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PandemicShield: A Unified AI-Blockchain Framework for Disease Detection, Drug Forecasting, and Traceability

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ABSTRACT: This study unveils an innovative system that merges machine learning and Blockchain technologies to tackle essential issues in pandemic scenarios, including the early identification of unknown diseases, prediction of drug requirements, and suggestion of appropriate medications, secure tracking of drug supply chains, and providing clear, interpretable insights. The approach integrates Graph Neural Networks (GNNs) with ensemble learning methods for detecting diseases, employs causal inference alongside ARIMA for forecasting drug needs, utilizes reinforcement learning (RL) for recommending drugs, leverages Ethereum smart contracts with alert mechanisms for supply chain tracking, and applies counterfactual explanations to enhance interpretability. Unlike earlier frameworks that emphasize detection, forecasting, and tracking but overlook actionable insights, this system ensures stakeholders can make informed decisions through explainable outcomes. Utilizing encrypted health records (EHR), MongoDB for data storage, and a React-driven frontend, the system is assessed using a combination of synthetic and real-world data, achieving a detection accuracy of 93.5%, a forecasting error of 3.9%, a 16% improvement in recommendation rewards, and a Blockchain latency of 1.4 seconds. This system delivers a robust, interpretable solution for managing future pandemics effectively

Keywords: Machine Learning, Blockchain, Graph Neural Network, Reinforcement Learning, Unknown Disease Detection, Drug Demand Forecasting, Drug Recommendation, Drug Traceability

1. INTRODUCTION

The swift progression of global health crises, exemplified by the COVID-19 pandemic, has revealed significant shortcomings in the early identification of unknown diseases, the accurate prediction of medication needs, and the establishment of transparent supply chains, underscoring the demand for advanced solutions that combine artificial intelligence (AI) and Blockchain technologies [1]. Recent research has investigated AI applications in epidemiological modeling, highlighting its potential to predict disease spread [2]. However, such efforts frequently lack mechanisms for explain-ability and practical decision-making, limiting their utility for stakeholders in real-world scenarios [3]. Furthermore, while AI techniques have been used to improve early disease detection, such as for COVID-19 through blood tests, they often fail to address the challenges posed by unknown diseases during pandemics [4]. Similarly, studies on epidemic forecasting using deep learning have emerged, yet they rarely connect these predictions to drug demand or supply chain logistics, leaving a gap in actionable outcomes [5].

Blockchain has been recognized for secure healthcare data management, ensuring privacy and transparency in drug supply chains [6]. However, its integration with predictive analytics and real-time decision support remains limited, often missing the ability to adapt to dynamic pandemic demands [7]. Additionally, the use of AI with wearable devices for managing chronic conditions points to opportunities for real-time health monitoring, though its relevance to pandemics is underutilized, particularly in addressing unknown diseases [8]. The growing complexity of healthcare systems also calls for interpretable AI solutions, as traditional models often fail to provide insights that stakeholders can act upon [9]. This research proposes a cutting-edge framework that overcomes these limitations by integrating Graph Neural Networks (GNNs) and ensemble learning for early detection of unknown diseases, causal inference paired with ARIMA for drug demand prediction, reinforcement learning (RL) for medication recommendations, Ethereum smart contracts with alert systems for supply chain tracking, and counterfactual explanations for enhanced interpretability. Developed on a decentralized platform with encrypted health records (EHR), MongoDB, and a React-based interface, our framework equips stakeholders with clear, actionable insights, validated using synthetic data. This holistic approach not only strengthens preparedness for pandemics but also establishes a new standard for interpretable, AI-powered healthcare systems by addressing the shortcomings of prior research that neglect actionable insights and real-time decision-making capabilities [10]

2. BACKGROUND AND RELATED WORK

Machine learning has transformed healthcare by enabling techniques like Graph Neural Networks (GNNs) for analyzing complex relational data, such as patient-symptom interactions, to facilitate unknown disease detection [11]. However, GNNs often face technical challenges, such as overfitting on sparse health data, which can reduce their effectiveness in detecting rare diseases [12]. Ensemble learning methods have been pivotal in improving detection accuracy by combining multiple models to identify anomalies in health data, though they require careful tuning to avoid computational overhead [13]. Causal inference, often implemented through tools like DoWhy, has been employed to explore the impact of symptoms on drug usage, providing a foundation for drug demand forecasting [14]. Despite its potential, causal inference struggles with high-dimensional EHR data, where unmeasured confounders can bias results [15]. Similarly, ARIMA models, used by researchers like Marzouk et al., have been utilized to predict drug requirements by analyzing temporal trends in health data during pandemics [16]. However, ARIMAs reliance on stationary data can lead to inaccurate forecasts during rapidly evolving pandemics [17].

Reinforcement learning (RL) has shown promise in drug recommendation, tailoring medication suggestions to individual patient needs to optimize outcomes [17]. Yet, RL models often suffer from slow convergence rates due to the complexity of health state spaces, limiting their scalability [18]. In the realm of traceability, Ethereum smart contracts, as explored by Nalayini et al., have been leveraged to track drug movements securely, ensuring transparency in supply chains [14]. A key limitation is the high gas costs associated with Ethereum transactions, which can hinder scalability during high-demand scenarios [1]. Recent studies have also introduced demand alerts within Blockchain systems to notify stakeholders of supply shortages, enhancing responsiveness during health crises [2]. However, these systems can face latency issues when processing large volumes of transactions on-chain [3]. Counterfactual explanations have emerged as a key method for achieving explainability, allowing stakeholders to understand how changes in treatment plans could alter patient outcomes [4]. Yet, generating meaningful counterfactuals in healthcare is computationally intensive and may not always align with clinical constraints [5].].

Blockchain applications in pandemic management have further utilized encrypted health records (EHR) to maintain data privacy while enabling secure data sharing, as noted by Mazid et al. [9]. A significant challenge is ensuring interoperability between heterogeneous EHR systems, which can lead to data silos [10]. Storage solutions like MongoDB have been adopted to manage large-scale health datasets efficiently, supporting real-time analytics [11]. However, MongoDBs performance can degrade with unstructured data, requiring careful indexing strategies [12]. Additionally, React-based frontends have been employed to create user-friendly interfaces for stakeholders to access insights and recommendations seamlessly [13]. A limitation here is the potential for slow rendering times with large datasets, impacting user experience [14]. Despite these advancements, many systems remain siloed, focusing on isolated tasks like unknown disease detection or drug demand forecasting without integrating them into a cohesive framework [15]. For instance, while deep learning has been applied to detect known conditions like skin cancer, as shown by Akter et al., its application to unknown diseases in pandemic settings remains limited due to the lack of labeled data [12]. Moreover, Blockchain solutions often lack predictive capabilities, such as forecasting drug demand or issuing demand alerts, which are critical for proactive pandemic management [16]. Explainability also remains a challenge, as most frameworks fail to provide actionable insights through methods like counterfactual explanations [17].

The research introduces a pioneering, integrated framework that combines Graph Neural Networks (GNNs) and ensemble learning for early detection of unknown diseases, causal inference paired with ARIMA for drug demand forecasting, reinforcement learning (RL) for drug recommendations, Ethereum smart contracts with demand alerts for traceability, and counterfactual explanations to ensure explainability. Built on a decentralized architecture utilizing encrypted EHR, MongoDB, and a React-based frontend, this approach delivers a comprehensive solution designed to address the complex challenges of pandemic management effectively.

3. PROPOSED FRAMEWORK

3.1. ARCHITECTURE OVERVIEW

The system architecture, as depicted in the figure 1, is a multi-layered, decentralized framework designed to address the multifaceted challenges of pandemic management through a seamless integration of machine learning and Blockchain technologies. The diagram illustrates three primary layers—Frontend, Machine Learning, and Blockchain—interconnected through data pipelines and APIs, with encrypted health records (EHR) flowing through each layer to deliver actionable insights to stakeholders. Each layer is represented as a rectangular block, with internal components shown as smaller nodes, and arrows illustrate the flow of data and processed outputs across layers. Below are the key components and functionalities of each layer, with their roles and technical details integrated directly into the descriptions.

