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# Strengthening HIV Surveillance Systems in Underserved U.S. Communities: A Review of Emerging Epidemiologic and Data-Driven Approaches

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**Abstract**: **Background:** As historically witnessed, HIV surveillance in the United States has often been dependent on traditional case reporting and demographic factors, but the existing disparities within underserved communities, such as rural areas, racial/ ethnic minorities, and people who inject drugs, continue to be a barrier to the efficacy of standard systems. **Purpose:** This narrative review is a synthesis of the recent developments (2020-present) in epidemiologic and data-driven methods of HIV surveillance, particularly in the underserved U.S. communities, with a critical analysis of how the advances can transform the way the population receives interventions. **Method:** We rely on peer-reviewed articles, policy reports, and health data on the population to infer the major emerging trends in molecular cluster detection, machine learning (ML) in incidence prediction, equity-oriented spatial mapping, and integration of social determinants. Rather than generalizing results from study after study, we portray the review in the shape of thematic trends without summarizing the strengths, limitations, and opportunities. **Findings:** Molecular cluster identification has become a national system, allowing quick detection of cross-jurisdictional transmission networks, and 404 clusters were detected during 2018-2023. The prediction of HIV incidence with high precision is now possible with the use of ML models trained on publicly available health databases of STIs, partly due to the efficacy of this feature as the social vulnerability index (SVI). Visual representation of surveillance data identifies locations with racial, geographic, and socioeconomic disparities. Nonetheless, there are still gaps in terms of delayed reporting of the sequence, low representation of the rural and marginalized populations, and a lack of integration of behavioral data. Inequalities in access to care and subjugation remain, particularly in rural counties in the group among patients who inject drugs (PWID). **Summary:** Integration of molecular epidemiology, ML, and equity-oriented data tools represents the beginning of a new era of HIV surveillance in the U.S. It will, however, be imperative to invest in capacity building, data infrastructure, and community engagement to ensure that the impact of these tools is maximized by ensuring that these underserved populations can access these tools. Improved surveillance can educate more objectively, expediently, and fair preventive activities and aid in eradicating chronic deficiencies in HIV care.

**Keywords:** HIV surveillance**,** molecular cluster detection**,** machine learning**,** health equity**,** and underserved communities.

## INTRODUCTION

Although much progress has been achieved in the prevention and treatment of HIV, more than 250,000 people continue to be greatly unequal in the United States, particularly the marginalized communities and underserved areas (Saunt *et al*., 2025). These endemic injustices underscore the necessity of sophisticated and progressive HIV surveillance methods that have the potential to fully capture and respond to the changing epidemic environment in these communities (Mann & Barocas, 2024). Despite the national surveillance data showing the trend of the overall reduction in new infections in certain classes of the age group and transmission types, the progress is uneven, and the disparities between the regions and population persist. These heterogeneities demonstrate that the aggregate statistics of the country mask local and network-level processes of transmission that lead to continued spread of HIV infection within marginalized groups (CDC, 2025).

The primary element of the traditional surveillance that has been employed to design the programs and distribute resources consists of the case reporting to the National HIV Surveillance System (NHSS), regular care continuum indicators surveillance, and occasional behavior surveillance (Cohen *et al*., 2014). These systems provide the population-level, standardized information concerning the diagnoses, the connection to the care, and the viral suppression. Yet, structural limitations such as reporting latencies, inhomogeneous coverage of laboratory sequence data, and gaps in behavioral connection and granularity to support local-level inference gradually limit their usefulness in responding to emergent transmission swiftly and support proactive and equity-oriented reactions (Mann & Barocas, 2024).

