



What Is Influenza?

NHS Trust Definitions in Response to Freedom of Information Requests: Research Report 1

Tom Jefferson, Carl Heneghan ^{1,2}

¹ Trust the Evidence

² University of Oxford

Abstract

Background: The term “active influenza” implies current infection, yet the criteria used by NHS organisations to distinguish active influenza from influenza-like illness or molecular detection are unclear. We examined how NHS organisations define an active case of influenza and establish its presence.

Methods: Freedom of Information responses from 161 NHS organisations in England, Scotland, Wales and Northern Ireland were analysed using a prespecified classification of response adequacy. A secondary analysis assessed responses across four evidential domains: clinical criteria, temporal/currentness criteria, influenza-specific laboratory evidence, and evidence of viral burden or virological activity.

Results: Of 161 responses, 2 (1.2%) were originally classified as operationally adequate, 30 (18.6%) as partially adequate, 102 (63.4%) as methodologically unsound, and 27 (16.8%) as non-responsive or information not held. The two operationally adequate responses incorporated a cycle-threshold (Ct) criterion (<30). In the secondary analysis, 26 responses (16.1%) combined clinical, temporal and laboratory criteria but provided no case-level viral-burden measure; 52 (32.3%) relied on qualitative laboratory confirmation without a complete clinical-temporal framework; 71 (44.1%) were non-operational; and 10 (6.2%) were non-responsive or unclear. No response incorporated all four proposed evidential domains.

Conclusions: NHS organisations showed no consistent operational definition of an active influenza case. Molecular assays reliably detect influenza-specific nucleic acid, but qualitative positivity alone does not confirm viral viability or infectiousness. The findings support clearer separation of clinical illness, currentness, influenza-specific detection and evidence of viral activity. We propose a four-domain working framework incorporating clinical, temporal, aetiological and viral-burden evidence. This framework is hypothesis-generating and requires influenza-specific validation.

Introduction

Influenza is among the most extensively studied respiratory viral infections and occupies a prominent place in both the scientific literature and public discourse. Between 2000 and 2025, 124,430 papers were indexed in PubMed using the search string *influenza[All Fields] AND 2000:2025[dp]*, while 101,026 were identified using the more focused search *influenza[Title/Abstract] AND 2000:2025[dp]*. This substantial literature reflects the enduring clinical and public-health importance of influenza and its considerable contribution to seasonal respiratory morbidity and mortality.

Despite this extensive scientific literature, terminology surrounding influenza is frequently imprecise. Influenza is commonly referred to by the colloquial term “flu”, including in some official and public-health communications. The terms, however, are not necessarily synonymous. In common usage, “flu” may describe a constellation of non-specific systemic and respiratory symptoms rather than infection with an influenza virus. Such symptoms may arise from numerous causes, including other respiratory viral infections, allergic disorders and, less commonly, the early manifestations of malignant, autoimmune, or cardiovascular disease. The indiscriminate use of “flu” can therefore obscure an important distinction between a defined viral infection and a non-specific clinical syndrome.

Accurate identification of influenza has important clinical, epidemiological, and public-health consequences. In particular, licensed influenza vaccines and antiviral agents are interventions directed specifically against influenza viruses rather than against “flu” as a broadly defined symptomatic illness. Estimates of vaccine and antiviral effectiveness therefore depend upon the accurate ascertainment of influenza infection. Failure to distinguish laboratory-confirmed influenza from clinically similar illnesses risks misclassification of outcomes and may consequently bias estimates of intervention effectiveness, disease burden, and associated healthcare utilisation.

The clinical signs and symptoms conventionally associated with influenza are not, however, specific to the causative agent. Patients may present with a syndrome commonly termed influenza-like illness (ILI), but the underlying aetiology cannot reliably be established from symptoms, clinical examination, or medical history alone [Call 2005]. A definitive diagnosis therefore requires evidence of influenza virus infection obtained through laboratory investigation of an appropriate clinical specimen. For the purposes of epidemiological and clinical assessment, influenza should consequently be distinguished from ILI and defined by compatible clinical illness together with laboratory evidence of active infection with influenza A or B virus.

This distinction has become increasingly important. The diagnostic challenges encountered during the COVID-19 pandemic demonstrated the limitations of assigning aetiology to respiratory illness on clinical grounds alone, particularly when multiple respiratory pathogens circulate simultaneously. At the same time, the increasing availability and sensitivity of molecular diagnostic methods, including multiplex respiratory pathogen assays, have substantially changed how respiratory infections are detected and classified. These developments, together with renewed attention to the seasonal burden of respiratory viral disease, raise a fundamental question concerning how a case of influenza should be defined and confirmed in contemporary clinical and epidemiological practice.