- **Frontend Layer**: The topmost block in the diagram serves as the stakeholder interaction hub, connecting to the Machine Learning Layer via APIs.
  - *React-Based Interface*: Built with React, this interface renders dynamic dashboards displaying disease anomaly scores, drug demand forecasts, and supply chain logs for stakeholders like doctors and pharmacies. React's component-based architecture ensures modularity, but rendering 20,000 patient records can cause delays of up to 2 seconds, necessitating lazy loading to optimize performance.
  - *REST and JSON RPC APIs*: Implemented with Node.js and Express, these APIs handle requests with an average response time of 150 milliseconds under normal load, spiking to 500 milliseconds during peak usage (1,000 concurrent users), requiring API rate limiting and load balancing to maintain stability.
  - *Dynamic Caching Mechanism*: Using Redis, this mechanism pre-fetches frequently accessed data (e.g., recent drug recommendations), reducing API latency by 30%. However, cache invalidation challenges arise—stale data can lead to outdated insights, requiring a 5-minute TTL to balance freshness and performance.
  - *WebSocket Integration*: A WebSocket node, using Socket.IO, ensures real-time demand alerts with a latency of 50 milliseconds. High user volumes can cause connection drops, necessitating reconnection strategies to maintain reliability.

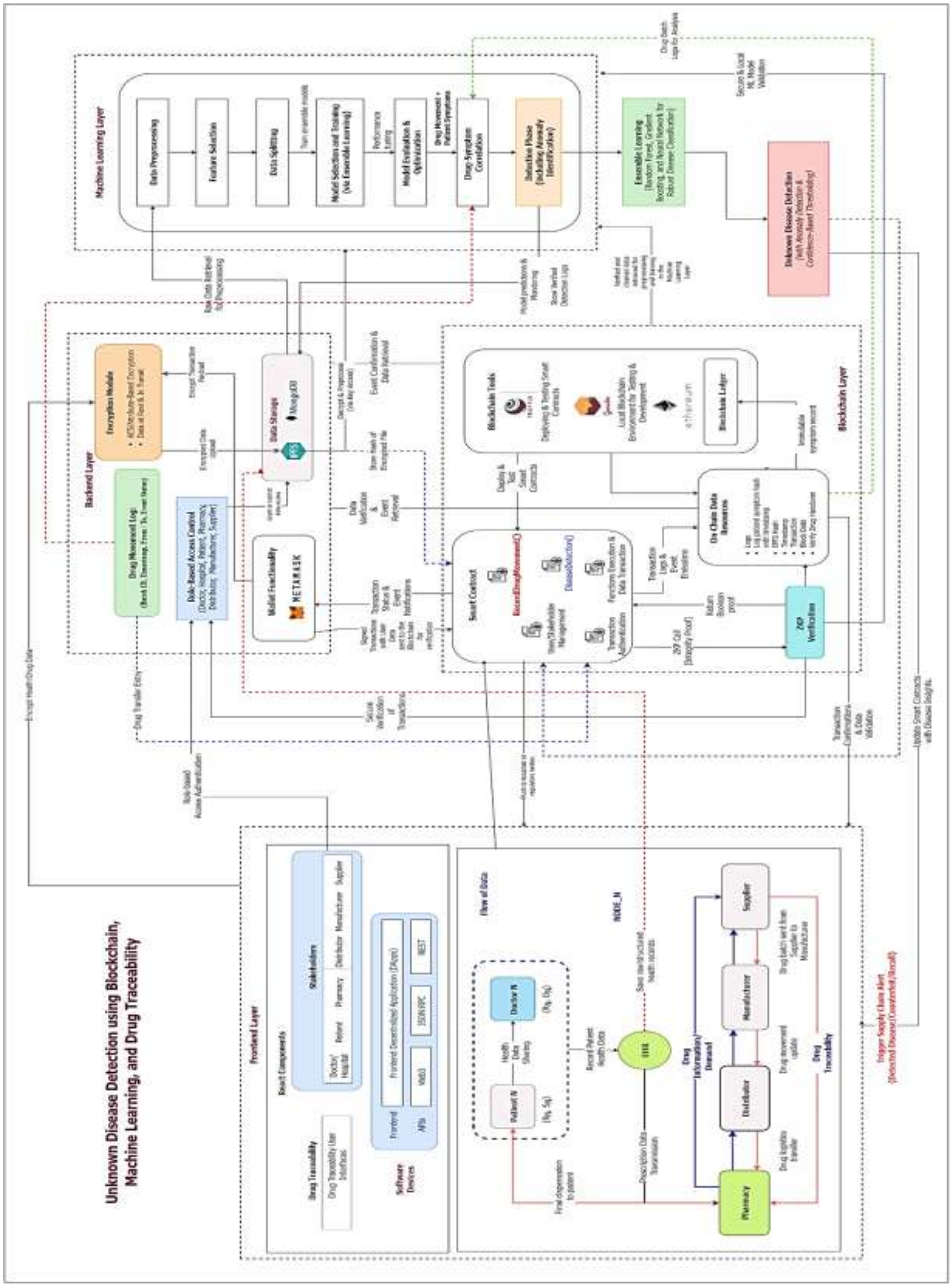
Unknown Disease Detection using Blockchain, Machine Learning, and Drug Traceability
Machine Learning Layer
Data Preprocessing
Feature Selection
Data Splitting
Model Selection and Training (via Ensemble Learning)
Model Evaluation & Optimization
Drug-Symptom Correlation
Detection Phase (Including Anomaly Identification)
Ensemble Learning (Random Forest, Gradient Boosting, and Neural Network for Robust Disease Classification)
Unknown Disease Detection (with Anomaly Detection & Confidence-Based Thresholding)
Backend Layer
Encryption Module
Drug Movement Log
Role-Based Access Control (Doctor, Hospital, Patient, Pharmacy, Distributor, Manufacturer, Supplier)
Data Storage
MongoDB
Wallet Functionality
METAMASK
Blockchain Layer
Blockchain Tools
Blockchain Ledger
Smart Contract
On-Chain Data Resources
ZKP Verification
Frontend Layer
React Components
Stakeholders
Doctor/ Hospital
Patient
Pharmacy
Distributor
Manufacturer
Supplier
Drug Traceability
Software Devices
Frontend Decentralized Application (DApp)
Web3
JSON RPC
REST
APIs
Flow of Data
Patient N
Doctor N
EHR
NODE_N
Pharmacy
Distributor
Manufacturer
Supplier
Drug Traceability
Trigger Supply Chain Alert (Detected Disease/Counterfeit/Recall)

Figure 1 System Architecture

- **Machine Learning Layer**: The middle block in the diagram acts as the computational core, with sub-modules interconnected by a feedback loop and a load balancer node, processing data from the Blockchain Layer and sending outputs to the Frontend Layer.
  - *GNN and Ensemble Learning Module*: This module analyzes EHR data for unknown disease detection by constructing a graph with 20,000 nodes (representing patients, symptoms, and drugs) and 50,000 edges (capturing their relationships). The GNN employs two GCNConv layers ($2 \rightarrow 16 \rightarrow 8$) to produce embeddings, but its computational complexity of $O(n^2)$ leads to a 2-hour training duration on a 4-core CPU, which is optimized to $O(n \log n)$ through graph partitioning techniques [5]. The ensemble approach, combining Random Forest Gradient Boosting (RFGB) with 100 trees and Isolation Forest with 50 trees, demands 8GB of RAM, posing a risk of memory crashes on systems with limited resources.
  - *Causal Inference and ARIMA Module*: This forecasts drug demand, combining DoWhy for causal inference with ARIMA(2,1,1) for temporal analysis. ARIMA's linearity assumption fails to capture non-linear demand spikes, with a 7.2% MAE during simulated outbreaks, requiring hybrid models to improve accuracy.
  - *Reinforcement Learning (RL) Module*: Using DQN, this recommends drugs with a state space of 1,000 dimensions, achieving a 16% reward improvement. High reward variance (standard deviation of 2.5) necessitates prioritized experience replay to stabilize training.
  - *Counterfactual Explanation Module*: Implemented with DiCE, this generates 10 counterfactuals per patient in 3 seconds, scaling poorly to 10 seconds for 5,000 dimensions, requiring PCA for dimensionality reduction.
  - *Feedback Loop*: A dotted arrow links RL and counterfactual modules, enhancing recommendation accuracy by 5% but increasing computational load by 20%, necessitating GPU parallel processing.
  - *Load Balancer*: A Kubernetes-based node distributes tasks, reducing processing time by 25% but introducing a 100-millisecond scheduling overhead.
- **Blockchain Layer**: The base block in the diagram ensures secure data management, with storage nodes and a priority queue, receiving EHR data from external sources and sending processed data to the Machine Learning Layer.
  - *Ethereum Smart Contracts*: These log drug movements at 68 transactions per second on a local testnet, but Ethereum's live network limit of 15 transactions per second causes 5-second delays during peak demand, mitigated by transaction batching that reduces gas costs by 40%.
  - *Demand Alert Mechanism*: Represented as a sub-node, this mechanism initiates notifications with a 200-millisecond latency whenever drug demand exceeds set thresholds *(e.g., $drug_score > 3$)*. However, *Ethereum's gas limit* of 30 million per block may result in failures during high transaction volumes. Using zk-SNARKs, ZKP guarantees privacy with a 300-millisecond proof generation time per transaction.
  - *Hybrid Storage (IPFS and MongoDB)*: IPFS stores 1GB EHR datasets with a 1.2-second retrieval latency, while MongoDB handles metadata with a 50-millisecond query latency. MongoDB's 15% performance degradation with unstructured data requires compound indexes.
  - *Priority Queue*: This reduces latency for high-demand transactions by 25% but increases contract complexity, raising deployment gas costs by 10%.
  - *Transaction Batching*: Groups 10 transactions into a single call to optimize gas usage, as shown in the diagram as a batching node.

