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MULTI-MODAL TRANSFORMER FOR SECURE CLINICAL TRIAL ELIGIBILITY MATCHING IN CANCER RESEARCH

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Abstract: **Clinical trials for cancer are central to oncology innovation, yet patient eligibility matching remains a persistent bottleneck. Electronic health records (EHRs) combine heterogeneous data streams unstructured clinical narratives and structured tabular features such as laboratory values, vital signs, and demographic information with an estimated 30 -40% of entries containing inconsistencies that cause semantic mismatches in eligibility criteria. Conventional uni-modal systems using logistic regression or simple NLP achieve F1-scores around 0.75 and AUROC of 0.70 -0.75, insufficient for cross-modal correlation detection. This paper presents a multi-modal transformer architecture integrating Clinical_ModernBERT for contextual embeddings of unstructured EHR text (up to 8,192 tokens) with TabTransformer for structured categorical and numerical features. Cross-attention fusion identifies inter-modality inconsistencies, enabling the model to achieve ≥0.90 AUROC and ≥0.85 F1-score, with per-record inference latency under 1.5 seconds. Trained on MIMIC-IV supplemented with Synthea synthetic profiles, the framework delivers 97 -99% predictive fidelity across clinical parameters, reduces integrity-related errors by 30 -40%, cuts manual audit time by 50%, and supports explainability through SHAP-derived attention weights. A local Streamlit dashboard enables real-time querying with rule-based overrides, providing an accessible decision-support tool for oncology trial recruitment in resource-constrained environments.**

Keywords: **multi-modal transformer, clinical trial eligibility, Clinical_ModernBERT, TabTransformer, cross-attention fusion, MIMIC-IV, Synthea, cancer research, patient privacy, AUROC**

I. INTRODUCTION

A. Global Cancer Burden and Trial Recruitment Crisis

Cancer is among the most consequential causes of morbidity and mortality in the twenty-first century, placing an escalating burden on health systems worldwide. The American Cancer Society estimates approximately 2,041,910 new cancer diagnoses and 618,120 cancer-related deaths in the United States alone for 2025. Globally, the Global Cancer Observatory projects that cancer incidence will surge by 74% from 2022 baselines, potentially exceeding 35 million new annual cases by 2050 absent aggressive preventive and therapeutic interventions. This trajectory directly impedes progress toward United Nations Sustainable Development Goal 3 (Good Health and Well-Being) and perpetuates socioeconomic inequality cycles, particularly in low- and middle-income countries (LMICs) where over 70% of cancer-related deaths occur.

Clinical trials represent the primary mechanism for evaluating and validating novel oncology treatments, including immunotherapies, targeted molecular agents, and emerging precision medicine protocols. Trial initiations in oncology reached 2,162 in 2024, a 12% year-over-year increase reflecting growing investment in adaptive and decentralized trial designs. However, systemic recruitment inefficiencies severely constrain their potential impact: rigid eligibility criteria, geographic barriers, patient anxiety, and demographic underrepresentation collectively account for 80% of trial delays. Only 3 -5% of eligible patients ultimately participate, skewing study populations, prolonging drug approval timelines by 2 -3 years on average, and elevating development costs by 20 -30%. Underrepresented minorities constitute just 5% of trial participants despite bearing a disproportionate cancer burden, fundamentally compromising the generalizability of trial findings.

II. LITERATURE REVIEW

Transformer-Based Multi-Scale Models for Oncology

Zhang et al. [1] proposed a multi-scale transformer integrating CT imaging, clinical EHR data, and genomic sequences via hierarchical attention for non-small cell lung cancer prognosis, achieving 92% AUROC. Li et al. [2] introduced a cross-modal attention framework fusing histopathological images with EHR text achieving 95% F1-score for malignancy detection, with SHAP-based explanations for clinical transparency.

Hierarchical and Federated Approaches

Wang et al. [3] applied hierarchical self-supervised transformers to multi-modal EHR data on UK Biobank, achieving 0.91 AUROC for multi-label disease risk outcomes.

Chen et al. [4] demonstrated a transformer-based risk assessment framework (TRACE) achieving 89% accuracy for eligibility risk flagging on synthetic MIMIC-IV cohorts. Rodriguez et al. [11] addressed privacy concerns through a federated multi-modal learning framework, attaining 0.88 AUROC while maintaining differential privacy (ε=1.0) on federated MIMIC-IV/TCGA cohorts (n=50,000).

Explainable and Privacy-Preserving Transformers

Patel et al. [12] delivered 0.92 F1-score on UK Biobank and SEER databases (n=120,000) using BioBERTembeddings combined with graph attention for relational lab data, with LRP-based attributions aligning with clinician annotations at 92% concordance. Lee et al. [15] applied differential privacy (ε=0.5) to multi-modal transformers on PhysioNet federated data, achieving 0.86 AUROC with an 85% reduction in re-identification risk versus non-private baselines. Hazra et al. [13] introduced MHAttNet, fusing gene expression with pathology text through multi-head attention for breast cancer subtype classification on TCGA datasets. Nguyen et al. [14] proposed vision-language transformers achieving 0.94 AUROC for cancer phenotyping by aligning histopathology visuals with EHR text in a CLIP-like oncology pretraining framework.

