections 3.5-3.14 present the design and development, and Sections 3.15-3.18 provide demonstration and evaluation.

3.2. Design Requirements

Requirements were derived from three sources: the deficiencies documented in Section 2, the constraints of standards conformance, and the operational realities of laboratory practice in resource-limited settings, including intermittent power and connectivity, mixed digital and paper workflows, and limited specialist informatics staffing (Aminu-Ibrahim, Ogbete & Ambali, 2018).

The resulting functional and non-functional requirements are summarised in Table 1.

Table 1. Design requirements for the proposed model

ID	Requirement	Type	Rationale
R1	Ingest results from analysers, LIS databases and manual entry without requiring replacement of existing systems	Functional	Incremental adoption
R2	Bind every incoming observation to LOINC and every organism and finding to SNOMED CT	Functional	Automated detection requires coded semantics
R3	Resolve patient identity across LIS, EMR and register sources	Functional	Enables trajectory-based detection
R4	Apply both deterministic case definitions and a probabilistic classifier to each candidate episode	Functional	Combines auditability with sensitivity
R5	Provide an explanation for every alert raised	Functional	Clinician trust and adoption
R6	Suppress duplicate and low-value alerts	Functional	Mitigates alarm fatigue
R7	Operate in degraded mode when connectivity is lost, with store-and-forward reconciliation	Non-functional	Infrastructure reality
R8	Maintain an immutable audit trail of all detections and overrides	Non-functional	Governance and validation
R9	Enforce role-based access and de-identification for secondary use	Non-functional	Privacy and legal compliance
R10	Complete detection and alerting within a defined latency budget from result verification	Non-functional	Timeliness is a component of accuracy

3.3. Data Sources and Variables

The model consumes five categories of input, set out in Table 2.

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DOI: https://doi.org/10.64388/IREV3I6-1723089

Table 2. Input data categories

Category	Representative elements	Typical source	Standard binding
Microbiology	Culture growth, organism identification, susceptibility, Gram stain	LIS microbiology module	SNOMED CT, LOINC
Molecular and serology	PCR target and cycle threshold, antigen and antibody results	LIS, analyser interface	LOINC
Haematology and chemistry	White cell count, differential, C-reactive protein, procalcitonin, lactate, creatinine, bilirubin	Analyser interface	LOINC, UCUM units
Clinical context	Vital signs, admission and discharge, ward, device presence, antimicrobial orders	EMR, nursing records	SNOMED CT, ATC for drugs
Demographic and administrative	Identifiers, age, sex, residence, facility	Registration system	Local plus national identifier

3.4. Evaluation Measures

Detection accuracy is operationalised across four dimensions.

Diagnostic accuracy. Sensitivity, specificity, positive predictive value, negative predictive value, F1 score and area under the receiver operating characteristic curve, computed against a reference standard established by expert adjudication of the full clinical record, following the reporting principles set out for diagnostic accuracy studies more generally (Bossuyt et al., 2015).

Timeliness. Detection latency, defined as the interval from the earliest time at which sufficient evidence existed in the data to the time the alert was raised, and lead time relative to the clinician's independent recognition of the infection. Lead time is the measure by which early warning models are conventionally judged (Henry et al., 2015; Nemati et al., 2018), and in sepsis it has a direct mortality interpretation (Seymour et al., 2017).

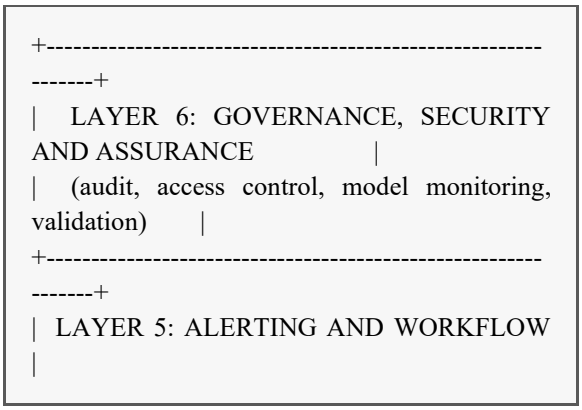
Completeness. The proportion of adjudicated true cases captured by the system, and the proportion of required data elements populated in each captured record. Completeness was the dimension on which early electronic reporting evaluations turned (Panackal et al., 2002).

Operational burden. Alerts per hundred patient days, the false alert ratio, and the override rate, which is the proportion of alerts dismissed by clinicians without action. Burden is included as a primary measure rather than a footnote because alert acceptance declines measurably with alert volume and clinician workload (Ancker et al., 2017).

