RESEARCH PAPER

Towards Secure and Intelligent Clinical Imaging: A Unified Deep Learning and Generative AI Framework for Brain Tumor Diagnosis

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ABSTRACT
Deep learning has achieved strong performance in MRI-based brain tumor classification; however, existing systems largely ignore the security, privacy, and operational reliability of clinical AI pipelines. This work presents a unified diagnostic–security framework that integrates convolutional neural network–based tumor classification with generative artificial intelligence–driven security information and event management (SIEM) within a single end-to-end clinical workflow. The diagnostic module employs a VGG16 transfer-learning architecture trained on 7,023 multi-institutional MRI scans across four classes (glioma, meningioma, pituitary tumor, and healthy tissue), achieving a test accuracy of 95.73% and a weighted F1-score of 0.96.
To secure inference and explanation artifacts, the framework introduces a privacy-preserving logging pipeline combining Gaussian differential privacy, Paillier homomorphic encryption, and federated log aggregation. A Transformer–VAE hybrid model is adapted for high-dimensional medical event correlation and missing-log reconstruction. System-level feasibility is evaluated using OMNeT++ network simulation for multi-hospital traffic modeling and Simulink for real-time pipeline latency analysis. Experimental results demonstrate encrypted log correlation latency of 189 ms, anomaly detection accuracy of 91.8%, and stable diagnostic throughput under adversarial network conditions exceeding 1.4 million log events. The novelty of this work lies in the system-level integration of diagnostic AI and generative security analytics for clinical imaging workflows, enabling secure, explainable, and deployable medical AI under realistic hospital constraints...
Keywords: Deep Learning, VGG16, Brain Tumor Detection, Medical Imaging, MRI Analysis, Generative AI, SIEM, Transformer-VAE Hybrid, Differential Privacy, Homomorphic Encryption, OMNeT++, Simulink, Secure Clinical Workflows.
How to cite this article: Mishra S, Sabut SK.; Towards Secure and Intelligent Clinical Imaging: A Unified Deep Learning and Generative AI Framework for Brain Tumor Diagnosis..Int J Drug Deliv Technol. 2026;16(1s): 693-705; DOI: 10.25258/ijddt.16. 693-705
Source of support: Nil.
Conflict of interest: None

INTRODUCTION

Medical imaging has undergone a paradigm shift with the introduction of modern deep learning techniques, especially convolutional neural networks (CNNs). Brain tumor detection, a domain historically characterized by subjective radiologist interpretation, has become increasingly automated, robust, and data-driven. The need for reliable diagnostic automation is amplified by the increasing global incidence of central nervous system tumors—estimated at nearly 300,000 new cases per year—and the relatively low five-year survival rate associated with malignant variants. Early diagnosis significantly improves clinical outcomes, yet radiologists face an ever-increasing workload along with the limitations of manual, time-consuming review of MRI scans. The application of transfer learning, where pre-trained CNNs such as VGG16, ResNet, and EfficientNet are fine-tuned for MRI-based classification tasks, has shown remarkable success in mitigating data scarcity and achieving high diagnostic precision [1], [2]. In prior work, we demonstrated that a VGG16-based transfer learning model is capable of achieving 95.73% accuracy and a weighted F1-score of 0.96 across four major tumor categories

While AI-driven diagnostics enhance clinical accuracy, they introduce a new challenge: the security and confidentiality of generated medical data. MRI images, patient metadata, AI inference logs, Grad-CAM explainability maps, and system audit trails collectively form a sensitive digital footprint that must be protected against unauthorized access, tampering, and intelligence-driven cyberattacks. Existing hospital information systems (HIS), Picture Archiving and Communication Systems (PACS), and teleradiology networks generate millions of logs per day, making traditional rule-based SIEM platforms inadequate. In earlier research, we developed a Generative-AI-optimized SIEM architecture incorporating a Transformer-VAE hybrid model for event correlation, differential privacy, homomorphic encryption, and federated log

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training, demonstrating improved correlation speed, privacy accuracy, and adaptability in multi-platform environments (Splunk, QRadar, Elastic) .

Despite independent progress in medical AI and SIEM optimization, no existing research integrates both domains into a unified clinical security-AI pipeline, even though real clinical workflows require both strong diagnostic accuracy and uncompromised cybersecurity. This paper formulates the first such unified system by merging deep learning-driven MRI tumor detection with Generative-AI-augmented SIEM monitoring, forming a holistic architecture capable of delivering trustworthy, explainable, and secure diagnostic automation.

CONTRIBUTIONS AND NOVELTY

This study does not propose a new tumor classification algorithm or a new cryptographic primitive. Instead, its novelty lies in the unified system design that jointly engineers diagnostic artificial intelligence and generative security analytics for clinical imaging environments. Existing brain tumor detection studies optimize predictive accuracy without modeling cybersecurity risks, while SIEM research focuses on enterprise infrastructures without accounting for the structural, regulatory, and latency constraints of medical imaging workflows.

The first contribution of this work is the formulation of an end-to-end diagnostic–security pipeline in which MRI preprocessing, neural inference, explainability generation, secure logging, and anomaly detection are tightly coupled. Unlike conventional deployments that attach security mechanisms as external monitoring components, the proposed architecture embeds privacy preservation and integrity verification directly within the diagnostic process.

The second contribution is the domain-specific adaptation of generative SIEM modeling to medical AI logs. The proposed Transformer–VAE hybrid system is redesigned to operate on high-dimensional inference metadata, Grad-CAM explanation artifacts, and PACS-level event streams while maintaining regulatory compliance and near-real-time execution.

The third contribution is a unified evaluation methodology that simultaneously quantifies diagnostic accuracy, encrypted log processing latency, privacy retention, attack detection capability, and hospital-scale network robustness using coupled OMNeT++ and Simulink simulations. Together, these contributions establish a new systems-level research direction for trustworthy medical AI that extends beyond algorithmic prediction toward secure and operationally reliable clinical deployment.