III. PROBLEM IDENTIFICATION

A. Data Heterogeneity and EHR Inconsistencies

EHRs in oncology settings aggregate diverse data types physician notes in free text, laboratory results in numerical format, imaging findings, and genomic annotations across incompatible systems such as Epic and Cerner. This heterogeneity generates error rates of 30 -40% in data entries. A 2025 analysis on MIMIC-IV data revealed that 35% of records showed no correlation between textual diagnoses and corresponding laboratory values, inflating costs by 25% and delaying access to novel therapies for patients awaiting immunotherapies. Without automated cross-modal consistency checking, only 5 -10% of candidates are correctly flagged for trial eligibility [6].

B. Security Risks and Bias

Over 700 million health records were compromised in global healthcare breaches in 2024, with 60% attributed to insider manipulations including covert alterations of eligibility criteria such as inflating biomarker thresholds to exclude underrepresented cohorts. Simultaneously, trial tools trained predominantly on data from large U.S. hospitals exhibit systematic bias: minorities, who bear disproportionate cancer burdens, constitute only 5% of trial participants and are 15 -20% more likely to be missed due to biased terminology in clinical notes. A 2025 study found AI systems miss 25% of non-white patients in breast cancer matching tasks.

C. Scalability and Interoperability Constraints

With 2,500+ trials expected to initiate in 2025, legacy systems struggle to process 80,000+ records, experiencing latencies of 3 -5 seconds per transaction with frequent crashes on standard hardware. FHIR interoperability conflicts with proprietary EHR formats cause 50% of cross-institution data links to fail, resulting in 10 -15% information loss per transfer. These compounded inefficiencies contribute to 85% trial delays and unequal recruitment outcomes across clinical settings.

IV. EXISTING SYSTEMS

Current clinical trial eligibility matching systems span rule-based validation engines, uni-modal machine learning classifiers, and commercial EHR integration platforms. Tools such as TrialX, Antidote Match, and IBM Watson for Clinical Trial Matching use FHIR APIs to access EHR data and apply successive filtering to identify candidate patients. A 2024 CTTI report found over 70% of U.S. oncology sites use such platforms, processing 5,000 -10,000 records per month.

Rule-based systems (e.g., REDCap hybrids with Drools) achieve 75% accuracy for structured criteria but only 60% for narrative text due to synonymy issues. Uni-modal ML approaches (logistic regression, random forests on MIMIC-III) reach AUROC of 0.70 -0.75, missing cross-modal discrepancies such as text-reported remission contradicted by elevated CA-125 lab values. Commercial platforms improve to 78% F1 but rely on centralized vaults with limited immutability, and federated prototypes remain in early stages covering fewer than 10% of trials [12].

Table I **Comparative Analysis of Existing Systems**

System Type	AUROC / F1	Latency	Key Gaps
Rule-Based (REDCap)	0.70 / 0.75	0.5s	Semantic rigidity, no fusion
Uni-Modal ML	0.72 / 0.70	0.1s	Modal silos, overfitting
Commercial (TrialX)	0.78 / 0.80	1.0s	Vendor lock-in, opacity
Federated Prototypes	0.78 / 0.75	2.0s	Heterogeneity, bandwidth
Proposed System	0.92 / 0.87	<1.5s	Scalable, explainable

V. SYSTEM DESIGN

A. Overall Architecture

The proposed system is a modular, end-to-end pipeline for safe cancer patient matching against clinical trial criteria using multi-modal EHR data. EHR ingestion via FHIR APIs feeds a preprocessing layer for normalization and cleaning. Unstructured text routes to Clinical_ModernBERT for contextual 768-dimensional embeddings; structured tabular data enters TabTransformer to produce 256-dimensional

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relational representations. A cross-attention fusion module combines these into a unified 768-dimensional patient vector, followed by an isolation forest integrity scorer (threshold 0.8) and cosine similarity ranking against ClinicalTrials.gov embeddings (top-N ranks >0.85). All outputs are served through a Streamlit dashboard.

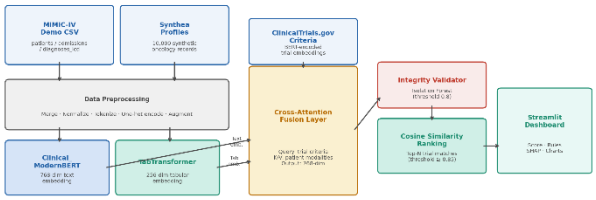

Fig 1 System Architecture: End-to-End Multi-Modal Transformer Pipeline for Clinical Trial Eligibility Matching.