These dimensions trade against one another. Lowering the alert threshold raises sensitivity and lowers latency while raising alert burden, and a model evaluated on sensitivity alone will always appear to improve as it becomes less usable.

3.5. Overview

The proposed model, the Integrated Laboratory Information System for Infection Detection Accuracy (ILIS-IDA), is organised into six layers. Each layer has a defined responsibility and a defined interface to its neighbours, so that layers can be implemented and validated independently.



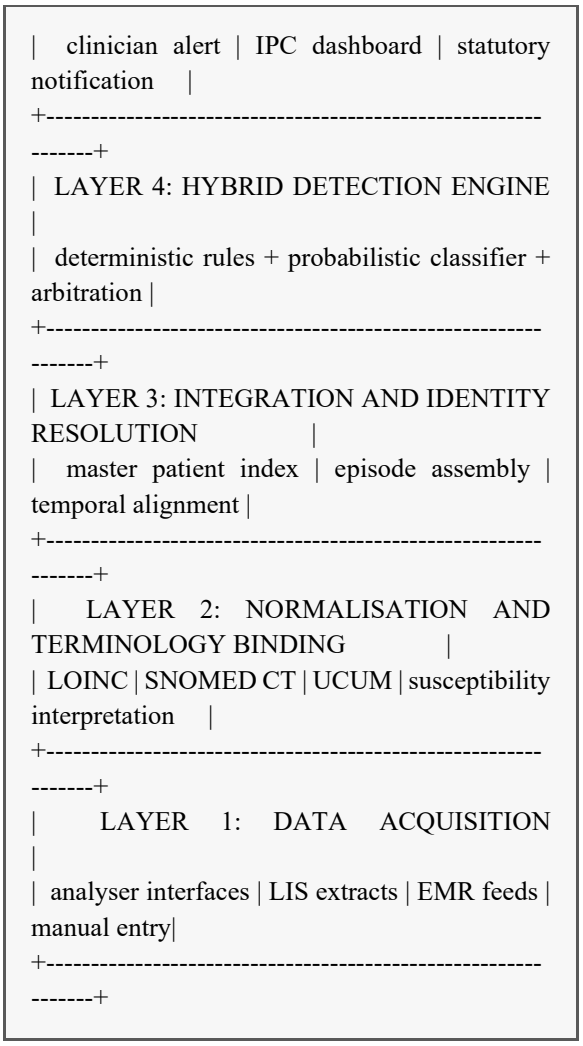


Figure 1. Layered architecture of the ILIS-IDA model

3.6. Layer 1: Data Acquisition

The acquisition layer is deliberately permissive, because the model is intended to be adopted without replacing incumbent systems. It supports four ingestion modes.

Analyser interfaces capture results directly from instruments using ASTM or HL7 v2 protocols, which removes transcription error at the earliest possible point. LIS extracts pull from the existing laboratory database, either through a vendor interface, an HL7 v2 outbound feed, or scheduled extraction from the underlying tables where no interface exists. EMR feeds supply clinical context variables, ideally through FHIR resources exposed by the record system (Bender & Sartipi, 2013; Mandel et al., 2016). Manual entry handles results produced outside any digital system, such as bench work recorded on worksheets, and is structured as a constrained form rather than a free text field, so that data enters the pipeline already partially coded.

Transport between components follows established messaging architecture practice rather than point-to-point coupling, so that adding a source does not require modifying the consumers (Ahmed & Odejobi, 2018a), and the extraction and transformation logic is specified declaratively in the manner of conventional integration pipelines (Badmus, Dosunmu & Ozowara, 2019a).

Every ingested item is written to an immutable staging store before any transformation, which preserves the original as received and makes all downstream processing reproducible and auditable. A store-and-forward queue satisfies requirement R7 by buffering locally when the network is unavailable and reconciling on restoration. Reconciliation on restoration is a control problem in its own right, since duplicate and out-of-order arrivals must be resolved deterministically rather than by arrival time (Dogbatsey, Ebhojie & Oyeleye, 2019).

Pre-analytical quality is captured at this layer rather than inferred later. Collection time, transport interval, container type and specimen adequacy are recorded as first-class fields, reflecting evidence that a disproportionate share of diagnostic error originates before analysis begins (Plebani & Carraro, 1997; Plebani, 2006).

3.7. Layer 2: Normalisation and Terminology Binding

This layer converts heterogeneous input into a single semantic representation, and it is the layer that most directly addresses the free text problem identified in Section 2.2.