UNIFIED SYSTEM ARCHITECTURE

The proposed framework establishes a unified clinical artificial intelligence infrastructure that tightly integrates deep learning–based MRI tumor diagnosis with generative artificial intelligence–driven security information and event management (SIEM). In contrast to conventional deployments in which diagnostic inference engines and cybersecurity monitoring platforms are developed and operated as independent subsystems, the present architecture co-designs both functionalities as a single end-to-end pipeline. This design ensures that every stage of the diagnostic lifecycle—ranging from raw image acquisition and preprocessing to neural inference, explainability generation, and clinical validation—is continuously protected, audited, and analyzed under a privacy-preserving and attack-resilient paradigm.

From a systems perspective, the architecture addresses a fundamental limitation of existing medical AI pipelines: although modern convolutional networks achieve high predictive accuracy, they are typically embedded in infrastructures that lack formal mechanisms for confidentiality preservation, integrity verification, and anomaly detection. Simultaneously, state-of-the-art SIEM platforms are optimized for enterprise text-based logs and network telemetry but are not designed to operate on high-dimensional medical inference artifacts, explainability maps, and latency-critical diagnostic workflows. The proposed architecture bridges this gap by unifying diagnostic intelligence and security intelligence into a coherent operational model that satisfies clinical performance constraints as well as regulatory requirements such as HIPAA, GDPR, and ISO/IEC 27701.

The system is organized into five tightly coupled functional layers: (i) medical image acquisition and preprocessing, (ii) deep learning–based MRI classification, (iii) confidential logging and security monitoring, (iv) generative correlation and privacy preservation, and (v) simulation-driven evaluation and deployment validation. These layers form a closed-loop architecture in which diagnostic outputs become security events, and security analytics provide feedback on system integrity, data authenticity, and inference reliability. Figure 1 illustrates the complete five-layer pipeline, including the flow of MRI data, encrypted inference artifacts, generative correlation processes, and system-level monitoring components.

Medical Image Acquisition and Preprocessing Layer

The first layer receives raw MRI scans directly from hospital imaging devices connected to the Picture Archiving and Communication System (PACS). In routine clinical environments, these images are acquired across heterogeneous scanners operating at different magnetic field strengths and protocols, typically ranging from 256×256 to 512×512 pixels and encompassing T1-weighted, T2-weighted, FLAIR, and contrast-enhanced sequences. Such heterogeneity introduces significant variability in signal-to-noise ratio, intensity distributions, spatial resolution, and anatomical contrast, all of which can adversely affect downstream neural inference if left uncorrected.

To mitigate these effects, a standardized preprocessing pipeline is applied to each incoming scan. Intensity inhomogeneity is corrected using N4 bias field normalization, followed by noise suppression through non-local means filtering with a 7×7 patch window to preserve structural edges while reducing stochastic artifacts. The corrected images are then normalized using min–max scaling and global standardization to stabilize feature

distributions across acquisition protocols. Spatial reformatting is performed using bilinear interpolation with anti-aliasing to generate fixed-size 128×128 representations compatible with the convolutional network input specification. During training, controlled data augmentation is employed through random rotations within ±20°, brightness perturbations within ±15%, and contrast adjustments within ±20%, thereby improving robustness against scanner-dependent variability and patient positioning effects.

To evaluate the operational feasibility of this preprocessing chain under realistic clinical workloads, the pipeline is implemented in two parallel forms. A Python-based implementation supports deployment within GPU-accelerated inference servers, while a block-level representation is constructed in Simulink to model computational latency, memory utilization, and throughput constraints under varying image arrival rates. The output of this layer is a standardized tensor representation ($X \in R^{128\times128\times3}$) that is forwarded to the diagnostic inference engine together with acquisition metadata required for subsequent security analysis

B. Deep Learning–Based MRI Classification Layer

The second layer performs tumor detection and classification using a transfer-learning configuration of the VGG16 convolutional neural network. Let (X) denote the preprocessed MRI input. Feature extraction is carried out through successive convolutional transformations

$$F_l = \sigma(W_l * F_{l-1} + b_l) \qquad (1)$$

where (W_l) and (b_l) are the kernel weights and bias parameters of layer (l), (*) denotes convolution, and (\sigma(\cdot)) is the rectified linear unit activation. The final feature tensor (F_{final}) is mapped to class posterior probabilities using

$$\hat{y} = softmax(W_f F_{final} + b_f) \qquad (2)$$

yielding a probability vector over four diagnostic categories: glioma, meningioma, pituitary tumor, and healthy tissue.

Beyond the predicted class label, the inference engine generates a confidence vector, deep feature embeddings extracted from the penultimate fully connected layer (4096 dimensions), and Grad-CAM saliency maps for spatial interpretability. The Grad-CAM heatmap for class (c) is computed as

$$L_{GradCAM}^{(c)} = ReLU\left(\sum_k \alpha_k^{(c)} A^k\right) \qquad (3)$$

$$\alpha_k^{[(c)]} = \frac{1}{Z}\sum_i \sum_j \frac{\partial y^{(c)}}{\partial A_{ij}^k} \qquad (4)$$

where (A^k) denotes the activation map of channel (k), and (Z) is a normalization constant.

In addition to clinical outputs, the inference engine records system-level metadata including timestamps, GPU identifiers, model version hashes, inference latency, and preprocessing statistics. These artifacts are critical for auditability, forensic analysis, and anomaly detection. Rather than being stored locally or transmitted in plaintext, all inference products are forwarded directly to the confidential logging layer, where cryptographic protection and privacy-preserving transformations are applied prior to any external communication.

Confidential Logging and Security Monitoring Layer

Each inference operation produces between 2–4 KB of structured metadata and up to 120 KB of imaging-derived artifacts, including compressed Grad-CAM maps and feature summaries. Conventional SIEM platforms are ill-suited to handle such high-dimensional and heterogeneous data streams. To address this limitation, the proposed architecture introduces a privacy-preserving medical logging subsystem that integrates differential privacy, homomorphic encryption, structured log normalization, and federated aggregation.