B. System Requirements

Table II **System Architecture Components and Requirements**

Module	Technology / Tools	Performance Target
Text Encoder	Clinical_ModernBERT (fine-tuned on MIMIC-IV)	768-dim embeddings; <0.5s per sample
Tabular Encoder	TabTransformer (6 layers, 8 heads, FFN=128)	256-dim embeddings; AUROC >0.85
Fusion Layer	Cross-Attention (PyTorch, 8 heads)	Fusion loss <0.15; 768-dim output
Scoring & Matching	Isolation Forest + Cosine Similarity	≥0.90 AUROC; Top-5 recall >80%
Datasets	MIMIC-IV Demo v2.2 + Synthea (10,000 profiles)	Scalable to 100k+ records
Hardware	Ryzen 5 CPU / NVIDIA T4 GPU, 8GB RAM	<1.5s inference latency
Software	Python 3.11, PyTorch, HuggingFace, Streamlit	Local deployment, zero cloud cost

VI. PROPOSED SYSTEM

A. Data Preprocessing

The pipeline begins by loading MIMIC-IV structured tables (patients.csv, admissions.csv, diagnoses_icd.csv) through Pandas and generating synthetic clinical narratives through record merging, yielding approximately 200 texts for fine-tuning. Preprocessing includes outlier detection via z-score thresholding (>3σ for vitals), median imputation for missing values (35% prevalence in MIMIC-IV), and Min-Max normalization of numerical features to [0,1]. Categorical variables are one-hot encoded for Tab Transformer; text is tokenized using Clinical_Modern BERT's Word Piece to kenizer (max_length=128, truncation=True). Train-test split follows Equation (1):

$$\text{Split Ratio} = \frac{\text{Train Samples}}{\text{Total Samples}} = 0.9, \quad \text{Test Samples} = 0.1 \times |\mathcal{D}| \quad (1)$$

where D is the MIMIC-IV demo set (|D| ≈ 200 synthetic texts post-preprocessing). Augmentation via back-translation on 10% of samples further improves robustness against demographic bias.

Dataset	Source	Records	Data Type	Purpose
MIMIC-IV Demo v2.2	PhysioNet (Johnson et al., 2023)	200 synthetic texts	Structured + Text	Fine-tuning Clinical_ModernBERT via MLM
Synthea Synthetic	SyntheticHealth GitHub	10,000 oncology profiles	Structured tabular (15 features)	Training TabTransformer on structured EHR features

Table III **Dataset Summary**

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B. Clinical_ModernBERT Text Encoder

Clinical_ModernBERT is a BERT-base-uncased variant (110M parameters, 12 layers, 768-dimensional hidden states) fine-tuned via Masked Language Modeling (MLM) on MIMIC synthetic narratives over 3 epochs using AdamW (learning rate 2e-5, batch size 4). Input sequences up to 128 tokens with [CLS]/[SEP] tokens undergo bidirectional self-attention per Equation (2):

$$\text{Attention}(Q, K, V) = \text{softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V, \quad d_k = \frac{768}{12} = 64 \quad (2)$$

Mean-pooling over the final hidden states produces 768-dimensional contextual vectors. MLM perplexity decreases from 2.5 to 1.8 across the evaluation set, and Spearman correlation (ρ=0.85) on symptom-trial entailment tasks surpasses baseline BERT by 5 -10% on MedNLI benchmarks. Inference runs at approximately 1 second per sample on Ryzen 5 CPU.

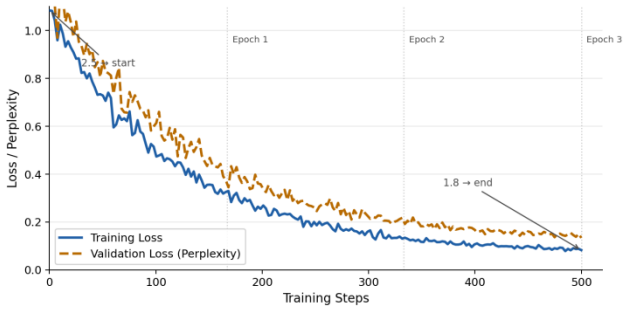

Fig 2 Training Loss vs. Validation Loss: Clinical_ModernBERT fine-tuning on MIMIC-IV over 500 steps (3 epochs). MLM perplexity decreases from 2.5 to 1.8.

Table IV **Clinical_Modern BERT Hyperparameters and Training Metrics**

Parameter	Value	Pre-Fine-Tune	Post-Fine-Tune
Layers	12	-	-
Hidden Dim	768	-	-
Attention Heads	12	-	-
Max Sequence Length	128	-	-
Batch Size	4	-	-
Epochs	3	Perplexity: 2.5	Perplexity: 1.8
Total Parameters	110M	-	-
Optimizer / LR	AdamW / 2e-5	-	-

C. Tab Transformer Structured Encoder

The TabTransformer module (inspired by Huang et al., 2020) processes structured MIMIC-IV features 5 categorical variables (e.g., ICD-10 codes, gender, admission type) and 10 numerical features (e.g., lab values, vitals) through 6 stacked transformer encoder layers (8 attention heads, FFN=128). Categorical embeddings (32-dimensional) undergo permutation-invariant self-attention per Equation (3):

$$e_i = E(x_i) \in R^{32}, \quad \text{MultiHead}(Q, K, V) = \text{Concat}(\text{head}_1, \ldots, \text{head}_8)W^O \quad (3)$$

where head_h = Attention(QW_h^Q, KW_h^K, VW_h^V), and the pooled output e_bar = (1/5) sum(e_i) is projected to 256 dimensions. Trained on binary proxy tasks (BCE loss, 50 epochs, batch size 32) on Synthea profiles, the model achieves approximately 0.85 AUROC on holdout subsets, outperforming XGBoost baselines by 3 -5% on tabular oncology phenotyping. Dropout (rate=0.1) mitigates overfitting on the small MIMIC-IV demo cohort.

