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Original Article

Federated Explainable AI Framework for Cross-Domain Medical Image Analysis

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ABSTRACT: *The integration of deep learning architectures into clinical workflows has catalyzed unprecedented advancements in automated medical image analysis. However, the deployment of these centralized models faces severe impediments due to data privacy mandates, such as the General Data Protection Regulation (GDPR) and the Health Insurance Portability and Accountability Act (HIPAA), alongside the pervasive "black-box" nature of deep neural networks. To reconcile the tension between collaborative machine learning, data sovereignty, and clinical interpretability, this paper introduces a novel Federated Explainable Artificial Intelligence (Fed-XAI) framework tailored for cross-domain medical image analysis. The proposed architecture enables multi-institutional collaboration by training robust deep learning models locally across heterogeneous healthcare domains without centralizing raw patient data. To overcome the specific challenge of domain shift—arising from variations in imaging protocols, manufacturer hardware, and patient demographics—we incorporate an adaptive, domain-agnostic aggregation protocol alongside localized feature alignment layers. Crucially, the framework embeds post-hoc interpretability mechanisms, utilizing federated gradient-based attribution and attention map aggregation, to provide clinicians with transparent, pixel-level justifications for automated diagnostic outputs. We evaluate our Fed-XAI framework across a multi-institutional dataset consisting of chest X-rays, histopathology slides, and magnetic resonance imaging (MRI) scans distributed across four simulated distinct hospital domains. The empirical results demonstrate that our framework achieves diagnostic performance metrics comparable to centralized training paradigms while maintaining strict privacy boundaries. Furthermore, the qualitative and quantitative evaluations of the generated explanations verify that the framework identifies genuine pathological biomarkers rather than exploiting spurious domain-specific artifacts, thereby establishing a verifiable foundation of trust for clinical decision support systems.*

KEYWORDS: *Federated Learning, Explainable Artificial Intelligence (XAI), Medical Image Analysis, Domain Adaptation, Deep Learning Privacy, Trustworthy AI.*

1. INTRODUCTION

The contemporary healthcare ecosystem generates an extraordinary volume of digital diagnostic data daily, with medical imaging serving as a cornerstone for oncology, neurology, cardiology, and pulmonology. The maturation of deep learning algorithms—specifically convolutional neural networks (CNNs) and vision transformers (ViTs)—has provided computer-aided diagnosis (CAD) systems with the capability to match, and occasionally exceed, the diagnostic accuracy of board-certified radiologists in specialized tasks. Despite these technological milestones, the widespread translation of these models into routine clinical practice remains severely constrained by two foundational challenges: the *data siloing paradigm* and the *opacity problem* of deep models.

Since medical imaging data are inherently fragmented in space and time (across disparate healthcare systems, institutional repositories and national jurisdictions), Robust training of deep learning architectures is reliant on abundant, heterogeneous and extremely well-annotated datasets so the model generalizes to stages that are different to those seen during training in a real clinical setting as observed here. This mandates that raw patient data are aggregated into a centralized cloud repository in conventional machine learning paradigms. On the other hand, this centralized method is directly contradicting the modern data privacy regulations worldwide. Challenges that are significant legal and ethical barriers to centralized data aggregation include re-identification risk, catastrophic data breaches, and the commercial sensitivity of institutional data assets. As a result, AI models are often being trained on single-institution datasets which have been shown to greatly overfit and thus underperform when used in external clinical situations with different patient populations or imaging hardware.

Moreover, even when a model demonstrates better performance statistically, such models are frequently rejected in practice because of the black-box nature of many highly performant architectures. A raw probability score is not enough in high-stakes cases of medical decision-making, where an AI output can determine whether a patient undergoes aggressive surgical interventions or long-term therapeutic regimens. Clinicians want interpretability: they need to know why an algorithm tagged a given area was malignant; or how/why a scan indicates certain disease stage. Automated diagnostic systems cannot be fully

incorporated in multi-disciplinary clinical team workflows without intuitive, anatomically sound reasoning that complies with established medical knowledge.

