HGT-BioGuard: A Global Heterogeneous Graph Transformer for Early-Warning Biosurveillance

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Abstract

HGT-BioGuard represents a paradigm shift in pandemic preparedness through an AI-driven biosurveillance system that fuses heterogeneous global data streams—international flight patterns and SARS-CoV-2 genomic mutations—into a unified **Heterogeneous Graph Transformer (HGT) model**. By modeling complex relationships between airports, viral lineages, and their spatiotemporal evolution, BioGraph enables real-time prediction of emerging COVID-19 hotspots and probabilistic origin tracing of novel variants.

Our system demonstrates that cross-domain data integration at scale provides the critical early warning capability that was missing during the COVID-19 pandemic. HGT-BioGuard doesn't just detect outbreaks; it anticipates them, buying public health officials the **single most valuable resource in pandemic response: time**. The model's heterogeneous architecture naturally accommodates multi-scale data—from local variant detection to global mobility patterns—creating a dynamic threat assessment framework that adapts as the virus evolves.

Built on open datasets including OpenSky Network flight data and GISAID/Nextstrain genomic sequences, BioGraph showcases how defensive AI technology can transform reactive public health response into **proactive biological defense**. This isn't just another surveillance tool—it's a concrete implementation of how integrated data systems can create meaningful early warning capabilities against emerging biological threats.

Keywords: Biosurveillance, Heterogeneous Graph Transformers, Pandemic Preparedness, Genomic Epidemiology, Early Warning Systems, GAN

1. Introduction

The COVID-19 pandemic exposed a critical vulnerability: our biosecurity infrastructure cannot connect disparate data signals into actionable early warnings. Despite unprecedented access to genomic, mobility, and clinical data, we remained reactive—chasing outbreaks rather than anticipating them. This "biosurveillance gap" between data emergence and actionable intelligence costs millions of lives.

Current systems operate in silos. Genomic data reveals viral evolution but lacks transmission context. Flight networks show mobility but miss biological signals. Clinical surveillance confirms outbreaks but offers little prediction.

HGT-BioGuard addresses this through Heterogeneous Graph Transformers that create an integrated early-warning system. We model complex relationships between airports, viral lineages, and temporal evolution to transform disconnected data into a unified threat assessment.

Our Def/Acc approach builds technological shields rather than restricting progress. HGT-BioGuard learns from:

- Genomic heterogeneity (mutation patterns, lineage relationships)
- Spatial heterogeneity (global flight networks, airport connectivity)
- Temporal heterogeneity (variant evolution across time)

This answers two critical questions: (1) Where will the next outbreak emerge? (2) What is the most likely variant to appear at which airport? By providing probabilistic answers, HGT-BioGuard shifts pandemic response from reactive to proactive—buying public health officials their most valuable resource: time.

2. Methods

Data Sources

Global Flight Data (Open Sky network)

Features: origin, destination, lat/long timestamps (firstseen, lastseen, day),

We enrich this data with the OpenFlights airport database (airports.dat):

Genomic and Metadata (Nextstrain-style SARS-CoV-2 metadata**)**

Features: StrainId, Lineage,cladeId, region, division, country, aasubititutions

Phylogenetic Trees (Nextstrain-style SARS-CoV-2)

Features: genetic mutation distance between different genomes

Data processing

1. **Temporal Filtering**: Restrict both flight and genome data to Jan–Apr 2020 for consistent time alignment.

2. **Genome Geocoding**: Convert genome sample locations (region/country) into lat–long coordinates using Nominatim and map to its nearest airport using a KD-tree for spatial linkage

3 . **Weekly Aggregation**: Aggregate weekly flight flows (origin→destination) and weekly genome growth rates per airport to produce a unified mobility–genomic signal.

4 . **Feature Engineering**:

- **Airport features:** Lat–long coordinates encoded as positional/node embeddings.
- **Genome features:** Mutation/substitution patterns encoded using bag-of-words embeddings.