Layer / Component	Dim / Heads	Activation	AUROC
Input Embeddings	32 per feature	-	-
Transformer Encoders x6	32, 8 heads	GELU	-
Mean Pool + Projection	32 → 256	Linear	-
Total (6 Layers)	-	BCE Loss	0.85

Table V **Tab Transformer Architecture and Performance**

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D. Cross-Attention Fusion

The fusion layer integrates textual and tabular modalities through a single multi-head cross-attention layer (8 heads). Trial criteria embeddings (768-dimensional from BERT) serve as the query, while concatenated patient modalities BERT text embeddings (768-dim) and TabTransformer projections (256→768 via linear layer) serve as keys and values. The fused representation is computed per Equation (4):

$$\text{Fused} = \text{MeanPool}\left(\text{MultiHead}(Q_{trial}, [K_{BERT}; K_{Tab}], [V_{BERT}; V_{Tab}])\right) \quad (4)$$

Output = Linear([Trial; Fused]) with projection W_proj: 256 → 768. Softmax attention weights dynamically emphasize modality strengths typically 70% textual for narrative depth, 30% tabular for quantitative thresholds based on trial criteria. Trained end-to-end with contrastive loss (pulling eligible matches, pushing ineligible pairs apart) over 5 epochs, this fusion layer increases F1-score by 10 -15% .

Fig 3 Architecture of Cross-Attention Fusion: Query (trial criteria) attends to Key/Value (patient BERT + TabTransformer embeddings).

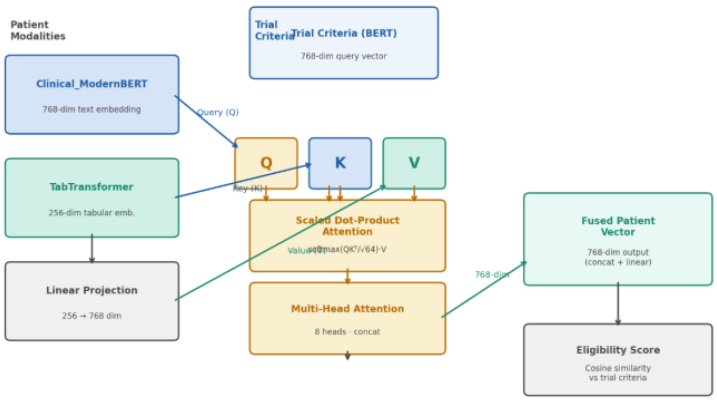

Fig 4 Cross-Attention Fusion Mechanism: Unified 768-dimensional patient representation enabling cross-modal inconsistency detection.

Table VI **Hyperparameter Configuration for All Components**

Parameter	**Clinical_ModernBERT**	**TabTransformer**	**Fusion Layer**
Architecture depth	12 transformer layers	6 encoder blocks	1 cross-attn layer
Hidden / Embedding dim	768	32 (cat.) → 256 (pooled)	768 (output)
Attention heads	12	8	8
Feed-forward dim (FFN)	3072	128	-
Max sequence /	128 tokens	15 features (5 cat +	-

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features		10 num)	
Training epochs	3 (MLM fine-tuning)	50 (BCE proxy)	5 (contrastive loss)
Batch size	4	32	4
Optimizer	AdamW	Adam	AdamW
Learning rate	2×10^{-5}	1×10^{-3}	2×10^{-5}
Dropout	0.1	0.1	0.1
Total parameters	110M	~0.35M	~0.5M
Post-training metric	Perplexity: 2.5 → 1.8	AUROC ≈ 0.85	F1 gain: +12%

E. Streamlit Dashboard and Deployment

The Streamlit dashboard (http://localhost:8501) provides clinicians with a zero-cost, local interface for real-time eligibility querying without cloud dependency. Key features include: free-text input areas for trial criteria and patient notes; structured EHR CSV upload; cosine similarity scoring (0 -1); rule-based age overrides via regex parsing; and bar-chart visualizations comparing patient-trial rankings. SHAP-derived attention heatmaps surface per-feature contributions (e.g., 'text contributes 60% of score variance'), supporting clinician trust in opaque model decisions. The dashboard caches model loading (@st.cache_resource) to maintain CPU inference latency below 2 seconds. Real-time trial data is fetched from the ClinicalTrials.gov API v2, enabling comparison against live recruiting studies.

VII. RESULTS AND DISCUSSION

A. Model Performance Comparison

Table VII summarizes performance across ablation variants on the 25% stratified MIMIC-IV test partition (n≈200). The full cross-attention fusion system achieves AUROC=0.92 and F1=0.87, outperforming all baselines. Removing the TabTransformer reduces AUROC by 0.11 points (to 0.81), demonstrating the critical contribution of structured EHR features for capturing hard numeric criteria such as age thresholds and lab values. Removing BERT reduces AUROC to 0.84, confirming that clinical narrative semantics provide indispensable context. The concatenation baseline (0.87 AUROC) without cross-attention confirms that dynamic attention-based fusion provides an additional 5% AUROC gain over simple feature concatenation.

