Optimising risk assessment of emerging threats in Africa through real-time ADAMS surveillance: the case of mpox 2025 in Sierra Leone

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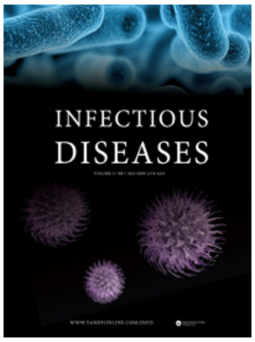

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COMMENT

Optimising risk assessment of emerging threats in Africa through real-time ADAMS surveillance: the case of mpox 2025 in Sierra Leone

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Background

On August 26, 2024, in response to the worsening global outbreak of mpox (MPXV virus), the World Health Organization (WHO) published a Global Strategic Preparedness and Response Plan [1]. The initiative followed the declaration of a State of Public Health Emergency of International Significance (PHEIC), proclaimed on August 14, due to the emergence of a new Clade Ib lineage, with epicenter in the Democratic Republic of Congo (DRC). The epidemic wave, in terms of spread and impact, has drawn international attention, recalling the global crises of 2022–2023 and reiterating the persistent vulnerability of health systems to re-emerging zoonoses, particularly in resource-limited settings. Nearly a year after the emergency was declared, the mpox virus continues to actively circulate. In Sierra Leone, the last quarter of 2025 saw a significant surge in cases, attributed mainly to Clade IIb: more than 4,000 confirmed cases, 91% of which were concentrated in the districts of Western Area Urban, Western Area Rural, and Bombali [2]. This trend reflects the tendency of the virus to spread in high-density urban environments, exacerbated by fragile health infrastructure and insufficient genomic surveillance.

Genomic analysis, while an essential tool for identifying mutations, reconstructing transmission chains, and monitoring viral evolution, remains fundamentally retrospective. Delays between sample collection, sequencing, and dissemination of results limit its effectiveness for timely interventions. To bridge these critical issues, it is crucial to integrate genomic surveillance with real-time epidemiological monitoring. This synergistic approach enables faster outbreak detection, better resource allocation, and more effective public health interventions.

Based on previous experiences in digital surveillance and epidemiological modelling [3,4], we present ADAMS (African Disease Analysis and Monitoring System), that is an open-source modular platform designed to support the collection, integration, and visualisation of epidemic data on the African continent. Although ADAMS is not intended to replace official surveillance systems, it is a complementary decision-support tool inspired by established models of digital epidemiology [5]. The platform aims to enhance visibility and timeliness in contexts where data are delayed or fragmented, providing a scalable, reproducible and economically sustainable solution for epidemic preparedness and response.

In rapidly changing epidemiological contexts, social media are proving to be valuable complementary sources for accessing real-time data [6]. In the current mpox outbreak in Sierra Leone, institutional updates disseminated by the National Public Health Agency (NPHA) via Channel X (formerly Twitter) enabled rapid mapping of areas of highest incidence. This initial level of information was then refined through more granular data from official sources and international databases, including verification of the availability of genomic sequences associated with new cases. The progressive integration of this information enabled a multidimensional analysis of the epidemic to support targeted resource allocation, on-the-ground interventions, and evidence-based and contextualized containment strategies.

ADAMS is proposed not only as a timely response to the mpox emergency, but also as a replicable model for strengthening epidemiological intelligence in resource-limited countries, where timeliness and

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data accessibility are often the main obstacles to effective outbreak management. Considering the growing threat posed by emerging pathogens, it is critical to promote innovative tools that can strengthen surveillance systems, improve outbreak management, and incentivize international cooperation. Only through adaptive approaches, based on integrated and transparent data, will it be possible to mitigate the health and social impact of future epidemic crises.

Materials and methods

ADAMS, available at the link: https://github.com/fbranda/ADAMS, aggregates real-time data from heterogeneous sources, including weekly and monthly epidemiological bulletins released by national and international health agencies such as the *Ministère de la Santé Publique, Hygiène et Prévention*, the Africa CDC, and the World Health Organization (WHO). These data include the number of suspected and confirmed cases, cumulative case counts, and geospatial distribution at subnational resolution. When available, demographic indicators (e.g. age, sex) and genomic data from platforms like GISAID (https://gisaid.org/) and Pathoplexus (https://pathoplexus.org/) are also incorporated. ADAMS adopts a modular architecture based on R packages such as *tidyverse* for data manipulation, *lubridate* for temporal processing, *sf* and *leaflet* for geospatial analysis, and *ggplot2* for visualisation. Installation instructions, system features, and usage documentation are detailed in the README (https://github.com/fbranda/ADAMS/blob/main/README.md). Among the next planned developments, the system will integrate *Shiny* for interactive dashboard creation and *RMarkdown* for automated report generation, further enhancing the platform's usability for real-time monitoring and evidence-based decision support.