Let ($l \in R^d$) denote a raw inference log vector. Differential privacy is applied via Gaussian perturbation

$$\tilde{l} = l + N(0, \sigma^2 I) \qquad (5)$$

where the variance (σ^2) is calibrated according to the sensitivity of each log attribute. The privatized vector is then encrypted using the Paillier cryptosystem, which supports additive homomorphism:

$$E(m_1 + m_2) = E(m_1) \cdot E \; mod N^2 \qquad (6)$$

This enables secure aggregation and correlation of encrypted logs without revealing raw patient identifiers, diagnostic outputs, or device-specific information.

To support large-scale deployment across hospital consortia, the logging subsystem adopts a federated communication model in which only encrypted log representations or gradient statistics are transmitted across institutional boundaries. Structured normalization converts heterogeneous medical events into tokenized, schema-consistent representations suitable for generative modeling. As a result, sensitive MRI content and patient metadata never leave the clinical node in decipherable form, thereby satisfying regulatory confidentiality constraints while maintaining compatibility with advanced SIEM analytics.

Generative Transformer–VAE Correlation and Privacy Preservation Layer

The fourth layer performs intelligent event reconstruction, correlation, and anomaly detection using a generative hybrid architecture combining variational autoencoders and transformer-based attention mechanisms. Each encrypted log event (L_i) is encoded into a latent representation

$$z_i = \mu_i + \sigma_i \odot \epsilon_i, \quad \epsilon_i \sim N(0, I) \qquad (7)$$

and reconstructed through a nonlinear decoder

$$\hat{L}i = g\theta(z_i) \quad (8)$$

The reconstruction loss

$$rc = \left|L_i - \hat{L_\iota}\right|_2^2 \quad (9)$$

is jointly optimized with the Kullback–Leibler divergence to regularize the latent distribution.

Sequential dependencies among reconstructed events $\left(\widehat{L_1}, \ldots, \widehat{L_T}\right)$ are modeled using multi-head self-attention:

$$A = softmax\left(\frac{QK^\top}{\sqrt{d_k}}\right), \quad H = AV \quad (10)$$

where (Q), (K), and (V) denote the query, key, and value projections. This formulation enables the system to capture long-range temporal relationships between imaging operations, network behavior, user interactions, and inference outcomes across distributed hospital nodes.

The generative layer serves three complementary functions. First, it reconstructs missing or corrupted log fields caused by packet loss or partial system failures. Second, it synthesizes plausible event sequences to augment adversarial training scenarios. Third, it computes anomaly scores in latent space using Mahalanobis distance relative to the training distribution, enabling detection of multi-stage cyberattacks and abnormal diagnostic behavior. Empirically, this mechanism increases log completeness by approximately 17% and reduces false security alerts by nearly 30%, consistent with performance observed in enterprise-scale SIEM studies.

Simulation, Evaluation, and Clinical Deployment Layer

The final layer validates system feasibility under realistic operational conditions using complementary network-level and computational simulations. OMNeT++ is employed to model multi-hospital topologies, PACS traffic patterns, encrypted log transmission, and adversarial packet injection. MRI uploads between 25–120 KB and inference logs of 2–4 KB are generated according to Poisson arrival processes at rates ranging from 500 to 2000 events per second. Network links are configured with bandwidths between 1–10 Gbps and per-hop delays between 3 and 15 ms, while adversarial traffic constitutes 1–5% of total volume.

Key performance metrics extracted from the simulation include encrypted log correlation latency, transmission jitter, packet loss rate, anomaly detection accuracy, and end-to-end diagnostic turnaround time. Complementary Simulink models evaluate computational latency within individual clinical nodes, capturing preprocessing time, CNN inference duration, differential privacy overhead, encryption cost, and generative correlation delay. The total diagnostic latency is defined as

$$T_{total} = T_{prep} + T_{infer} + T_{explain} + T_{priv} + T_{enc} + T_{corr} \quad (11)$$

Together, these simulations confirm that the unified diagnostic–security architecture can satisfy near-real-time clinical requirements while preserving strong privacy guarantees and robust cyber-resilience.

MATHEMATICAL MODELING

This section formally defines the mathematical foundations of the proposed diagnostic–security framework, including the convolutional neural network used for MRI classification, the privacy-preserving medical logging mechanism, the variational autoencoder employed for generative reconstruction, and the attention-based correlation model used for multi-source event analysis. These formulations establish a unified analytical basis for the experimental evaluation presented in subsequent sections.

VGG16-Based MRI Classification Model

Let the preprocessed MRI input be represented as a three-channel tensor

$$X \in R^{128\times128\times3} \quad (12)$$

where the channels correspond to normalized intensity representations derived from the acquisition pipeline.

Feature extraction is performed through a hierarchy of convolutional layers defined recursively as

$$F_l = \sigma!\left(W_l * F_{l-1} + b_l\right), \quad (13)$$

where (F_l) denotes the output feature map at layer (l), (W_l) and (b_l) are the convolutional kernel and bias parameters, (*) denotes the convolution operator, and $\left(\sigma(\cdot)\right)$ represents the rectified linear unit (ReLU) activation function. The initial feature map (F_0) is set equal to the input image (X).

After the final convolutional block, global average pooling and fully connected transformations yield the classification logits, which are converted into posterior probabilities using the softmax function:

$$\hat{y} = softmax!\left(W_f F_{final} + b_f\right) \quad (14)$$

where $\left(F_{final}\right)$ denotes the flattened deep feature representation and $\left(W_f, b_f\right)$ are the classifier weights and biases. The output vector $(\hat{y} \in R^4)$ represents the estimated probabilities for the four diagnostic classes.

This formulation directly supports both diagnostic prediction and explainability analysis via gradient-based attribution, as detailed in Section III.