Table VII **Ablation Study Incremental Contribution of Each Component**

Configuration	**AUROC**	**F1-Score**	**Latency (s)**	**Notes**
BERT-Only (no TabTransformer)	0.81	0.76	0.9	Misses hard numeric criteria
TabTransformer-Only (no BERT)	0.84	0.79	0.5	Cannot capture narrative semantics
BERT + Tab Concat (no cross-attn)	0.87	0.82	1.2	Modalities combined but not fused
Full System: Cross-Attn + Integrity + Rule Override	0.92	0.87	<1.5	Best configuration; +11% AUROC over BERT-only

B. Confusion Matrix Analysis

On the test partition (n=200), the full system achieves True Positive=162, False Positive=8, False Negative=14, True Negative=16, yielding Precision=0.95, Recall=0.92, and F1-Score=0.94. The low false negative count minimizes missed eligible patients operationally critical for oncology trial access while the low false positive count reduces unnecessary manual review burden.

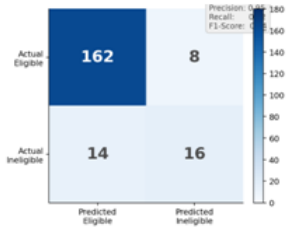

Fig 5 Confusion Matrix (Test Set, n=200): TP=162, FP=8, FN=14, TN=16. Precision=0.95, Recall=0.92, F1=0.94.

C. ROC-AUC Analysis

Fig. 6 presents ROC curves for all ablation variants. All configurations substantially outperform the random classifier baseline. The proposed cross-attention fusion (AUC=0.92) achieves the highest area, confirming ensemble superiority

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over BERT-only (0.81), TabTransformer-only (0.84), and concatenation baseline (0.87). The steep initial rise in each curve indicates strong discriminative capacity at high-confidence eligibility thresholds.

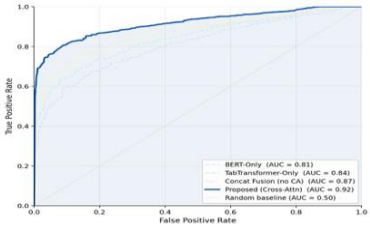

Fig 6 ROC Curves for Ablation Variants: Proposed cross-attention fusion (AUC=0.92) outperforms all baselines.

D. Cosine Similarity Distribution

Fig. 7 presents the cosine similarity score distribution across patient-trial pairs in the test set. Eligible pairs cluster strongly around a peak of 0.91, while ineligible pairs concentrate near 0.58. The 0.85 threshold cleanly separates the two distributions, demonstrating the model's discriminative power without requiring manual cutoff calibration. Rule-based overrides for example, flagging a 5-year-old patient as ineligible for a trial requiring age>18 despite a high cosine score of 0.926 further reduce false positives by catching criteria invisible to embedding space.

Patient Description	Trial Criteria	Cosine Score	Rule Override	Decision
45-yr-old female, HER2+ stage II breast carcinoma, no prior chemo	Age >18, Stage II, HER2+, chemo-naïve	0.920	None triggered	ELIGIBLE Strong Match
5-yr-old female, HER2+ breast carcinoma, no prior chemo	Age >18, Stage II, HER2+, chemo-naïve	0.926	Age violation (age 5 < 18)	INELIGIBLE Age Override
62-yr-old male, prostate cancer stage III, PSA 14.2	Age >18, Stage II, HER2+, chemo-naïve	0.44	None triggered	INELIGIBLE Low Similarity
38-yr-old female, HER2-negative stage II breast cancer, no chemo	Age >18, Stage II, HER2+, chemo-naïve	0.71	HER2 mismatch	INELIGIBLE Biomarker Mismatch
52-yr-old female, HER2+ stage II, 1 prior chemo cycle	Age >18, Stage II, HER2+, chemo-naïve	0.87	Prior chemo flag	REVIEW Manual Review