Test code binding. Each local test code is mapped to a LOINC code through a maintained mapping table (McDonald et al., 2003). Mapping is a curated activity performed once per test per laboratory and reviewed when the test menu changes. Unmapped codes are routed to a review queue rather than silently discarded, and the size of that queue is itself a monitored quality indicator.

Unit harmonisation. Numeric results are converted to UCUM-conformant units with explicit conversion factors. Where a laboratory reports in units that cannot be converted without assumption, the result is flagged rather than coerced.

Organism and finding coding. Organism identifications are bound to SNOMED CT concepts. Where microbiology results arrive as free text, a two-stage process applies: a dictionary and fuzzy-matching pass resolves the common cases, including standard abbreviations and known misspellings, and residual text is queued for human coding. The hierarchical structure of the terminology is retained so that detection rules can be written at whatever level of generality is appropriate, which is one of the properties a controlled vocabulary is expected to supply (Cimino, 1998).

Susceptibility interpretation. Raw minimum inhibitory concentrations and zone diameters are stored alongside the interpretive category, with the interpretive standard and version recorded explicitly. This makes it possible to re-interpret historical data when breakpoints change, which is essential for any longitudinal analysis of resistance and for linking detection output to stewardship programmes.

Quality flagging. Each normalised record carries a data quality vector recording completeness, whether values fall within plausible physiological range, whether the collection to receipt interval was acceptable, and whether contamination indicators are present, for instance a single positive blood culture bottle growing a common skin commensal. These flags are consumed downstream by the detection engine as features, so that data quality informs the confidence of the detection rather than being assessed separately.

3.8. Layer 3: Integration and Identity Resolution

Detection accuracy depends on seeing a patient's results as a connected trajectory rather than as isolated events. This layer performs three functions.

Master patient index. Records from different sources are linked using probabilistic record linkage over name, date of birth, sex, national or hospital identifier and contact details, with the classical theory of record linkage supplying the weighting scheme and the decision rule (Fellegi & Sunter, 1969). Match, possible match and non-match thresholds are set so that possible matches are routed for clerical review. Under-linkage fragments a patient's history and depresses sensitivity, while over-linkage merges distinct patients and creates spurious findings, so the thresholds are treated as tuned parameters subject to periodic audit. Access control over who may perform and review merges is governed at Layer 6, and where several institutions share an index the federated identity case applies rather than the single-domain one (Oshoba, Hammed & Odejobi, 2019; Mbonu et al., 2019a).

Episode assembly. Linked records are grouped into care episodes bounded by admission and discharge, or by a defined window for outpatient encounters. Each episode carries the full sequence of laboratory results, clinical observations, device exposures and antimicrobial administrations, time-ordered. Episode boundaries drawn on administrative transfers frequently fragment what is clinically a single episode, and the model therefore permits configurable merging across transfers within a facility.

Temporal alignment. Laboratory results carry several timestamps: collection, receipt, analysis and verification. The model uses collection time as the physiological anchor for feature construction and verification time as the operational anchor for latency measurement. Confusing the two is a common source of optimistic bias in retrospective evaluation, because features appear in the analysis dataset earlier than they would have been available in practice.

3.9. Layer 4: The Hybrid Detection Engine

This is the analytic core of the model, and its central design decision is that no single method is trusted alone.

3.9.1. Deterministic component

A rule engine evaluates each episode against codified case definitions. Rules are expressed declaratively against the normalised, coded representation, which allows them to be written and maintained by clinical microbiologists and infection control practitioners rather than programmers. A rule for laboratory-confirmed bloodstream infection, for example, tests for a recognised pathogen isolated from one or more blood cultures, or a common commensal isolated from

two or more separately drawn cultures accompanied by supporting clinical signs. This is the established basis of automated healthcare-associated infection surveillance (Klompas & Yokoe, 2009; van Mourik et al., 2012).

The deterministic component produces a binary determination together with the specific criteria satisfied. Its outputs are used directly for statutory notification, where the legal requirement is conformance to a published definition rather than probabilistic likelihood.

3.9.2. Probabilistic component

A supervised classifier estimates the probability that the episode represents a true infection of a given class. Gradient boosted decision trees are the recommended default (Chen & Guestrin, 2016). The justification is practical rather than theoretical: they handle heterogeneous tabular features and missing values natively, they train on the modest dataset sizes typical of a single institution, and they support per-prediction attribution through additive feature attribution methods, which satisfies the explanation requirement R5 (Lundberg & Lee, 2017). Interpretability is not a presentational nicety here, since deployed sepsis models have found attribution necessary for clinician acceptance (Nemati et al., 2018).