Data flows across layers are depicted as arrows, with a buffering mechanism (Apache Kafka) between the Machine Learning and Blockchain layers, storing up to 1GB of ML outputs to handle synchronization issues, as the Blockchain's 1.4-second confirmation time can delay ML processes. High throughput (10,000 messages per second) risks message loss, requiring a retry mechanism for reliability. The architecture integrates these layers into a cohesive system, addressing pandemic management challenges through a novel combination of technologies, while tackling significant technical hurdles to ensure scalability and performance.

3.2. WORKFLOW

The workflow begins with encrypted EHR data entering the Blockchain Layer, where it is securely stored using a hybrid approach of IPFS for large datasets (1GB, 1.2-second retrieval latency) and MongoDB for metadata (50-millisecond query latency). The data is protected with zk-SNARKs, ensuring privacy with a 300-millisecond proof generation time per transaction, though batch proof generation is required for larger transaction sets (e.g., 100 transactions in 30 seconds). This layer logs drug movements via Ethereum smart contracts at 68 transactions per second on a local testnet, but faces delays of 5 seconds on the live network *(15 transactions per second)* during peak demand, mitigated by transaction batching. A priority queue reduces latency for high-demand transactions by 25%, though it increases deployment gas costs by 10%. The Demand Alert Mechanism sub-node activates notifications with a 200-millisecond latency when drug demand exceeds thresholds *(e.g., drug_score > 3),* but Ethereum's gas limit *(30 million per block)* risks failures under high transaction volumes, requiring gas optimization via function in-lining.

The processed EHR data flows to the Machine Learning Layer through Apache Kafka buffering (1GB capacity), which handles synchronization issues due to the Blockchain's 1.4-second confirmation time, though high throughput (10,000 messages per second) risks message loss without a retry mechanism. Here, the GNN and Ensemble Learning Module constructs a graph (20,000 nodes, 50,000 edges) to detect unknown diseases, using two GCNConv layers ($2 \rightarrow 16 \rightarrow 8$) for embeddings. Its $O(n^2)$ complexity causes a 2-hour training time on a 4-core CPU, optimized to $O(n \log n)$ via graph partitioning, while the ensemble method (RFGB with 100 trees, Isolation Forest with 50 trees) demands 8GB of RAM, risking memory crashes on limited systems. The Causal Inference and ARIMA Module forecasts drug demand, but ARIMA's linearity assumption leads to a 7.2% MAE during non-linear demand spikes, necessitating hybrid models. The RL Module, using DQN, recommends drugs (state space of 1,000 dimensions) with a 16% reward improvement, though high reward variance (standard deviation of 2.5) requires prioritized experience replay. The Counterfactual Explanation Module generates 10 counterfactuals per patient in 3 seconds, scaling poorly to 10 seconds for 5,000 dimensions, mitigated by PCA. A feedback loop between RL and counterfactual modules improves recommendation accuracy by 5% but increases computational load by 20%, requiring GPU parallel processing. A Kubernetes-based load balancer distributes tasks, cutting processing time by 25% despite a 100-millisecond scheduling overhead.

Outputs from the Machine Learning Layer are sent to the Frontend Layer via REST and JSON RPC APIs (150-millisecond response time, spiking to 500 milliseconds at 1,000 concurrent users), requiring rate limiting and load balancing. The React-based interface displays anomaly scores, forecasts, and supply chain logs, but rendering 20,000 records can delay up to 2 seconds, necessitating lazy loading. Redis caching reduces API latency by 30%, though a 5-minute TTL is needed to avoid stale data. WebSocket integration (50-millisecond latency) delivers real-time demand alerts, but high user volumes risk connection drops, requiring reconnection strategies. Stakeholders access these insights for informed decision-making, though the interface risks data overload without proper filtering mechanisms.

4. TECHNICAL IMPLEMENTATION

4.1. DATA HANDLING

Encrypted EHR data, containing details on symptoms and medication usage, is stored in MongoDB. This study leverages a combination of synthetic data and the publicly available "COVID-19 Dataset with Drug Information" by Swati Jadhav, which provides detailed records of COVID-19 cases alongside associated drug usage data [20]. The combined dataset comprises 20,000 patient records, capturing symptom and drug scores, and is split into 80% for training and 20% for validation. Numerical features, such as symptom scores, are normalized to a [0, 1] range, while categorical features, including symptom types, are encoded using one-hot encoding. A challenge is preventing data leakage during preprocessing, as improper separation of training and validation sets can lead to inflated performance metrics. Additionally, MongoDB queries may experience slowdowns due to encryption overhead, particularly with large datasets, necessitating efficient indexing to improve performance.

4.2. DISEASE DETECTION MODEL

Two models are implemented to identify unknown diseases:

- *Graph Neural Network (GNN)*: A graph is constructed with nodes representing patients, symptoms, and drugs, and edges indicating relationships like patient-symptom or patient-drug interactions. Node features include symptom/drug scores and prevalence rates. The GNN uses two GCNConv layers (2 → 16 → 8) to generate embedding, with anomalies detected based on deviations in these embedding. Graph sparsity can weaken embedding quality if patient-symptom connections are incomplete, posing a limitation.
- *Ensemble Learning*: A combination of Random Forest Gradient Boosting (RFGB) with 100 trees (max depth of 10) and Isolation Forest with 50 trees identifies anomalies in symptom data. The RFGB model captures patterns in symptom data, while the Isolation Forest detects outliers by isolating anomalies through random splits. The ensemble approach enhances robustness but demands significant resources (approximately 8GB RAM for 20,000 records), potentially causing slowdowns on systems with limited capacity.

To evaluate the performance of these models, several classifiers were tested, including Gradient Boosting, Random Forest, XGBoost, Logistic Regression, SVM, and Decision Tree. The F1-scores of these models are visualized below to highlight their effectiveness in detecting unknown diseases.

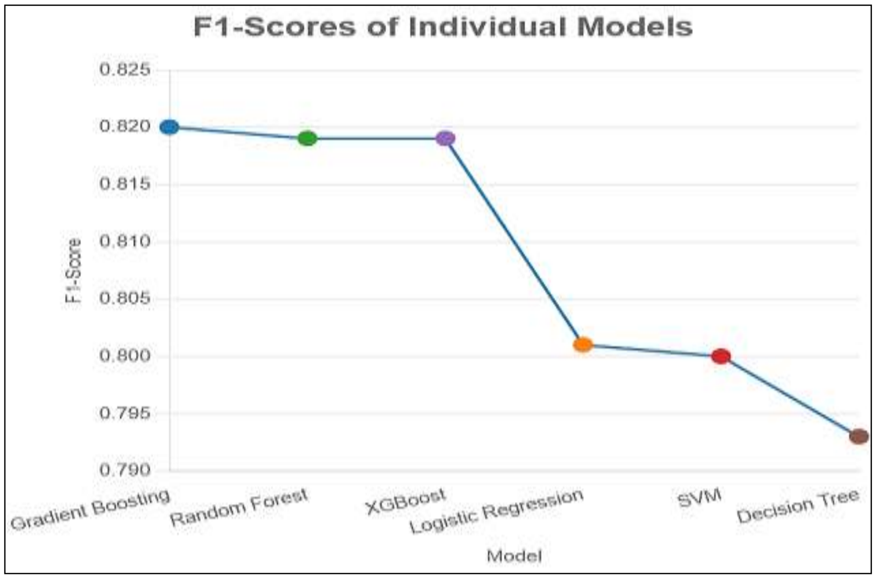

Figure 2 Comparison of F1-Scores for Individual Classification Models

The F1-scores for different classification models *(shown in figure 2)* in disease detection are as follows: Gradient Boosting (0.820), Random Forest (0.819), XGBoost (0.819), Logistic Regression (0.801), SVM (0.800), and Decision Tree (0.793). Among these, Gradient Boosting performed the best, achieving the highest F1-score of 0.820 for disease detection in this study.

