

**Review Article**

# Artificial Intelligence and Predictive Analytics for HIV Surveillance: From Retrospective Monitoring to Anticipatory Outbreak Response

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**Received:** 12.09.2026;**Accepted:** 20.10.2026;**Published:** 31.10.2026 © 2026 by the author's. The terms and conditions of the Creative Commons Attribution (CC BY) license apply to this open access article.**Abstract**

Despite major advances in HIV testing, antiretroviral therapy (ART), pre-exposure prophylaxis (PrEP), and surveillance, ongoing transmission and persistent gaps across the HIV care continuum remain important public-health challenges. Most surveillance systems, however, remain predominantly retrospective: they describe diagnoses, transmission clusters, care disengagement, and viral non-suppression after these patterns have already emerged. Artificial intelligence (AI) and predictive analytics offer the possibility of shifting surveillance toward earlier identification of emerging risks, but improved predictive performance does not necessarily translate into effective prevention. This critical narrative review examines the evolving role of AI in HIV surveillance, integrating evidence across routine surveillance and care-continuum data, molecular and genomic surveillance, clinical and electronic health records, and behavioral, social, geographic, and mobility information. Particular attention is given to data latency, prediction horizon and lead time, concept drift, transportability, multimodal integration, the prediction-to-response gap, and ethical and equity concerns. The review argues that the central challenge is no longer simply whether HIV-related outcomes can be predicted, but whether predictions provide sufficiently early, validated, interpretable, equitable, and actionable intelligence to change public-health decisions and outcomes. To address this gap, I propose an AI-enabled anticipatory HIV surveillance framework organized around OBSERVE → INTEGRATE → DETECT → PREDICT → VALIDATE → PRIORITIZE → RESPOND → EVALUATE → LEARN. Future progress should therefore be evaluated by the ability of predictive surveillance to generate meaningful lead time and enable interventions that improve HIV prevention and care.

**1. Introduction**

HIV surveillance has evolved from the simple counting of reported diagnoses into a much richer system for monitoring transmission, treatment, and population-level outcomes. Routine diagnosis reporting remains fundamental, but it is increasingly complemented by viral-load surveillance, antiretroviral resistance monitoring, and care-continuum indicators that track progression from diagnosis and linkage to care through treatment and viral suppression [1]. Geographic surveillance further identifies areas with disproportionate disease burden or gaps in service delivery, while molecular surveillance can identify genetically related infections and rapidly growing clusters that may

warrant public-health investigation [2]. Together, these approaches provide a considerably more detailed picture of the epidemic than diagnosis counts alone.

Yet greater surveillance resolution does not necessarily mean greater anticipation. Most established indicators become observable only after an epidemiologically important event has occurred. A diagnosis follows infection and testing; viral non-suppression is recognized after laboratory measurement; disengagement becomes visible after missed care or absent clinical information; and a molecular cluster must contain enough diagnosed and sequenced infections to become detectable [3]. Geographic concentrations of diagnoses or poor care-continuum outcomes similarly reveal patterns that have already developed. Reporting, laboratory processing, data integration, and analytical delays can further widen the interval between a change in transmission or care and its recognition by the surveillance system [4].

The limitation is therefore not that contemporary HIV surveillance lacks useful information. Rather, much of its strength lies in describing and detecting existing epidemiological conditions. This creates a persistent temporal gap between the emergence of risk and the point at which that risk becomes sufficiently visible to trigger response [5]. Closing that gap requires surveillance capable not only of recognizing where transmission or care failures are occurring, but of identifying credible indications of where they are likely to emerge or intensify next [6].

### 1.1. Why Anticipatory Surveillance Matters

The value of anticipatory surveillance lies in creating time for intervention before an emerging pattern becomes an established public-health problem. Earlier identification of increasing transmission risk could prompt intensified testing in affected populations or locations, allowing infections to be diagnosed and treated sooner. It could also support more targeted deployment of pre-exposure prophylaxis (PrEP) and other prevention resources where risk is expected to increase rather than where high transmission has already been documented [7]. Similarly, early indications of declining engagement in care or increasing risk of viral non-suppression could support linkage and re-engagement efforts before prolonged treatment interruption occurs [8].

At the population level, anticipatory intelligence could help determine when a molecular or epidemiological signal warrants accelerated cluster investigation and where limited personnel, testing capacity, prevention services, and outreach resources should be concentrated [9]. The objective is not to predict every individual infection. It is to provide sufficiently credible information, sufficiently early, to change the timing or targeting of intervention. In this sense, the practical value of anticipation is measured by the decision time it creates between recognition of emerging risk and the point at which preventable transmission or care disruption has already occurred [10].

### 1.2. The Emergence of AI and Predictive Analytics

Artificial intelligence and predictive analytics have created new possibilities for extracting such forward-looking information from HIV surveillance data. Machine-learning methods can identify complex relationships among demographic, clinical, behavioral, and service-use variables and estimate risks such as treatment disengagement, viral non-suppression, or other adverse outcomes [11]. Network-based approaches can examine relationships within transmission or contact structures, while spatiotemporal models can identify geographic patterns and estimate how risk may change across locations and over time [12].

Natural-language processing extends analysis to unstructured information contained in clinical notes and other text-based records that conventional surveillance databases may not capture readily [13]. Multimodal approaches go further by combining information from different sources, including routine surveillance, clinical records, molecular data, geographic information, and social or contextual indicators [14]. These developments potentially expand HIV surveillance from observing established patterns toward identifying emerging ones. Their significance, however, depends on whether they provide genuinely prospective information that improves public-health decisions, rather than simply applying more sophisticated algorithms to classify risks that are already visible in historical data.

### 1.3. Central Argument and Review Objective

The central argument of this review is that technological sophistication should not be mistaken for anticipatory surveillance. Monitoring is not prediction, prediction is not early warning, and early warning is not response. Monitoring establishes what is occurring or has occurred; prediction estimates what may happen next; early warning requires that a prediction be sufficiently timely, credible, and specific to inform a decision; and response requires that this intelligence be translated into an appropriate intervention [15]. Failure to distinguish these functions can lead to AI systems being described as predictive or anticipatory when they primarily classify existing risk using historical data [16].

This review therefore critically examines whether AI and predictive analytics are genuinely shifting HIV surveillance from retrospective monitoring toward anticipatory outbreak response. It evaluates the principal analytical approaches and prediction targets, the integration of clinical, molecular, geographic, and population-level data, and the methodological and implementation barriers separating model performance from public-health impact [13]. Particular attention is given to whether predictive systems provide meaningful lead time, remain reliable as epidemic conditions change, and generate information that can be validated and acted upon [17]. Ultimately, the review asks a more demanding question than whether AI can predict HIV-related outcomes: can predictive intelligence enable earlier action capable of changing the trajectory of transmission or care failure?

## 2. What Does “Prediction” Mean in HIV Surveillance?

### 2.1. Descriptive Surveillance

Descriptive surveillance provides the empirical foundation for understanding the HIV epidemic by establishing what has already happened. Routine systems document diagnoses, prevalence and incidence patterns, viral-load outcomes, treatment uptake, viral suppression, mortality, and other indicators across populations, locations, and time [5]. These data allow public-health agencies to characterize disease burden, identify persistent disparities, monitor progress along the HIV care continuum, and determine whether prevention and treatment goals are being achieved [1].