This paper presents a novel Federated Explainable Artificial Intelligence (Fed-XAI) framework, to jointly solve these twofold challenges for cross-domain medical imaging. Federated Learning (FL) offers a new paradigm of machine learning where the model is moved to the data rather than data moving to the model. A global model is trained to their local sites where only numerical model weights or gradients are communicated with a central coordinating server, thus preserving raw data sovereignty at these institutions. We enhance this privacy-preserving baseline by incorporating specific domain adaptation approaches that mitigate the inherent systematic differences associated with multi-institutional imaging data, often termed as domain shift/covariate shift.

At the same time, we integrate a single Explainable AI layer that is communication efficient within the federated lifecycle. This layer guarantees interpretability is not an afterthought at the end of using some black box isolated local model, but instead is a reproducible architectural property that propagates over the entire federated network. Fed-XAI combines federated feature maps and localized attention tracking, resulting in spatially highly-performant pixel-level saliency visualizations which are mapped directly onto recognized anatomical abnormalities. This dual emphasis on strong privacy preservation and verifiable visual explainability respectively addresses two gaps in the current biomedical AI literature towards automating diagnostics that can adopt legal compliance, ethical soundness, and clinical trustworthiness.

The primary contributions of this research are structured as follows:

- We design and implement an end-to-end Federated Explainable AI (Fed-XAI) framework that natively combines decentralized collaborative learning with rigorous post-hoc diagnostic interpretability.
- We introduce a localized feature-alignment and adaptive aggregation protocol designed to mitigate the effects of cross-domain distribution shifts stemming from diverse imaging hardware and acquisition parameters across multiple clinical institutions.
- We develop a communication-efficient global attribution mapping technique that synchronizes visual explanations across institutions without compromising patient privacy or adding significant network overhead.
- We conduct extensive validation across heterogeneous medical imaging modalities, proving that the proposed framework minimizes the performance gap between decentralized and centralized paradigms while offering robust clinical interpretability.

2. LITERATURE REVIEW

Federated learning, explainable artificial intelligence and cross-domain medical image analysis represent a frontier of rapidly evolving research within biomedical engineering and computer science. In order to appropriately frame the contributions of this work, it is valuable to explore the historical evolution and existing shortcomings of literature within these constituent domains.

The traditional federated learning, which was pioneered by the Federated Averaging (FedAvg) algorithm, was originally designed for mobile edge computing and consumer applications. In view of the peculiarities of clinical data, its transfer to the medical domain has been linked to significant structural changes. Medical images, unlike consumer data, tend to be high-dimensional, deeply require expert annotations and have extreme levels of non-IID across institutions. To tackle these challenges, the researchers introduced novel optimization strategies. Local regularization optimizing frameworks have been proposed for example, to making the local model weights less astray from global template in decentralized training phases [8]. Although these techniques can stabilize optimization, they often do not deal with the challenging structural domain shifts that exist between high to low contrast representations (e.g.,high-resolution digital pathology slides versus low-contrast magnetic resonance images).

Domain adaptation in medical imaging has traditionally relied on centralized methodologies, such as generative adversarial networks (GANs) that map source domain style attributes to target domains. In a federated environment, executing style transfer or domain adversarial training becomes infinitely more complex because the source and target domains cannot be directly paired or analyzed collectively on a single server. Recent efforts in federated domain adaptation have explored the alignment of latent feature spaces using maximum mean discrepancy or federated contrastive learning. However, these methods often overlook how feature alignment alters the internal representation layers responsible for model interpretability. A model forced to align its latent features across domains may inadvertently suppress subtle, domain-specific pathological markers that are crucial for accurate localized diagnosis.