Feature construction draws on five groups:

- *Static features:* age, sex, admission type, comorbidity indicators.
- *Laboratory features:* most recent value, direction and rate of change, and time since last measurement for each key analyte. Explicit missingness indicators are included rather than imputed away, because the fact that a test was not ordered is itself informative.
- *Microbiological features:* organism concept and its terminological ancestors, specimen type, time to positivity, contamination flags.
- *Contextual features:* device presence and duration, ward-level recent incidence of the organism, prior colonisation history.
- *Data quality features:* the quality vector from Layer 2.

Training uses a reference standard produced by expert adjudication of full records. Class imbalance is addressed through class weighting rather than synthetic oversampling, since synthetic minority samples in clinical data frequently generate physiologically implausible combinations. Validation is performed with temporal splitting, training on earlier periods and testing on later ones, because random splitting leaks information across time and inflates apparent performance. Where an institution lacks sufficient local data, external validation experience suggests that a model transferred from elsewhere requires local updating rather than direct application (van Mourik et al., 2012).

3.9.3. Arbitration

The arbitration function combines the two components. Four states are possible, and each is handled differently, as shown in Table 3.

Table 3. Arbitration logic

Rule outcome	Classifier probability	Action	Rationale
Positive	High	Confirmed detection; alert and notify	Concordant evidence
Positive	Low	Alert with discordance flag; queue for review	Possible contamination or data error
Negative	High	Advisory alert; queue for review	Possible emerging case not yet meeting definition
Negative	Low	No alert; retained for surveillance aggregation	Concordant absence

The two discordant states are where the model earns its value. A rule-positive, probability-low result frequently indicates contamination or a data quality problem, and routing it to review prevents an unnecessary treatment cascade. A rule-negative, probability-high result is the early warning case, where evidence is accumulating but has not yet crossed a categorical threshold, and this is precisely where lead time is gained. This state typically arises when the trend and rate-of-change features and the time-since-last-measurement features constructed in Section 3.9.2 cross a learned risk pattern before the discrete count or threshold criteria in the rule definition are met, since the classifier has access to trajectory information the rule engine does not use. This differs from the triage arrangement in semi-automated surveillance, where the algorithm only ever narrows the set of records a human must read (Sips, Bonten & van Mourik, 2017).

3.9.4. Alert burden control

Three mechanisms address requirement R6. Deduplication suppresses repeat alerts for the same episode and organism within a configurable window unless the probability increases by a material margin, addressing the repetition effect that drives alert dismissal (Ancker et al., 2017). Threshold calibration sets the operating point using the precision-recall curve rather than the ROC curve, because at the low prevalence typical of specific infections the ROC curve substantially overstates usable performance (Saito & Rehmsmeier, 2015). Feedback capture records every clinician override with a structured reason, and these overrides become labelled data for periodic retraining, so that precision improves through use. Retrained models reach production through a controlled release path rather than in-place substitution, so that the active version is always identifiable and reversible (Badmus, Dosunmu & Ozowara, 2018).

3.10. Layer 5: Alerting and Workflow

Detection has no value unless it reaches a person who can act, in a form that supports action. The layer routes output along three channels.

The clinical channel delivers the alert to the treating team, showing the probability, the contributing evidence ranked by attribution, the relevant results with their timestamps, and, where susceptibility data exists, the implied therapeutic options.

The infection prevention and control channel aggregates detections by ward, organism and device, and applies aberration detection across time and space to surface clusters. This is the output that automated surveillance programmes consume, and presenting it at the level of the unit rather than the individual patient is what allows it to drive prevention rather than only treatment (Klompas & Yokoe, 2009; van Mourik et al., 2018).

The public health channel generates statutory notifications from the deterministic component, formatted according to the receiving authority's specification, with a queue and retry mechanism and a paper fallback consistent with the recommendation that electronic systems retain backup transmission methods (M'ikanatha, Southwell & Lautenbach, 2003).

3.11. Layer 6: Governance, Security and Assurance

The governance layer spans the others. It enforces role-based access control and audit logging of every access and every override, drawing on log analytics and incident response practice from enterprise environments (Mbonu et al., 2019b). It manages consent and de-identification for secondary use of data within the compliance framework applicable to the jurisdiction, which for a system operating across sites or borders may involve reconciling several regimes at once (Mbonu et al., 2019a). Access rights are administered through the directory infrastructure the institution already operates, with periodic offline assessment of that infrastructure rather than reliance on its default configuration (Ladapo, Jooda, Dosunmu & Abolaji, 2019; Ladapo, Dosunmu, Jooda & Abolaji, 2018), and the threat model gives explicit weight to authorised users acting outside their remit, which is the dominant exposure for clinical records (Akeju et al., 2018).