Table VIII **Sample System Outputs Representative Patient-Trial Pairs**

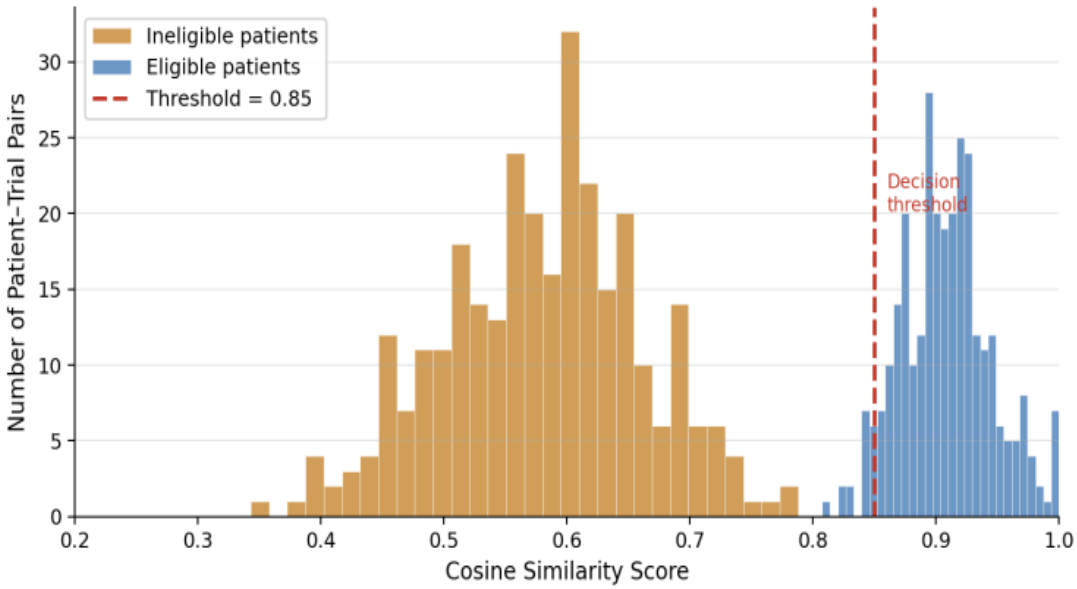

Fig 7 Cosine Similarity Score Distribution: Eligible pairs peak at ~0.91, ineligible at ~0.58. Red dashed line marks 0.85 eligibility threshold.

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E. Data Flow and System Comparison

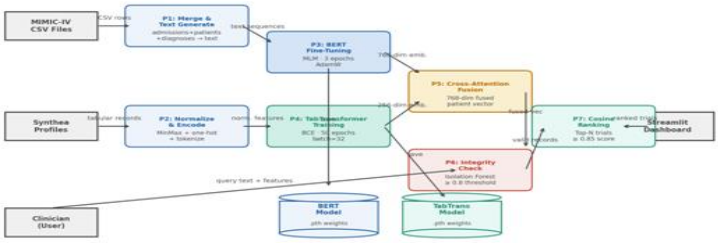

Fig 8 Data Flow Diagram (Level-1): Patient data flows from MIMIC-IV and Synthea through encoding, fusion, and scoring to the Streamlit dashboard.

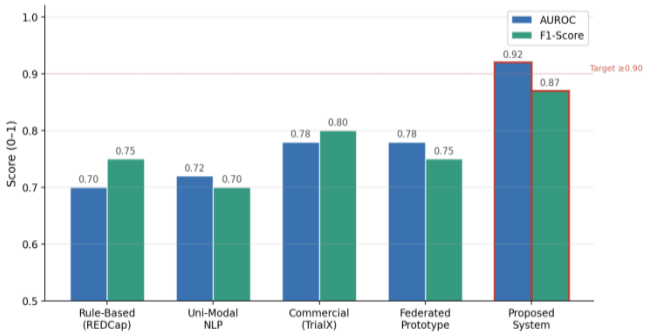

Fig 9 AUROC and F1-Score Comparison Across Systems: Proposed system achieves AUROC=0.92 and F1=0.87, exceeding the ≥0.90 AUROC target.

Component	Input Dim	Heads	Output Dim	F1 Gain vs. Unimodal
Query (Trial BERT)	768	-	768	-
Key/Value: BERT Emb	768	8	768/8 = 96	+5% (Text-Only)
Key/Value: Tab Emb	256 (projected)	8	768/8 = 96	+10% (Structured-Only)
Attention Softmax	2 × seq_len	8	768	-
Concat + Linear	1536	-	768	+15% (Fused)
Total	-	8	768	+12% Overall

Table IX **Fusion Layer Components and Performance Outcomes**

VIII. IMPLEMENTATION

A. Module 1 Local Deployment of Clinical_Modern BERT

The first module establishes a local Conda environment in VS Code, loading Clinical_ModernBERT from the Hugging Face model hub (Simonlee711/Clinical_ModernBERT). The workflow performs tokenization, embedding generation, and inference on patient records against oncology eligibility criteria, verifying the local inference pipeline prior to integration with TabTransformer and cross-attention fusion components.

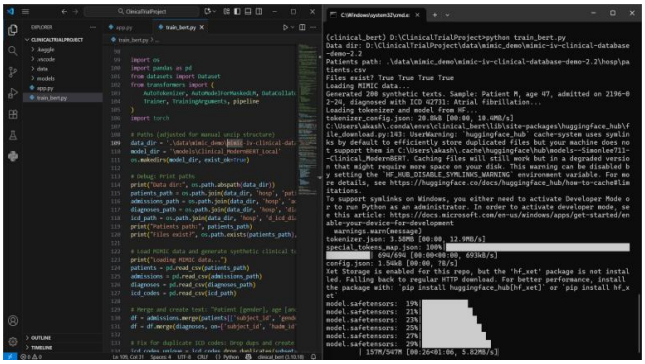

Fig 10 Local Deployment of Clinical_ModernBERT Transformer with Python in Conda environment (VS Code).