We therefore sought to determine what constitutes an active case of influenza in the United Kingdom, with particular attention to the clinical, laboratory, and epidemiological criteria used to distinguish laboratory-confirmed influenza infection from influenza-like illness and other causes of acute respiratory disease.

Methods

Using the publicly accessible platform [WhatDoTheyKnow](#) (WDTK), we wrote FOI requests to every NHS Trust and Health Board in the UK. We also wrote the same request to the United Kingdom Health Security Agency (UKHSA). The latter will be the subject of another paper.

We asked the 161 NHS Trusts and Boards in the UK the same two questions (Q):

Q1. What is your definition of an active case of influenza?

Q2. What are your methods used to confirm an influenza case and distinguish it from other acute respiratory infections?

In Question 1, the crucial word is “active”. By this we mean a patient with influenza-like symptoms in whom influenza A or B virus is actively replicating, causing illness, possible complications and potentially enabling viral transmission to others. If interventions are intended to interrupt or reduce transmission, these are the cases that matter.

The question aimed at identifying infectious cases. [The International Health Regulations](#) [IHR 2005] clearly state: “infection” means the entry and development or multiplication of an infectious agent in the body of humans and animals that may constitute a public health risk. So multiplication- or replication-competent microorganisms are the ones that pose a threat.

Question 2 explores how Trust laboratories and clinicians determine and confirm the presence of influenza viruses in the specimen, and whether influenza viruses are actively replicating and, if so, how they measure the quantity of virus present.

The two questions are inseparable because they form part of the same clinical continuum. ILI symptoms cannot reliably be attributed to influenza viruses without a validated diagnostic test. Likewise, antiviral drugs are licensed only for laboratory-confirmed influenza, not for the loosely defined condition “flu” or ILI. The same applies to influenza vaccines.

Initial Grading of Answers

The initial responses were entered into a Google Sheet, and each Trust or Board response was then classified independently by CH and TJ into a hierarchy of evidential claims based on the question being able to answer the question:

Does the response correctly distinguish clinical suspicion, detection of influenza material, evidence of replication-competent virus, and actual infectiousness?

Question 1

Grade: Scientifically rigorous. The response explicitly distinguishes:

- influenza-like illness from confirmed influenza;
- detection of viral RNA or antigen from active replication, preferably from serial observations;
- active replication from infectiousness or transmissibility;

- current infection from residual molecular positivity.

This definition of “active influenza” includes a compatible acute illness with contemporaneous laboratory evidence of influenza, while acknowledging that routine tests do not definitively establish active replication or transmission.

Grade: Operationally adequate. The response defines an active case as:

- compatible symptoms plus a positive PCR or other validated laboratory test; or
- a laboratory-confirmed case during an acute illness with at least one estimate of viral load

The definition does not definitively distinguish between RNA detection, viable virus, and infectiousness, but it provides a reasonable estimate of viral load.

Grade: Partially adequate. The response treats any positive influenza PCR or antigen result as an active case, without qualification.

The first two may be acceptable for administrative or surveillance purposes, but they are methodologically overconfident. The third is clearly unsupported unless qualified.

Grade: Methodologically unsound. The grade applies to responses which equate the clinical syndrome (ILI) to influenza diagnosis or attribute predictive diagnostic power to various symptoms

The response defines an active case primarily through symptoms, such as:

- fever, cough and myalgia;
- influenza-like illness;
- a clinician’s diagnosis of “flu”;
- epidemiological linkage alone.

This confuses a syndromic or suspected case with virologically confirmed influenza.

Grade: No definition or non-responsive answer. This Grade applies to responses in which the Trust states lack of definition or refers only to national guidance without answering, supplies an infection-control policy but no case definition, or states the information is not held.

Question 2

Grade: Scientifically rigorous - Fully differentiated diagnostic account

This grade applies to responses which identify the methods used and correctly explain what each establishes. An ideal answer distinguishes:

- RT-PCR or another NAAT for viral RNA detection;
- rapid antigen testing for viral antigen detection;
- viral culture for replication-competent virus;
- quantitative PCR for RNA quantity, if validated and calibrated;

- Ct values for assay-dependent and not, by themselves, an absolute viral load;
- multiplex PCR or parallel testing for differentiation from other respiratory pathogens;
- Sequencing for identification or characterisation, but not viral viability;
- Serology provides retrospective evidence but not contemporary proof of active infection.