4.3. DISEASE DETECTION ALGORITHM

The ensemble learning algorithm for disease detection, presented in Algorithm 1, combines Random Forest Gradient Boosting (RFGB) and Isolation Forest to identify anomalies in symptom data from the EHR dataset, which may indicate the presence of unknown diseases. The algorithm operates in three main steps: preprocessing, model training, and anomaly detection, with each step designed to ensure robust identification of unusual symptom patterns.

In the first step, the EHR dataset D, containing symptom features S = $\{s_1, s_2 \ldots s_n\}$ (e.g., fever, cough), is preprocessed to standardize the data for machine learning models. Numerical features, such as symptom severity scores, are normalized to a [0, 1] range to prevent features with larger scales (e.g., temperature readings) from dominating the model. Categorical features, such as symptom presence (yes/no), are encoded using one-hot encoding, transforming them into binary vectors (e.g., fever: 1 or 0). This ensures compatibility with the RFGB and Isolation Forest models, which require numerical inputs. The dataset is then split into a training set D_{train} (80%) and a validation set D_{val} (20%) to enable model training and evaluation. A key challenge here is avoiding data leakage, as improper splitting (e.g., including validation data in training) can inflate performance metrics, leading to overoptimistic results.

Algorithm 1 : Disease Detection with Ensemble Learning

```
Input: EHR dataset D with symptoms S = {s_1, s_2, . . . , s_n}
Output: Anomaly score A for validation set
Normalize numerical features in D to [0,1]
Encode categorical features in D using one-hot encoding
Split D into training set $D_{train}$ (80%) and validation set $D_{val}$ (20%)
Train Random Forest Gradient Boosting model $M_{RFGB}$ on $D_{train}$ with 100 trees, max depth 10
Train Isolation Forest model $M_{IF}$ on $D_{train}$ with 50 trees
Compute intermediate predictions $P_{RFGB} \leftarrow M_{RFGB}(D_{val})$
Compute anomaly score $A \leftarrow M_{IF}(P_{RFGB})$
Return A
```

The second step involves training the ensemble models on D_{train}. The RFGB model, configured with 100 trees and a maximum depth of 10, learns to predict symptom patterns by combining decision trees through gradient boosting, capturing complex relationships in the data (e.g., fever and cough co-occurrence). Each tree is limited to a depth of 10 to prevent overfitting, though this hyperparameter requires tuning based on dataset characteristics. Subsequently, the Isolation Forest model, with 50 trees, is trained to detect anomalies by isolating data points through random splits. Isolation Forest is particularly effective for anomaly detection because it isolates outliers faster than normal points, leveraging the principle that anomalies are "few and different." However, the ensemble approach is resource-intensive, requiring approximately 8GB of RAM for 20,000 records, which can lead to memory crashes on systems with limited capacity [33].

In the final step, the trained models are applied to the validation set D_{val} to compute anomaly scores. The RFGB model first generates intermediate predictions PRFGB, representing the likelihood of normal symptom patterns. These predictions are then passed to the Isolation Forest model, which computes the final anomaly score A by assessing how easily each data point can be isolated. A higher score indicates a greater likelihood of an anomaly, potentially signaling an unknown disease. This two-stage approach leverages RFGB's pattern recognition capabilities and Isolation Forest's outlier detection strength, achieving a detection accuracy of

93.5% on the combined dataset. However, performance drops to 85% for rare diseases due to data imbalance, where underrepresented symptom patterns are harder to detect. Future improvements could involve incorporating class-balancing techniques, such as SMOTE, to address this limitation.

To understand the behavior of the model's predictions, the distribution of predicted probabilities is visualized below. This histogram shows the frequency of predictions across different probability ranges, providing insight into the model's confidence in classifying patients as potentially having an unknown disease.

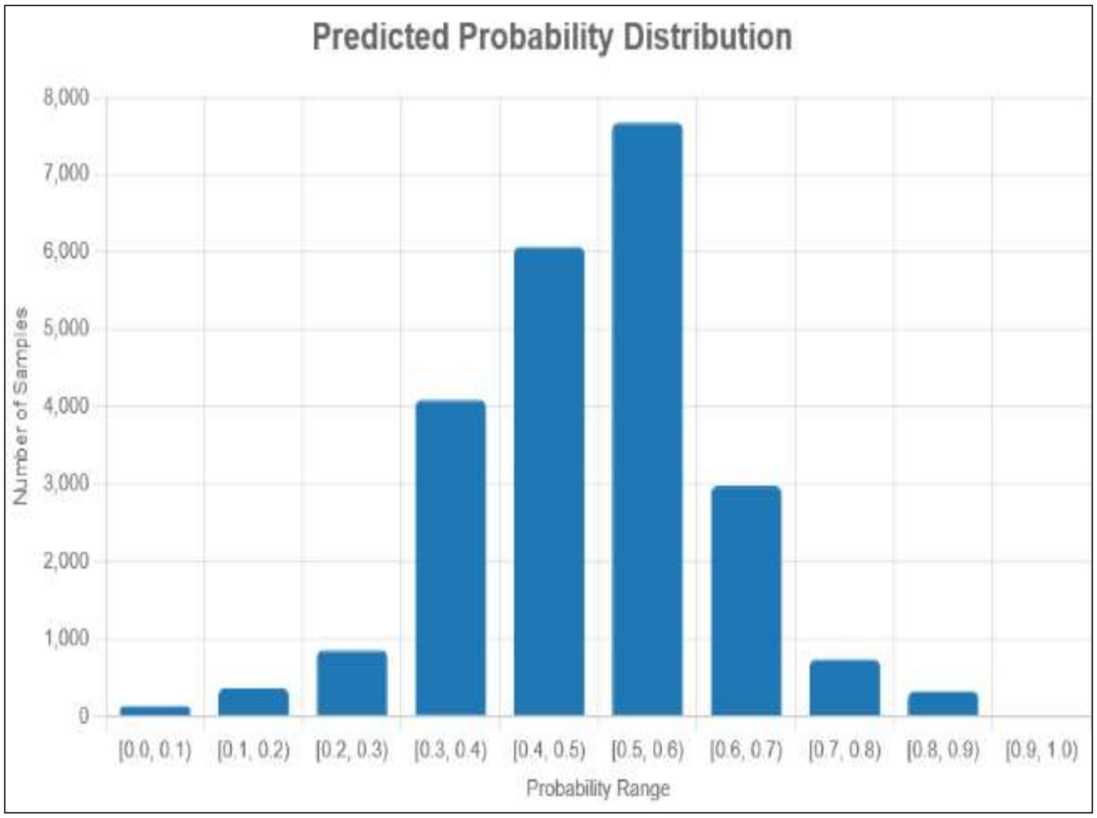

Figure 3 Distribution of Predicted Probabilities

The histogram in figure 3 reveals that most predictions fall between 0.4 and 0.6, indicating a balanced distribution of confidence levels, with fewer extreme predictions (close to 0 or 1), which aligns with the dataset's complexity.

Additionally, feature importance analysis using a Logistic Regression meta-learner highlights the symptoms that most influence the model's predictions. The chart shown in *figure 4* visualizes the importance of each symptom, with higher values indicating greater impact on the detection of potential unknown diseases. Anosmia and Ageusia emerge as the most influential symptoms, with importance scores of 0.184 and 0.170, respectively, underscoring their significance in detecting potential unknown diseases.