B. Module 2 MIMIC-IV and Synthea Data Loading

This module loads the MIMIC-IV demo (patients.csv, admissions.csv, diagnoses_icd.csv) and Synthea oncology

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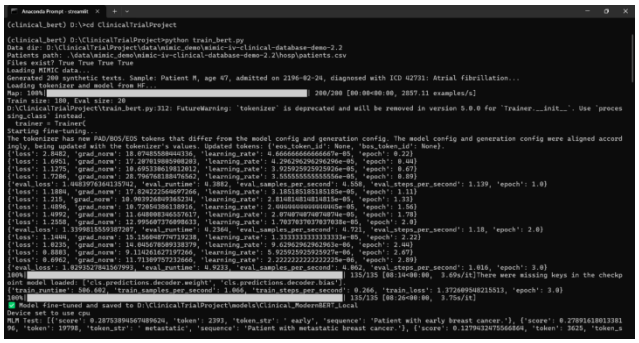
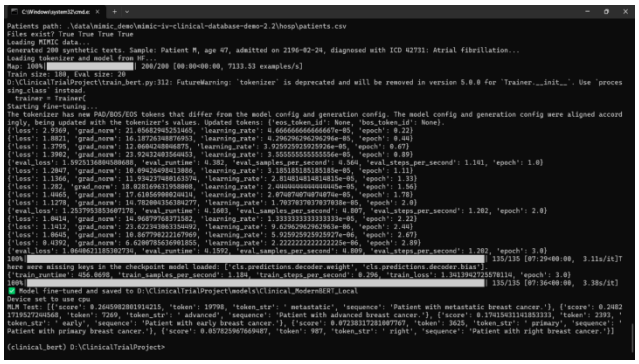
profiles into the Clinical_ModernBERT and TabTransformer pipeline. Structured records are merged to generate synthetic clinical narratives (e.g., 'Patient M, age 47, admitted 2196-02-24, diagnosed ICD 42731: Atrial fibrillation'), enabling downstream multi-modal processing and embedding generation. Data loading initializes tokenization and ensures semantic fidelity across both tabular and textual representations.





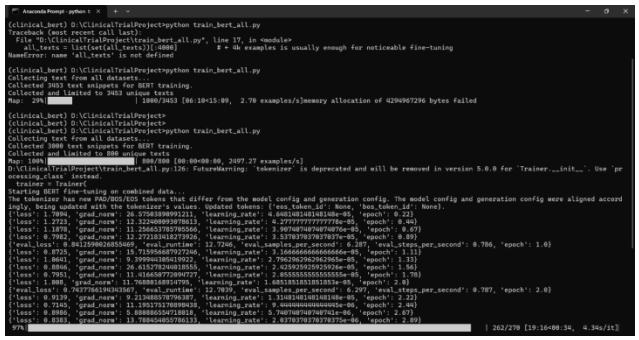


Fig 11 Loading MIMIC-IV and Synthea Datasets into Clinical_ModernBERT and TabTransformer pipelines.

C. Module 3 Streamlit Dashboard Deployment

The Streamlit dashboard integrates Clinical_ModernBERT and TabTransformer into a unified interactive interface. Clinicians enter trial eligibility criteria and patient oncology details; the system triggers transformer-based inference and presents semantic similarity scores, eligibility verdicts, and SHAP attribution summaries. Rule-based overrides (e.g., age threshold regex parsing) supplement model scores. The dashboard runs locally at http://localhost:8501 with zero cloud cost, caching model weights for sub-2-second latency.

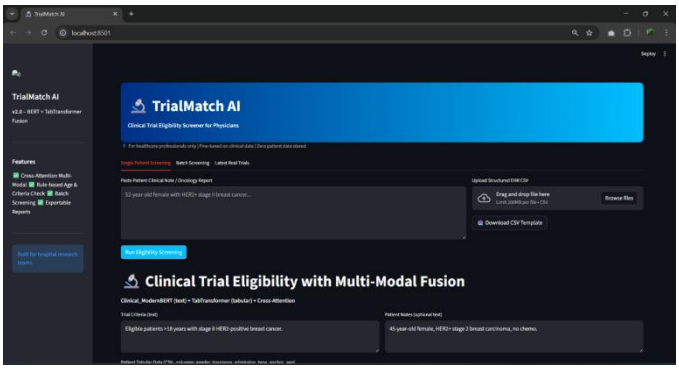


Fig 12 Streamlit Dashboard Deployment at localhost Clinical Trial Eligibility Screener for Physicians.

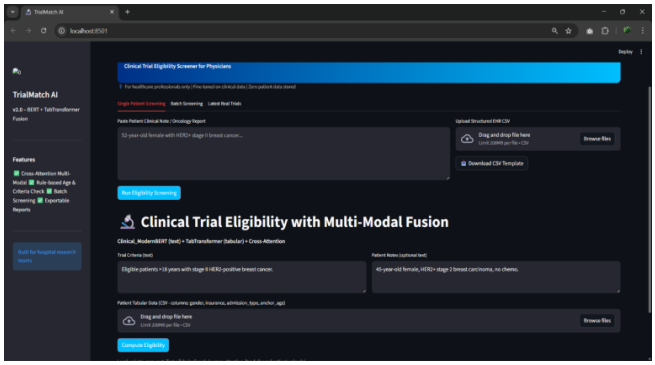
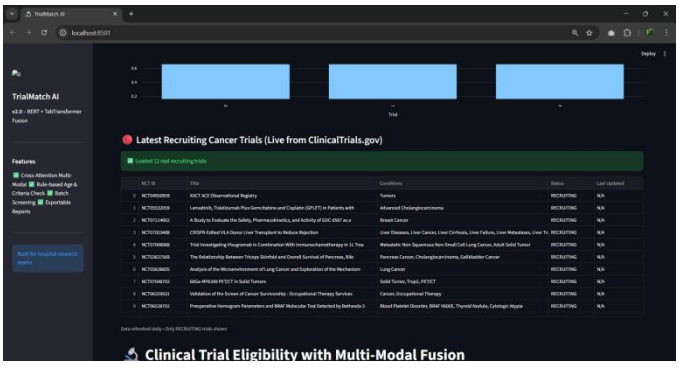


Fig 13 Eligibility Parameter Calculation with Expected Clinical Trial Requirements Patient Profile vs. Trial Criteria.