Its principal limitation is temporal. Most descriptive indicators become visible only after the underlying event has occurred and entered the surveillance system [4]. A reported diagnosis follows infection and testing, while changes in viral suppression or treatment engagement are recognized only after relevant clinical information becomes available. Descriptive surveillance can therefore reveal where transmission or care failures have occurred, but it does not inherently indicate what will happen next. This distinction provides an important baseline for evaluating AI-based approaches: using sophisticated algorithms to describe historical patterns more precisely does not, by itself, transform retrospective surveillance into prediction [16].

## 2.2. Detection and Risk Identification

Detection moves surveillance from describing accumulated outcomes toward recognizing what is changing now and where risk is concentrated. In HIV surveillance, this may involve identifying an unexpected increase in diagnoses, deterioration in viral suppression, geographic concentrations of poor care outcomes, or rapid growth within a molecular cluster [2]. Risk-identification models can similarly distinguish individuals, populations, or locations whose observed characteristics are associated with greater vulnerability to infection, disengagement from care, or treatment failure [18].

The distinction from prediction is important. A system may accurately identify a population experiencing elevated risk without demonstrating that the adverse outcome will increase in the future. Likewise, detecting a rapidly growing molecular cluster establishes evidence of ongoing transmission rather than necessarily forecasting its subsequent expansion [19]. Detection and risk stratification can therefore improve the targeting of surveillance and intervention, but they remain principally concerned with present epidemiological conditions. Labeling these functions as predictive simply because machine learning is used can overstate how far surveillance has moved toward anticipation [13].

## 2.3. Prediction

Prediction asks a different question: what is likely to happen next? A predictive HIV surveillance system uses information available at a defined point in time to estimate an outcome that has not yet occurred. Relevant targets might include future disengagement from care, viral non-suppression, growth of a transmission cluster, geographic increases in diagnoses, or changes in population-level transmission risk [20]. Genuine prediction therefore requires a clearly defined future outcome and prediction horizon [21].

This temporal distinction is fundamental. A model that identifies individuals already showing evidence of disengagement or locations where transmission has already increased may be useful, but it provides limited anticipatory value. The stronger test is whether the model recognizes emerging risk before the outcome becomes evident through conventional surveillance [15]. Predictive performance should consequently be considered alongside the amount of useful time gained. For HIV surveillance, the objective is not merely to forecast correctly, but to forecast sufficiently early for the information to create an opportunity for prevention or intervention [16].

## 2.4. Early Warning

Early warning begins where prediction becomes relevant to a decision. A model may correctly estimate that HIV transmission, viral non-suppression, or cluster growth is likely to increase, but that estimate constitutes an early warning only if it is generated with sufficient confidence and lead time to justify action [22]. Timing is therefore fundamental. A highly accurate forecast delivered after transmission has accelerated or care disruption has become established offers little advantage over conventional surveillance [4].

Confidence is equally important because acting on uncertain predictions carries costs. An overly sensitive system may generate repeated false alarms and divert limited prevention resources, whereas an overly conservative system may fail to identify emerging threats while intervention is still possible [3]. Early-warning systems must therefore balance timeliness against reliability and communicate uncertainty rather than presenting risk estimates as certainty [23]. The relevant question is not simply whether an outcome can be predicted, but whether the prediction crosses a defensible threshold at which public-health investigation or intervention should begin.

## 2.5. Anticipatory Outbreak Response

Anticipatory outbreak response represents the point at which predictive intelligence changes practice. A warning should create an opportunity to intervene before substantial additional transmission occurs, whether through intensified testing, targeted PrEP delivery, rapid cluster investigation, linkage or re-engagement in care, community-based prevention, or redistribution of public-health resources [3]. This requires predefined connections between particular warnings and feasible response options. Without such pathways, even an accurate early-warning system may produce information without producing public-health benefit [15].

The distinction between prediction and response is therefore critical. A machine-learning model that produces a risk score is not, by that fact alone, an anticipatory surveillance system [24]. Its value depends on whether the prediction provides credible additional lead time, supports an appropriate response, and ultimately creates an opportunity to prevent transmission or avert deterioration in HIV care [17].

# 3. The Emerging AI Toolkit for HIV Surveillance

## 3.1. Supervised Machine Learning

Supervised machine learning represents one of the most established applications of AI in HIV research because many surveillance and clinical datasets contain defined outcomes that can be used to train predictive models. Algorithms learn relationships between observed characteristics and outcomes such as HIV acquisition, treatment disengagement, viral non-suppression, or loss to follow-up [25]. At the population level, similar approaches can classify geographic areas according to expected HIV burden or future risk. The appeal is clear: surveillance systems routinely collect large numbers of demographic, laboratory, clinical, and service-use variables, and machine learning can identify interactions among these variables that may be difficult to specify in advance using conventional statistical models [26].

For anticipatory surveillance, however, the important issue is not simply whether individuals or locations can be classified accurately. The timing of the predictors relative to the outcome is critical. A model that identifies patients at high risk of disengagement only after missed visits have accumulated may formalize a problem that is already apparent to clinicians [8]. Similarly, geographic models trained on historical diagnoses may reproduce established patterns of HIV burden without demonstrating where transmission will increase next. Models predicting viral non-suppression or HIV acquisition are more useful when they identify risk sufficiently early for prevention, treatment support, or outreach to alter the expected outcome [18].

Supervised learning should therefore be evaluated according to the prospective information it contributes beyond existing surveillance indicators and clinical judgment [27]. Discrimination measures may demonstrate that a model separates higher- from lower-risk observations, but they do not establish that its predictions create a useful intervention window [23]. For HIV surveillance, predictive utility depends on combining accurate risk estimation with a clearly defined prediction horizon and sufficient time for prevention, treatment support, or outreach. This provides a more meaningful benchmark than increasingly sophisticated classification of risks that are already apparent within existing surveillance systems.

### 3.2. Unsupervised Learning and Anomaly Detection

Unsupervised learning offers a different surveillance function because it does not require a predefined outcome for every observation. Instead, algorithms search for structure within the data, identifying groups, relationships, or observations that differ from established patterns. In HIV surveillance, this capability may be useful for identifying previously unrecognized population clusters, unusual combinations of clinical or behavioral characteristics, and changes in surveillance patterns that would not necessarily trigger conventional thresholds [13]. Anomaly-detection methods extend this principle by identifying observations or temporal changes that deviate substantially from what is expected [22].

This flexibility makes unsupervised approaches attractive for detecting emerging events that were not specified in advance. However, statistical novelty is not equivalent to epidemiological importance. An apparent anomaly may reflect changes in testing, reporting, data completeness, laboratory practices, or service utilization rather than a genuine change in HIV transmission [4]. Unsupervised systems therefore require epidemiological verification and comparison with independent evidence. Their strongest role may be as signal-generating tools that direct attention toward patterns requiring investigation, rather than systems that independently determine whether an outbreak is occurring [3].

### 3.3. Temporal and Spatiotemporal Modelling

Temporal and spatiotemporal models add a dynamic dimension to HIV surveillance by examining how epidemiological outcomes change across time and, where relevant, geographic space, consistent with broader efforts to develop more responsive and integrated mathematical-modelling approaches for infectious-disease epidemiology [28]. These approaches can be used to forecast incidence or diagnoses, anticipate changes in viral suppression, estimate future testing or service demand, and identify locations where HIV burden may increase [22]. Incorporating spatial relationships is particularly important because neighboring areas are not epidemiologically independent; transmission and service-use patterns may extend across administrative boundaries through population movement, social networks, and healthcare access [12].