Over the past five years, the supplementary epidemiologic and data-driven innovations have begun to transform the HIV surveillance in the U.S (Saldana *et al* 2024). Three key advances stand out. First is a molecular cluster detection, in which HIV genetic sequence information is utilized to approximate probable new transmission networks that have been scaled by the country. Recent CDC analyses have also revealed hundreds of priority

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clusters in 2018-2023, with many of them cutting across jurisdictions, thereby revealing transmission patterns that could not be observed using geographically siloed case counts. Such an approach is likely to enable quicker and more precise outbreak detection and targeting resources (CDC, 2025). Second, machine learning (ML) and predictive analytics using regular public health data, including STI diagnoses, provider diagnoses, and community vulnerability data, is becoming a tool to predict HIV incidence at sub-jurisdictional levels. Models of the U.S. South off the counties show that ML can predict imminent HIV diagnoses increases, which provide early warning features with the potential to improve surveillance by turning it into a forward-looking process instead of the backward one (Saldana *et al*., 2024). Third, the development of spatial and equity-driven visualization tools has rendered finer maps of the social determinants highly available to the public health practitioners, policymakers, and local partners. These tools explain geographic and sociodemographic differences in incidence, testing, PrEP uptake, and viral suppression, which connect the epidemiologic data to the contextual indicators, including poverty and insurance coverage, to further clarify the target of interventions and advocate for resources.

A combination of molecular epidemiology, predictive modeling, and equity-based spatial analytics are likely to give rise to a more responsive, network-conscious, and socially mindful surveillance system (Rennie *et al*., 2025). However, this aspiration has not been fulfilled in most of the underserved communities with a number of challenges that have continued to persist (Saunt *et al*, 2025). J Jurisdictional data completeness and representativeness Data completeness and representativeness of margins and rural populations Data may be underrepresented in molecular data due to reduced care access and sequencing (CDC, 2025). Isolation of data types prevents the integration of behavioral, molecular and predictive data, which restricts actionable insights (CDC, 2025). These limitations are the capability of these analytic tools to be applied, due to restrictions in the infrastructure available across health departments, especially in resource-limited environments (Saldana *et al*., 2024). Molecular surveillance is further complicated by ethical issues such as privacy, risk of criminalization, and stigma (Saunt *et al*, 2025). Unless there is a clear governance and community involvement, these issues may further fuel mistrust and decrease participation in prevention and care (Abboah-Offei, 2025). These barriers demonstrate a gap in research and practice: despite the availability of novel molecular and analytic tools that allow detecting and predicting HIV transmission at increasingly finer scales, there is no evidence available on how to equitably deploy these instruments in underserved communities of the United States, how to integrate behavioral and social determinants to present actionable insights, and on how to establish governance mechanisms that balance privacy and the need to take action on public health (Mann *et al*., 2024). The technical development and descriptive mapping process lack a synthesis of the current literature in terms of local programs to an equity-focused and operation-based roadmap (CDC, 2025).

This is a narrative review that synthesizes peer-reviewed literature published in 2020 and beyond, presenting a critical review of emerging epidemiologic and data-driven HIV surveillance strategies in the U.S. It evaluates their implications for underserved communities and recommends priorities for research, governance, capacity building, and implementation. The review will aim to direct the future policy and practice by forecasting trends, problems, and meanings of challenges in a manner that will promote both equity, as well as, effectuality in the surveillance modernization process.

## EMERGING TRENDS AND THEMATIC ANALYSIS (RESULTS)

This section synthesizes major recent trends reshaping HIV surveillance for underserved U.S. communities, organized into four thematic subsections: (1) Scaling molecular cluster detection and its equity implications, (2) Predictive analytics and machine learning for early warning, (3) Integrating spatial, behavioral, and multilevel data to reveal structural drivers, and (4) Governance, ethics, capacity, and implementation challenges. Each subsection compares and contrasts relevant studies published from 2020 onward, highlights unresolved controversies, and offers expert interpretation of the field's trajectory.

### Theme 1: Scaling Molecular Cluster Detection: Promise, Performance, and Equity Implications

Molecular cluster detection (MCD) that uses HIV genetic sequence data, mostly collected through the pol gene by standard genotypic resistance testing, has graduated to the level of near-national implementation, explicitly embedded in federal programs, such as Ending the HIV Epidemic (EHE) (France *et al*., 2025; CDC, 2024). National CDC reports reveal identification of over 400 priority molecular clusters during 2018-2023, with 80% crossing multiple jurisdictions, highlighting the critical need for coordinated, multi-jurisdictional surveillance and response strategies (France *et al*., 2025).