It also recognises that none of these routine methods directly proves person-to-person infectiousness.

Grade: Operationally adequate - Good routine laboratory answer

The response states that influenza is confirmed using PCR or a multiplex respiratory panel and differentiated from other pathogens through pathogen-specific targets. It may discuss specimen type, collection timing and test limitations, but does not address viability, viral culture or the limitations of Ct values. This is a strong operational answer, even if it falls short of proving active viral replication.

Grade C: Partially adequate - The test is named, but its evidential meaning not explained

This applies to responses that mention PCR, multiplex PCR, antigen testing, or laboratory testing. It provides little or no explanation of: what the test detects; whether the test is qualitative or quantitative; how influenza is distinguished from other infections; whether positivity implies replication or infectiousness. This category is technically responsive but analytically weak.

Grade D: Methodologically unsound - Unsupported inference from routine testing

This applies to responses that claim that PCR positivity proves active viral replication; measure infectious virus; establish that the patient is contagious; or directly measure “viral load” from Ct without validation or calibration. Or simply answer “PCR test”. This type of response represents a significant methodological error with absolute inference based on insufficient evidence.

Grade E: Not responsive - No confirmatory method or non-responsive answer

This applies to reliance solely on symptoms (thereby not answering question 2); no laboratory testing available; referral to another organisation or external guideline without explaining local practice; or when information is not held.

To synthesise our assessment, we unified the responses into one overall classification

Overall grade	Meaning
1 – Scientifically rigorous	Clearly distinguishes syndrome, infection, RNA detection, viable virus and infectiousness
2 – Operationally adequate	Gives a defensible routine case definition and valid diagnostic methods, but does not fully discuss replication or transmission
3 – Partially adequate	Names appropriate tests but conflates some concepts or omits major limitations

4 – Methodologically unsound	Equates symptoms or PCR positivity with active replication or infectiousness
5 – Non-responsive / information not held	Does not provide an answer capable of scientific assessment

We did not aim to downgrade a response based on non-use of viral culture, but on whether the respondent understands the limits of the method used (e.g., PCR) and its reporting.

The difference can be shown in two different possible responses:

“We confirm influenza by PCR, but PCR detects viral RNA and does not by itself prove infectious virus”

Or:

“We use PCR, which confirms that the virus is actively replicating and that the patient is infectious.”

The first is methodologically careful. The second makes statements beyond what is reported.

We expected Polymerase Chain Reaction (PCR) to be the most widely used test. In the correct clinical context and with repeated observations, PCR can provide indications on the clinical course of viral disease [Rosca 2026], provided its serial observations are reported alongside an estimate of viral load and a summary of the clinical picture. In the absence of specimen contamination, decreasing viral loads and symptom relief are correlated with convalescence and with an increase in the acute replicating phase of the infection. Provided the kit primers are validated against influenza culture, then PCR is highly predictive of infection status.

Data analysis

Freedom of Information responses from 161 NHS organisations across England, Scotland, Wales and Northern Ireland were analysed descriptively according to the prespecified response classification. Country and response category frequencies were summarised as counts and percentages.

We collated FOI responses from 161 UK organisations: primary protocol analysis and secondary methodological analysis. Two Trusts had dual roles (for example, teaching and healthcare delivery) under slightly different names, so we excluded them to avoid double-counting replies.

A secondary methodological analysis was undertaken using ChatGPT (OpenAI) to systematically review the free-text responses against a predefined four-domain framework comprising: (1) clinical criteria, (2) temporal/currentness criteria, (3) influenza-specific laboratory evidence, and (4) evidence of viral burden or virological activity. Responses were subsequently grouped into five mutually exclusive methodological levels: viral-burden-qualified laboratory definition; clinically and temporally operational but without viral-burden measurement; qualitative laboratory-defined; non-operational; and non-responsive/unclear.

ChatGPT was used as a secondary analytical and coding tool, not as a source of primary data. The underlying responses, coding rules and resulting classifications were reviewed by the investigators, with particular attention to ambiguous responses and to distinguishing molecular detection from evidence of current infection, viral viability and infectiousness.

Counts and percentages are derived from an FOI workbook entered into Google Sheets and converted to Excel. Country assignment was based on the recipient/organisation names in the UK response list.