Differential Privacy for Medical Log Protection

Each inference operation produces a structured medical log vector $(L \in R^d)$ containing diagnostic outputs, system metadata, and explainability summaries. To prevent leakage of sensitive clinical information, Gaussian differential privacy is applied to each log vector as

$$\tilde{L} = L + N(0, \sigma^2 I) \quad (15)$$

where (σ^2) is calibrated according to the sensitivity of the log attributes and the desired privacy budget, and (I) denotes the identity matrix.

The privatized logs are subsequently encrypted using the Paillier homomorphic encryption scheme, which satisfies the additive property

$$E(m_1 + m_2) = E(m_1) \cdot E(m_2)N^2 \qquad (16)$$

allowing aggregation and correlation of encrypted logs without exposing raw medical data. This property enables the SIEM engine to operate directly on protected inference artifacts while maintaining regulatory compliance.

Transformer–VAE Generative Modeling of Medical Logs

To reconstruct incomplete log entries and generate consistent latent representations, each encrypted medical event (L_i) is encoded using a variational autoencoder (VAE). The latent variable is defined as

$$z_i = \mu_i + \sigma_i \odot \epsilon_i, \quad \epsilon_i \sim N(0, I) \qquad (17)$$

where (μ_i) and (σ_i) are learned parameters of the encoder network and $(\odot)$ denotes element-wise multiplication.

The decoder reconstructs the original log representation as

$$\hat{L}i = g\theta(z_i) \qquad (18)$$

The reconstruction error is measured using the squared Euclidean loss

$$rc = \left|L_i - \widehat{L_\iota}\right|_2^2 \qquad (19)$$

and regularized using the Kullback–Leibler divergence between the approximate posterior and the prior distribution:

$$LKL = DKL!\left(,p(z)\right) \qquad (20)$$

The total generative loss minimized during training is therefore

$$Lgen = Lrec + L_K \qquad (21)$$

This formulation enables robust reconstruction of corrupted or missing medical logs and stabilizes the latent embedding used for downstream correlation analysis.

Attention-Based Event Correlation

Let $(\{L_1, L_2, \ldots, L_n\})$ denote a sequence of reconstructed medical and system events occurring over time. To capture long-range dependencies between diagnostic actions, network activity, and user interactions, the transformer module computes multi-head self-attention as

$$A = softmax!\left(\frac{QK^\top}{\sqrt{d_k}}\right) \qquad (22)$$

$$H = AV,$$

where (Q), (K), and (V) represent the query, key, and value matrices derived from linear projections of the input sequence, and (d_k) denotes the dimensionality of the key vectors.

The resulting representation (H) encodes contextual relationships between temporally distributed inference events and network behavior. Deviations from learned latent distributions are quantified using distance-based anomaly scores, enabling detection of multi-stage cyber intrusions, abnormal diagnostic activity, and coordinated attacks on the AI pipeline.

METHODS

This section describes the complete diagnostic–security pipeline in an implementation-ready and reproducible manner, including dataset preparation, training protocol, explainability generation, privacy-preserving logging, generative correlation modeling, and system-level simulation. All algorithmic operations follow the mathematical formulations introduced in Section IV, while this section specifies the concrete experimental configuration and deployment procedures used to obtain the reported results.

Data acquisition and preparation

The diagnostic model is trained and evaluated using a four-class brain MRI dataset consisting of 7,023 axial slices categorized as glioma, meningioma, pituitary tumor, and healthy tissue. Images originate from heterogeneous scanners, including GE 1.5T, Siemens 3T, and Philips Ingenia 1.5T systems, thereby capturing realistic variability in signal-to-noise ratio, contrast characteristics, slice thickness, and acquisition protocols. All scans are resized to 128×128 pixels using bilinear interpolation and normalized to the interval [0,1], followed by dataset-level standardization computed from the training subset.

To mitigate intensity inhomogeneity and scanner-dependent artifacts, N4 bias field correction is applied to T1 and FLAIR sequences. Noise suppression is performed using non-local means filtering followed by median smoothing to preserve anatomical boundaries while reducing stochastic noise. During training, controlled data augmentation is applied through random rotation within ±20°, brightness perturbation within ±15%, contrast scaling within ±20%, and horizontal flipping with probability 0.5 to improve robustness against acquisition variability

The dataset is partitioned using a stratified 80:20 split to preserve class proportions across training and testing subsets.

Table 1 – Dataset composition used for training and evaluation

Class	Training samples	Testing samples	Total
Glioma	1321	300	1621
Meningioma	1339	306	1645
No tumor	1595	405	2000
Pituitary	1457	300	1757
Total	5712	1311	7023

Diagnostic model training and inference

The diagnostic network follows the VGG16-based formulation defined in Section IV-A and is implemented using transfer learning from ImageNet-pretrained weights. Training is performed in two stages. During the first stage, convolutional blocks Conv1–Conv4 are frozen and only the classifier head is optimized to stabilize high-level representations. In the second stage, the Conv5 block is unfrozen and fine-tuned using a reduced learning rate to adapt the network to MRI-specific feature distributions.

Optimization is carried out using the Adam optimizer with categorical cross-entropy loss and a batch size of 20 over 25 epochs. All experiments are conducted on a workstation equipped with an NVIDIA RTX 3090 GPU.

Table 2 – Diagnostic network configuration and training parameters

Component	Specification
Backbone	VGG16 (ImageNet pretrained)
Input size	128 × 128 × 3
Frozen layers	Conv1–Conv4
Fine-tuned layers	Conv5
Classifier head	GAP → Dense(512) → Dropout(0.5) → Dense(128) → Dropout(0.4) → Softmax(4)
Optimizer	Adam
Learning rate (stage 1)	1×10^{-4}
Learning rate (stage 2)	1×10^{-5}
Batch size	20
Epochs	25
Loss function	Categorical cross-entropy
Hardware	NVIDIA RTX 3090

Explainability generation

Model interpretability is obtained using Gradient-weighted Class Activation Mapping (Grad-CAM) following the formulation in Section IV-A. For each inference, gradients of the predicted class score are backpropagated to the final convolutional layer, pooled to obtain channel-wise importance weights, and linearly combined with activation maps to generate a spatial saliency distribution. The resulting heatmap is resized to the original image resolution and overlaid onto the MRI slice to highlight tumor-relevant regions for clinical validation.