Their contribution to anticipatory surveillance lies in identifying where and when risk is likely to change, rather than reproducing maps of established disease burden. Prospective hotspot models should therefore identify locations likely to experience increasing risk during a specified future period [9]. Their performance should be evaluated according to prediction horizon, calibration, geographic resolution, and stability as epidemic conditions change [29]. From a public-health perspective, their value ultimately depends on whether emerging changes are identified early enough to influence the deployment of testing, prevention, treatment, and surveillance resources.

### 3.4. Network and Graph-Based Approaches

HIV transmission is inherently relational, making network-based methods particularly relevant to surveillance. Sexual and social networks can represent connections through which exposure may occur, while molecular data can identify groups of genetically related infections that suggest epidemiological connectivity [30]. Network analysis can examine characteristics such as connectivity, clustering, and changes in network structure to identify parts of a population in which transmission may be concentrated or expanding [31]. Graph-based machine-learning methods extend this approach by learning from both individual characteristics and relationships among connected observations.

For anticipatory surveillance, these methods may help estimate which networks or clusters are most likely to expand, allowing epidemiological investigation or prevention resources to be prioritized earlier. Such predictions require careful interpretation, however. Molecular similarity does not establish direct transmission, and observed networks remain incomplete because undiagnosed, untested, or unsequenced individuals are absent [32]. Network models can therefore inherit biases in the surveillance systems from which their connections are constructed. Their outputs are best treated as evidence for further epidemiological investigation rather than complete representations of transmission.

### 3.5. Natural-Language Processing

A substantial amount of potentially relevant HIV information exists outside structured surveillance fields. Electronic health records and clinical notes may contain information on treatment interruptions, barriers to care, medication use, social circumstances, symptoms, and clinician assessments that is difficult to represent using routinely coded variables [8]. Natural-language processing (NLP) can convert portions of this unstructured text into information that can be incorporated into surveillance or predictive models. Similar methods can potentially extract epidemiologically relevant information from public-health reports and other text-based sources [13].

The potential advantage is not simply access to more data, but access to information that may appear before an outcome is formally recorded in structured surveillance systems. Clinical documentation of difficulties maintaining treatment, for example, could contain early indications of subsequent disengagement. Yet NLP introduces important problems of its own. Clinical language varies across practitioners

and institutions, documentation may be incomplete, and models trained on one health system may perform poorly elsewhere [33]. Free-text records may also contain highly sensitive information whose secondary use raises privacy concerns [17]. NLP should therefore be judged by whether the additional information it extracts improves the timeliness and reliability of prediction beyond structured data, rather than by its ability to process large volumes of text alone.

### 3.6. Deep Learning and Multimodal AI

Deep learning extends predictive analytics by learning complex representations from high-dimensional data, while multimodal AI seeks to combine information that would otherwise be analyzed separately. More broadly, advances in precision medicine demonstrate the increasing value of integrating high-dimensional multi-omic data to characterize complex biological states and identify clinically relevant patterns [34]. In HIV surveillance, such systems could integrate clinical histories, laboratory results, molecular data, geographic information, care-utilization patterns, and other population-level indicators within a common predictive architecture [14]. This is potentially important because emerging transmission or deterioration in care may not be adequately represented by any single data source. Patterns that appear weak in isolation may become more informative when interpreted alongside complementary signals [35].

Greater computational complexity, however, should not be treated as evidence of greater surveillance value. Deep models often require large training datasets and substantial computational resources, and their internal reasoning may be difficult to interpret [36]. These limitations become particularly important when models are transferred across populations or health systems with different patterns of testing, treatment access, documentation, and surveillance coverage [33]. Multimodal systems also introduce practical challenges because their component datasets may be collected at different frequencies, geographic scales, and levels of completeness. Missing one data stream may substantially alter performance, particularly in settings with limited molecular or digital surveillance infrastructure.

The appropriate benchmark is therefore incremental public-health value rather than computational sophistication. A complex multimodal model should outperform simpler alternatives in ways that matter operationally: earlier identification of emerging risk, better calibration, useful gains in lead time, improved targeting of intervention, or more equitable allocation of resources [27]. If additional complexity produces only a small increase in conventional predictive metrics while reducing interpretability, transportability, or feasibility, its contribution to HIV surveillance may be limited. The objective is not to build the most technically elaborate model, but to identify the least complex approach capable of producing sufficiently reliable and timely intelligence to improve public-health action [15]. The principal AI and predictive-analytics approaches used in HIV surveillance differ in their applications, data requirements, and limitations. Table 1 summarizes these approaches and their potential contribution to anticipatory surveillance.

**Table 1:** AI and predictive-analytics approaches in HIV surveillance: applications, data requirements, strengths, and limitations

| Approach                       | HIV surveillance applications                                          | Data requirements                                              | Strengths                                               | Key limitations                                                                          |
|--------------------------------|------------------------------------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------|------------------------------------------------------------------------------------------|
| Supervised ML                  | HIV acquisition, disengagement, viral non-suppression, geographic risk | Labeled clinical, laboratory, behavioral, or surveillance data | Risk prediction and stratification                      | Historical bias; limited generalizability; classification may not equal forecasting [18] |
| Unsupervised learning          | Emerging clusters and unusual patterns                                 | Unlabeled surveillance or clinical data                        | Detects unexpected patterns without predefined outcomes | Anomalies may lack epidemiological significance [4]                                      |
| Temporal/spatiotemporal models | Incidence, diagnoses, viral suppression, demand, hotspots              | Longitudinal and geographic data                               | Forecasts when and where risk may change                | Sensitive to data latency and changing epidemic conditions [22]                          |
| Network/graph methods          | Transmission networks, molecular clusters, cluster expansion           | Network, molecular, and epidemiological data                   | Captures relational transmission patterns               | Incomplete networks; molecular links do not prove direct transmission [30]               |
| NLP                            | EHRs, clinical notes, public-health reports                            | Unstructured text                                              | Extracts information absent from structured fields      | Documentation variability, privacy, and transportability [8]                             |
| Deep/multimodal AI             | Integrated prediction across multiple surveillance streams             | Large, heterogeneous datasets                                  | Models complex interactions across data sources         | Data intensive, less interpretable; added public-health value may be uncertain [27]      |

## 4. What Should AI Actually Predict?

### 4.1. Individual-Level Deterioration

One of the most immediate targets for predictive HIV surveillance is deterioration in an individual's position along the care continuum, where breakdowns in diagnosis, linkage, retention, treatment, and viral suppression can undermine both individual outcomes and population-level HIV control [1, 37]. This includes future disengagement from care, treatment interruption, viral non-suppression, and related outcomes that may increase morbidity and create conditions for onward transmission [1]. Clinical histories, laboratory results, appointment patterns,

medication records, and previous patterns of care engagement can potentially be used to identify patients whose outcomes are likely to worsen before conventional indicators clearly establish that deterioration has occurred [11].

The public-health value of such prediction depends heavily on when risk becomes identifiable. Predicting treatment interruption after repeated missed appointments or predicting viral non-suppression after a worsening laboratory trajectory may offer little additional time for intervention [25]. More useful systems would recognize combinations of earlier signals that identify increasing vulnerability while adherence support, re-engagement, or other interventions can still prevent the anticipated outcome [8].