Assurance is scheduled rather than incidental. Security audit and enterprise risk assessment provide the periodic external check (Dosunmu & Ogundele, 2019), technology-enabled internal audit makes the routine checks continuous rather than annual (Akomolafe & Agu, 2018), and availability is treated

as a first-class security property alongside confidentiality and integrity, since a detection system that is offline is not merely inconvenient but silently insensitive (Fadayomi et al., 2019). Platform change control follows the governance practice established for regulated healthcare deployments (Badmus, Dosunmu & Ozowara, 2019b). Legal and ethical obligations are represented as modelled design constraints rather than as a checklist applied after the fact (Mbonu et al., 2018).

The layer maintains version control over rules, terminology mappings and trained models, so that any historical detection can be reproduced with the exact logic that produced it. It monitors the deployed classifier for drift, comparing the distribution of incoming features and output probabilities against the training distribution, and triggering review when divergence exceeds a threshold. And it schedules periodic revalidation against freshly adjudicated samples, since a model validated once and never revisited is a liability rather than an asset, a point reinforced by external validation studies in which transferred models required updating before they performed acceptably (van Mourik et al., 2012).

3.12. Phased Deployment

The layered structure permits incremental implementation, which matters because most facilities cannot suspend operations for a system transition, and because technical capability delivered ahead of organisational capability tends not to change outcomes (Ilodigwe & Adesemoye, 2019b). A four-phase sequence is proposed.

Phase one implements Layers 1 and 2 only, achieving structured, coded capture of laboratory data with quality flagging. This phase delivers value independently through improved reporting and reduced transcription error, and it establishes the data foundation without which later phases cannot function.

Phase two adds Layer 3 and the deterministic component of Layer 4, together with the notification channel of Layer 5. At this point the facility has automated, standards-conformant electronic laboratory reporting with linked patient records.

Phase three introduces the probabilistic component. This requires a labelled dataset, which the preceding phases will have been accumulating, and it should run in shadow mode, generating predictions that are logged but not surfaced, for a period sufficient to establish performance before any alert reaches a clinician.

Phase four activates full arbitration and clinical alerting, with threshold settings initially conservative and adjusted on the basis of observed override rates.

3.13. Constraints in Resource-Limited Settings

Several constraints deserve explicit attention.

Infrastructure. Intermittent power and connectivity require local processing and store-and-forward queuing rather than a purely centralised design. The detection engine should be capable of running on modest local hardware, which is a further argument for gradient boosted trees over deep architectures (Chen & Guestrin, 2016). Facility-level infrastructure planning, including power resilience and environmental control, is a precondition rather than a detail (Aminu-Ibrahim, Ogbete & Ambali, 2018; Ogbete, Aminu-Ibrahim & Ambali, 2019). Power resilience in particular deserves treatment as a design input rather than a site condition: hybrid solar installations with optimised load distribution have been shown to be viable in developing economies (Sunday & Omoegun, 2019; Sunday & Omoegun, 2018), and voltage stability in the presence of distributed generation determines whether sensitive analysers and servers tolerate the resulting supply (Oshevire, Eyenubo & Amayo, 2017). Connectivity quality is a parallel constraint, and deployment planning should be informed by the realities of local network provision rather than assuming metropolitan bandwidth (Amayo & Popoola, 2017b). Where the platform is hosted rather than local, capacity planning under concurrency and query optimisation for the underlying data store become the determinants of whether the latency budget in R10 is met (Odejobi & Ahmed, 2018b; Odejobi, Hammed & Ahmed, 2019; Ahmed, Odejobi & Oshoba, 2019). These constraints are the present-day form of a problem flagged at the policy level over a decade ago: the argument that laboratory systems and services are critical to global health yet have been chronically neglected specifically named infrastructure and human resources, not

diagnostic algorithms, as the binding constraint (Nkengasong et al., 2010), and the case for treating national strategic planning as a precondition for laboratory strengthening in resource-poor settings, rather than a downstream administrative step, was made on the same grounds (Nkengasong et al., 2009). The phased deployment sequence in Section 3.12 follows the precedent set by the regional accreditation process developed for the WHO African region, which demonstrated that laboratories operating under exactly these infrastructure constraints could still be brought to a defined quality standard through a stepwise pathway rather than an all-at-once upgrade (Gershy-Damet et al., 2010).