We posted our protocol on the Open Science Framework: Heneghan, C., Professor, & Jefferson, T. (2026, July 30). What Is Influenza? Examining NHS Trust Definitions in Response to Freedom of Information Requests. <https://doi.org/10.17605/OSF.IO/WZ5PG>

Results

Baseline characteristics and original protocol classification

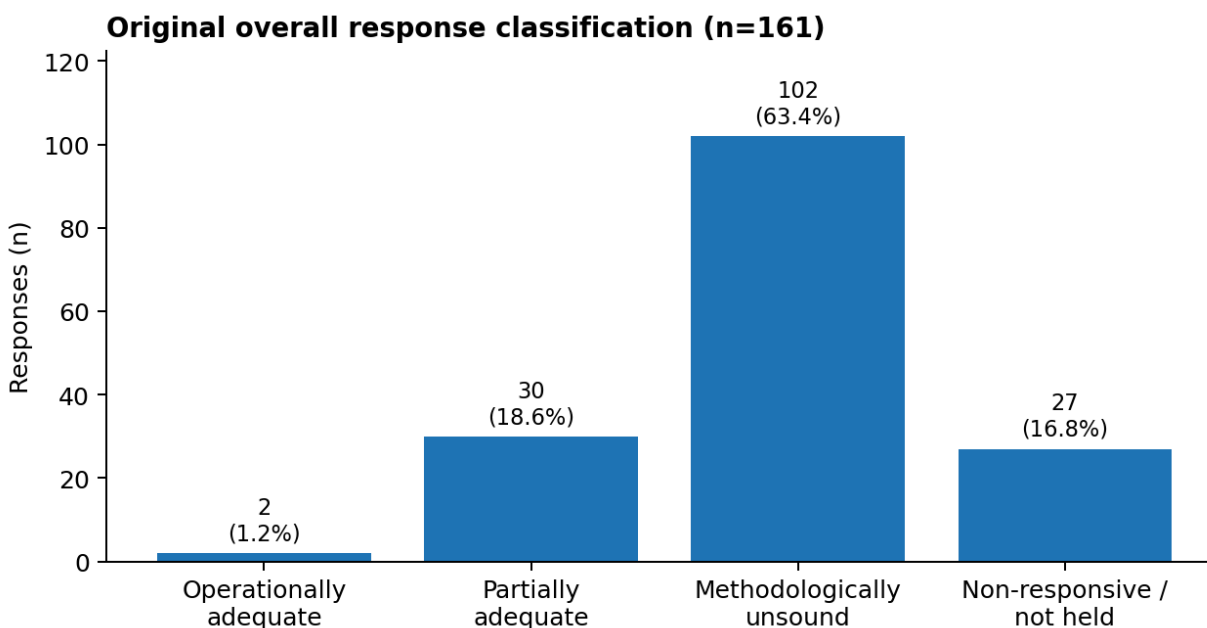
Of the 161 UK recipients, 136 (84.5%) were from England, 13 (8.1%) from Scotland, 7 (4.3%) from Wales and 5 (3.1%) from Northern Ireland. The country distribution was therefore highly concentrated in England and was used descriptively rather than as a basis for comparative inference.

Table 1. Country of response among the 161 UK recipients

Country	n	%
England	136	84.5%
Scotland	13	8.1%
Wales	7	4.3%
Northern Ireland	5	3.1%
Total	161	100.0%

Original response classification

Across the 161 UK responses, 2 (1.2%) were classified as operationally adequate, 30 (18.6%) as partially adequate, 102 (63.4%) as methodologically unsound, and 27 (16.8%) as non-responsive or information not held. Thus, 129/161 (80.1%) fell within the original categories 4 or 5.



Inter-assessor agreement on the overall classification was 144/145 (99.3%). The only disagreement concerned University Hospital Southampton NHS Foundation Trust, which TJ classified as grade 4 and CH as grade 5. There were no disagreements involving grades 1–3.

The country-specific analysis shows the same broad pattern, with category 4 the most frequent classification in England, Scotland, Wales and Northern Ireland; however, the small denominators outside England make percentage comparisons unstable.

Table 2. Original overall classification by country, n (%) within country

Country	Operationally adequate	Partially adequate	Methodologically unsound	Non-responsive / not held	Total
England	2 (1.5%)	24 (17.6%)	89 (65.4%)	22 (16.2%)	136
Wales	0 (0.0%)	2 (28.6%)	2 (28.6%)	3 (42.9%)	7
Scotland	0 (0.0%)	3 (23.1%)	7 (53.8%)	2 (15.4%)	13
Northern Ireland	0 (0.0%)	1 (20.0%)	4 (80.0%)	0 (0.0%)	5
Total	2 (1.2%)	30 (18.6%)	102 (63.4%)	27 (16.8%)	161

Figure 1. Distribution of the original overall response classifications.