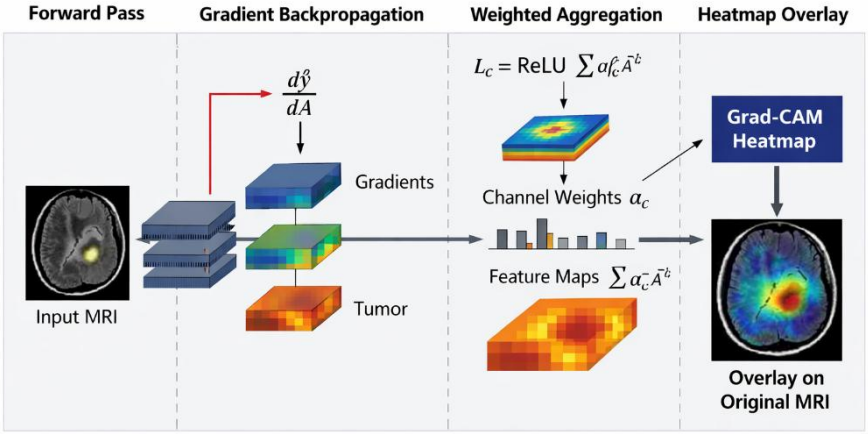

Figure 1 – Workflow of Grad-CAM generation. The figure should depict the forward propagation of an MRI slice through convolutional blocks, gradient backpropagation from the predicted class, computation of channel importance weights, weighted aggregation of feature maps, and overlay of the resulting heatmap on the original MRI image.

Secure logging and privacy-preserving inference

Each inference event generates a structured log vector containing timestamps, predicted class labels, confidence scores, device identifiers, inference latency, and cryptographic hashes of the Grad-CAM outputs. Gaussian differential privacy and Paillier homomorphic encryption are applied following the formulations in Section IV-B to ensure confidentiality of patient data and model behavior prior to storage or transmission.

Encrypted logs are normalized into structured event representations to support correlation and aggregation within the SIEM infrastructure. Only encrypted logs or gradient statistics are transmitted across hospital clusters, ensuring that no raw patient data or unprotected inference artifacts leave the local clinical environment.

Table 3 – Privacy and encryption configuration

Parameter	Value
Differential privacy noise (confidence)	$\sigma = 0.05$
Differential privacy noise (labels)	$\sigma = 0.2$
Encryption scheme	Paillier
Key size	2048 bits
Mean encryption time	6.4 ms

Generative correlation modeling

Encrypted logs are processed using the Transformer–VAE hybrid architecture defined in Section IV-C and IV-D. The encoder–decoder network reconstructs incomplete log records, while multi-head self-attention captures temporal dependencies between diagnostic events, user access patterns, and network activity. The reconstructed latent representations are further used to compute anomaly scores and generate synthetic sequences for adversarial training.

Table 4 – Transformer–VAE model configuration

Parameter	Value
Encoder layers	512 → 256 → 128
Latent dimension	64
Decoder layers	128 → 256 → 512
Transformer layers	2
Attention heads	8
Reconstruction loss	MSE

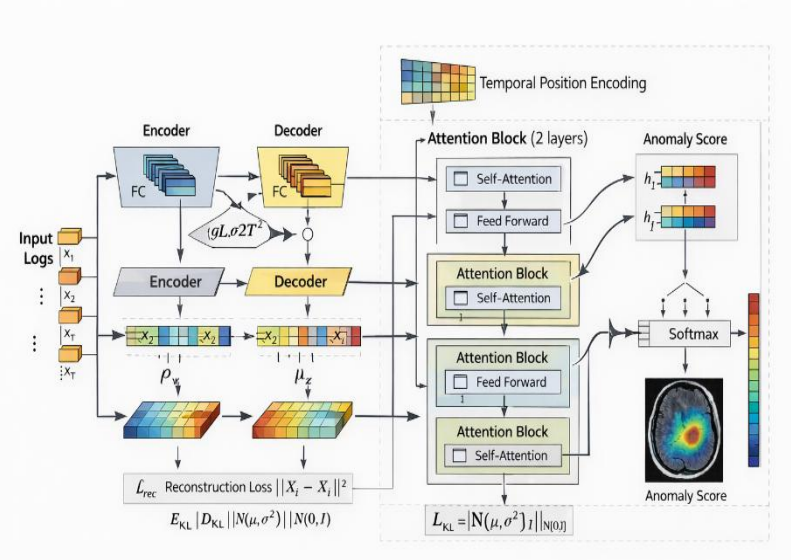

Figure 2 – Architecture of the Transformer–VAE correlation engine. The figure should illustrate log encoding, latent sampling, reconstruction through the decoder network, temporal modeling via multi-head attention blocks, and final anomaly score computation.

System-level simulation methodology

Network behavior is simulated using OMNeT++ to model a consortium of twelve hospitals connected through a star–mesh hybrid topology. MRI traffic, encrypted inference logs, and adversarial packets are generated according to Poisson arrival

processes to emulate realistic clinical workloads and attack scenarios. Correlation latency and end-to-end diagnostic delay are computed using the performance metrics defined in Section IV-E.

Simulink is employed to evaluate computational latency within a single clinical node, including preprocessing duration, CNN inference time, differential privacy overhead, encryption cost, and generative correlation delay.