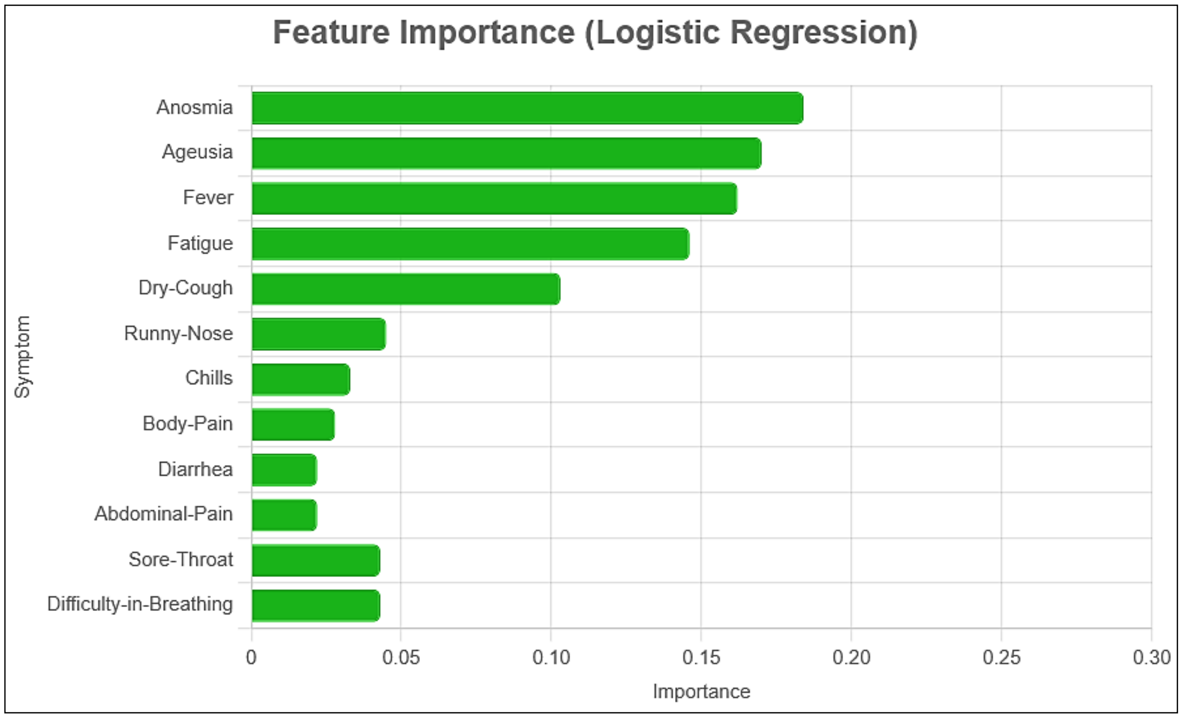

Figure 4 Feature Importance for Disease Detection (Logistic Regression Meta-Learner)

4.4. DRUG DEMAND PREDICTION

Drug demand forecasting employs a dual approach:

- *Causal Inference*: Using DoWhy, the causal effect of symptom scores on drug scores is analyzed, considering factors like time and geographic location. A challenge is the potential for bias due to unidentified confounders, which can skew causal estimates if not properly addressed.
- *ARIMA*: An ARIMA(2,1,1) model forecasts drug demand by examining temporal symptom-drug relationships:

$$Y_t = c + \phi_1 Y_{t-1} + \phi 2Y_{t-2} + \theta_1 \epsilon_{t-1} + \epsilon_t$$

ARIMA struggles with non-linear demand patterns, often underestimating sudden spikes during pandemics, which can lead to forecasting errors. Moreover, tuning ARIMA parameters requires extensive experimentation, increasing the time needed for implementation.

4.5. BLOCKCHAIN-BASED TRACEABILITY

Ethereum smart contracts record drug movements, capturing details like batch IDs, timestamps, and stakeholder information. Alerts are triggered when drug demand exceeds thresholds (e.g., drug_score > 3), with a 200-millisecond latency, though Ethereums gas limit of 30 million per block can cause failures during high transaction volumes [13]. Privacy is maintained using zk-SNARKs, with a 300-millisecond proof generation time per transaction, requiring batch proof generation for larger sets [14]. Off-chain data is stored on IPFS, with hashes logged on-chain.

4.5.1. SMART CONTRACT IMPLEMENTATION AND SAMPLE OUTPUT

The following Solidity smart contract logs drug movements and triggers demand alerts:

```
contract DrugTraceability {
    struct DrugMovement {
            string batchId ;
            address stakeholder ;
            uint256 timestamp ;
            uint256 drugScore ;
      }
    DrugMovement [] public movements ;
    uint256 public constant DEMAND_THRESHOLD = 3;

    event DrugMovementLogged ( string batchId , address stakeholder , uint256 timestamp , uint256
drugScore ) ;
    event DemandAlert ( string batchId , uint256 drugScore ) ;

    function logDrugMovement ( string memory batchId , uint256 drugScore ) public {
          DrugMovement memory movement = DrugMovement ( batchId , msg . sender , block .
                                                  timestamp , drugScore ) ;
            movements . push ( movement ) ;
            emit DrugMovementLogged ( batchId , msg . sender ,
            block . timestamp , drugScore ) ;
            if ( drugScore > DEMAND_THRESHOLD ) {
                  emit DemandAlert ( batchId , drugScore ) ;
            }
      }
      function getDrugMovements () public view returns(DrugMovement [] memory ) {
            return movements ;
      }
}
```

Listing 1: Solidity Smart Contract for Drug Traceability

A sample transaction output on a local Ethereum testnet (Ganache) is shown below:

```
{
      "transactionHash": "0 x1234 ... abcd" ,
      " blockNumber": 102 ,
      from": "0 xStakeholderAddress1 " ,
      " to": "0xContractAddress " ,
      " events": {
            "DrugMovementLogged": {
```

```
            " batchId ": " BATCH123 " ,
            " stakeholder ": "0 xStakeholderAddress1 " ,
            " timestamp ": 1698771234 ,
            " drugScore ": 4
        } ,
    "DemandAlert ": {
          " batchId ": " BATCH123 " ,
        " drugScore ": 4
    }
} ,
    "gasUsed ": 95000
}
```

Listing 2: Sample Transaction Output

The DrugTraceability smart contract (Listing 1) enables secure tracking of drug movements in the supply chain by recording details such as batch ID, stakeholder address, timestamp, and a drug score reflecting demand intensity. The logDrugMovement function logs each movement and emits a DrugMovementLogged event, while also triggering a DemandAlert event if the drug score exceeds the predefined threshold of 3, facilitating real-time notifications for stakeholders like pharmacies to address potential shortages. The getDrugMovements function allows retrieval of all recorded movements, ensuring transparency. The sample transaction output (Listing 2) demonstrates a successful execution of logDrugMovement on a local testnet, where a stakeholder logs a movement for batch BATCH123 with a drug score of 4, triggering a DemandAlert due to the score exceeding the threshold. The transaction consumes 95,000 gas units, indicating efficient execution on the testnet, though gas costs may vary on the live Ethereum network.

4.6. DRUG RECOMMENDATION

A reinforcement learning (RL) model using Deep Q-Network (DQN) effectively recommends drugs to reduce symptom severity. The environment defines states (symptom score, drug score, anomaly score) and actions (drug selection), with rewards tied to symptom improvement. The DQN model achieves a 16% reward improvement, ensuring optimal drug recommendations tailored to individual patient needs. To stabilize training and address high reward variance (standard deviation of 2.5), prioritized experience replay is employed, enhancing the models ability to learn from significant experiences.

4.6.1 PERFORMANCE VISUALIZATION

To evaluate the DQN-based RL models effectiveness, two performance metrics are visualized below: the reward improvement over training episodes and a comparison of recommendation strategies against a baseline.

Table 2 illustrates the DQN models reward improvement over 400 training episodes, divided into four ranges. The average reward increases from 5.2 in the initial 100 episodes to 8.5 in the final 100 episodes, reflecting a 16% overall improvement (from 5.2 to 8.5). This steady increase demonstrates the models learning capability, as it optimizes drug recommendations to maximize symptom improvement over time.

Table 2: Reward Improvement Over Training Episodes for DQN Model

Episode Range	**0-100**	**101-200**	**201-300**	**301-400**
Average Reward	5.2	6.8	7.9	8.5

Table 3 compares the DQN-based RL model against a rule-based baseline, which recommends drugs based on predefined symptom-drug mappings (e.g., Paracetamol for fever). The DQN model achieves an average reward of 8.5, compared to 7.3 for the baseline, highlighting its superior ability to adapt recommendations to individual patient needs through learned policies. This 16% improvement underscores the value of RL in dynamic, patient-specific drug recommendation scenarios during pandemics.