Only 2 of 161 organisations (1.2%) were classified as operationally adequate under the prespecified assessment. Both incorporated a semiquantitative molecular measure into their definition rather than relying solely on qualitative PCR positivity.

Clatterbridge Cancer Centre defined an active case as a positive respiratory specimen with a cycle threshold (Ct) value <30. Chelsea and Westminster Hospital NHS Foundation Trust similarly defined an active case as the detection of a significant amount of influenza A or B RNA in a respiratory specimen, typically using a Ct value <30.

These two responses were distinctive because they were the only organisations in the dataset to incorporate a case-level Ct threshold into their operational definition. However, neither provided the complete combination of clinical syndrome, temporal/currentness criteria, influenza-specific laboratory confirmation, and viral burden assessment subsequently specified in our four-domain evidential framework. They should therefore be interpreted as viral-burden-qualified laboratory definitions, rather than as complete reference definitions of active influenza.

Secondary methodological analysis

The secondary analysis recoded the raw Q1 and Q2 answers using a stricter five-level framework designed to distinguish: (A) a case definition incorporating a viral-burden criterion; (B) a clinically and temporally operational definition without a viral-burden measure; (C) a qualitative laboratory-defined or insufficiently qualified definition; (D) a non-operational or insufficiently specified response; and (E) a non-responsive or unclear response. Figure 1 is an example of a D-type response in which presence or frequency of certain symptoms is used to infer clinical entities which are not defined. This framework was applied to all 161 UK responses independently of the original overall classification.

Table 3. Secondary methodological classification of all 161 responses

Strict level	Definition	n	%
A	Case-level Ct/Cq, quantitative viral-load criterion, or clearly specified influenza culture criterion in the case definition.	2	1.2%
B	Clinical criteria + influenza laboratory evidence + explicit currentness/temporality, without a case-level viral-burden measure.	26	16.1%
C	Laboratory positivity/confirmation is part of the case definition, but the clinical-temporal framework and/or viral-burden requirement is incomplete.	52	32.3%
D	Relevant information is provided, but no reproducible case definition that meets the stricter framework can be constructed.	71	44.1%
E	No usable substantive methodological response, or available text is administrative-only/insufficient to code.	10	6.2%

Direct comparison of Levels A, B and C

Because Levels A-C represent the responses for which a substantive case-definition or laboratory framework could be reconstructed, these groups were examined directly for the components most relevant to the meaning of “active” case: clinical criteria, temporal/currentness, influenza-specific laboratory evidence, assay characteristics, and viral-burden information. The three groups were intentionally kept separate because they represent different methodological strengths and weaknesses rather than a simple linear scale.

Table 4. Clinical, temporal and viral-burden components in Levels A-C

Component	Level A n=2	Level B n=26	Level C n=52	A+B+C n=80	Interpretation
Clinical criteria	0	26 (100%)	32 (61.5%)	58 (72.5%)	Present in every Level-B response; not present in the two Ct-based Level-A responses.
Case-defining laboratory result	1 (50.0%)	26 (100%)	52 (100%)	79 (98.8%)	Laboratory evidence is central to B and C; coding is constrained in Level A because its definition is predominantly laboratory/viral-burden based.
Temporal/currentness	0	26 (100%)	7 (13.5%)	33 (41.3%)	Temporal operationalisation is the defining strength of B and is uncommon in C.
Viral-burden criterion	2 (100%)	0	0	2 (2.5%)	Only the two Level-A responses provide a case-level viral-burden measure.
Ct/Cq specifically	2 (100%)	0	0	2 (2.5%)	Both are Ct-based; no other response supplies Ct/Cq as a case-defining criterion.
Influenza culture specifically	0	0	0	0	No response uses routine influenza culture as the case-defining criterion.
Explicit active-case wording	0	20 (76.9%)	25 (48.1%)	45 (56.3%)	The strongest clinical-temporal group most often explicitly answers the “active case” question.

Assay information supplied

Assay information was heterogeneous but overwhelmingly molecular. Among Levels A-C, the Q2 text frequently mentioned PCR/RT-PCR or another molecular nucleic acid method, often as part of multiplex respiratory testing. Rapid point-of-care or antigen methods were also described, generally

as adjuncts or alternatives to laboratory molecular testing. No Level A, B, or C response relied on routine influenza culture as the principal method of clinical confirmation.