Human capacity. Terminology mapping and clerical review of possible matches require trained staff. The realistic approach is to train existing laboratory scientists in these functions rather than to assume dedicated informatics personnel, and to design review interfaces accordingly. This follows the precedent of an innovative training approach that accelerated laboratory accreditation across developing-country laboratories by building the capability of existing quality management system staff rather than adding a parallel specialist workforce (Yao et al., 2010), and it is consistent with evidence that measurable improvement in laboratory quality management systems follows from strengthening the people already in post (Sisay et al., 2015).

Legacy and paper. Many facilities will retain paper workflows for some tests indefinitely. The structured manual entry path in Layer 1 exists for this reason and should be designed for speed, using constrained pick lists derived from the terminology binding so that entry and coding occur in a single action.

Cost. Open standards and open source components substantially reduce licensing exposure. LOINC is freely available, and SNOMED CT is available at no charge in member countries and to low income countries under the licensing arrangements of SNOMED International, though the licensing position should be verified for any specific jurisdiction. Broader financing considerations, including how diagnostic investment is justified against competing priorities and how it is paid for, follow the logic of the health financing literature in emerging markets (Ilodigwe & Adesemoye, 2019a). Procurement practice determines how much of the budget reaches capability rather than margin, and structured procurement optimisation offers a transferable method (Okonkwo, Ogunwole & Okeke, 2018a). Consumable availability should be planned on the same footing, since detection stops entirely when reagents run out (Okonkwo, Ogunwole & Okeke, 2018b).

Equity of benefit. Improved detection concentrated in tertiary urban facilities widens rather than narrows disparity, so deployment planning should consider the distribution of diagnostic capacity as well as its total (Aminu-Ibrahim, Ogbete & Ambali, 2018).

3.14. Ethical and Legal Considerations

The model processes identifiable health data, and its deployment must be grounded in the applicable legal framework, which in Nigeria includes the Nigeria Data Protection Regulation and in other jurisdictions may include the General Data Protection Regulation, HIPAA or equivalent instruments. Comparative treatment of these regimes matters wherever a platform spans jurisdictions or relies on hosted infrastructure (Mbonu et al., 2019a). Three points are particularly relevant.

Statutory notification generally proceeds under a legal mandate rather than individual consent, and this basis should be documented. Secondary use for model training requires either consent or a lawful basis such as de-identification with governance approval, and the obligations attaching to that use are better modelled at design time than asserted afterwards (Mbonu et al., 2018). And the model must not be permitted to substitute for clinical judgement: alerts are advisory, the clinician retains the decision, and the override mechanism must be frictionless enough that overriding is genuinely available.

A fourth consideration concerns fairness. A classifier trained on data from a population that is unevenly served will encode that unevenness, so subgroup performance should be reported alongside aggregate performance as a standing requirement rather than an occasional audit.

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DOI: https://doi.org/10.64388/IREV3I6-1723089

3.15. Purpose and Scope of the Simulation

This section demonstrates how the evaluation framework of Section 3.4 would be applied. The data used is synthetic, generated to exhibit the structural properties described, and the figures below illustrate the method rather than reporting empirical findings. No claim is made about the model's performance in clinical use; that requires prospective validation, identified in Section 4 as the necessary next step. The framework itself is designed for STARD-compliant reporting (Bossuyt et al., 2015) once prospective, non-synthetic data become available, so that a future validation study can be reported against an established checklist rather than an ad hoc structure.

3.16. Simulation Design

A synthetic cohort of 10,000 care episodes was specified, with a true infection prevalence of 6 percent, distributed across bloodstream, urinary tract and respiratory infections. Data degradation was applied to reflect realistic conditions: 18 percent of organism identifications recorded as free text, 12 percent of episodes with unlinked prior results, and missingness in inflammatory markers ranging from 20 to 45 percent depending on the analyte.

Three configurations were compared. The baseline represents current practice, applying deterministic rules to unnormalised data with no identity resolution. Configuration A applies deterministic rules to fully normalised and linked data, isolating the contribution of Layers 2 and 3. Configuration B is the full model, adding the probabilistic component and arbitration.

3.17. Illustrative Results

Table 4. Illustrative comparison across configurations (synthetic data)

Metric	Baseline	Configuration A	Configuration B
Sensitivity	0.61	0.79	0.89
Specificity	0.94	0.96	0.95
Positive predictive value	0.39	0.56	0.53
F1 score	0.48	0.66	0.66
Median detection latency (hours)	26.5	9.2	6.1
Case capture completeness	0.63	0.86	0.91
Alerts per 100 patient days	4.1	4.4	6.8