Individual prediction nevertheless has an important conceptual boundary. A person identified as having a high probability of viral non-suppression or disengagement is not necessarily someone who will contribute disproportionately to future population-level transmission. Transmission depends on additional biological, behavioral, network, and contextual factors [31]. Individual vulnerability models should therefore be evaluated according to the outcomes they were designed to predict rather than interpreted automatically as models of epidemic risk. This distinction becomes particularly important when AI-generated individual risk scores are used to inform broader surveillance or resource-allocation decisions [24].

## 4.2. Population-Level Transmission Risk

Population-level prediction asks whether HIV transmission is likely to increase within a particular geographic area, demographic group, or other defined population [20]. This differs fundamentally from identifying individuals with elevated vulnerability. Surveillance data on diagnoses, testing, viral suppression, prevention coverage, demographic patterns, and contextual conditions can potentially be combined to estimate where transmission risk may intensify during a defined future period [12].

The distinction between **current burden and future transmission** is especially important. Areas with historically high numbers of diagnoses may remain priority locations, but identifying them does not constitute prediction [6]. A genuinely prospective system should detect changes suggesting that transmission is likely to accelerate in populations or locations that may not yet appear exceptional using conventional indicators. Such information could provide a basis for earlier allocation of testing, prevention, and outreach resources [5].

Population-level models must also account for surveillance visibility. An apparent low-risk area may reflect limited testing, incomplete reporting, or weak engagement with health services rather than genuinely low transmission [10]. Predictions should therefore be interpreted within the context of how completely the underlying population is represented in available data. The objective is not simply to produce increasingly detailed risk maps, but to identify credible changes in population-level transmission early enough to support preventive action [16].

## 4.3. Emerging Transmission Clusters

Molecular and epidemiological surveillance has strengthened the ability to identify HIV transmission clusters, but **detecting a cluster and predicting its future growth are different analytical tasks**. Cluster detection establishes that a group of related infections or epidemiological connections is already observable [2]. Anticipatory surveillance should instead ask which newly detected or evolving clusters are likely to expand rapidly and therefore warrant accelerated investigation or intervention [19].

Prediction of cluster growth could incorporate characteristics such as recent growth patterns, network structure, timing of diagnoses, molecular information, geographic distribution, and relevant epidemiological characteristics [9]. The intended output would not simply classify a cluster as present or absent, but estimate its probability or trajectory of subsequent expansion within a specified prediction horizon. This distinction matters because public-health agencies may identify multiple clusters while having limited capacity to investigate all of them with equal intensity [3].

However, observed cluster growth is partly determined by testing, diagnosis, sequencing, and reporting practices. A cluster may appear stable because new infections remain undiagnosed or unsequenced, while increased testing may produce apparent acceleration without an equivalent change in underlying transmission [30]. Predictive models must therefore distinguish changes in observed cluster membership from changes in transmission itself. The practical goal is to identify clusters for which earlier intervention could plausibly prevent additional infections, rather than merely providing a more sophisticated description of transmission that has already occurred [31].

## 4.4. Prevention and Service Demand

Prediction can also support HIV surveillance by anticipating **where prevention and care resources will soon be needed**. Rather than forecasting transmission as an end in itself, these models could estimate future demand for HIV testing, PrEP, treatment outreach, linkage or re-engagement services, and other interventions [7]. Such forecasts may help public-health agencies position resources before increases in need become evident through service utilization or diagnosis data [6].

This application is particularly relevant where resources are constrained. However, predicted demand should not be equated with underlying need. Service utilization is influenced by accessibility, awareness, stigma, affordability, and healthcare infrastructure [1]. Populations with substantial unmet need may therefore generate relatively little observable demand. AI systems trained primarily on previous utilization could reproduce these disparities by directing resources toward populations already well represented in service data [17]. Forecasting should consequently incorporate indicators of epidemiological need and service gaps rather than simply extrapolating historical patterns of use.

## 4.5. Outbreak Escalation

Perhaps the most demanding prediction target is whether an emerging signal will develop into a transmission event requiring rapid public-health response. Surveillance systems routinely encounter fluctuations in diagnoses, cluster size, testing positivity, viral suppression, and other indicators. Not every increase represents sustained transmission, and responding intensively to every deviation would be inefficient [4]. The predictive challenge is therefore to distinguish transient variation from signals indicating likely escalation [3].

An effective model would estimate whether an emerging pattern is likely to persist, expand, or produce substantial additional transmission within a meaningful time horizon [19]. This requires combining the magnitude and trajectory of the signal with its epidemiological context

and determining whether the resulting risk exceeds a predefined threshold for action. Such prediction could help prioritize which signals require immediate investigation and which can continue under enhanced surveillance [9].

Outbreak-escalation models must also distinguish individual vulnerability from population-level transmission risk. Aggregating individual risk scores does not automatically produce an accurate forecast of transmission because epidemic dynamics reflect interactions among individuals, networks, prevention coverage, service access, and broader epidemiological conditions [20]. Anticipatory surveillance must therefore specify the outcome being predicted, the population or level of analysis, the prediction horizon, and the public-health decision the forecast is intended to inform [6].

## 5. From Retrospective Data to Anticipatory Intelligence

### 5.1. The Problem of Historical Training Data

AI models do not learn HIV risk independently of the surveillance systems that generate their training data. They learn from records of who was tested, diagnosed, linked to care, retained in treatment, sequenced, and successfully captured by existing reporting systems [24]. Consequently, historical datasets contain not only epidemiological information but also the accumulated effects of healthcare access, testing practices, service availability, reporting completeness, and previous public-health priorities [17].

This creates a fundamental problem for anticipatory surveillance. Populations that interact frequently with healthcare systems may generate rich longitudinal data and therefore appear highly visible to predictive models. In contrast, populations experiencing limited testing, unstable access to care, migration, stigma, or other barriers may be poorly represented [1]. Missing information is therefore not always random; it may indicate precisely the forms of marginalization that increase vulnerability while simultaneously reducing surveillance visibility. A model trained on such data can learn patterns of observation as well as patterns of HIV risk [33].

Historical training data can also constrain prediction to relationships that were important under previous epidemic conditions. Even technically strong models may reproduce established geographic or demographic patterns rather than identify genuinely emerging ones [29]. The central question is therefore not simply whether historical data are sufficiently large for machine learning, but whether they adequately represent the populations and processes about which future predictions will be made. Anticipatory HIV surveillance requires explicit attention to missingness, selection mechanisms, and unequal surveillance coverage; otherwise, AI may reinforce the blind spots of the system it is intended to improve [15].

### 5.2. Data Latency

The usefulness of predictive surveillance depends not only on what data are available, but also on how quickly those data become available. HIV surveillance information may pass through multiple stages between the underlying event and its availability for analysis, including testing, laboratory processing, clinical documentation, reporting, data linkage, and database updating [4]. Consequently, a model can be technically accurate while operating on information that already represents conditions from weeks or months earlier [2].

This creates a distinction between predictive accuracy and operational timeliness. A model that forecasts cluster expansion using delayed diagnosis or sequence data may identify future growth relative to its dataset while providing little warning relative to transmission occurring in real time [9]. Similar problems arise when predicting geographic increases or deterioration in care from records that are updated infrequently. Data latency therefore reduces the effective intervention window and may convert an apparently prospective model into a largely retrospective surveillance tool [19].

For anticipatory HIV surveillance, timeliness should consequently be treated as a property of the entire data pipeline, not merely the algorithm [15]. Improving computational performance cannot compensate for surveillance inputs that arrive too late to support meaningful action [3].