The application of MCD has been shown to be useful in informing rapid responses to health crises, such as responding to people who inject drugs (PWID) and containing outbreaks (Bonavitacola 2025; CDC, 2024). Nonetheless, there are three driving operational metrics that affect performance, which are sequence coverage, reporting timeliness, and analytic definitions. The level of sequence completeness differs across the board; relatively resource-limited and rural jurisdictions, in turn, tend to become underrepresented in the marginalized communities and possibly blind in detecting the clusters (France *et al*., 2025). Delays between sample collection and sequence receipt (median = 34 days) limit rapid action, although improvements in local sequencing infrastructure show promise (CDC, 2024). The divergent cutoffs of analytical thresholds (e.g., 0.5% reduced genetic distance cutoff introduced by the CDC) affect sensitivity-specificity tradeoffs and make comparisons across studies difficult (Broshkevitch *et al*., 2025). Of primary concern is the equity issues. Limited access to healthcare, like uninsured rural residents, the homeless, and racial/ethnic minorities, has a risk of not being represented in molecular datasets, which can conceal the transmission in underserved populations (France *et al*., 2025). This presents problems of forming coordinated response efforts in the absence of data-sharing systems because of cross-jurisdictional transmission network mobility (CDC, 2024). The privacy concerns and the potential risk of not identifying anyone unintentionally, namely in small communities, call into question the need to have strong community involvement and deterrents (Schuster *et al*., 2025). It is important to mark that the evidence of the effects of routine MCD on incidence reduction on the population level is rather scarce, which is why the study is urgently needed (CDC, 2024). Expert recommendations emphasize investments to improve sequencing accessibility in underserved settings, development of cross-jurisdictional data sharing agreements, and coupling molecular data with behavioral and social context to tailor equitable interventions.

## Predictive Analytics and Machine-Learning: From Forecasting to Decision Support

This has been done over the past five years, where the movement of machine learning (ML) and predictive analytics applications to public health HIV surveillance data has proliferated exponentially. Research is starting to rely on notifiable STI histories, sociodemographic, and geospatial variables such as the CDC Social Vulnerability Index (SVI) to predict future HIV incidence and high-risk populations (Saldana *et al*., 2024). One of them is the ML model created in Fulton County, GA, which uses gradient boosting algorithms on STI registries and community-based SVI data in the future to predict HIV diagnosis with a high level of discrimination (Saldana *et al*., 2024). The input data can be diverse, such as electronic health records or community indices on a community scale; ensemble tree-based models are usually effective in comparison with other models because they are resilient to missingness and nonlinear trends (Saldana *et al*., 2024). ML models operate across a prediction continuum from individual risk assessment for case-finding to community-level risk for targeted resource allocation (Saldana *et al*., 2024).

These methods create early-warning features that allow adopting a surveillance paradigm that views surveillance no longer as an act of retrospective examination but as a proactive preventative measure (Saldana *et al*., 2024). ML strategies can improve resource-constrained departments by using routinely assembled public health statistics. Nevertheless, there are still considerable limitations: models tend to remain unvalidated in the real world, current data quality may be biased, and missingness causes bias, and practitioners might have little or no confidence in their use over time due to the lack of their interpretability (Saldana *et al*., 2024). Such critical controversies as the possible support of inequities by relying on biased historical data, and ambiguous operational mechanisms of converting the results of ML into the actions of the health community (Saldana *et al*., 2024). Professionals support the idea of external validation, interpretability improvements, equity audits, and incorporation into human-centered decision-making processes in order to maximize the benefits.

