On 20 January 2026, GISAID published a statement (archived link) titled "*Facts surrounding data-related complaints*", citing four examples to justify recent termination on access to its data feeds. Although presented as matters involving "*Individual*"(s), each of these examples refer to open-source platforms or national public health responses, in which individuals **representing our respective teams** made agreements with GISAID to serve the broader public health community: (**1**) COG-UK [1], (**2**) outbreak.info [2], (**3**) Cov-Spectrum [3], and (**4**) Nextstrain [4]. At no point did we intentionally operate outside the scope of the terms in these agreements.

In their post – and a related, 28 September 2025 post (archived link) – GISAID states that the termination of data access occurred because "*some of them were found to have considerably encroached on the rights of GISAID's data contributors, which resulted in the termination of their data feed and the supplementary agreement with GISAID, given their usage had significantly deviated from the manner they promised to make use of the data feed.*" Further, GISAID accuses us variously of: (**1**) "*spreading disinformation*", (**2**) engaging in "*fraudulent activities*", (**3**) having "*violated the terms of [our] access Agreement and misused the data shared via GISAID*", (**4**) having "*abused the GISAID data sharing process*", (**5**) "*mischaracterized [our] engagement with GISAID*", (**6**) "*misrepresented GISAID's actions in public*", and (**7**) engaged in communications that were "*dangerously misleading*".

The allegations are serious; however, they are **false and misrepresent known facts.** Since the beginning of the COVID-19 pandemic, we, along with many other scientists, have had repeated engagements with GISAID staff and leadership. As has been extensively reported, there have been repeated disputes involving GISAID surrounding these engagements, including on matters of transparency around data access and reuse, as well as historical events. GISAID leadership has also threatened junior scientists who did not support its version of events and even fabricated personas to communicate with scientists. Finally, scientists in our wider teams and networks were not granted access to requested GISAID data, hampering extension of our dashboards to additional pathogens.

As previously reported, GISAID terminated access to outbreak.info on 11 January 2025, Nextstrain on 1 October 2025, CoV-Spectrum on 12 October 2025, and COG-UK in January 2025. In addition to the four data feeds cited by GISAID, **several other feeds supporting external analysis and visualization resources were also terminated** over the course of 2025, including COVID CG and COVID-19 Viral Genome Analysis Pipeline, each time with shifting and often vague justifications such as "*resource limitations.*"

Contrary to GISAID's claims, the affected **platforms were largely not informed** in advance of these terminations, and repeated emails and messages to GISAID staff and leadership went **unanswered for weeks to months** [5]. We submitted separate appeals seeking reinstatement of access for our platforms, however, these were all denied, with no further mechanism for review or reinstatement. Taken together, these actions point to a **systematic withdrawal of support** for external, community-run dashboards and analyses in favor of a closed, internally controlled approach to genomic surveillance. This shift is difficult to reconcile with GISAID's own mission statement (archived link), which states that "*GISAID actively promotes the development of novel research tools for the analysis of genomic data and helping developers facilitate the integration, or connection of their tools to analyze GISAID data*".

In addition to falsely accusing us of fraudulent activities, GISAID claims to ensure "*equitable access to outbreak data to meet the needs of the global community, and not just a select few in economic privileged*

settings". Further, GISAID describes us and other members of the scientific community as a "*small – but vocal group of individuals*". The implication that the platforms we developed primarily benefit us "*in economic privileged settings*" by exploiting others' data is factually incorrect and deeply misleading. In contrast, by providing timely information on pathogen spread, dynamics, and evolution, our platforms have consistently **provided critical support for public health** with **tens of millions of users over the course of the pandemic** across all resources. Additionally, several of us are also **among the largest generators of viral genomic data worldwide**, having produced and openly shared hundreds of thousands of SARS-CoV-2 genomes, and thus among the largest contributors to GISAID itself. We developed our platforms – as well as the **main protocols used for viral sequencing**, including SARS-CoV-2 – to support genomic surveillance and make it broadly accessible, regardless of economic setting. Beyond this work, we have **collaborated for decades with colleagues globally**, including many in low- and middle-income countries **to strengthen genomic surveillance**, work that continues today.

We agree with the principle that GISAID purports to uphold: **protecting the rights** of data generators and **ensuring equitable benefit sharing**. However, we believe that the misrepresentations of facts and opaque processes GISAID uses to govern data access are at odds with that goal. In addition, GISAID has, on a routine basis, ingested sequence data from other public databases, including data generated by projects in which we have been heavily involved, without labeling of data provenance, without explicit consent from data producers, and without proper acknowledgements. Further, by assigning new GISAID-specific sequence identifiers while omitting previous identifiers, traceability to the original source effectively becomes impossible.

These practices are **inconsistent with ongoing efforts** to adopt the World Health Organization's Pathogen Access and Benefit-Sharing ([PABS](#)) system, which emphasizes proper attribution of data producers, transparency in governance, and **accountable oversight of data stewards**. Providing multiple pathways for pathogen data sharing, including mechanisms that respect data sovereignty while enabling timely global access, is essential to maintaining trust and scientific integrity. Any organization stewarding pathogen data **must demonstrate adherence to [agreed principles](#)** of transparency, interoperability, equitable access, and data provenance and access. No database should operate in a manner that concentrates unilateral control without transparency or accountability. Rather, as a community, our focus should be on creating tools, analyses, and insights that strengthen trust, enable equitable science, and improve our collective ability to effectively respond to infectious disease threats.

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[1] The COVID-19 Genomics UK (COG-UK) Consortium was launched in 2020 as a UK-wide partnership of public health agencies, academic institutions, the NHS, and sequencing centres to sequence and analyse SARS-CoV-2 genomes at scale. Its aim was to track how the virus spread and evolved, identify and monitor new variants, and provide genomic evidence to inform public health responses across the UK. By the end of 2020 the consortium had contributed over 180,000 SARS-CoV-2 genomes to global databases including GISAID.

[2] outbreak.info was launched in March 2020 by researchers at Scripps Research in the US in response to the COVID-19 pandemic to provide near real-time access to epidemiological and genomic surveillance data. The platform integrates epidemiological data on cases and deaths with spatiotemporal genomic data on SARS-CoV-2 variants, enabling users to track lineage and mutation dynamics across space and time. In addition, outbreak.info provides a searchable, curated research library, including publications, preprints, clinical trials, datasets, and protocols, through a common schema and public API.

[3] Cov-Spectrum is an interactive dashboard for identifying and tracking SARS-CoV-2 variants. Launched in May 2021, it enabled researchers, public health professionals and citizen scientists to rapidly search millions of available sequences and perform detailed analysis. Until December 2025, it was available for both GISAID and INSDC data; since the removal of the GISAID instance, it only serves data from INSDC.

[4] Nextstrain was launched in 2015 to provide a continually updated, near real-time phylogenetic analyses of pathogen sequence data to support public health response to novel outbreaks and endemic viruses.

[5] Communications between GISAID staff and representatives of our platforms can be found on Github: https://github.com/andersen-lab/2026_gisaid_response