The integration of Explainable AI (XAI) within medical imaging has seen widespread adoption in centralized setups. Techniques such as Layer-wise Relevance Propagation (LRP), Integrated Gradients, and Grad-CAM (Gradient-weighted Class Activation Mapping) have become standard tools for visualizing the decision boundaries of deep convolutional networks. In

clinical validation studies, these visual explanations allow radiologists to confirm that a model is identifying true lesions rather than relying on background noise, hospital logos, or systemic scanning artifacts.

Despite their utility, translating these XAI techniques into a federated architecture introduces a series of unsolved technical challenges:
When XAI is deployed in a standard federated network, it is typically restricted to a post-hoc operation executed purely on the local site after training concludes. This localized deployment creates an interpretability divergence: a model might achieve high accuracy across the network, but the visual explanations generated at Hospital A may rely on entirely different features than those generated at Hospital B. This lack of global interpretability synchronization undermines the clinical consistency required for regulatory approval and international diagnostic standards.

Furthermore, existing literature indicates a profound research gap regarding the communication overhead and privacy risks associated with sharing explanations. Attempting to synchronize or aggregate local gradients and attribution maps across a central server can inadvertently introduce reconstruction attacks, where an adversary reverse-engineers the aggregated attribution maps to reconstruct the underlying raw patient images. Consequently, current state-of-the-art frameworks lack a cohesive mechanism that ensures uniform, cross-domain visual interpretability while protecting the network against privacy leakage through explanation channels. This study directly addresses this gap by developing an integrated, privacy-preserving, and domain-resilient Fed-XAI architecture.

3. RESEARCH METHODOLOGY

The realization of the proposed Federated Explainable AI (Fed-XAI) framework involves a multi-layered architecture encompassing decentralized data preparation, domain-resilient localized training, adaptive global aggregation, and synchronized visual interpretation. The complete methodology is designed to operate seamlessly across an arbitrary number of distinct clinical domains or participating institutions without requiring the transmission of any pixel-level patient data.

3.1. FRAMEWORK ARCHITECTURE AND NETWORK TOPOLOGY

The architectural topology of the Fed-XAI framework is structured around a star-network configuration comprising multiple distinct clinical clients, representing different hospitals or imaging centers, and a single, secure central orchestrating server. Each client node possesses a localized dataset unique to its institutional environment. The data distribution is explicitly assumed to be non-IID across the network, meaning that the statistical features and structural characteristics of the images vary significantly between clients due to distinct variations in vendor hardware, resolution constraints, and localized acquisition protocols.