### 5.3. Prediction Horizon and Lead Time

Prediction horizon specifies how far into the future an outcome is being estimated, whereas lead time reflects how much usable time the prediction provides before that outcome becomes evident or requires intervention [16]. Both are central to determining whether an AI system contributes meaningfully to anticipatory HIV surveillance. A model predicting viral non-suppression within six months, for example, has a different operational purpose from one estimating cluster expansion over the next several weeks [11].

The critical question is: how early is early enough to change an HIV response? There is no universal answer. Useful lead time depends on the predicted event and the intervention it is intended to trigger. Re-engagement in care, targeted testing, PrEP outreach, cluster investigation, and redistribution of prevention resources each require different amounts of time to organize and implement [3]. Predictions made too late may leave insufficient opportunity for action, while predictions made too far in advance may become less reliable and generate unnecessary interventions [4].

Lead time should therefore be evaluated alongside discrimination and calibration as a substantive measure of predictive utility [23]. The relevant benchmark is not the longest possible forecast horizon, but whether the system provides enough reliable advance notice for a feasible intervention to alter the anticipated outcome. This shifts evaluation from asking how accurately AI predicts future HIV-related events to asking whether it predicts them early enough to matter [15].

### 5.4. Concept Drift

Predictive relationships in HIV surveillance are unlikely to remain stable indefinitely. Concept drift occurs when relationships learned from historical data change as the epidemiological, clinical, or social environment evolves [29]. Expanded PrEP uptake, increasing ART coverage, changes in testing practices, migration, shifts in sexual networks, changes in service access, and new public-health policies can all alter the relationship between predictors and outcomes [16]. Variables that strongly predicted HIV acquisition, viral non-suppression, or cluster growth during one period may therefore become less informative later.

This creates a particular challenge for models deployed over extended periods. Strong performance during initial validation does not guarantee continued reliability as prevention coverage and epidemic conditions change. Anticipatory systems consequently require ongoing performance monitoring and periodic recalibration or retraining [23]. Importantly, deterioration in model performance should not automatically be interpreted as technical failure; it may indicate that the population or epidemic itself has changed. Surveillance systems must therefore be designed to detect changes not only in predicted risk, but also in the validity of the predictive relationships on which those estimates depend [33].

## 5.5. External Validation and Transportability

A second challenge is whether models developed in one setting can perform reliably elsewhere. HIV epidemics differ substantially across cities, populations, and health systems in transmission patterns, demographic composition, testing coverage, treatment access, prevention uptake, surveillance infrastructure, and data completeness [12]. A model trained in one jurisdiction may therefore learn relationships that reflect local conditions rather than generalizable predictors of future HIV outcomes [33].

Internal validation alone cannot establish transportability. Models intended for broader surveillance use should be evaluated in independent populations and, where possible, across different geographic and temporal settings [21]. Performance should also be examined across relevant population groups rather than reported only as an overall average. Poor transportability may require local recalibration, modification of predictors, or development of setting-specific models [18]. The practical question is therefore not simply whether an algorithm performs well where it was developed, but whether its predictions remain reliable in the population in which public-health decisions will actually be made.

## 5.6. Prediction Without Action

The most important limitation of predictive HIV surveillance may arise after an accurate prediction has already been produced. A model can discriminate effectively between higher- and lower-risk observations yet contribute little to prevention if its output is not connected to a feasible intervention [15]. In this sense, AUC is not public-health impact. Measures such as discrimination, sensitivity, specificity, and calibration characterize predictive performance, but they do not demonstrate that using the model reduces transmission, improves viral suppression, or strengthens engagement in care [24].

For prediction to influence outcomes, model outputs must reach appropriate decision-makers and connect to predefined response pathways. Alerts must be interpretable within their epidemiological context, linked to interventions that can realistically be delivered, and generated while sufficient time remains for action [17]. Even a technically strong model may provide little practical advantage when alerts arrive too late, appropriate resources are unavailable, or public-health teams lack a clear mechanism for responding [35].

The relevant standard is therefore whether predictive surveillance adds practical value to existing practice [16]. Without a credible pathway from prediction to intervention, increasingly accurate algorithms risk becoming sophisticated descriptions of risk rather than instruments of anticipatory public-health action [13].

# 6. Integrating AI with Molecular, Clinical, and Population Surveillance

## 6.1. Routine Surveillance and Care-Continuum Data

Routine HIV surveillance provides the foundation for anticipatory intelligence because it captures changes in diagnoses, linkage to care, treatment engagement, viral load, viral suppression, and other outcomes across time [1]. AI can potentially extract greater prospective value from these longitudinal data by identifying combinations of changes that precede clinically or epidemiologically important events. Rather than waiting until disengagement or viral non-suppression is established, for example, predictive systems could identify trajectories suggesting that deterioration is becoming increasingly likely [11].

However, routine surveillance reflects what the health system is able to observe. Individuals who remain undiagnosed, test infrequently, move between jurisdictions, or have limited contact with care may be weakly represented precisely when their risks are increasing [10]. Apparent stability in surveillance indicators therefore does not necessarily indicate epidemiological stability. AI cannot eliminate this limitation simply by modelling existing data more intensively. Routine surveillance should instead serve as an **anchor for prediction**, providing longitudinal evidence that becomes more informative when interpreted alongside molecular, clinical, behavioral, social, and geographic signals [6].

## 6.2. Molecular and Genomic Surveillance

Molecular and genomic surveillance adds information that routine clinical reporting cannot provide by revealing patterns of genetic relatedness among diagnosed infections. These data can support identification of rapidly growing clusters and help public-health teams recognize transmission patterns that may not be apparent from diagnosis counts alone [2]. For anticipatory surveillance, however, the more important opportunity is not simply to detect clusters earlier, but to estimate which emerging clusters are most likely to expand and therefore warrant prioritized investigation [19].

AI and network-based methods could combine sequence relationships with cluster growth, timing of diagnoses, geographic patterns, and epidemiological characteristics to distinguish signals requiring urgent attention from those less likely to escalate [9]. Yet molecular data provide an incomplete view of transmission. Undiagnosed or unsequenced infections remain invisible, sequencing coverage varies across populations and jurisdictions, and genetic similarity does not establish direct transmission between individuals [30]. Molecular signals should therefore be treated as one layer of epidemiological evidence rather than definitive representations of transmission. Their greatest anticipatory value emerges when they are interpreted alongside independent clinical and population-level information.

### 6.3. Clinical and Electronic Health Data

Clinical and electronic health records can add a level of detail that routine surveillance datasets often lack. The broader digital transformation of healthcare, including increasingly automated monitoring, connected clinical technologies, and data-driven hospital systems, is expanding the volume and diversity of information potentially available for intelligent health applications [38]. Medication histories, appointment patterns, laboratory trajectories, comorbidities, previous treatment interruptions, and clinical documentation may reveal deterioration before it appears in formal surveillance indicators, which is particularly important where delayed recognition and treatment failure can contribute to advanced HIV disease and preventable adverse outcomes [8, 39]. AI can integrate these longitudinal signals to identify patients whose probability of disengagement or viral non-suppression is increasing, potentially creating an earlier opportunity for adherence support, re-engagement, or other intervention [25].

Yet greater clinical detail does not automatically produce better surveillance. Electronic health records are designed primarily for care delivery rather than epidemic forecasting, and documentation practices, data completeness, and interoperability vary across institutions [33]. They also disproportionately represent people who interact with healthcare services. Clinical data are therefore most valuable when treated as a complementary early signal, not as a complete representation of population-level HIV risk [18].