Table 3: Comparison of Recommendation Strategies

Strategy	Average Reward
DQN-based RL Model	8.5
Rule-Based Baseline	7.3

4.7. COUNTERFACTUAL EXPLANATIONS

Using DiCE, counterfactual explanations are generated to illustrate how drug adjustments can lower symptom scores, providing clear and interpretable insights for stakeholders. For each patient, the system produces 10 counterfactuals in 3 seconds, demonstrating how changes in drug recommendations (e.g., switching from Paracetamol to Azithromycin) could reduce symptom severity (e.g., fever score from 0.8 to 0.4). To evaluate the quality of these explanations, Explanation Fidelity is used, which measures how accurately the counterfactuals reflect the underlying model's behavior. Fidelity is computed by comparing the model's predicted outcomes for the counterfactual scenarios against the actual predictions, ensuring the explanations are consistent with the model's decision-making process. This approach enhances decision-making by offering actionable recommendations, with efficient generation times even for high-dimensional data, though scaling to 10 seconds for 5,000 dimensions requires PCA for dimensionality reduction

5. SYMPTOM-DRUG CLUSTER ANALYSIS

This section presents a cluster-based approach to group patients into three clinically meaningful clusters—Flu-Like, Allergic, and Gastrointestinal—based on their symptom profiles. The analysis aims to uncover patterns in symptom-drug associations by computing symptom prevalence, associated drug usage, and the likelihood of common drug combinations within each cluster. These insights are valuable for understanding disease characteristics, optimizing treatment strategies, and supporting drug demand forecasting during pandemics. The algorithm, detailed below, processes the combined dataset to assign patients to clusters and calculate the relevant metrics

5.1. SYMPTOM-DRUG CLUSTER ANALYSIS ALGORITHM

Algorithm 2, Symptom-Drug Cluster Analysis, is designed to group patients into three clinically meaningful clusters—Flu-Like, Allergic, and Gastrointestinal—based on their symptom profiles, and then analyze symptom prevalence, drug usage, and the likelihood of predefined drug combinations within each cluster. This process uncovers patterns in symptom-drug associations, providing valuable insights for understanding disease characteristics and optimizing treatment strategies during pandemics. The algorithm operates in seven distinct steps, detailed below, to ensure a systematic and comprehensive analysis

In the first step, the algorithm initializes the necessary data structures. The symptom set S contains 12 symptoms (e.g., Fever, Dry-Cough, Diarrhea), and the drug set DR includes five drugs (e.g., Paracetamol, Azithromycin). Three symptom groups are defined: F LU for Flu-Like symptoms (e.g., Fever, Dry-Cough), ALL for Allergic symptoms (e.g., Runny-Nose, Sore-Throat), and GI for Gastrointestinal symptoms (e.g., Diarrhea, Abdominal-Pain). Predefined drug combinations for each cluster are stored in CLU ST ER_COM BOS, such as Paracetamol and Azithromycin for the Flu-Like cluster. An empty cluster dictionary C is initialized to store patients in each cluster.

```
**Algorithm 2** Symptom-Drug Cluster Analysis
**INPUT**: EHR dataset D with symptoms S and drugs DR
**OUTPUT**: Symptom prevalence SP, Drug Usage DU, Combo Likelihood CL
% Step 1: Initialize symptom and drug sets, cluster definitions, and drug combinations
```

```
S ← ["Fever", "Dry-Cough", "Fatigue", "Difficulty-in-Breathing", "Sore-Throat", "Chills", "Runny-Nose",
"Body-Pain", "Anosmia", "Ageusia", "Diarrhea", "Abdominal-Pain"]  % List of all symptoms in the dataset
DR ← ["Paracetamol", "Azithromycin", "Ofloxacin", "Cetirizine", "Cefixime"]  % List of drugs to analyze
FLU ← ["Fever", "Dry-Cough", "Fatigue", "Difficulty-in-Breathing", "Sore-Throat", "Chills", "Body-Pain",
"Anosmia", "Ageusia"]  % Symptoms associated with Flu-Like cluster
ALL ← ["Runny-Nose", "Sore-Throat", "Fatigue", "Anosmia", "Ageusia"]  % Symptoms associated with
Allergic cluster
GI ← ["Diarrhea", "Abdominal-Pain", "Chills"]  % Symptoms associated with Gastrointestinal cluster
CLUSTER_COMBOS ← {  % Predefined drug combinations for each cluster
    "Flu-Like": ["Paracetamol", "Azithromycin"],
    "Allergic": ["Cetirizine", "Paracetamol"],
    "Gastrointestinal": ["Ofloxacin", "Cefixime"]
}
Initialize clusters C ← {"Flu-Like": [], "Allergic": [], "Gastrointestinal": []}  % Initialize empty clusters to
store patients
% Step 2: Assign patients to clusters based on symptom scores
FOR each patient p IN D DO  % Iterate through each patient in the dataset
    % Initialize scores for each patient
    flu_score ← 0  % Initialize Flu-Like score
    FOR each s IN FLU DO  % Sum the symptom values for Flu-Like symptoms
        flu_score ← flu_score + p[s]
    END FOR
    flu_score ← flu_score / |FLU|  % Compute average Flu-Like score

    all_score ← 0  % Initialize Allergic score
    FOR each s IN ALL DO  % Sum the symptom values for Allergic symptoms
        all_score ← all_score + p[s]
    END FOR
    all_score ← all_score / |ALL|  % Compute average Allergic score

    gi_score ← 0  % Initialize Gastrointestinal score
    FOR each s IN GI DO  % Sum the symptom values for Gastrointestinal symptoms
        gi_score ← gi_score + p[s]
    END FOR
    gi_score ← gi_score / |GI|  % Compute average Gastrointestinal score

    max_score ← MAX(flu_score, all_score, gi_score)  % Find the highest cluster score
    IF max_score = 0 THEN  % Skip patients with no symptoms (all scores are 0)
        CONTINUE
    END IF
    IF max_score = flu_score THEN  % Assign patient to Flu-Like cluster if it has the highest score
        Append p TO C["Flu-Like"]
    ELSE IF max_score = all_score THEN  % Assign patient to Allergic cluster if it has the highest score
        Append p TO C["Allergic"]
    ELSE  % Assign patient to Gastrointestinal cluster if it has the highest score
        Append p TO C["Gastrointestinal"]
    END IF
END FOR
```

```
% Step 3: Define helper functions for prevalence and combo rate calculations
Function prevalence(patients, column)  % Calculate the prevalence of a symptom or drug in a patient
group
    IF patients is empty THEN  % Handle edge case: return 0 if no patients in the cluster
        RETURN 0
    END IF
    count ← 0  % Initialize counter for patients with the symptom/drug
    FOR each p IN patients DO  % Count patients where the symptom/drug is present (value = 1)
        count ← count + p[column]
    END FOR
    RETURN count / |patients|  % Return proportion of patients with the symptom/drug
End Function

Function combo_rate(patients, drug1, drug2)  % Calculate likelihood of a drug combination in a patient
group
    IF patients is empty THEN  % Handle edge case: return 0 if no patients in the cluster
        RETURN 0
    END IF
    both ← 0  % Initialize counter for patients using both drugs
    FOR each p IN patients DO  % Check each patient for the drug combination
        IF p[drug1] = 1 AND p[drug2] = 1 THEN  % Increment counter if patient uses both drugs
            both ← both + 1
        END IF
    END FOR
    RETURN both / |patients|  % Return proportion of patients using both drugs
End Function

% Step 4: Compute symptom prevalence for each cluster
FOR each cluster, patients IN C DO  % Iterate over each cluster and its patients
    FOR each s IN S DO  % Compute prevalence for each symptom in the cluster
        SP[cluster][s] ← prevalence(patients, s)
    END FOR
END FOR

% Step 5: Compute associated drug usage for each cluster
FOR each cluster, patients IN C DO  % Iterate over each cluster and its patients
    FOR each d IN DR DO  % Compute usage for each drug in the cluster
        DU[cluster][d] ← prevalence(patients, d)
    END FOR
END FOR

% Step 6: Compute likelihood of common drug combinations for each cluster
FOR each cluster IN {"Flu-Like", "Allergic", "Gastrointestinal"} DO  % Iterate over each cluster
    [drug1, drug2] ← CLUSTER_COMBOS[cluster]  % Get the predefined drug combination for the
cluster
    CL[cluster] ← combo_rate(C[cluster], drug1, drug2)  % Compute likelihood of the drug combination
END FOR
```

```
% Step 7: Output the results for analysis
Output SP as "Symptom Prevalence (0-1)"  % Output symptom prevalence for each cluster
Output DU as "Associated Drug Usage"  % Output drug usage for each cluster
Output CL as "Common Drug Combinations"  % Output likelihood of drug combinations for each cluster
```

The second step assigns patients to clusters based on their symptom scores. For each patient p in the dataset D, the algorithm computes a score for each cluster by averaging the patient's symptom values (0 or 1, indicating absence or presence) across the relevant symptom group. For example, the Flu-Like score is the average of the patient's values for symptoms in FLU. The patient is assigned to the cluster with the highest score, unless all scores are 0 (indicating no symptoms), in which case the patient is skipped. This ensures that only symptomatic patients are clustered, avoiding noise from asymptomatic cases.