## Multilevel Integration: Spatial Mapping, Behavioral Data, and Social Determinants

More recent initiatives focus on the combination of molecular, behavioral, and social determinant data to produce broad insights to inform targeted interventions. Such websites as AIDSVu have increased to include county- and ZIP-level maps superimposing HIV data with poverty level, insurance coverage, and PrEP adoption, making it easy to engage a community and take action (AIDSVu, 20222024). Behavioral surveillance surveys including the National HIV Behavioral Surveillance (NHBS) augment this data with individual risk behavior, testing and prevention behavior information (Gallagher *et al*., 2007). Connection of social determinants through indices such as SVI strengthens the understanding of structural determinants, housing instability, insurance cover, substance use services, and biomedical intervention as essential areas of intervention in addition to biomedical intervention (Saldana *et al*., 2024). Combined modes of molecular-behavior provide the understanding of the transmission context, sexual or injection networks and establish appropriate response customization.

There are barriers of law and privacy that prevent the connecting of disparate data sources, the inability of small populations to identify variation in the data, and lags in the use of updates to the denominator (Garcia *et al*., 2023). The professional advice given is the construction of safe data pipelines with effective governance, using sophisticated statistical smoothing methods of small-area forecasts and linking the mapping deliverables to stakeholder engagement structures to ethically implement them effectively.

### Governance, Ethics, and Implementation: The Human Systems that Enable Surveillance

The technical capacity has grown so fast that it has exceeded the consensus on the governance, consent, and ethical protection. The research on the stakeholders shows conflicting priorities: certain officials of the public health department focus on utility, whereas the representatives of the community focus on the possible risks, such as privacy invasion, stigma, and threat of criminal prosecution due to the HIV criminalization legislation (Schuster *et al*., 2025). Consent models are controversial scenarios, and there is a conflict between the attitudes of mixed communities regarding the use of clinical sequencing data to conduct surveillance without clear consent (Schuster *et al*., 2025).

The implementation faces workforce limitations and uneven bioinformatics capacity, which is particularly a restraint to rural and resource-limited health departments (Purcell *et al*., 2025). The presence of a significant lack of implementation science research assessing the translation of molecular and predictive surveillance into better outcomes in practical situations is significant (Abboah-Offei, 2025).

It is recommended that clear data governance structures should be established with legal safeguards, criminalization prohibited by law enforcement should be barred, and open practices should promote trust in the community. The focus of staff development in the areas of bioinformatics and privacy would be essential (Schuster *et al*., 2025).

**Table 1.** Summary of Emerging Approaches to Strengthen HIV Surveillance in Underserved U.S. Communities

| **Study/Source (Year)** | **Type/Setting** | **Key Methods** | **Main Findings** |
|---|---|---|---|
| France AM *et al*. (CDC EID, 2025) | National program/USA | NHSS sequences; Secure HIV-TRACE; national vs. state comparisons | 404 priority clusters (2018–2023); 80% multijurisdictional; median sample-to-sequence: 34 days (2023) |
| Saldana *et al*. (Clin Infect Dis, 2024) | County-level ML/Fulton Co., GA | Gradient boosting ML on STI registries + SVI | High-accuracy HIV incidence prediction; SVI/prior STI strongest predictors |
| RI Public Health–Academic Partnership (2023/2024) | State case study/RI | Monthly conferences; reinterviews; data pipelines | Integration beneficial; mixed reinterview acceptability; data silos/jurisdictional limits |
| CDC Science Brief (2024) | Policy synthesis | Evidence review for CDR outcomes | CDR improves prevention/care; clusters signal service gaps; best practices recommended |
| Schuster *et al*. | Ethics | Best-worst scaling | "Harms" vs. "Utility" classes; |

| | | | |
|---|---|---|---|
| (BMC Public Health, 2024) | prioritization | (practitioners/researchers) | stigma/prosecution concerns; need community engagement |
| AIDSVu (2022–2024 updates) | Data visualization platform | County/ZIP maps; SDOH overlays; PrEPVu | Small-area HIV/SDOH maps for advocacy/program targeting |

NHSS = National HIV Surveillance System; ML = machine learning; SVI = Social Vulnerability Index; CDR = cluster detection and response; RI = Rhode Island; SDOH = social determinants of health.