### 6.4. Behavioral, Social, Geographic, and Mobility Information

HIV transmission occurs within social and geographic contexts that clinical and laboratory records capture only partially. Changes in sexual networks, prevention uptake, housing stability, healthcare access, migration, population movement, and local service availability may alter transmission risk before those changes become visible in diagnosis or viral-load data [20]. Geographic and mobility information can further show how risk extends across administrative boundaries and how connections between communities may shape emerging transmission patterns [12].

Integrating these signals could therefore improve the contextual interpretation of conventional surveillance. A rise in diagnoses, for example, may have different implications when considered alongside changes in testing access, PrEP coverage, population movement, or other local conditions [10]. These data also require caution. Behavioral information may be incomplete or selectively reported, social indicators can become outdated, and mobility patterns should not be treated as direct evidence of transmission. Their value lies in providing context for emerging signals, helping distinguish epidemiologically meaningful change from patterns produced by healthcare utilization, reporting, or surveillance coverage [4].

### 6.5. Multimodal Predictive Systems

The greatest opportunity for anticipatory HIV surveillance may lie in combining data sources that capture different dimensions of the epidemic. Routine surveillance can reveal changes in diagnoses and care outcomes; molecular data can identify emerging transmission

**Table 2:** HIV surveillance data streams and their potential contribution to anticipatory intelligence

| Data stream                                  | Information captured                                                                            | Potential contribution to anticipatory intelligence                                                             | Key limitations                                                                                                 |
|----------------------------------------------|-------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|
| Routine surveillance and care-continuum data | Diagnoses, CD4 counts, linkage, retention, viral suppression                                    | Detects changing trends and trajectories in transmission and care outcomes                                      | Reporting delays; incomplete representation of undiagnosed or poorly engaged populations [1]                    |
| Molecular and genomic data                   | Viral sequences, genetic relatedness, molecular clusters, cluster growth                        | Identifies emerging transmission structures and supports prediction of cluster expansion                        | Unequal sequencing coverage; incomplete networks; genetic similarity does not establish direct transmission [2] |
| Clinical and electronic health data          | Laboratory histories, appointments, medications, treatment interruptions, clinical notes        | Provides early signals of deteriorating engagement, treatment interruption, or viral non-suppression            | Inconsistent documentation; interoperability problems; dependence on healthcare contact [25]                    |
| Behavioral and social data                   | Prevention uptake, healthcare access, housing instability, socioeconomic and behavioral factors | Provides context for changing vulnerability, prevention gaps, and barriers to care                              | Measurement and self-report bias; incomplete data; privacy concerns [26]                                        |
| Geographic and mobility data                 | Spatial distribution, population movement, service locations, accessibility                     | Detects geographic shifts in risk and potential mismatches between emerging need and available services         | Spatial aggregation may obscure heterogeneity; mobility does not establish transmission [12]                    |
| Integrated multimodal data                   | Combined routine, molecular, clinical, behavioral, social, and geographic signals               | Triangulates complementary signals and may strengthen early identification and prioritization of emerging risks | Data linkage, asynchronous reporting, accumulated biases, interpretability, and governance challenges [35]      |

structures; clinical records can capture early deterioration in health and engagement; and behavioral, social, and geographic information can provide context for changing risk [14]. Multimodal systems may strengthen prediction by identifying patterns that remain weak or ambiguous when individual data streams are considered separately [35].

The value of such integration lies in triangulation rather than algorithmic substitution. AI can help identify concordant or conflicting signals and direct attention toward patterns requiring further investigation, while epidemiological, clinical, and community expertise remains necessary for interpretation [24]. For example, a prediction supported by changes in care outcomes, molecular-cluster growth, and relevant population-level indicators may warrant greater concern than an isolated algorithmic alert [3].

Integration, however, does not eliminate the limitations of the underlying data. Different sources vary in timeliness, completeness, coverage, and reliability [14]. Multimodal systems should therefore preserve these uncertainties rather than collapse heterogeneous evidence into an apparently authoritative risk score. Their contribution is strongest when complementary signals support earlier identification of emerging risk, followed by epidemiological verification and proportionate public-health action [17]. The principal data streams and their potential contributions to anticipatory surveillance are summarized in Table 2.

## 7. The Prediction-to-Response Gap

### 7.1. When Should a Prediction Trigger Action?

A prediction becomes useful to public health only when it can support a defensible decision about whether and when to intervene. This creates a difficult threshold problem. Acting on every elevated risk estimate would consume limited resources and could expose communities to unnecessary surveillance, while waiting for near certainty may eliminate the very lead time that makes prediction valuable [4]. The appropriate threshold therefore cannot be determined by model performance alone [23].

Instead, thresholds should reflect the predicted probability and severity of the outcome, uncertainty around the estimate, available lead time, feasibility of intervention, and consequences of acting or not acting [15]. A moderate probability of rapid cluster expansion, for example, may justify investigation when the potential intervention is timely and relatively low burden, whereas more intrusive actions should require stronger supporting evidence. Predictions should also be interpreted alongside epidemiological and contextual information rather than converted automatically into interventions. The purpose of an AI-generated alert is therefore not to make the decision itself, but to identify situations in which the evidence has become strong enough to warrant structured public-health assessment and, where justified, earlier action [3].

### 7.2. False Alarms Versus Missed Transmission Events

Any early-warning system must negotiate a trade-off between detecting emerging threats and generating unnecessary alerts. Lowering the threshold for action may identify more transmission events early, but it also increases false alarms, potentially diverting testing, outreach, and investigative capacity from other priorities. Repeated false alerts may also produce alert fatigue and weaken confidence in the system [22]. Conversely, a highly conservative threshold may improve specificity while allowing important transmission signals to remain undetected until opportunities for early intervention have narrowed [10].

The appropriate balance is therefore context dependent. Errors should be evaluated according to their public-health consequences, not simply their statistical frequency [23]. Missing a rapidly expanding cluster may carry greater consequences than investigating a signal that ultimately does not escalate. Thresholds should consequently reflect available resources, intervention burden, uncertainty, and the relative costs of false-positive and false-negative decisions [19].

### 7.3. Who Receives the Alert?

Even a timely and accurate prediction has limited value if it does not reach someone positioned to interpret and act on it. Predictive surveillance therefore requires clearly defined alert ownership and accountability [15]. Depending on the signal, recipients may include surveillance epidemiologists, molecular cluster-response teams, clinicians, prevention programs, or local public-health authorities [3].

Importantly, alerts should not move directly from an algorithm to intervention without appropriate interpretation. The recipient must be able to examine the underlying evidence, assess uncertainty, compare the prediction with other epidemiological information, and determine whether escalation is justified [36]. Systems should also specify who is responsible when signals cross organizational or geographic boundaries. Without predefined pathways for receiving, reviewing, and escalating alerts, predictive surveillance can generate information without producing a coordinated response [17].

### 7.4. What Intervention Follows?

The response to a predictive signal should reflect the outcome being forecast, the location and population affected, and the mechanisms contributing to the identified risk [16]. A forecast of increasing diagnoses in a geographic area might prompt intensified testing or PrEP outreach, whereas predicted expansion of a molecular cluster may justify accelerated epidemiological investigation and rapid-response activities informed by cluster-detection and contact-tracing approaches [40]. Signals of impending treatment disengagement or viral non-suppression may instead require ART adherence support or re-engagement in care [8].