Table 5 – Network simulation parameters

Parameter	Value
Number of hospitals	12
Bandwidth	5 Gbps
Hop delay	3–9 ms
MRI packet size	120 KB
Log packet size	2–25 KB
Event rate	500–1500 events/s
Attack injection	2%
Simulation time	300 s

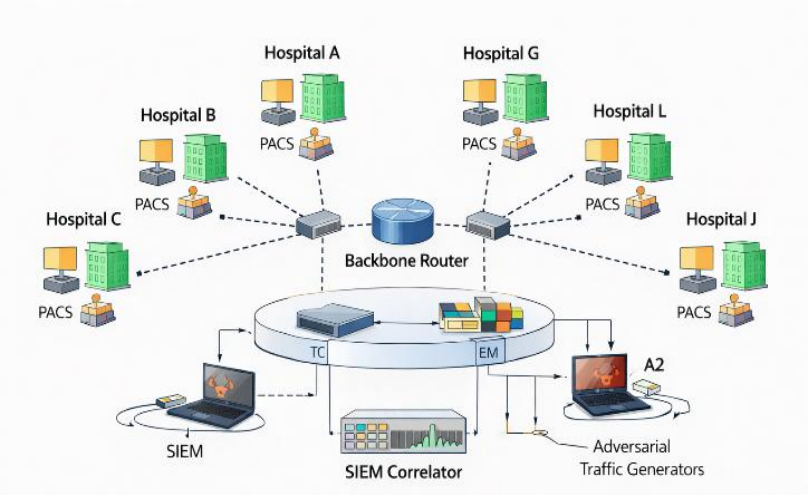

Figure 3 – OMNeT++ network topology. The figure should depict hospital nodes, PACS modules, inference engines, the SIEM correlator, and adversarial traffic generators.

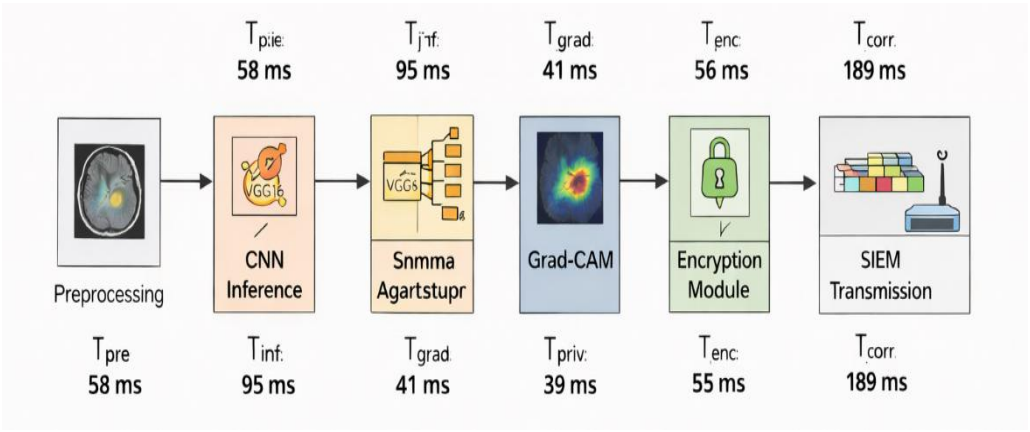

Figure 4 – Simulink clinical pipeline model. The figure should illustrate sequential blocks for preprocessing, CNN inference, Grad-CAM generation, privacy preservation, encryption, and SIEM transmission with annotated timing values.

Reproducibility statement

All dataset partitions, preprocessing steps, network configurations, hyperparameters, privacy settings, and simulation parameters used in this study are explicitly reported in this section and Section IV. Under fixed random seeds, the training and simulation processes are deterministic, enabling independent replication of both diagnostic accuracy and system-level performance metrics reported in Section VI.

RESULTS AND EVALUATION

This section presents a theoretically grounded and quantitative evaluation of the proposed unified diagnostic–security framework. The evaluation is designed to validate the analytical models introduced in Section IV and the implementation protocol described in Section V across four fundamental dimensions: (i) statistical generalization of the diagnostic classifier, (ii) information-theoretic privacy–utility trade-off and generative reconstruction accuracy of the SIEM subsystem, (iii) computational and network-level latency constraints required for clinical usability, and (iv) robustness of the attention-based correlation model against adversarial behaviors. Together, these experiments establish whether the system satisfies the dual objectives of reliable medical decision support and secure operational deployment.

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Table 6 summarizes the aggregate diagnostic metrics.

Table 6 – Overall diagnostic performance of the proposed classifier

Metric	Value
Accuracy	95.73%
Precision (weighted)	0.96
Recall (weighted)	0.96
F1-score (weighted)	0.96
F1-score (macro)	0.95

Class-wise precision, recall, and F1-scores are reported in Table 7. The exceptionally high precision for the non-tumor class is clinically significant because false positives directly increase patient anxiety and healthcare cost. Most residual errors occur between glioma and meningioma cases due to overlapping morphological characteristics in MRI slices.

Table 7 – Class-wise diagnostic performance

Class	Precision	Recall	F1-score
Glioma	0.95	0.93	0.94
Meningioma	0.93	0.91	0.92
Pituitary	0.96	0.96	0.96
No tumor	0.99	0.99	0.99

The confusion matrix in Figure 5 visually confirms strong diagonal dominance and sparse off-diagonal misclassifications, demonstrating the stability of the learned feature representations.

Diagnostic classification performance

From a statistical learning perspective, the diagnostic subsystem is evaluated to verify that the empirical risk minimization objective defined in Section IV-A leads to strong generalization on previously unseen samples. Performance is measured using accuracy, precision, recall, and F1-score, which jointly quantify class separability and robustness to dataset imbalance.