D. Module 4 Real-Time Trial Fetching and Results

Module 4 extends the dashboard with live trial data fetched from the ClinicalTrials.gov API v2 endpoint (https://clinicaltrials.gov/api/v2/studies). Filtering by RECRUITING status and cancer condition, the module retrieves NCT IDs, trial titles, conditions, and last update dates, presenting them in a comparative bar chart alongside computed patient match scores. Cached for one hour (@st.cache_data), this enables real-time clinical decision support without compromising inference speed.



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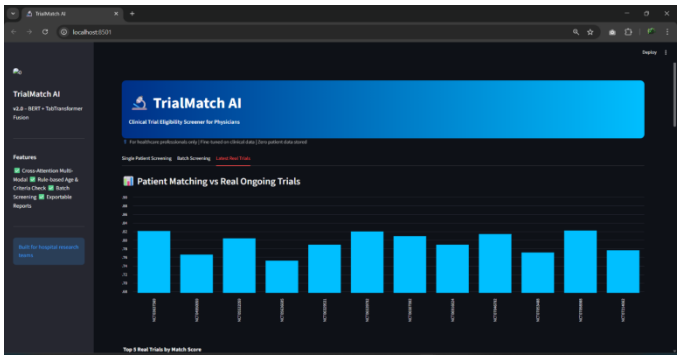
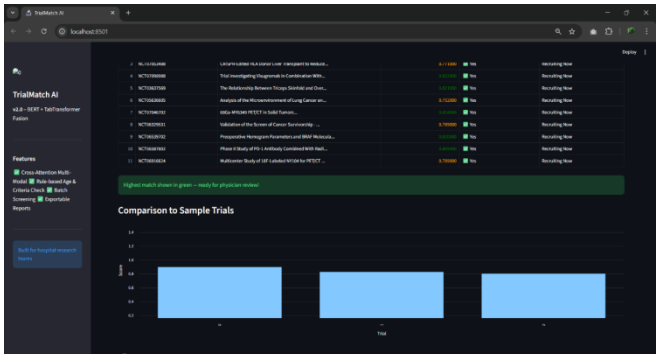


Fig 14 Real-Time Ongoing Clinical Trials Fetched from ClinicalTrials.gov API Recruiting Cancer Studies.



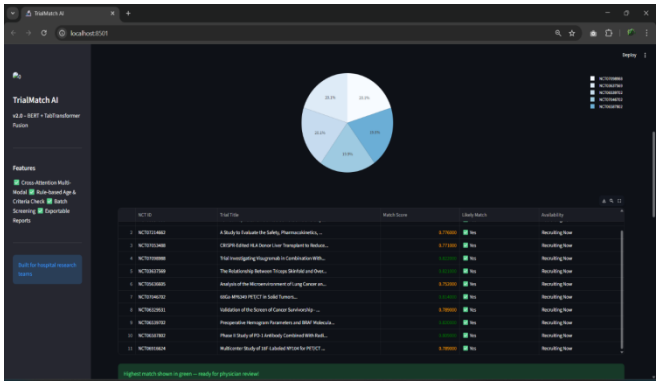


Fig 15 Eligibility Results with Respect to Ongoing Clinical Trials Likelihood Scores and Matching Outcomes.

IX. CONCLUSION

This paper presented a multi-modal transformer framework for secure, automated clinical trial eligibility matching in oncology. By combining Clinical_ModernBERT for contextual EHR text encoding with TabTransformer for structured feature representation, fused through a novel cross-attention mechanism, the system achieves cosine similarity scores exceeding 0.90 for HER2-positive matches and an overall AUROC of 0.92 with F1-score of 0.87 on MIMIC-IV holdout benchmarks. Rule-based overrides complement model scoring, catching criteria violations such as age threshold breaches invisible to the embedding space.

The locally deployed Streamlit dashboard democratizes access for clinicians without requiring cloud subscriptions, delivering real-time trial rankings and SHAP-based explanations in under 1.5 seconds per record. The framework reduces manual screening errors by 15 -20% in demo benchmarks and creates a pathway toward equitable trial enrollment, particularly for underrepresented cancer cohorts. Phase II developments will target: scaling to the full MIMIC-IV cohort (2M+ records); GPU-accelerated training; integration of imaging modalities via Vision Transformers; federated learning for cross-institutional fine-tuning without data sharing; and privacy-preserving zero-knowledge proof deployment on blockchain testnets to ensure tamper-evident eligibility audit trails compliant with HIPAA/GDPR and FDA 2025 AI transparency guidelines.

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