Table 5. Assay characteristics mentioned in Q2 among Levels A-C

Assay characteristic	Level A n=2	Level B n=26	Level C n=52	Comment
Molecular PCR/NAAT	2 (100%)	21 (80.8%)	38 (73.1%)	Mentions are not mutually exclusive; one response can name more than one method.
Rapid antigen/POC	0	11 (42.3%)	12 (23.1%)	Mentions are not mutually exclusive; one response can name more than one method.
Multiplex respiratory panel	1 (50.0%)	5 (19.2%)	18 (34.6%)	Mentions are not mutually exclusive; one response can name more than one method.
Culture	0	1 (3.8%)	1 (1.9%)	Mentions are not mutually exclusive; one response can name more than one method.

Named platforms across Levels A-C included GeneXpert / Xpert Xpress (n=10), BIOFIRE / FilmArray (n=7), Roche cobas (n=5), QIAstat-Dx (n=3), Abbott Alinity (n=2), ID NOW (n=1), Healgen Flu/Covid LFD (n=1), RIDA Plex / AusDiagnostics (n=1), LumiraDx (n=1). These counts represent mentions in free-text Q2 answers and are not mutually exclusive.

The revised evidential model for an active case

The direct comparison indicates that the most reliable responses are strongest in different domains. The two Level-A responses uniquely incorporate a case-level Ct threshold, but neither supplies a complete clinical-temporal definition. Neither suggested repeated observations to assess the infection's clinical course.

The 26 Level-B responses provide the most coherent clinical definition of current illness—each specifies clinical criteria, laboratory confirmation, and currentness/temporality—but none provides a measure of viral burden. Level C is dominated by qualitative laboratory confirmation: all 52 contain a case-defining laboratory result, but only 32 (61.5%) provide clinical criteria and 7 (13.5%) an explicit temporal/currentness criterion.

Table 6. Revised evidential model for an active influenza case

Domain	Minimum information sought	Why it matters
Clinical illness	Compatible acute influenza-like illness/signs and symptoms	Anchors the laboratory finding to a clinical episode rather than detection alone.
Temporal/currentness	Defined symptom onset, ongoing illness, or another explicit time criterion	Makes “active” an operational time-dependent construct.
Aetiological evidence	Influenza-specific diagnostic evidence where confirmation is required	Distinguishes influenza from other respiratory infections.
Viral-burden/activity evidence	Ct/Cq, quantitative viral load (preferably serial), or culture where the purpose is to assess ongoing viral activity/infectious potential	Adds information about burden/activity that qualitative PCR alone cannot provide.
Interpretive separation	Do not equate nucleic-acid detection automatically with viability or infectiousness	Avoids over-interpreting a qualitative molecular result.

None of the 161 responses included all four evidential domains. Two responses (1.2%) supplied a case-level viral-burden criterion, but lacked a complete clinical-temporal definition; 26 (16.1%) supplied clinical, temporal and laboratory components but no viral-burden measure; 52 (32.3%) were qualitatively laboratory-defined or insufficiently qualified; 71 (44.1%) were non-operational; and 10 (6.2%) were non-responsive or unclear.

Discussion

In this national Freedom of Information analysis of 161 responses from NHS organisations across England, Scotland, Wales and Northern Ireland, we found substantial heterogeneity in how an “active case” of influenza was defined and, more importantly, substantial absence of an explicit operational definition. Under the original protocol classification, only 2 responses were classified as operationally adequate, 30 (19%) as partially adequate, 102 (63%) as methodologically unsound, and 27 (17%) as non-responsive or with information not held. Thus, 159 of 161 responses (98.8%) did not meet the prespecified operationally adequate category.

The secondary analysis provided a more granular explanation for this finding. Responses varied across four evidential domains: clinical criteria, temporal/currentness, influenza-specific laboratory evidence, and evidence related to viral burden or virological activity. Only two organisations reported a case-level Ct threshold as part of their definition. A further 26 responses combined clinical criteria, temporal information and laboratory confirmation, but did not report a measure of viral burden. Fifty-two were predominantly qualitative laboratory definitions, while 71 did not provide a sufficiently reproducible operational definition and 10 were non-responsive or unclear. Importantly, none of the 161 responses contained all four elements of the proposed evidential framework simultaneously.

These findings suggest that the principal methodological problem is not a lack of access to molecular diagnostic technology. Rather, it is the absence of a consistent conceptual and operational link between clinical illness, timing of illness, laboratory detection and evidence of ongoing viral activity.

Interpretation

A positive molecular assay indicates that the assay target has been detected in the specimen under the test conditions. It does not, by itself, establish that the detected material is replication-competent virus, that it is responsible for the patient's clinical illness, or that the patient remains capable of transmitting infection. Consequently, a qualitative statement such as “influenza A PCR positive” is not, in isolation, a complete definition of an active case.