Core analytical capabilities include: (i) Predictive analytics using statistical time-series models (e.g. ARIMA, exponential smoothing) with machine learning techniques implemented through libraries like *caret* and *randomForest*. (ii) Geospatial visualisations including dynamic choropleths and hotspot maps with interactive overlays. (iii) Temporal monitoring tools, such as rolling incidence curves, case fatality rate trends, and reproduction number (Rt) estimations. (iv) Network analysis, to explore spatial-temporal links between cases and clusters.

An overview of the structure and content of the ADAMS database used for the collection and monitoring of mpox surveillance data, is provided in Table 1, which outlines directory structure, file naming conventions, and detailed field specifications (name, description, format, and example) to support standardised data collection and integration across geographic and temporal dimensions.

Example application

Epidemiological situation at a glance in Sierra Leone

Between 16 January and 19 June 2025, a total of 4,221 confirmed mpox cases have been reported in Sierra Leone by the National Public Health Agency (NPHA), as shown in Figure S1 (A), with 2,008 cases in female individuals and 2,213 in male individuals. During this period, 26 deaths were recorded, corresponding to a case fatality rate (CFR) of 0.6%. The first confirmed cases appeared on 16 January ($n = 4$), followed by a gradual increase through late January and February. A significant surge was observed from mid-April, particularly during the week of 15–21 April (59 new cases), peaking on 4 May with 119 new confirmed cases. By 19 June, 173 new cases were reported. As of that date, 3,501 individuals had recovered and 694 remained active cases. All cases are presumed to be locally acquired, with no imported cases detected. Daily surveillance and reporting began in January and continued uninterrupted, contributing to timely case detection and response. The data indicate ongoing community transmission with a moderate burden and low but measurable fatality, peaking in intensity during April and May.

The geographical distribution of cases reveals a pronounced concentration in the Western Area, with Western Urban accounting for 2,459 confirmed cases—nearly 59% of the national total—and Western Rural reporting an additional 851 cases as of June 19, 2025 (Figure S1(B)). These two districts together represent the epicenter of the outbreak, with sustained transmission documented from the first day of reporting (16 January) through to the latest surveillance date (19 June). Bombali (243 cases) and Port

Table 1. Data dictionary for national- (A) and subnational-level (B) mpox surveillance datasets available in the ADAMS repository.

A. National-level surveillance data

Directory: surveillance/yyyy/Mpox/country (where yyyy indicates the year of surveillance)

Filename: Surveillance-data-mpox-outbreak-yyyy-by-country.csv

Field Name	Description	Format	Example URL / Value
Source	Source document containing the original data	PDF	Link
DateOfIssue	Date of publication of the surveillance report	Date (YYYY-MM-DD)	2024-08-23
Country	Country where the cases were reported	Text	Sierra Leone
Latitude	Latitude of the reporting country	Numeric	−3.9416119
Longitude	Longitude of the reporting country	Numeric	11.0375552
NewSuspectedCases	Newly suspected cases reported since the previous bulletin	Numeric	582
TotalSuspectedCases	Cumulative suspected cases as of the report date	Numeric	5000
NewProbableCases	Newly probable cases since the previous bulletin	Numeric	10
TotalProbableCases	Cumulative probable cases as of the report date	Numeric	100
NewConfirmedCases	Newly confirmed cases since the previous bulletin	Numeric	200
TotalConfirmedCases	Cumulative confirmed cases as of the report date	Numeric	500
TotalActiveCases	Number of active confirmed cases at the time of reporting	Numeric	385
NewRecoveredCases	Newly recovered cases since the previous bulletin	Numeric	30
TotalRecoveredCases	Cumulative recovered cases as of the report date	Numeric	100
NewConfirmedDeaths	Newly confirmed deaths since the previous bulletin	Numeric	2
TotalConfirmedDeaths	Cumulative confirmed deaths as of the report date	Numeric	15
CFR	Case Fatality Rate (TotalConfirmedDeaths / TotalConfirmedCases)	Numeric	8.0

B. Subnational-level weekly data

Directory: surveillance/yyyy/Mpox/country

Filename: track-outbreak-country-yyyy-by-district.csv

Field Name	Description	Format	Example
Source	Source document containing the original data	PDF	Link
DateOfIssue	Date of publication of the surveillance report	Date (YYYY-MM-DD)	2024-08-23
District	Name of the reporting district	Text	Bo
Latitude	Latitude of the district	Numeric	3.6682004
Longitude	Longitude of the district	Numeric	22.4296578
NewSuspectedCases	Newly suspected cases since the previous bulletin	Numeric	582
TotalSuspectedCases	Cumulative suspected cases in the province	Numeric	5000
NewConfirmedCases	Newly cases since the previous bulletin	Numeric	582
TotalConfirmedCases	Cumulative confirmed cases in the province	Numeric	500
NewConfirmedDeaths	Newly reported confirmed deaths in the province	Numeric	2
TotalConfirmedDeaths	Cumulative confirmed deaths in the province	Numeric	15
Lethality	Ratio: NewConfirmedDeaths / TotalSuspectedCases	Numeric	0.04