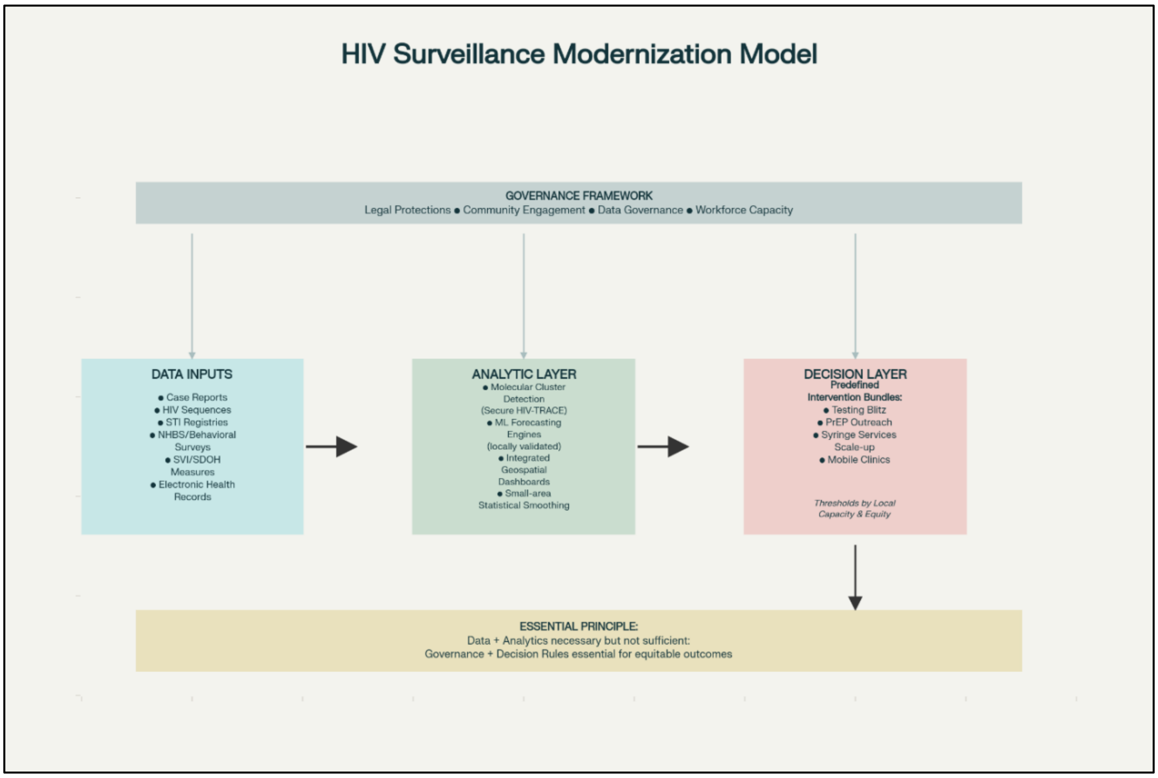

**Figure 1:** Conceptual Model: HIV Surveillance Modernization in Underserved U.S. Communities
Source: Author's Construct, 2025.

## Future Directions and Research Gaps

The development and dissemination of molecular epidemiology, machine learning, and geospatial technologies in the surveillance of HIV have a transformative potential in the prevention activities of underserved populations in the United States, where the centers of transmission frequently indicate unmet care and service needs (Wilbourn *et al.*, 2021). Nationwide analyses indicate that there is significant progress in detecting clusters with priority in 20182023, with 404 priority clusters identified through routine sequencing and programs such as Secure HIV-TRACE (Dennis *et al*, 2020), but with an uneven pattern in coverage across the nation and of the groups with disrupted access to care (France *et al.*, 2025). This imperfection is the reverse skewness of network inferences, and there can be concealed transmission paths, imposing disproportionately Black, Hispanic, and rural communities with lower coverage rates, as shown in research in Houston and elsewhere where sampling gaps during network reconstruction may change reconstruction (Mazrouee *et al.*, 2021). The solution to these gaps can be found in optimised routine sequencing of all new diagnoses through automated reflex workflows and commercial laboratories, as well as methods of methodology, such as Bayesian imputation or the use of phylogenetic, social network, and mobility data to reduce bias and protect privacy by methods such as differential privacy (Hughes *et al.*, 2019).