This distinction is particularly important in the context of the questions posed to NHS organisations. Many responses addressed the narrower question of whether influenza could be detected but did not fully answer the broader question of whether infection should be regarded as currently active. The common inferential sequence of molecular detection to active infection therefore appears to have been used without consistently specifying the clinical and temporal conditions under which that inference should apply.

The secondary evidential framework was motivated by our previous work showing that molecular detection should be interpreted in relation to viral burden, time and clinical context. Rosca et al. reported in a 2026 systematic review of SARS-CoV-2 that culture positivity declined with increasing cycle threshold and increasing time from the first PCR, and that serial Ct values, interpreted alongside clinical and epidemiological information, may assist in assessing infectious potential. Jefferson et al., in a systematic review of transplant populations, similarly considered viral culture, Ct values, and viral load estimation together when assessing infectiousness. These studies provide a methodological rationale for considering viral burden and temporal context, but they are SARS-CoV-2 studies and do not establish an influenza-specific Ct threshold.

PCR and multiplex molecular assays are appropriate and widely used tools for detecting influenza nucleic acid and for differentiating influenza from other respiratory pathogens. The methodological concern is instead the generalisability of the inference drawn from a positive result when the question concerns whether infection is active and potentially transmissible.

Detection is not synonymous with biological activity

The distinction between detection and activity is central to interpreting these results. A qualitative molecular assay is fundamentally a detection method. Where a Trust uses a positive molecular result as the operational definition of an active case, the definition risks conflating the presence of detectable nucleic acid with an ongoing biological process.

The two organisations using a Ct threshold illustrate an attempt to address this problem by incorporating a semiquantitative measure of viral burden. However, these responses did not provide a complete clinical-temporal framework. Conversely, the 26 responses classified as clinically and temporally operational incorporated the clinical episode and timing of illness but did not report a case-level viral-burden measure. The findings therefore expose a complementary gap: some responses quantify laboratory signals without fully defining the clinical and temporal context, whereas others define the clinical episode without measuring viral burden.

This supports a four-domain model in which an “active” case is considered using clinical, temporal, aetiological and virological-activity evidence, rather than being defined by any single component. Such a model is intended as a working evidential framework rather than a validated influenza standard.

The problem of syndromic terminology

The findings also highlight the limitations of syndromic terminology. Influenza-like illness is useful for surveillance and initial clinical assessment, but fever, cough, myalgia, and other respiratory symptoms are not specific to influenza. A definition based primarily on a generic respiratory syndrome, therefore, answers a different question than whether influenza A or B is present.

Conversely, a definition based predominantly on a positive molecular assay may have the opposite problem: it may increase specificity for influenza detection while failing to distinguish current clinically relevant infection from residual or low-level nucleic-acid detection. The methodological challenge is therefore not simply to maximise sensitivity or specificity, but to ensure that the definition being used corresponds to the construct it purports to measure.

Implications for surveillance, forecasting and clinical interpretation

These findings have direct implications for the use of the term “influenza” in NHS surveillance, infection prevention and control, service planning, forecasting and evaluation of interventions. Where “active influenza” is used as an analytical or operational category, the evidential basis for assigning that label should be explicit.

In particular, a positive molecular assay should not automatically be treated as synonymous with an active or infectious case. A clinically useful operational definition can legitimately combine compatible

acute illness with contemporaneous influenza-specific laboratory detection. However, where the objective is to make a stronger assertion about current biological activity or infectious potential, additional information on viral burden and timing is relevant, and a qualitative molecular result alone is insufficient to support that stronger inference.

This distinction also matters for downstream analyses. If counts labelled as “influenza” combine clinically suspected cases, laboratory-confirmed cases, historical molecular positivity and currently symptomatic infections without a consistent definition, then apparently precise trends may conceal substantial heterogeneity in what is actually being counted. Any forecasting, burden estimation or comparison of interventions that relies on such data therefore inherits uncertainty from the underlying case definition.

Proposed four-domain working definition

On the basis of the present analysis, we propose a working evidential definition for NHS use rather than a validated diagnostic standard:

An active case of influenza is an individual with a current clinically compatible acute illness, occurring within a defined temporal relationship to symptom onset, in whom influenza virus has been specifically detected and in whom the laboratory result is accompanied, where technically available and validated, by quantitative or semiquantitative evidence of viral burden compatible with current active infection.