Median detection latency in Table 4 uses the end-to-end anchor defined in Section 3.4, measured from the earliest time sufficient evidence existed in the data to the time the alert was raised; the R10 latency budget introduced in Table 1 is a narrower processing interval nested within this end-to-end figure, covering only the interval from result verification to alert, rather than an alternative measure of the same quantity. The pattern these figures are constructed to display is consistent with the argument of the paper. The largest single gain in sensitivity and the largest reduction in latency come from the move from baseline to Configuration A, that is, from normalisation and linkage rather than from any analytic sophistication. The addition of the probabilistic layer in Configuration B adds a further increment in sensitivity and completeness and a further reduction in latency, but at the cost of a higher alert rate and slightly lower positive predictive value. This trade-off is the central operational decision facing an implementing institution. It is not resolved by choosing the configuration with the best headline metric. It is resolved by asking what the institution can absorb: a unit with adequate staffing and a strong stewardship programme may accept the higher alert volume of Configuration B in exchange for earlier detection, while a unit already carrying a heavy alert load may be better served by Configuration A operating reliably, since acceptance of any individual alert falls as volume rises (Ancker et al., 2017).

3.18. Sensitivity to Data Quality

A secondary simulation varied the proportion of free text organism identifications from 0 to 40 percent

while holding all else constant. Detection sensitivity in the full model degraded approximately linearly with this proportion, passing through the 0.89 sensitivity reported for Configuration B in Table 4 at the 18 percent free-text level that characterises the main synthetic cohort: sensitivity fell below that figure as the free-text proportion rose toward 40 percent and rose above it as the proportion fell toward 0 percent. The implication is that the terminology binding layer is not a supporting component but a determinant of overall accuracy, and that investment in coding discipline at the point of result entry yields returns no downstream algorithm can replicate. This mirrors the finding that free text, rather than transmission failure, accounted for most cases missed by early electronic laboratory reporting (Panackal et al., 2002).

IV. DISCUSSION AND CONCLUSION

The model advanced here rests on a claim that runs against a common assumption in health informatics: that detection accuracy is primarily an algorithmic problem. The evidence assembled in Section 2 points elsewhere, while the simulation in Sections 3.15-3.18 illustrates how the same conclusion would manifest in the proposed measurement framework. Evaluations of electronic laboratory reporting located the dominant failure mode in free text rather than in transmission or logic (Panackal et al., 2002; Effler et al., 1999). The machine learning literature reports strong retrospective discrimination alongside uneven deployment experience, and attributes the gap to alert burden, interpretability and data availability rather than to modelling technique (Ancker et al., 2017; Nemati et al., 2018). In both bodies of work the binding constraint is the quality and integration of the data pipeline, a conclusion reached independently from the health system delivery side (Ilodigwe & Adesemoye, 2019b).

The layered design responds by treating semantic standardisation and identity resolution as first-class architectural concerns with their own validation criteria, rather than as preprocessing. The hybrid detection engine responds to a second observation, that rules and learned models fail in complementary ways, by keeping both and treating their disagreement as information rather than as noise to be resolved arbitrarily. Relative to conventional electronic laboratory reporting, the model adds the analytic and arbitration layers, extending its function from notification of confirmed cases to earlier identification of probable ones. Relative to semi-automated surveillance, in which the algorithm serves only to reduce the volume of manual review, arbitration assigns a substantive interpretation to each of the four concordance states rather than treating the algorithm as a filter (Sips, Bonten & van Mourik, 2017). Relative to standalone machine learning detection, it adds the normalisation, linkage and governance layers that address the data quality and accountability problems limiting deployment. A further comparator, though not surveyed at length in Section 2, is the integrated commercial platform that some institutions might procure instead of building toward this model: relative to such platforms, the practical advantage of the present approach is that it does not require replacement of the incumbent LIS and can be adopted in phases, which is decisive where wholesale replacement is not financially or operationally feasible (Aminu-Ibrahim, Ogbete & Ambali, 2018).

Several implications follow for practice and policy. Laboratory data quality standards deserve regulatory attention equal to that given to analytical quality. Accreditation frameworks assess whether a laboratory produces correct results; they less often assess whether those results are produced in a form downstream systems can use. Requiring LOINC and SNOMED CT binding as a condition of accreditation would address the single largest source of detection error identified here (McDonald et al., 2003). Procurement policy should require open, standards-conformant interfaces from LIS vendors, since a closed system is not merely inconvenient but forecloses the integration on which detection accuracy depends, and substitutable application platforms demonstrate that this is achievable rather than aspirational (Mandel et al., 2016; Okonkwo, Ogunwole & Okeke, 2018a). National surveillance architecture should be designed to receive coded data rather than documents, because investment in transmission infrastructure without corresponding investment in semantic standards will reproduce, at higher speed, the ambiguity of the paper systems it replaces.