These response options should be defined before deployment rather than determined only after an alert occurs [9]. Intervention intensity should also remain proportionate to the strength, urgency, and uncertainty of the evidence. Predictive surveillance is most useful when it enables public-health systems to intervene earlier and more selectively, rather than simply increasing the number of alerts generated [4].

## 7.5. How Should Success Be Measured?

The evaluation of AI-enabled HIV surveillance must extend beyond conventional measures of predictive performance. AUROC, sensitivity, and specificity establish whether a model can discriminate between outcomes, but they do not establish whether its use improves public health [15]. A model can perform well statistically while providing insufficient warning, producing alerts that cannot be acted upon, or directing interventions that fail to reach the populations for whom they are intended [35].

Evaluation should instead examine the consequences of using predictive surveillance in practice. Lead time establishes whether a signal arrives early enough to alter the course of events, while calibration determines whether predicted probabilities correspond to observed risks [23]. Actionability and intervention uptake further indicate whether predictions support feasible decisions and whether resulting responses reach their intended populations. The strongest evidence, however, comes from transmission and care outcomes: whether acting on predictions reduces new infections, prevents disengagement, improves viral suppression, or produces other measurable benefits compared with existing practice [24].

These benefits must also be assessed through an equity lens [5]. Overall improvement can conceal poorer performance, disproportionate alerts, or unequal intervention benefits across populations [17]. Success should therefore be judged across lead time, calibration, actionability, intervention uptake, health outcomes, and equity, with the ultimate standard being whether predictive surveillance enables earlier, effective, and equitable public-health action [13].

## 8. Ethics, Equity, and the Risks of Predictive HIV Surveillance

### 8.1. Privacy, Molecular Surveillance, and Potential Misuse

Predictive HIV surveillance creates substantial privacy concerns because linking clinical, molecular, geographic, and behavioral data can make individuals increasingly identifiable [17]. Molecular surveillance requires particular caution: genetic similarity can reveal transmission clusters, but it cannot establish who transmitted HIV to whom, and incomplete sequencing means observed networks represent only part of transmission [32].

These limitations become especially important where HIV exposure or transmission is criminalized [3]. Data collected for public-health purposes could potentially be interpreted or used beyond their original purpose, creating legal, social, or stigmatizing consequences. Predictive systems therefore require strong safeguards governing data linkage, access, interpretation, sharing, and secondary use. Greater predictive capability should not come at the cost of privacy or produce transmission inferences that the underlying evidence cannot support [30].

### 8.2. Algorithmic Bias and Surveillance Inequality

Algorithmic bias in HIV surveillance can arise before an AI model is developed because the underlying data are produced by unequal systems of testing, diagnosis, treatment, and reporting [1]. Populations with frequent healthcare contact may generate detailed longitudinal records, while people facing barriers to testing or care may appear only intermittently or remain absent altogether, a concern that is particularly important for surveillance systems serving underserved communities [41]. Models trained on these data may therefore learn patterns of surveillance visibility alongside patterns of HIV risk [24].

This creates a critical interpretive problem: low predicted risk may reflect low surveillance visibility rather than low HIV transmission risk. Limited testing can reduce documented diagnoses, poor engagement with care can produce incomplete clinical histories, and unequal sequencing coverage can make some transmission networks less visible than others [2]. Missingness should therefore not automatically be treated as random or epidemiologically neutral [17].

The central equity question is consequently not only who is classified as high risk, but who is absent from the data? Predictive systems should assess differences in data coverage, missingness, and model performance across populations before deployment [21]. Otherwise, AI may reproduce existing surveillance inequalities while presenting them as objective estimates of future risk [33].

### 8.3. Community Trust, Transparency, and Governance

Anticipatory HIV surveillance depends on community trust because predictive systems may influence how individuals, networks, or communities are prioritized for intervention. A technically effective system can still cause harm if affected communities do not understand how their data are used or perceive surveillance as intrusive [3]. Community involvement should therefore extend beyond consultation to meaningful participation in decisions about acceptable data use, prediction targets, and response strategies [17].

Transparency and accountability are equally important. Public-health agencies should clearly define how predictions are generated, who receives alerts, and what actions may follow [36]. Human oversight should remain central, particularly when predictions involve uncertain or sensitive information. Strong governance should also establish limits on data access, retention, sharing, and secondary use. Ultimately, trust should be treated as part of surveillance effectiveness: predictive intelligence has limited public-health value if the system producing it undermines the communities whose participation makes surveillance possible [35].

## 9. A Framework for AI-Enabled Anticipatory HIV Surveillance

### 9.1. Proposed Anticipatory HIV Surveillance Framework

The evidence synthesized in this review suggests that anticipatory HIV surveillance requires more than adding predictive algorithms to existing surveillance systems [15]. Prediction must be embedded within a pathway that connects diverse data, emerging signals, epidemiological interpretation, and public-health response [6]. I therefore propose an AI-Enabled Anticipatory HIV Surveillance Framework organized

around nine linked stages:

OBSERVE → INTEGRATE → DETECT → PREDICT → VALIDATE → PRIORITIZE → RESPOND → EVALUATE → LEARN

OBSERVE represents continuous collection of complementary information from routine HIV surveillance, care-continuum indicators, molecular and genomic surveillance, clinical records, and relevant geographic and social data [14]. The purpose is not to assume that more data automatically improve prediction, but to capture different dimensions of transmission, prevention, and engagement in care [1].

INTEGRATE involves linking these data while assessing completeness, timeliness, missingness, and differences in population coverage [21]. This step is critical because combining biased or delayed datasets does not eliminate their limitations [24]. Instead, integration should make those limitations visible before predictive modelling begins.

DETECT identifies meaningful deviations from expected patterns, such as unusual changes in diagnoses, viral suppression, care engagement, or molecular-cluster growth [2]. PREDICT then moves beyond detecting what is already occurring to estimating what may happen next within a defined prediction horizon. Potential outcomes include future cluster expansion, increasing geographic transmission, treatment disengagement, or viral non-suppression [11].

Prediction alone, however, should not trigger intervention. VALIDATE requires algorithmic signals to be examined against additional epidemiological, clinical, molecular, and contextual evidence [35]. This step creates an important boundary between automated prediction and public-health decision-making. PRIORITIZE then determines whether the validated signal is sufficiently urgent, credible, and actionable to cross a predefined response threshold. Prioritization should consider predicted risk, uncertainty, available lead time, intervention feasibility, resource constraints, and potential consequences of action or inaction [4].

RESPOND connects the warning to an appropriate intervention. Depending on the predicted outcome, this could involve targeted testing, PrEP outreach, cluster investigation, ART re-engagement, community-based intervention, or redistribution of prevention resources [3]. EVALUATE determines whether the response actually changed meaningful outcomes rather than merely whether the original prediction was accurate. Finally, LEARN feeds implementation experience back into the surveillance system through model recalibration, threshold adjustment, improved data collection, and modification of response strategies [29].

The framework therefore conceptualizes anticipatory surveillance as a continuous learning cycle rather than a prediction endpoint [13]. AI contributes most when it creates useful lead time within this larger system. Its value ultimately depends on whether emerging risk can be identified, validated, and converted into intervention before the anticipated adverse outcome becomes established [16].