The four domains are therefore: (1) clinical illness, (2) temporal/currentness, (3) influenza-specific laboratory evidence, and (4) viral-burden or virological-activity evidence. A Ct or other quantitative measure should be interpreted in relation to the assay, specimen, timing and clinical context rather than through a universal numerical threshold. Viral culture or another validated measure of replication competence may provide stronger evidence when the specific question is whether a viable (replication competent) virus is present.

This framework should also preserve separate concepts of laboratory-confirmed influenza infection, active influenza, and infectiousness. These terms should not be used interchangeably.

Limitations

Several limitations require consideration. First, the analysis evaluates what organisations reported in response to two specific questions; it is not a direct audit of laboratory protocols, assay validation, patient management or transmission events. Freedom of Information responses may have been prepared by information governance or administrative teams rather than by the clinicians, microbiologists, or laboratory scientists responsible for day-to-day influenza diagnosis. Responses may therefore incompletely describe actual practice.

Second, the dataset contains administrative complexities, including duplicate acknowledgement entries and at least one response that relates to more than one Trust. These were addressed in the revised

analysis, but residual ambiguity is possible. The country comparison is also dominated by England due to the substantially larger number of English responses; consequently, country-specific percentages should not be overinterpreted.

Third, the stricter viral-burden framework was developed as a secondary analytical construct. The two principal studies supporting the framework concern SARS-CoV-2. Rosca et al. showed associations between serial Ct values, time and culture positivity and emphasised the value of integrating Ct trajectories with clinical and epidemiological information. Jefferson et al. synthesised evidence from culture, Ct, and viral load in immunocompromised transplant populations. Neither study establishes a universal influenza Ct threshold, and Ct values are influenced by assay platform, specimen characteristics and laboratory methodology.

Fourth, the secondary coding was undertaken with the assistance of ChatGPT as a structured text-analysis tool. This improved consistency in reviewing a large volume of free-text responses, but does not constitute independent validation of the coding hierarchy. The classification rules were investigator-defined and placed particular emphasis on explicit recognition of the distinction between molecular detection and biological activity. Future work could assess inter-rater reproducibility using independent assessors and, ideally, blinding to organisation identity.

Finally, even a four-domain definition should be regarded as an operational framework rather than a direct measure of infectiousness. Neither a single Ct value nor a quantitative viral load estimate is equivalent to the demonstration of replication-competent virus. The relationship between viral burden, viable virus and transmissibility is influenced by timing, host factors, specimen characteristics and assay methodology.

Implications for practice and policy

The principal practical implication is the need for clearer and more standardised terminology. NHS organisations should distinguish explicitly between: (1) influenza-like illness or suspected influenza; (2) laboratory-confirmed influenza infection; (3) active influenza infection; and (4) potentially infectious influenza.

For operational surveillance and clinical reporting, organisations should record symptom onset or another appropriate temporal marker alongside the laboratory result wherever feasible. Where quantitative molecular data are available, Ct/Cq or viral load information should be retained rather than immediately reduced to a binary positive/negative variable, while recognising that thresholds must be assay-specific and validated for their intended use. A universal Ct cutoff should not be adopted without influenza-specific validation.

For policy and surveillance systems, case definitions should be stated explicitly whenever aggregated data are used for forecasting, trend analysis, infection-control decisions, vaccine-effectiveness studies, or evaluations of antiviral interventions. In particular, the label “influenza case” should not conceal

whether the underlying numerator represents symptomatic illness, laboratory detection, current infection or presumed infectiousness.

The findings therefore support a move away from a binary concept of influenza based on test positivity alone towards a transparent evidential framework in which the intended construct is stated, and the limitations of the underlying measurements are acknowledged.

Conclusion

The principal finding of this study is that there is no consistent, scientifically explicit operational definition of an “active case” of influenza across the NHS responses examined. Routine molecular testing is widespread and appropriate for influenza detection, but the transition from detection to claims about current activity and infectious potential is inconsistently specified. None of the 161 responses combined clinical, temporal, influenza-specific laboratory and viral-burden evidence in the manner proposed by our secondary framework.

A standardised working definition that explicitly separates clinical illness, currentness, influenza detection, and evidence of viral activity would improve the transparency and interpretability of NHS surveillance and other analyses that use the term “active influenza”. This framework should be regarded as a hypothesis-generating proposal requiring influenza-specific validation rather than as a currently established diagnostic standard.

Our findings show that any influenza report should be disregarded as unverified until NHS operators learn the strengths and limitations of clinical significance in the tests they routinely use.

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