Loko (155 cases) were also notably affected, with both districts experiencing early case emergence in late January. In contrast, other districts such as Kenema, Kono, and Koinadugu reported later onset of cases, with first detections occurring in mid-April to early May, indicative of progressive geographic spread. While all 16 districts eventually reported mpox cases, the intensity and onset timing varied, reflecting both differential transmission dynamics and potential delays in detection or reporting. This district-level analysis underscores the importance of targeted interventions and resource allocation to high-burden areas, particularly in densely populated urban centers.

The genome-based analyses performed including viral sequences isolated in Sierra Leone between January and June 2025, together with all isolates collected worldwide since October 2017, in order to place the genetic variability of the Sierra Leonean isolates in a global context. The phylogenomic tree showed in Figure S1(C) shows a co-circulation of lineages already documented during the 2022–2023 outbreaks. Isolates form Sierra Leone belong to the lineage A.2.2 (Clade IIa), except for two 'unassigned' isolates, and clustered together with isolates from Europe and North America. The lack of a private clade could be the result of a scenario depicted by an initial introduction of the virus (imported through travel or international exchanges), followed by local spread in an uncontrolled manner, especially in areas with limited surveillance and public health infrastructure, facilitating sustained transmission within the community. The presence of 'unassigned' sequences further corroborates this scenario, suggesting the emergence of unpublished or poorly sampled evolutionary lineages, that could be explained as a result of secondary transmission in under-supervised populations. This scenario is in line with what has been reported by Isidro et al. [7] and from the data described by Dumonteil et al. [8], which show an unexpected accumulation of mutations—likely attributable to APOBEC3-mediated editing—and the occurrence of microevolution during community transmission. Furthermore, the study [9] describes positive amino acid selection in viral proteins critical for immune evasion, confirming the presence of selective adaptation within clade IIb. The topology of the tree reveals multiple co-circulating sub-lineages with branching patterns consistent with a bit higher-than-usual rapid higher than usual diversification and local evolution under host-mediated pressures.

Supporting this, the entropy plot displayed in Figure S1(D) highlights specific genomic regions characterized by higher variability. These peaks in sequence entropy are concentrated in discrete loci, which in several cases may correspond to genomic regions involved in viral replication or immune evasion, potentially indicating hotspots of adaptive evolution or sites under selection. The coexistence of multiple expanding lineages and high-entropy regions reinforces the view of a dynamic evolutionary landscape, shaped by continuous transmission, immune pressure, and limited containment. The absence of evidence of new introductions reinforces the hypothesis of established autochthonous transmission, supported by genetically related temporal and geographic clusters. These findings underscore the need for an integrated genomic and epidemiological surveillance system to intercept emerging variants early and effectively target control strategies.

Discussion

In conclusion, this study provides a concrete example of how the integration of genomic analysis, real-time epidemiological data, and unconventional digital sources can significantly enhance the surveillance and management of infectious disease outbreaks. The documented experience with the ADAMS system during the mpox outbreak in Sierra Leone—alongside previous public health emergencies such as the Ebola outbreaks in Uganda in 2022 [10] and 2025 [11]—demonstrates the effectiveness of an integrated, multidimensional approach. Such a strategy can help overcome the limitations of traditional data collection channels, which are often fragmented or delayed in resource-limited settings, ultimately supporting more agile and evidence-based outbreak responses.

With its open-source architecture, ADAMS stands out as a flexible, scalable tool that can be easily adapted to different epidemic scenarios, providing practical support to researchers, policymakers, and health workers. Its ability to rapidly visualize data, monitor the geographic and temporal evolution of cases, and integrate genomic analysis with epidemiological indicators enables more targeted, efficient, and evidence-based interventions. This interdisciplinary, data-driven approach is a valuable resource for strengthening the responsiveness of health systems and improving preparedness for future epidemic threats.

Authors' contribution

Francesco Branda: Conceptualisation, Formal analysis, Data curation, Resources, Visualisation, Investigation, Writing - Original Draft, Writing - Review & Editing. Massimo Ciccozzi: Validation, Supervision, Writing - Original Draft, Writing - Review & Editing. Fabio Scarpa: Data curation, Visualisation, Investigation, Writing - Original Draft, Writing - Review & Editing

Disclosure statement

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