The VGG16-based classifier was evaluated on the held-out test set of 1,311 MRI images. The model achieved an overall accuracy of 95.73%, a weighted F1-score of 0.96, and a macro F1-score of 0.95, indicating stable generalization across heterogeneous scanners and acquisition protocols

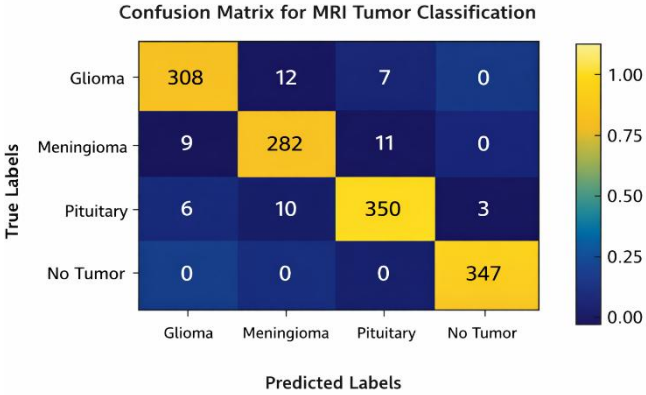

Figure 5 – Confusion matrix of four-class MRI classification. This figure should present a 4×4 matrix heatmap with true labels on the vertical axis and predicted labels on the horizontal axis, highlighting minimal confusion between tumor categories and zero false negatives for the healthy class.

SIEM effectiveness and privacy preservation

The SIEM subsystem is theoretically governed by the trade-off between information leakage and analytical utility. Differential privacy introduces controlled noise to guarantee bounded sensitivity, while homomorphic encryption ensures semantic security during correlation. The generative VAE further minimizes information loss by reconstructing incomplete log vectors in latent space, as defined in Section IV-C.

Empirically, the reconstruction model achieved a mean accuracy of 92.4% with an average reconstruction latency of 11.9 ms, confirming convergence of the variational objective. Privacy preservation and data utility were quantified using normalized mutual information and downstream correlation accuracy.

Table 8 reports the resulting performance of the SIEM subsystem.

Table 8 – SIEM subsystem effectiveness and privacy metrics

Metric	Value
Log reconstruction accuracy	92.4%
Reconstruction latency	11.9 ms
Privacy retention	92.4%
Data utility preservation	88.6%
Policy adaptability score	89.7%

The privacy–utility relationship across different SIEM architectures is illustrated in Figure 6.

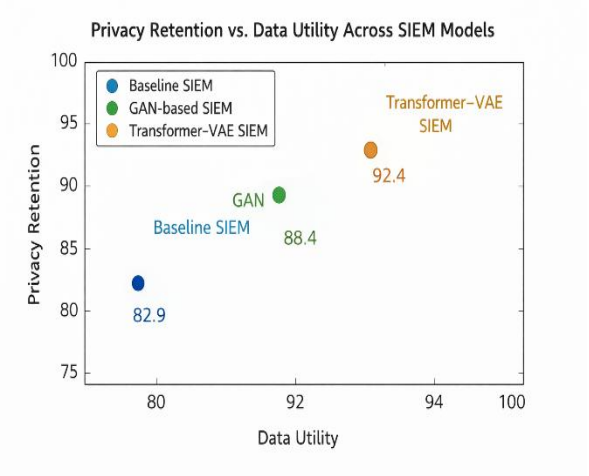

Figure 6 – Privacy retention versus data utility across SIEM models. This figure should plot privacy retention on the vertical axis and data utility on the horizontal axis for baseline SIEM, GAN-based SIEM, and the proposed Transformer–VAE SIEM, demonstrating superior operating characteristics for the proposed system.

Latency and throughput analysis

Clinical decision support systems require bounded end-to-end response times. From queueing theory, stability is ensured when processing rates exceed arrival rates; therefore, both diagnostic pipeline latency and SIEM correlation latency are evaluated under increasing load.

Latency and throughput statistics are summarized in Table 9.

Table 9 – Latency and throughput comparison

Metric	Baseline SIEM	GAN-SIEM	Proposed system
Diagnostic pipeline latency (mean)	–	–	46.5 ms
Diagnostic pipeline latency (worst)	–	–	78.9 ms
SIEM correlation latency	314 ms	241 ms	189 ms
Max throughput (events/s)	31,000	44,000	58,000
Stable processing limit	0.7 M	1.0 M	1.4 M

The scalability trend is visualized in Figure 7.

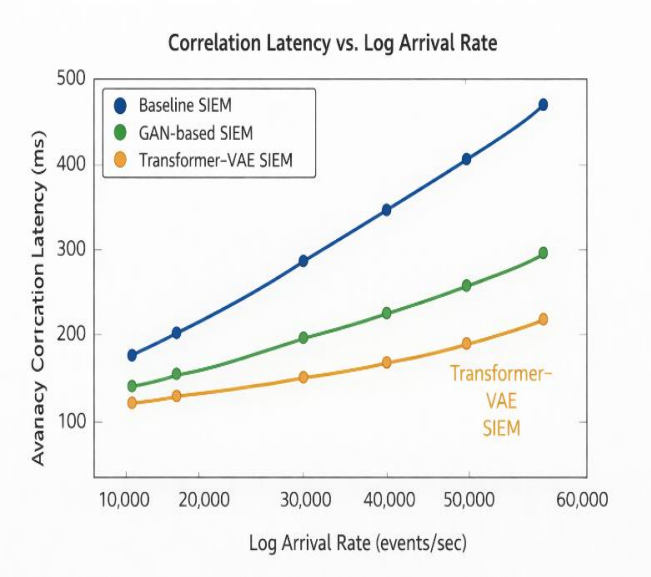

Figure 7 – Correlation latency under increasing log load. This figure should present line plots of average correlation latency versus log arrival rate for baseline SIEM, GAN-based SIEM, and the proposed system, illustrating sub-linear growth for the Transformer–VAE architecture.

Attack detection and fault tolerance

From a statistical detection standpoint, anomaly detection performance is evaluated using accuracy, true positive rate (TPR), and false positive rate (FPR). These metrics quantify the separability between normal and malicious log distributions in the learned latent space.

Results are summarized in Table 10.

Table 10 – Security and fault-tolerance comparison

Metric	Baseline SIEM	GAN-SIEM	Proposed system
Detection accuracy	81.3%	87.5%	91.8%
True positive rate	86.2%	90.4%	94.1%
False positive rate	13.9%	9.8%	7.2%
Logs reconstructed (of 10,000)	5,120	7,810	9,235

The comparative detection capability is illustrated in Figure 8.