At facility level the sequencing matters as much as the components. Terminology binding is the first step

rather than a later refinement: mapping the local test menu to LOINC and the organism dictionary to SNOMED CT should precede any analytic project, and the proportion of results entered as free text should be measured, published and targeted for reduction. Equal attention belongs to the pre-analytical phase, where a large share of error originates (Plebani & Carraro, 1997). Administrators should implement in phases with each phase demonstrating value before the next begins, and should budget for security and governance as part of the system rather than as an addition to it (Mbonu et al., 2018). Clinicians and infection control teams should participate in defining alert thresholds and in the structured override process, since the system's precision depends on the feedback it receives and unrecorded dismissal of alerts is a loss of information.

Several limitations should be stated plainly. The evaluation presented is a simulation, and simulations reflect the assumptions built into them; the figures in Table 4 demonstrate a method and cannot substitute for prospective measurement. The model presumes an adjudicated reference standard for training, and constructing one is labour-intensive and subject to inter-rater variability. Classifier performance depends on local case mix and will not transfer unchanged between institutions, so each deployment requires local calibration at minimum, as external validation work has shown (van Mourik et al., 2012). The economics of implementation, including hardware, training and ongoing maintenance, are not analysed here and would materially affect feasibility assessments (Ilodigwe & Adesemoye, 2019a). Finally, the model addresses detection and does not extend to whether earlier detection changes patient outcomes, which requires a different study design and depends on treatment availability as much as on diagnosis.

Four directions for further work follow. Prospective multi-site validation is the immediate requirement, with pre-registered protocols measuring all four accuracy dimensions and reporting override rates and subgroup performance alongside discrimination metrics. Learning across institutions without pooling identifiable data would address both privacy and the transferability problem, and decentralised training methods now make this technically plausible (McMahan et al., 2017). Extension to antimicrobial resistance surveillance is a natural adjacent application, given that the susceptibility data required already flows through Layer 2, and given the supply-side determinants of treatment quality that surround it (Aneke & Adesemoye, 2019). That picture is complicated further by antimicrobial use that never reaches a laboratory or pharmacy record at all: traditional and alternative preparations with demonstrated antimicrobial activity remain in routine use in some of the same low-resource settings this model targets, and a surveillance system built only on formal laboratory and prescribing data will not see the resistance pressure this consumption exerts (Gbadamosi & Obogo, 2013). And evaluation of downstream clinical and economic outcomes would establish whether the detection gains modelled here translate into benefit for patients and health systems.

4.1. Conclusion

This paper has developed a model for improving infection detection accuracy through integrated laboratory information systems. Reviewing work on electronic laboratory reporting, interoperability standards, diagnostic infrastructure, automated surveillance of healthcare-associated infections, computational detection and health data protection, it identified five recurring weaknesses: semantic fragmentation, identity fragmentation, reliance on single detection methods, narrow measurement of accuracy, and governance treated as an afterthought. In response it specified ILIS-IDA, a six-layer architecture comprising data acquisition, normalisation and terminology binding, integration and identity resolution, a hybrid detection engine, alerting and workflow, and governance and assurance, together with an evaluation framework spanning diagnostic accuracy, timeliness, completeness and operational burden, demonstrated on synthetic data.

The central conclusion is that detection accuracy is an emergent property of an integrated pipeline. The largest available gains lie in ensuring that laboratory data enters the pipeline coded, complete and linked to the right patient. Analytic sophistication compounds those gains but cannot substitute for them, and a system that improves the algorithm while leaving the pipeline untouched will deliver faster ambiguity rather than better detection.

Declarations

Ethics approval and consent to participate: Not applicable. This is a conceptual model paper; no human participants, human tissue, or identifiable patient data were used. The illustrative evaluation in this paper uses only synthetic data generated for demonstration.

Consent for publication: Not applicable.

Availability of data and materials: Not applicable. No new datasets were generated; the synthetic data used for the illustrative evaluation is described in the manuscript and no primary datasets require deposition.

Competing interests: The authors declare no competing interests.

Funding: This research received no external funding.

Authors' contributions: Kazeem Abdulrazaq conceived the model, led its architectural design, and drafted the manuscript. Habeeb Damilola Yusuf contributed to the design requirements and the illustrative evaluation, and critically reviewed the manuscript. Helen Ekwi Osinem contributed to the literature review and the governance and assurance considerations, and revised the manuscript for important intellectual content. Florence Eribenne contributed to the implementation considerations and reviewed the manuscript. All authors read and approved the final manuscript.

Acknowledgments: None.

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