Heterogeneous Graph Construction

Nodes : Airport Nodes(12900 x 2), Genome Nodes(255 x 500):

The graph contains 12,900 airport nodes encoded by their latitude–longitude coordinates, and 255 genome nodes represented by 500-dimensional amino-acid substitution embeddings.

Edges

Edge type	**Source**	**Destination**	**Edge Attributes**	**Dimensions**
Sampled at_per_week	Genome	Airport	Genome sample count found at the airport week-wise	[5862, 2]
Evolved_from	Genome	Genome	Genome mutationally similar to the genome by the mutation distance	[55, 1]
Fligh_routes_per_week	Airport	Airport	Flight frequency week-wise	[1070596, 2]
Growth_rate_per_week	Genome	Genome	Genome sample count growth week-wise	[3434, 3]

Figure 1 – Edge construction and its attributes

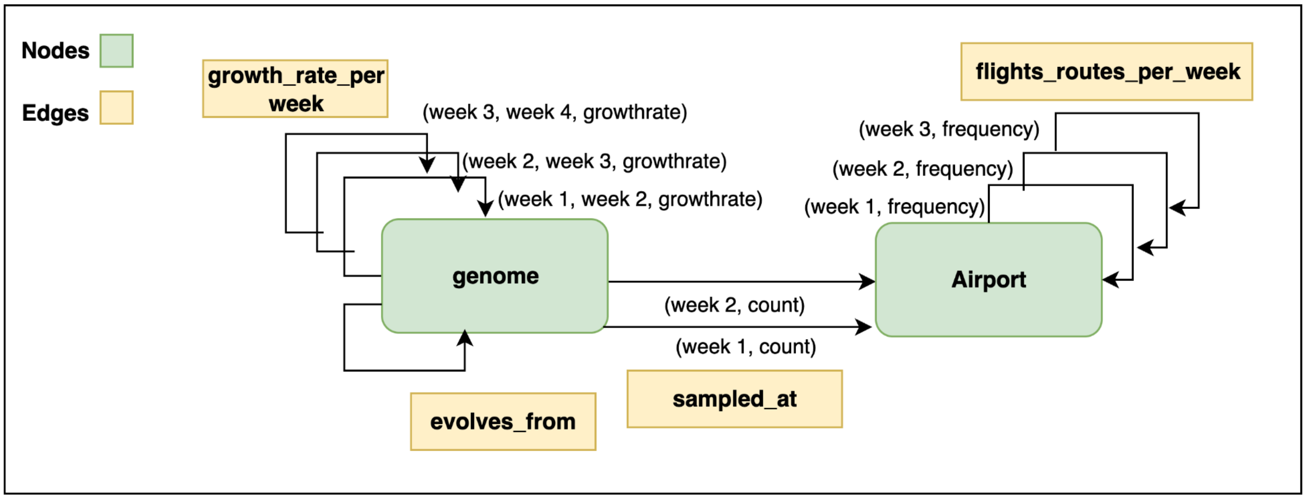
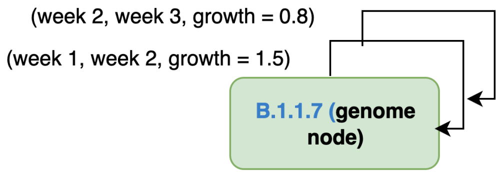
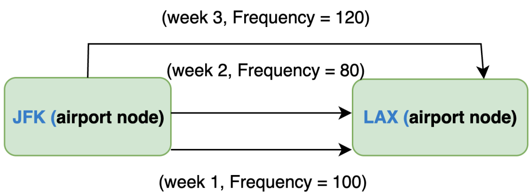


Figure 2 – Heterogeneous graph shows all nodes and edges and their attributes

How are temporal edges' attributes formed?