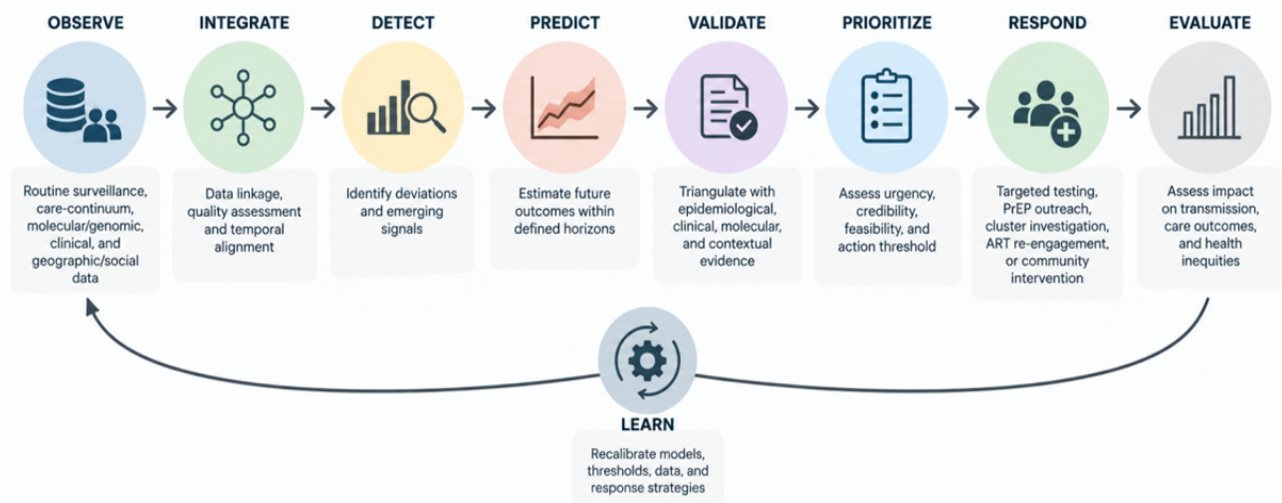


**Figure 1:** AI-Enabled Anticipatory HIV Surveillance Framework

The framework conceptualizes anticipatory surveillance as a continuous cycle in which multimodal HIV data are observed and integrated to detect emerging signals, predict future risks, validate and prioritize alerts, guide targeted responses, evaluate public-health outcomes, and support iterative learning and recalibration Figure 1.

## 9.2. Principles for Responsible Implementation

Successful implementation of anticipatory HIV surveillance requires more than technical model performance. Predictive systems should satisfy five connected requirements: they must be timely, validated, interpretable, equitable, and actionable [17]. Timeliness means that predictions must provide sufficient lead time for an intervention to occur before the anticipated outcome becomes established. This requires attention not only to computational speed but also to delays in testing, reporting, data integration, and alert delivery [4].

Predictions must also be validated and interpretable. Model outputs should be evaluated against independent epidemiological and contextual evidence before triggering consequential action, particularly when uncertainty is high [23]. Decision-makers should be able to understand what outcome is being predicted, over what time horizon, which information contributed to the prediction, and how confident the system is [36]. Interpretability is therefore important not simply for technical transparency, but for determining whether an alert has a plausible epidemiological basis.

Finally, predictive surveillance must be equitable and actionable. Performance should be assessed across populations and surveillance contexts to identify whether unequal data coverage produces systematically different errors or benefits [24]. At the same time, every operational prediction should correspond to a feasible response pathway, with clear responsibility for reviewing the alert and predefined intervention options [15]. Together, these principles shift the standard for responsible AI from producing accurate predictions to generating timely, trustworthy, equitable, and usable intelligence that can support meaningful public-health action. Effective implementation may also depend on coordination and collaboration across institutions and public-health stakeholders, reflecting broader evidence that partnerships can strengthen infectious-disease prevention and control efforts [42].

## 10. Research Agenda

The next phase of research should determine whether AI provides meaningful lead time, rather than simply improving retrospective identification of HIV risk. Studies should compare AI-enabled approaches directly with conventional surveillance and establish how much earlier relevant events can be identified [13]. Importantly, useful lead time should be defined in relation to specific interventions. Predicting cluster expansion several weeks earlier, for example, matters only if that interval is sufficient to initiate investigation, expand testing, strengthen PrEP outreach, or redirect prevention resources [19]. Future evaluations should therefore report not only predictive accuracy, but also the time gained between an actionable warning and the outcome it is intended to prevent.

A second priority is determining whether multimodal integration provides genuine incremental predictive value. Combining molecular, clinical, routine surveillance, geographic, behavioral, and social data may improve situational awareness, but greater data complexity does not necessarily produce better prediction [27]. Research should identify which combinations contribute information beyond simpler surveillance models and whether they improve prediction of outcomes that matter operationally. A particularly important test is whether AI can predict future cluster expansion, rather than simply identify clusters that have already grown sufficiently to become detectable [2].

The durability and transportability of these models also remain unresolved. Relationships learned in one jurisdiction or historical period may change as PrEP uptake, ART coverage, testing practices, population movement, and service access evolve [29]. Models should therefore undergo temporal and external validation, with explicit examination of performance across settings and populations [21]. Research is also needed to determine how frequently models should be recalibrated, how concept drift should be detected, and when local adaptation is preferable to transferring an existing model.

Most importantly, the field needs to move from retrospective model development toward prospective evaluation in functioning public-health systems. Studies should test whether AI-generated warnings change decisions, trigger earlier interventions, and ultimately improve transmission or care outcomes compared with existing surveillance practice [15]. These evaluations should also examine false alarms, missed events, intervention uptake, resource requirements, and differential performance across populations. Equity must be treated as an outcome rather than an assumption: improved overall performance should not conceal poorer detection or disproportionate surveillance among particular communities [17]. The decisive research question is therefore no longer simply whether HIV-related outcomes can be predicted, but whether acting on those predictions produces earlier, measurable, and equitable public-health benefit.

## 11. Conclusion

Artificial intelligence creates an opportunity to move HIV surveillance beyond documenting transmission and care outcomes after they have occurred [13]. Yet the value of this transition will depend less on the sophistication of individual algorithms than on whether prediction can be translated into earlier and more effective public-health action [16]. This requires surveillance systems that can move from retrospective monitoring toward the timely identification, validation, and response to emerging risks.

Achieving this transition requires predictive systems that operate within, rather than apart from, existing surveillance infrastructure. Signals must arrive with sufficient lead time, remain reliable as epidemic conditions change, be validated against complementary epidemiological evidence, and connect to clearly defined interventions [35]. Equally important, predictive systems must recognize that surveillance data reflect unequal patterns of testing, diagnosis, healthcare access, and molecular sequencing. Without attention to these inequalities, AI may reproduce existing surveillance blind spots while giving them an appearance of computational objectivity [24].

The future of AI-enabled HIV surveillance should therefore be judged by a higher standard than predictive accuracy alone. Its success will depend on whether it generates timely, validated, interpretable, equitable, and actionable intelligence that improves decisions and outcomes compared with existing practice [17]. Ultimately, AI will have transformed HIV surveillance only when earlier prediction enables interventions that prevent transmission, treatment disengagement, or viral non-suppression that might otherwise have occurred [5].

## Article Information

**Ethical Approval:** Not applicable.

**Consent to Participate:** This article is a narrative review based exclusively on previously published literature and did not involve the recruitment of human participants, collection of primary human data, use of identifiable personal information, or involvement of animal subjects.

**Consent for Publication:** Not applicable.

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