Machine learning models have potentially useful predictive performance, and incidence spikes that could be used to target PrEP have been shown to be accurately predicted in the context of the southern United States using gradient boosting algorithms using STI registries and social vulnerability indices, and historical diagnoses (Mazrouee *et al.*, 2024; Saldana *et al.*, 2024). Nevertheless, external verification in a variety of regions is insufficient, operational decision-points of interventions are non-clinical, and risks of bias of socioeconomic or policing data incorporated in inputs are present, thus necessitating explainable AI, hybrid mechanistic models, and co-constructed assessment frameworks of how cost-effective and actionable interventions are in a public health report (Bonavitacola *et al*., 2025; Schuster *et al*., 2025). The issue of ethics also complicates adoption because the concept of molecular surveillance arouses concerns of invasion of privacy, stigma, and criminalization of its use under state HIV exposure laws, and research involving communities has found specific stakeholder priorities of harms versus utility, particularly with LGBTQ+ populations, people who use drugs, and communities of color with historic historical mistrust (Schuster *et al*., 2024).

The innovations that need to be scaled involve strengthening infrastructure and labor capability because the rural health departments do not have staff and equipment to perform big-data analytics, and the ratio of clinicians to HI cases is significantly less beyond cities (Quinn *et al*., 2022). This can be met at regional centers of analysis, cloud computing, and fellowship training, as well as unified federal systems, in order to enjoy the benefits of economies of scale. Including social determinants of health, e.g., poverty, housing instability, stigma, has been a key frontier of the problem, making it possible to infer causally as to whether upstream factors are causing molecular clusters or equity metrics to reduce rather than augment disparities in surveillance (Kulohoma & Wesonga, 2025). Finally, the translation of indicators into action requires the implementation frameworks that help to connect siloed systems with rapid responses, such as testing blitzes or PrEP outreach that should be implemented by a trusted community member in underserved places to support equitable and long-lasting reduction of HIV incidence (Abboah-Offei, 2025).

## CONCLUSION

Currently, the U.S. HIV surveillance environment is developing exponentially with the help of molecular epidemiology, predictive analytics, and geospatial applications, which provide new opportunities to focus on the early detection of outbreaks and fair prevention of HIV in underserved communities in a disproportionate. These innovations do not substitute the old systems, they enlarge them. Molecular cluster identification through the use of Secure HIV-TRACE is accurate with regard to identifying rapid transmission networks, though it requires full sequence information and effective response capabilities, whilst machine learning models can indicate incidence by using the STIs registries and social vulnerability indices, and require prospective validation and reduction of bias. The AIDSVu is one of the geospatial platforms that democratize access to small-area HIV statistics superimposed with social determinants, and entire communities can be acted upon in coordination with local capacity. Technology is not the major challenge, but infrastructure gaps, such as data fragmentation and ethical governance, are the major challenges. Poor sequencing in rural communities, Black/Latino communities, and unstable care settings biases cluster inferences, and disparate behavioral, structural, and molecular data inhibit full risk profiling. Ethical issues, privacy invasion, stigma, and fear of criminalization under state laws, weaken trust in LGBTQ+, PWUD, and communities of color, threatening the increase in disparities unless the community is offered protection. The work ahead to be done would focus on modernizing infrastructure using automated reflex sequencing, robust cross-jurisdictional exchange, and cloud analytics available to small departments; justifiable ML with practical application; and community governance entrenching transparency and non-criminalization norms. Interoperable tools that preserve privacy and are privacy constrained will be created in the industry, bridging gaps in federal funding of bioinformatics workforce training, regional hubs, and equity measures. This is in line with the Ending the HIV Epidemic objectives that move surveillance in anticipatory and justice-based paradigms. The current-day urgency of modernizing HIV surveillance is a public-health priority that requires ethical responsibility, cooperation, and equity to ensure that the signals are translated into a lower incidence. These tools can ensure an accurate, fair system that supports national HIV-eradication by 2030 and further through dedication in all the sectors.

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