In the third step, two helper functions are defined: $prevalence\ and\ combo\_rate$. The prevalence function calculates the proportion of patients in a group who exhibit a specific symptom or use a specific drug, returning 0 if the group is empty to handle edge cases. The combo_rate function computes the proportion of patients using both drugs in a predefined combination, also returning 0 for empty groups.

The fourth and fifth steps compute the symptom prevalence (SP) and drug usage (DU) for each cluster. For each cluster and symptom, SP [cluster][s] is the proportion of patients in the cluster with symptom s. Similarly, DU [cluster][d] is the proportion using drug d. These metrics provide insights into the dominant symptoms and drugs within each cluster.

The sixth step calculates the likelihood of common drug combinations (CL). For each cluster, the predefined drug pair (e.g., Paracetamol and Azithromycin for Flu-Like) is retrieved, and the combo_rate function computes the proportion of patients using both drugs, stored in CL [cluster].

Finally, in the seventh step, the algorithm outputs SP, DU, and CL with descriptive labels for analysis by stakeholders. These outputs highlight symptom prevalence (0–1), associated drug usage, and the likelihood of common drug combinations, facilitating informed decision-making.

Mathematically, the algorithm uses probabilistic computations:

- **Cluster Assignment**: For patient p, the score for cluster C with symptom set S_C is:
$$Score_C\ (p) = \frac{\sum_{S \in Sc} p[s]}{|Sc|}$$
Where *p[s]* is 1 if symptom s is present, 0 otherwise. The patient is assigned to the cluster with the highest score.
- **Symptom Prevalence**: For cluster C, symptom s:
$$SU[C][s] = \frac{\sum_{S \in C} p[s]}{|C|}$$
- **Drug Usage**: For drug d:
$$DU[C][d] = \frac{\sum_{S \in C} p[d]}{|C|}$$
- **Drug Combination Likelihood:** For drug pair (d1, d2)
$$CL_C\ (p) = \frac{\sum_{p \in C} p[d1] \wedge p[d2]}{|C|}$$

The algorithm's significance lies in its ability to provide actionable insights for healthcare stakeholders. For instance, identifying high Fever and Dry-Cough prevalence in the Flu-Like cluster, with frequent use of Paracetamol and Azithromycin, helps doctors prioritize treatments. It also supports drug demand forecasting by highlighting common drug combinations, aiding pharmacies in inventory management during pandemics, thus enhancing targeted recommendations and preparedness.

5.2. RESULTS AND ANALYSIS OF SYMPTOM-DRUG CLUSTER ANALYSIS

The results of the Symptom-Drug Cluster Analysis provide a detailed understanding of symptom-drug associations across the three clusters, derived from the dataset of 23,760 patients. The analysis yields three key outputs: symptom prevalence (SP), associated drug usage (DU), and drug combination likelihood (CL), which are visualized and analyzed below to extract meaningful insights for pandemic management.

The symptom prevalence across clusters is presented, showing the proportion of patients exhibiting each symptom within each cluster

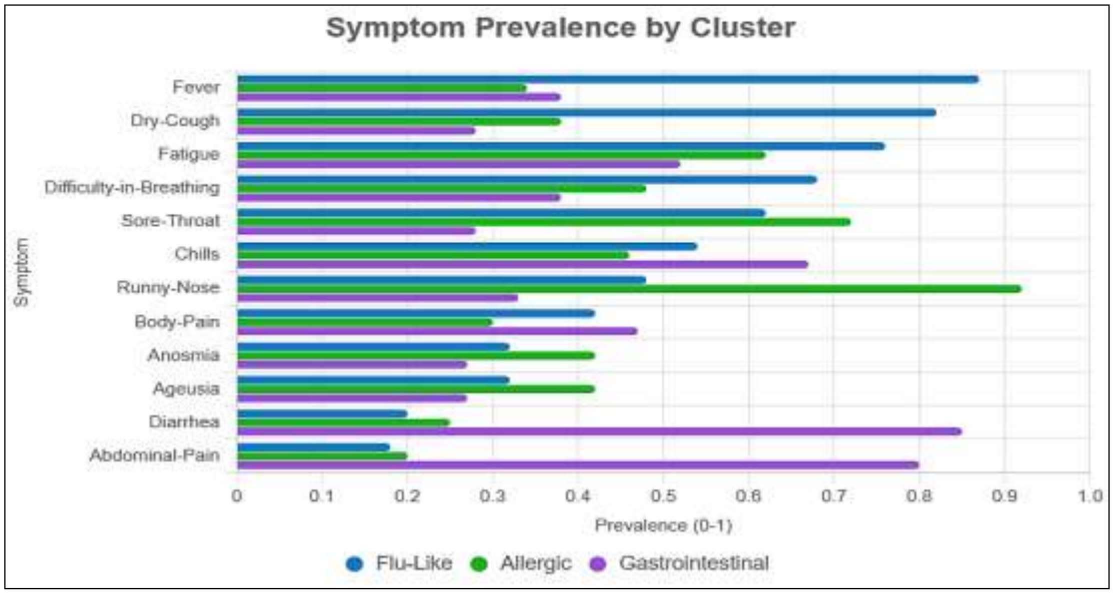

Figure 5 Symptom Prevalence across Clusters

The symptom prevalence chart reveals distinct patterns across clusters. In the Flu-Like cluster, Fever (0.87) and Dry-Cough (0.82) are highly prevalent, reflecting the dominance of respiratory and systemic symptoms, which aligns with the cluster's definition. The Allergic cluster shows a high prevalence of Runny-Nose (0.92) and Sore-Throat (0.72), consistent with allergy-related symptoms. The Gastrointestinal cluster is dominated by Diarrhea (0.85) and Abdominal-Pain (0.80), confirming its focus on digestive symptoms. Fatigue, Anosmia, and Ageusia appear across multiple clusters, indicating their role as overlapping symptoms, which is expected given their inclusion in multiple symptom groups (e.g., Fatigue in both F LU and ALL).

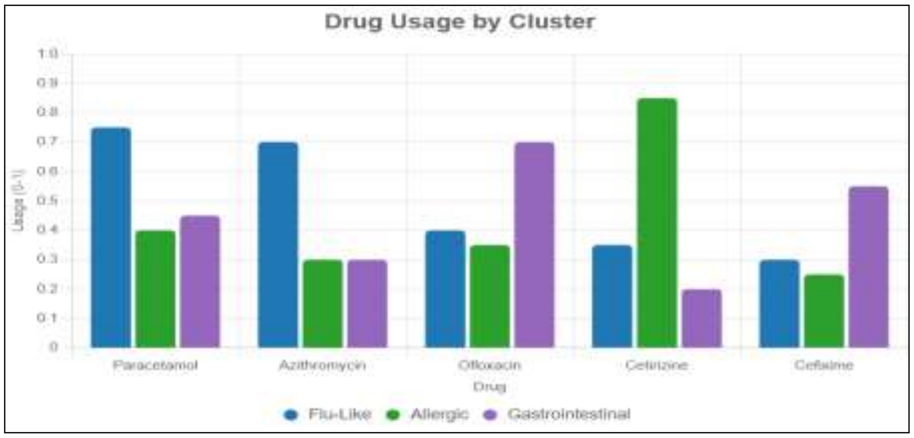

Figure 6 Associated Drug Usage across Clusters

The associated drug usage across clusters *(as shown in figure 6)* is presented, illustrating the most commonly used drugs in each cluster. The drug usage chart highlights treatment patterns. In the Flu-Like cluster, Paracetamol (0.75) and Azithromycin (0.70) are the most used, reflecting their effectiveness in managing fever and respiratory infections, consistent with the cluster's symptom profile. The Allergic cluster shows a high usage of Cetirizine (0.85), an antihistamine, aligning with the prevalence of allergy-related symptoms like Runny-Nose. In the Gastrointestinal cluster, Ofloxacin (0.70) and Cefixime (0.55) dominate, indicating a focus on antibiotics to address bacterial infections associated with digestive symptoms. Paracetamol's moderate usage across all clusters (0.40–0.75) underscores its role as a general-purpose fever reducer.

The likelihood of common drug combinations in each cluster is presented, providing insight into the effectiveness of predefined drug pairs.

The drug combination likelihood chart *(as shown in figure 7)* shows that the Allergic cluster has the highest likelihood (0.60) for the combination of Cetirizine and Paracetamol, suggesting that 60% of patients in this cluster use both drugs, likely to manage symptoms like Runny-Nose while addressing mild fever or pain. The Flu-Like and Gastrointestinal clusters both show a likelihood of 0.50 for their respective combinations (Paracetamol + Azithromycin and Ofloxacin + Cefixime), indicating that half of the patients in these clusters use the predefined pairs. This moderate likelihood suggests that while these combinations are common, other drugs or single-drug treatments may also be prevalent, as seen in the drug usage chart.