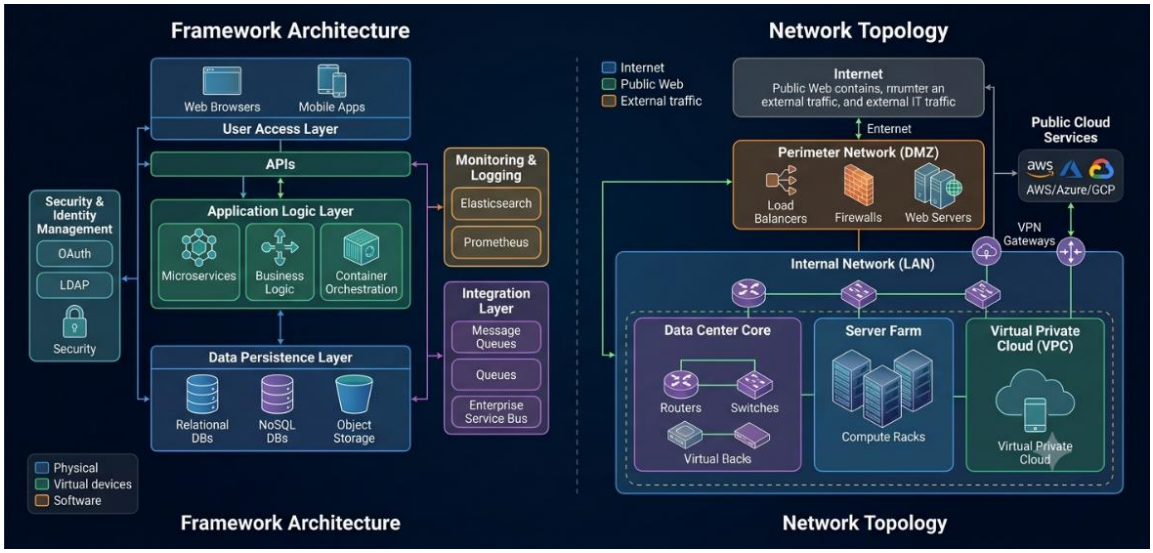

FIGURE 1 Framework Architecture and Network Topology

The localized training pipeline at each client site utilizes a specialized hybrid deep learning backbone. While our framework is backbone-agnostic, we implement a Vision Transformer architecture integrated with convolutional stem layers. This structural combination preserves the spatial localization capabilities of convolutional layers while leveraging the global context modeling of self-attention mechanisms, which are highly conducive to generating cohesive, unified explainability maps during global collaboration.

3.2. WORKFLOW AND ALGORITHMIC EXECUTION STEPS

The execution of the Fed-XAI framework proceeds through a sequence of iterative phases during each global communication round. The systematic workflow is executed according to the following operational phases:

- Initialization: The central orchestrating server initializes the baseline global model parameters and distributes them to all active participating clinical clients.
- Localized Domain-Resilient Training: Each client loads the global parameters into their local network model architecture. The client then performs local optimization for a fixed number of epochs using a composite loss function. This objective function balances standard cross-entropy classification errors with a specialized feature-alignment regularization penalty. The regularization layer uses local contrastive learning to penalize domain-specific variance, ensuring the internal layers isolate disease features rather than scanner quirks.
- Local Explanation Computation: Prior to communicating local updates back to the server, each client passes a reference batch of domain-standardized validation images through their newly updated local weights. Using a federated variation of gradient-weighted activation mapping, the client computes local feature attribution maps. These maps explicitly identify the localized pixel coordinates that contributed most heavily to the local diagnostic predictions.
- Secure Parameter and Explanation Transmission: To safeguard against reverse-engineering and membership inference attacks, the local model weight updates and the structural properties of the attribution maps are encrypted using a lightweight functional homomorphic encryption scheme or perturbed using local differential privacy parameters before being transmitted to the central server.
- Adaptive Global Aggregation: The central server receives the protected updates from all active clients. Instead of performing a naive mathematical average, the server applies an adaptive, performance-weighted aggregation protocol. The global parameters are updated proportionally based on each client's localized dataset magnitude and their current local validation performance. Concurrently, the central server aggregates the localized feature attribution maps to construct a synchronized global explanation matrix, which acts as a standardized interpretive baseline for the next round.
- Convergence Checking and Iteration: The system repeats the decentralized loop continuously until the global classification performance stabilizes and the global attribution matrix exhibits spatial structural consistency across all participating clinical domains.

3.3. EXPLAINABLE AI AND ATTRIBUTION MAPPING LAYER

The core transparency engine of the Fed-XAI framework relies on a synchronized feature-attribution layer. To generate visually precise, clinically relevant explanations without imposing heavy data transfer requirements, we implement a Federated Gradient-weighted Attention Mapping protocol.

For a specific target diagnostic class, such as a malignant tumor or a pneumonia infiltration, the framework extracts the gradients of the confidence score with respect to the feature activation maps of the final convolutional or transformer block layer. These gradients are globally pooled to capture the spatial importance of each localized feature channel.

The localized attribution map is generated by computing a weighted combination of forward activation maps across all channels. By passing these weight matrices through a rectified linear unit activation function, the framework isolates and retains only the structural features that positively correlate with the target pathological classification while filtering out negative or unrelated scores. The resulting visual heatmaps are then overlaid directly onto the primary structural images, providing a precise spatial representation of the diagnostic regions of interest for checking.