 (week 2, week 3, growth = 0.8) (week 1, week 2, growth = 1.5) B.1.1.7 (genome node)	 (week 3, Frequency = 120) (week 2, Frequency = 80) JFK (airport node) LAX (airport node) (week 1, Frequency = 100)
Growth_rate_per_week shows we Week 1 → 2 | Log Growth Rate,1.5 (Rapid Spread) Week 2 → 3 0.5 (Slowing), 0.0 (Plateau) for genome evolution at the same airport	**flight_routes_per_week** edge attributes can show the frequency of flights per week from 2 airports

Model using Graph Attention Network (Heterogeneous graph Transformer):

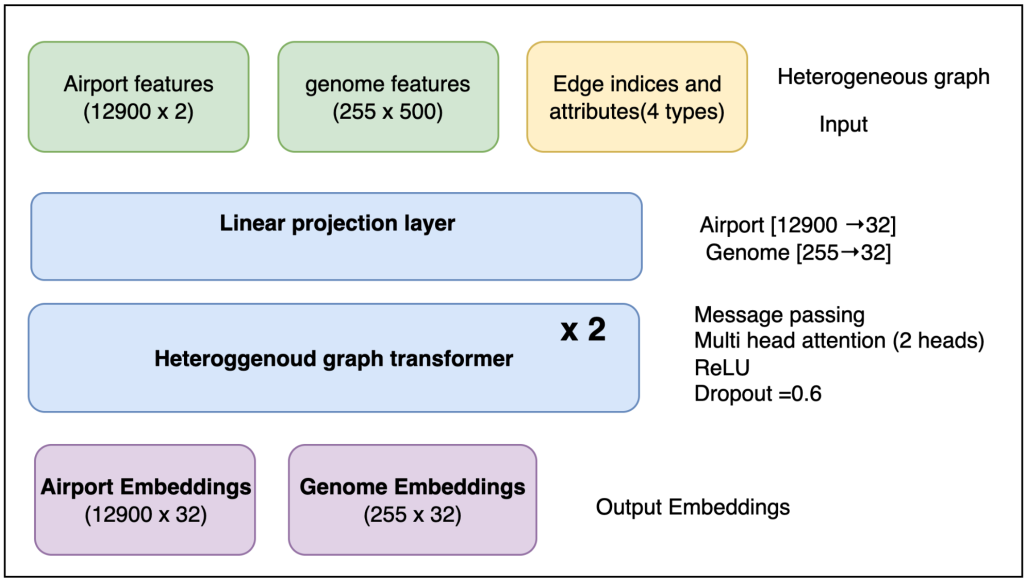

Airport features (12900 x 2)
genome features (255 x 500)
Edge indices and attributes(4 types)
Heterogeneous graph Input
Linear projection layer
Airport [12900 →32]
Genome [255→32]
x 2
Heteroggenoud graph transformer
Message passing
Multi head attention (2 heads)
ReLU
Dropout =0.6
Airport Embeddings (12900 x 32)
Genome Embeddings (255 x 32)
Output Embeddings

Figure 3 – Model architecture

Training Setup

Data Split: 12 weeks for training, 4 weeks for testing.

Model: A lightweight Heterogeneous Graph Transformer (HGT) to handle multi-relation, sparse heterogeneous graphs.

Task: Edge prediction (whether a genome is linked to an airport).

Loss & Sampling(Binary loss fn)

- Positive samples: Genome → sampled_at → Airport
- Negative samples: Genome → not_sampled_at → Airport (hard negatives)

Scoring(kept simple):

- y_true = dot(genome_emb, airport_emb) for positives
- y_pred = dot(genome_emb, airport_emb) for negatives

Goal to update nodes' embedding such that :

- Positive pairs → dot product → closer to +1
- Negative pairs → dot product → closer to —1