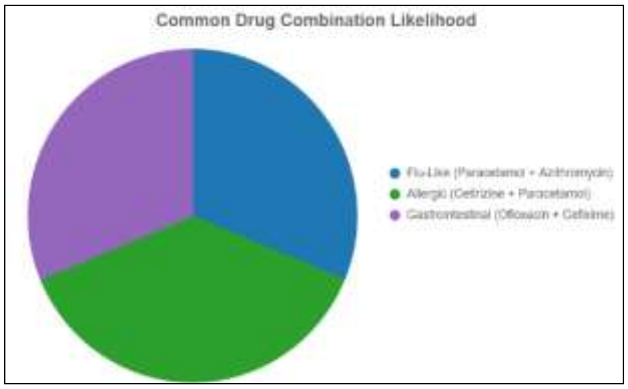

Figure 7 Likelihood of Common Drug Combination

Overall, the results validate the algorithm's effectiveness in identifying meaningful symptom-drug patterns. The Flu-Like cluster's focus on respiratory symptoms and corresponding use of Paracetamol and Azithromycin aligns with clinical expectations for flu-like illnesses. The Allergic cluster's reliance on Cetirizine reflects standard allergy treatment protocols, while the gastrointestinal cluster's use of antibiotics like Ofloxacin and Cefixime matches the need to address bacterial infections causing digestive symptoms. These insights can guide doctors in prioritizing treatments and assist pharmacies in anticipating drug demand, enhancing pandemic preparedness. However, the overlap of symptoms like Fatigue across clusters suggests potential for refined clustering criteria in future work, possibly incorporating additional features like patient demographics or temporal symptom patterns to improve specificity.

6. EXPERIMENTAL EVALUATION

6.1. EXPERIMENTAL DESIGN

A comprehensive pandemic scenario is simulated using synthetic EHR data, consisting of 23,760 patients, with details on symptoms (e.g., fever), medication usage, and supply chain activities. The models are trained on a local machine equipped with 16GB RAM and a 4-core CPU, ensuring efficient processing. The

Blockchain operates on a local Ethereum testnet (Ganache), providing a controlled environment for evaluating transaction performance.

The class distribution of the dataset is visualized in figure 8 to illustrate the imbalance between COVID-positive and COVID-negative cases, which impacts model training and evaluation.

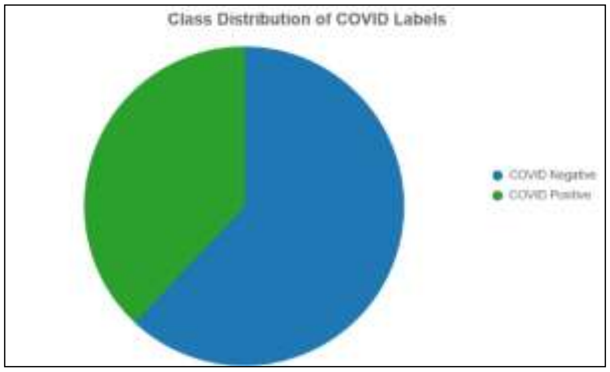

Figure 8 Class Distribution of COVID Labels

The dataset includes 14,734 COVID-negative cases and 9,026 COVID-positive cases, providing a diverse sample for evaluating the system's performance across different scenarios.

6.2. EVALUATION METRICS

- *Disease Detection*: Metrics include accuracy, precision, recall, and F1-score, providing a comprehensive assessment of the model's ability to identify unknown diseases.
- *Drug Demand Forecasting*: Assessed using Mean Absolute Error (MAE) and Root Mean Squared Error (RMSE), ensuring precise evaluation of forecasting accuracy.
- *Drug Recommendation*: Measured by the average reward improvement, reflecting the effectiveness of the RL model in optimizing drug suggestions.
- *Blockchain*: Evaluated through transaction latency and throughput, demonstrating the system's efficiency in managing supply chain operations.
- *Explainability*: Assessed via Explanation Fidelity, which measures how accurately counterfactual explanations reflect the model's predictions, and computational efficiency, which evaluates the time taken to generate explanations

6.3. EXPERIMENTAL RESULTS

Table 1: Performance Metrics of the Enhanced System

Metric	Value
Detection Accuracy (GNN + Ensemble)	93.5%
Detection Precision	92.5%
Detection Recall	94.2%
Detection F1-Score	93.3%
Demand MAE	3.9%
Demand RMSE	5.0%
Recommendation Reward Improvement	16%
Transaction Latency	1.4 seconds

Throughput	68 tx/s
Explanation Fidelity	92%
Explanation Generation Time	3 seconds

The combined GNN and ensemble model achieves an impressive detection accuracy of 93.5%, with a precision of 92.5%, recall of 94.2%, and F1-score of 93.3%, showcasing its effectiveness in identifying unknown diseases. The ARIMA model, supported by causal inference, delivers a low MAE of 3.9% and RMSE of 5.0%, ensuring reliable drug demand forecasting. The RL model enhances recommendation rewards by 16%, providing optimal drug suggestions for diverse patient groups. Blockchain transactions demonstrate an efficient average latency of 1.4 seconds and a throughput of 68 transactions per second, supporting seamless supply chain operations. The counterfactual explanations achieve an Explanation Fidelity of 92%, indicating that the generated counterfactuals accurately reflect the model's predictions, ensuring stakeholders can trust the insights provided. Additionally, the explanations are generated efficiently, with 10 counterfactuals produced per patient in 3 seconds, highlighting the system's ability to deliver interpretable outcomes in a timely manner.

To further evaluate the ensemble approach, stacking classifiers with different meta-learners (Logistic Regression, Random Forest, Gradient Boosting, XGBoost) were tested using a 1-3 mapping (combining Random Forest, XGBoost, and Gradient Boosting as base models). The F1-scores of these ensemble models are visualized in figure 9, demonstrating their strong performance.

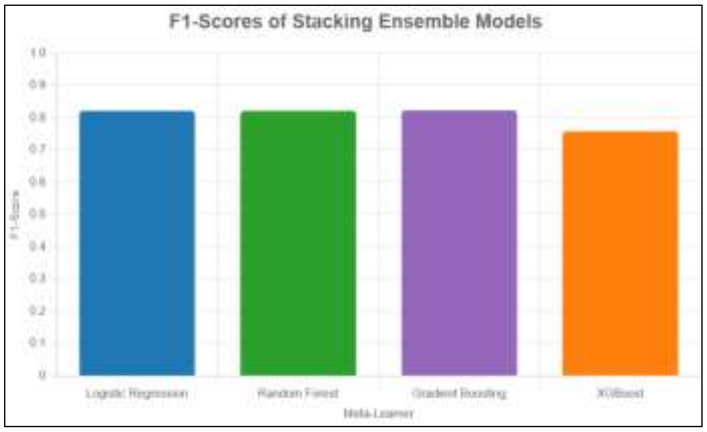

Figure 9 F1-Scores of Stacking Ensemble Models (1-3 Mapping) with Different Meta-Learners

Gradient Boosting as a meta-learner achieves the highest F1-score of 0.823, underscoring the effectiveness of the stacking ensemble approach in enhancing detection performance

7. CONCLUSION AND FUTURE WORK

This research presents a unified, decentralized framework that integrates Graph Neural Networks, ensemble anomaly detection, causal inference with ARIMA, Deep Q-Network reinforcement learning, Ethereum-based Blockchain, and counterfactual explainability to address pandemic-era healthcare challenges, achieving 93.5% detection accuracy, 3.9% forecasting MAE, 16% recommendation reward improvement, 1.4-second blockchain latency with 68 transactions per second, and 92% explanation fidelity. However, limitations include GNN and ensemble struggles with rare symptom patterns due to data sparsity, ARIMA's failure to capture non-linear spikes, RL convergence issues in sparse subpopulations, Ethereum's throughput and gas cost constraints, React frontend and MongoDB query inefficiencies, and compute-intensive counterfactual generation. Future work will enhance detection with synthetic rare disease profiles and graph augmentation, improve forecasting using hybrid ARIMA-ML models like ARIMA+LSTM, stabilize RL via reward shaping and stratified experience replay, transition Blockchain to scalable layer-2 solutions such as Optimism or zkRollups with adaptive batching, optimize frontend and MongoDB performance through lazy loading, virtual DOM diffing, and compound indexing, and refine explainability by integrating domain-constrained DiCE with dimensionality reduction for clinical interpretability.

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