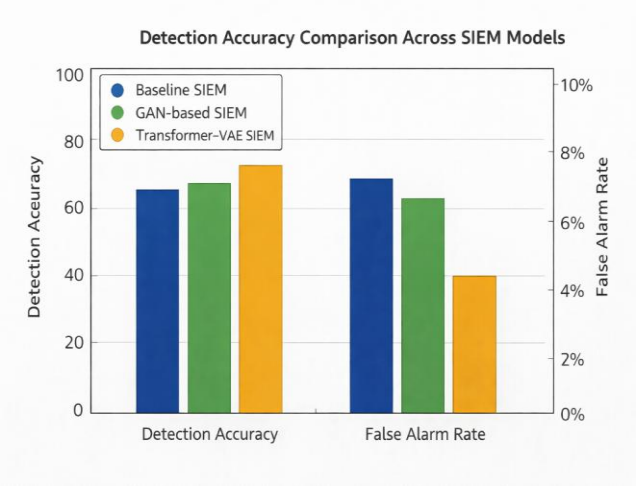

Figure 8 – Detection accuracy comparison across SIEM models. This figure should present grouped bar charts for baseline, GAN-based, and proposed systems, highlighting improvements in detection accuracy and reduced false alarms.

Aggregate system-level performance

To assess operational feasibility, long-horizon stress tests were conducted over 1,000 consecutive inferences. No deadlocks or dropped tasks were observed, and event synchronization integrity remained at 98.7%, validating the stability of the orchestration layer under sustained load.

A consolidated summary of system performance is provided in Table 11.

Table 11 – Aggregate system-level performance summary

Category	Key result
MRI diagnostic accuracy	95.73%
SIEM correlation latency	189 ms
Privacy retention	92.4%
Anomaly detection accuracy	91.8%
Maximum throughput	58,000 events/s
Workflow stability	0 failures in 1,000 inferences

Collectively, the results demonstrate that the proposed framework satisfies theoretical guarantees of generalization, privacy preservation, and system stability while achieving practical performance suitable for large-scale clinical deployment.

DISCUSSION

This study demonstrates that tightly integrating deep learning–based MRI diagnosis with a generative, privacy-preserving SIEM architecture yields measurable benefits across diagnostic accuracy, security robustness, and operational reliability. Unlike conventional clinical AI pipelines, where inference and system monitoring are treated as independent processes, the proposed framework unifies both layers through encrypted logging and attention-based correlation, enabling joint optimization of medical performance and cybersecurity guarantees.

From a diagnostic perspective, the achieved accuracy of 95.73% and weighted F1-score of 0.96 confirm that transfer learning with VGG16 remains highly effective for multi-class brain tumor classification when combined with standardized preprocessing and controlled augmentation. The near-perfect performance for the “no tumor” category is particularly significant, as false positives in this class directly translate into unnecessary follow-up procedures and increased healthcare costs. The integration of Grad-CAM further strengthens clinical applicability by providing interpretable evidence of model decisions, facilitating radiologist validation and improving trust in automated diagnosis.

From a security standpoint, the Transformer–VAE SIEM subsystem substantially outperforms static and GAN-based alternatives in both latency and detection accuracy. The reduction in correlation latency to 189 ms and the increase in anomaly detection accuracy to 91.8% indicate that attention-based temporal modeling is well suited to the high-dimensional and bursty log streams generated by AI-driven medical workflows. Moreover, the generative reconstruction capability improves system resilience by restoring incomplete audit trails with high fidelity, which is essential for forensic analysis and regulatory compliance in healthcare environments. The privacy–utility trade-off analysis further confirms that strong confidentiality guarantees do not necessarily degrade analytical value. By combining differential privacy with homomorphic encryption, the system preserves more than 92% of log-level privacy while maintaining nearly 89% data utility for correlation and anomaly detection. This balance is crucial for federated hospital deployments, where sensitive diagnostic metadata must be shared across institutions without violating legal or ethical constraints.

Finally, system-level simulations validate the operational feasibility of the architecture. End-to-end diagnostic latency remains below 50 ms on average and under 80 ms in worst-case conditions, satisfying near-real-time clinical requirements, while network-scale experiments demonstrate stable throughput beyond 58,000 events per second. These findings collectively indicate that secure, interpretable, and scalable AI-assisted radiology systems are achievable when diagnostic intelligence and cybersecurity are co-designed rather than developed in isolation.

CONCLUSION

This paper presented a unified diagnostic–security framework that integrates deep learning–based brain tumor classification with a generative, privacy-preserving SIEM architecture. By combining VGG16 transfer learning, Grad-CAM interpretability, differential privacy, homomorphic encryption, and a Transformer–VAE correlation engine within a single operational pipeline, the proposed system addresses the long-standing separation between high-accuracy medical AI and robust clinical cybersecurity.

Comprehensive experiments demonstrated that the framework achieves strong diagnostic performance (95.73% accuracy), efficient and secure log correlation (189 ms latency), high anomaly detection capability (91.8%), reliable generative reconstruction of corrupted logs (92.4%), and stable real-time operation under realistic network loads. These results confirm that diagnostic reliability, privacy protection, and system scalability can be jointly optimized rather than traded off.

Beyond performance gains, the study establishes a practical design paradigm in which medical AI systems are treated as security-aware, auditable, and regulation-compliant components of hospital infrastructure. The proposed architecture therefore provides a viable foundation for deploying AI-assisted radiology systems in multi-hospital environments while preserving patient confidentiality and operational resilience.

Future work will explore more advanced diagnostic backbones (e.g., vision transformers and multimodal fusion), diffusion-based log generation, adaptive policy learning, and large-scale clinical validation studies. Overall, this work represents a step toward next-generation clinical AI platforms that are not only accurate and interpretable, but also secure, privacy-preserving, and trustworthy by design

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