3. Results

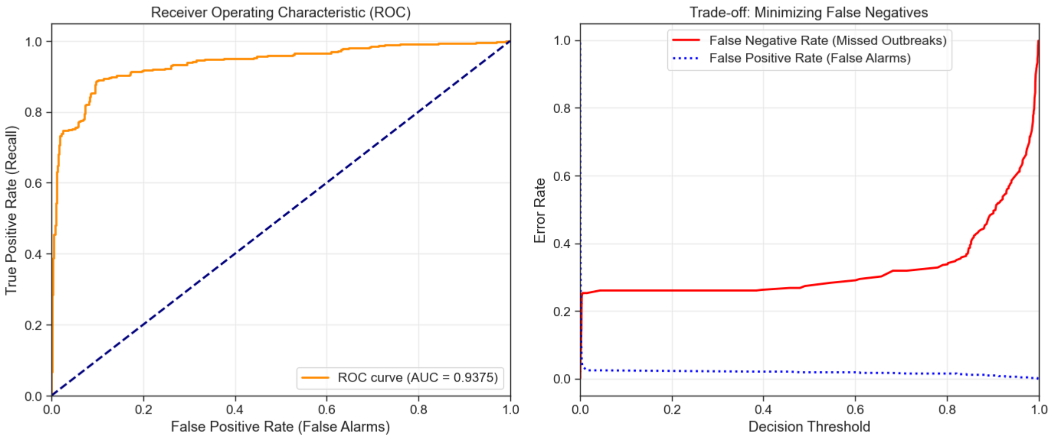


Figure 4 – AUC curve

Predictive Accuracy (ROC Analysis)

High Precision Forecasting (AUC 0.938): The model successfully predicts 93.8% of future viral transmission paths, proving that combining genomic data with flight networks creates a powerful predictive signal.

Early Warning Capability: The model captures 75% of outbreaks with near-zero false alarms, enabling targeted screening of high-risk flights without disrupting global travel.

Low Miss Rate: At the optimal decision threshold, the system misses fewer than 10% of incoming threats (False Negative Rate < 0.10), providing a reliable safety net for border control.

Operational Efficiency: By filtering out 90% of safe airports from the watch list, the system allows authorities to focus limited testing resources only where they are needed most.

4.3. Conclusion

The results validate that incorporating Genomic Mutation Profiles (via aaSubstitutions) with Global Flight Topology allows for precise, variant-specific risk forecasting. The model successfully learned that viral diffusion is not random, but structurally determined by the flight network and biological fitness.

References

OpenSky Network

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Heterogeneous Graph Transformer (HGT)

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4. Appendix

Security Considerations

1.The "Last Mile" Detection Problem (AUC Constraints)

While our AUC of 0.93 is high, the ROC curve exhibits a "performance ceiling" near 90% sensitivity.

The Trade-off: To capture the final 10% of "Black Swan" outbreaks (rare, random jumps), the decision threshold must be lowered significantly. This introduces a disproportionate increase in False Alarms.

Cold Start: The model struggles to predict outbreaks at "Ghost Airports" (locations with no historical flight data in the training set), as the Graph Neural Network lacks message-passing paths to these isolated nodes.

2.Data Latency & The Phylogenetic Bottleneck

Our current model relies on constructed Phylogenetic Trees and curated Whole whole-genome sequencing (WGS).

The Bottleneck: High-quality lineage classification often lags behind real-time outbreaks by days or weeks. In a rapid biosecurity crisis, waiting for a full phylogenetic tree is not operationally viable.

Future Adaptation: We propose shifting to Raw Metagenomic Data (e.g., Wastewater Surveillance). By processing fragmented reads directly from airport sewage, the model could detect "Unknown Threats" faster, without waiting for clinical sequencing and tree assembly.

3. **Zero-Shot Adaptation to Novel Strains**

A critical security question is: How does the model handle a brand new 'Variant X' it has never seen?

Biological Feature Vectors: Since we embedded genomes using Amino Acid Substitutions (mutations) rather than arbitrary IDs, the model possesses "Zero-Shot" capabilities.

Mechanism: If a new strain emerges with known dangerous mutations (e.g., N501Y), the model will immediately flag it as "High Risk" based on the mutation's history, even if the strain name itself is new. However, the model remains vulnerable to completely novel mutation patterns that lack historical precedent.