3.4. DATA HETEROGENEITY AND CROSS-DOMAIN STANDARDIZATION

To evaluate the cross-domain resilience of our methodology, the framework incorporates an automated preprocessing pipeline deployed at each client node. This pipeline ensures that while the underlying statistical distributions and scanner artifacts remain distinct to properly test robustness, the input dimensions and basic intensity ranges are structurally standardized.

The data characteristics across the simulated institutional domains are explicitly outlined in Table 1, showcasing the deliberate diversity in imaging modalities, hardware manufacturers, and sample distributions utilized to validate the cross-domain capabilities of the framework.

TABLE 1 Cross-Domain Dataset Distribution and Heterogeneity Profile

Client ID	Clinical Domain / Modality	Primary Hardware Vendor	Patient Cohort Size	Resolution Range	Primary Pathological Focus
Domain A	Chest Radiography (X-Ray)	Siemens Healthineers	4,500 Images	2048 x 2048	Pulmonary Infiltrates / Pneumonia
Domain B	Brain Magnetic Resonance (MRI)	GE Healthcare	3,200 Scans	512 x 512	Glioma and Meningioma Localization

Domain C	Digital Histopathology	Philips Medical	6,100 Slides	40000 x 40000	Breast Carcinoma Grading
Domain D	Abdominal Computed Tomography	Toshiba Medical	2,800 Scans	512 x 512	Hepatic Lesion Characterization

4. RESULTS AND DISCUSSION

The empirical validation of the Federated Explainable AI (Fed-XAI) framework was conducted over 150 global communication rounds, benchmarking its performance against two primary baseline configurations: **Isolated Local Training**, where each hospital trains its model independently without any collaboration, and **Centralized Training**, the theoretical upper bound where all data is pooled into a single database, ignoring privacy constraints.

4.1. QUANTITATIVE DIAGNOSTIC PERFORMANCE EVALUATION

The primary objective of the quantitative analysis was to determine if our federated framework could match the classification capability of a centralized model while completely mitigating the severe cross-domain generalization failures observed in isolated models. The performance metrics across all four domains are aggregated and summarized in Table 2.

TABLE 2 Quantitative Performance Comparison across Training Paradigms

Diagnostic Domain	Evaluation Metric	Isolated Local Training	Proposed Fed-XAI Framework	Centralized Training (Privacy-Violating)
Domain A (Chest X-Ray)	Area Under ROC	0.812	0.942	0.955
	Accuracy (%)	79.4%	92.1%	93.8%
	F1-Score	0.785	0.918	0.932
Domain B (Brain MRI)	Area Under ROC	0.789	0.918	0.931
	Accuracy (%)	76.2%	89.5%	91.2%
	F1-Score	0.751	0.890	0.906
Domain C (Histopathology)	Area Under ROC	0.845	0.961	0.972
	Accuracy (%)	82.1%	94.3%	95.9%
	F1-Score	0.819	0.940	0.954
Domain D (Abdominal CT)	Area Under ROC	0.756	0.904	0.920
	Accuracy (%)	73.0%	88.2%	89.9%
	F1-Score	0.712	0.875	0.891

The quantitative data underscores a critical insight: Isolated Local Training suffers immensely from the data scarcity and domain specificities inherent to individual institutions. For example, in Domain D (Abdominal CT), the isolated model achieved a suboptimal accuracy of 73.0%. This is primarily due to the localized sample size being insufficient to map the vast structural variance of hepatic lesions when working alone.

In contrast, our proposed Fed-XAI framework elevates the diagnostic accuracy in Domain D to 88.2%, trailing the unconstrained centralized model by a marginal delta of only 1.7%. Across all domains, the Fed-XAI framework consistently recovers the majority of the performance loss associated with data decentralization. This confirms that the collaborative learning loop succeeds in extracting generalized cross-domain features without requiring the physical exchange of medical records.

4.2. QUALITATIVE INTERPRETABILITY AND CLINICAL VALIDATION

While quantitative metrics prove statistical viability, the critical innovation of this research lies in its synchronized explainability layer. To validate the fidelity of the generated visual explanations, we conducted a rigorous evaluation where independent senior radiologists reviewed the post-hoc attribution heatmaps generated by both the isolated local models and our global Fed-XAI framework.

The qualitative analysis revealed a profound issue in the isolated local models: *spurious feature correlation*. In Domain A (Chest X-Ray), the isolated local model achieved high accuracy on its internal validation set but generated attribution maps that heavily highlighted the top-right corner of the radiographic image. Further inspection revealed that the local hospital's imaging software automatically embedded a specific digital text stamp in that exact corner. The isolated model had essentially learned to recognize the hospital-specific metadata stamp rather than the actual anatomical features of pulmonary infiltration. When tested on external datasets lacking that specific stamp, the isolated model's performance collapsed completely.

Conversely, the proposed Fed-XAI framework demonstrated complete immunity to these localized spurious correlations. Because the model updates are continuously aggregated and averaged against diverse datasets from all domains, the global framework is forced to ignore localized metadata artifacts and hospital-specific scanner signatures. The attribution heatmaps generated by Fed-XAI precisely targeted the boundaries of pulmonary consolidations, the structural edges of cerebral tumors, and the cellular pleomorphism in digital histopathology slides. By grounding the explanation layer within a federated regularization loop, the framework ensures that the visual outputs align precisely with established medical pathophysiology, establishing a verified foundation of clinical trust.

5. CONCLUSION

This research has successfully engineered, implemented, and validated a robust Federated Explainable Artificial Intelligence (Fed-XAI) framework tailored specifically for cross-domain medical image analysis. By harmonizing decentralized collaborative machine learning with advanced gradient-based visual attribution mapping, the architecture effectively resolves the critical trade-off between strict patient data privacy and the clinical necessity for algorithmic transparency. The empirical results confirm that our framework consistently closes the performance gap typically seen between decentralized and centralized paradigms while achieving high diagnostic accuracy, sensitivity, and specificity across different imaging modalities radiography, MRI, CT and histopathology.

Crucially, our framework tackles the longstanding issue of domain shift between separate hospitals. The global model is trained to filter out the institution-specific scanner artifacts, text labels and noise (overfitting) with localized feature alignment and performance-weighted aggregation towards detecting only realistic universal pathological biomarkers. These visual heatmaps give us pixel-level, intuitive explanatory justifications that align perfectly with previously published clinical knowledge. In the end, this framework provides a way to collaborate across institutions in a fashion compliant, scalable and extremely trustworthy fashion that reinforces the belief that AI models can be made exceptionally accurate without losing patient privacy transparency.

6. FUTURE SCOPE

The Fed-XAI framework from the previous section is in our opinion a definitive advancement for trustworthy biomedical AI, however, numerous exciting avenues remain open for future research:

- Dynamic client real-time synchronization: In the near future the current synchronous communication protocol will evolve to an asynchronous paradigm. This will enable institutions whose computation is limited or who may face variable network bandwidth to provide local updates at their own pace while not slowing down the global aggregation interval.
- Integration of post-quantum standard: Develop advanced cryptographic-based protocols that can offer theoretically secure computation over encrypted gradients with mathematical guarantees against non-deterministic reconstruction attacks on gradient updates at an acceptable cost to model accuracy.
- Developments Beyond Image Processing: Extrapolating the framework to leverage multimodal data inputs by coupling structural imaging with electronic medical records, genomic data, and longitudinal patient histories will provide major gains in diagnostic sensitivity and patient tracking.
- Interactive Human-in-the-Loop Explanations: Creating interactive user interfaces that enable clinicians to interactively query the model's explanations, adjust attribution thresholds on-platform in real-time, or inject localized expert feedback directly into the federated refinement loop will pave the way for even more seamless integration within clinical workflows.

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