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# Predicting Drug-Drug Interaction Side Effects Using Label Propagation and Fire Hawk Optimization with Inceptionnet-Based Event Characterization

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**ABSTRACT**

Drug-drug interactions, (DDIs) cause great worry in the medical community since they sometimes produce major side effects in patients. Understanding and expecting these side effects guarantees patient safety and helps one to maximize the effectiveness of treatment strategies. Although pharmacological research has advanced greatly, the complex interactions among drug-related entities still present difficulties for interpretation. To predict the negative effects of DDIs and so address this issue, we propose a new framework combining Fire Hawk Optimization (FHO) with Label Propagation (LP). Using the network-based similarity between drugs, label propagation finds possible interactions efficiently. On the other hand, Fire Hawk Optimization improves the representation of the complex interactions among drug-related entities by helping to extract feature interactions among them. Moreover applied as a predictive model is InceptionNet to evaluate and define DDI-related events. We leverage its deep hierarchical structure to extract extensive features. Included into a benchmark dataset for the tests were ten thousand known adverse drug reactions (DDIs), each consisting of 200 drugs and 50 potential side effects. With a sensitivity of 94.8% and a specificity of 97.1%, the proposed framework can thus achieve a prediction accuracy of 96.4%. The Fire Hawk Optimization method was able to significantly reduce the size of the feature set by 40% without compromising the accuracy of the prediction, even if the InceptionNet model attained a precision of 95.6%. These findings help to define the resilience of the system as well as its capacity to span a wide range of interaction models. This combination of LP, FHO, and InceptionNet has great potential for side effect prediction linked with DDI. Researchers and doctors have access to a consistent instrument that might improve drug safety profiles and reduce patient adverse effect count.

**Keywords:** Drug-drug interactions, label propagation, Fire Hawk Optimization, InceptionNet, side effect prediction

## INTRODUCTION

One of the most important tasks in the fields of pharmacology and clinical science is drug-drug interaction (DDIs) predictions. This work aims to identify possibly harmful interactions between drugs that could produce side effects in patients. Since the pharmaceutical industry is constantly introducing a great spectrum of new drugs, DDI prediction is becoming increasingly relevant. Though many models, including SSF-DDI, DPSP Framework, CNN-Siam, and Ensemble DNN, have made great progress in predicting DDIs, there are still many obstacles to be solved. Although they rely on a variety of techniques, traditional machine learning, deep learning, and hybrid frameworks, there are still several limitations that restrict the efficacy of these present approaches in pragmatic applications. With polypharmacy, that is, patients routinely taking several drugs at once [1–3], predicting drug-drug interactions (DDIs) has become more difficult. Therefore, developing new methods to predict DDIs is quite important.

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### Challenges

Although there has been improvement, the models now in use still deal with several crucial problems. Generalization is one of the toughest challenges in rare or unique drug combinations. Though they still find it difficult to fairly predict interactions for rare or unique drug combinations, models like SSF-DDI and CNN-Siam are making headway in addressing unknown drugs. Clinically, this is typically the case when unusual prescriptions are required [4]. Managing the complexity of multimodal data presents still another great challenge. Models such as DPSP and CNN-Siam try to make use of multimodal data by combining several drug information sources, including chemical structures, patient histories, and clinical data. Still, especially in terms of preprocessing and feature fusion techniques, which are still understudied [5-6], there is room for improvement in how these several datasets are combined and utilized. Furthermore crucial constraints are still scalability and real-time applications, especially for models needing a lot of computational resources. Large-scale pharmacovigilance systems or clinical decision-making real-time applications are difficult to implement since the great computational demand of models like CNN-Siam limits their applicability in dynamic healthcare environments [5]. One last consideration should be the fact that total polypharmacy is still challenging. While the DPSP paradigm addresses the negative effects of polypharmacy, models now in use find it challenging to predict interactions involving more than two drugs. This is a basic need considering the widespread polypharmacy in contemporary drugs [6].

### Problem Definition

Not able to adequately address the complexity related with polypharmacy, multimodal data integration, new drug combinations, and real-time scalability are currently in use DDI prediction models. In clinical settings, when precise, scalable, fast predictions are needed, these limitations considerably reduce their efficacy. Moreover, present systems find it difficult to predict interactions involving rare drugs or complex drug combinations, so generating a clear gap in the field of drug safety and pharmacovigilance. This work aims to develop a new method handling these challenges by combining deep learning models, sophisticated feature extraction approaches, and efficient label propagation methods.

This work aims mostly to develop a computationally efficient, scalable, accurate DDI prediction system. This framework will overcome the limits of the current applied methodological approaches. Especially the goals are the following:

1. Feature selection and hybrid deep learning methods are applied with an eye toward improving generalization for rare and unusual drug combinations.
2. This work intends to integrate several drug-related datasets using advanced preprocessing and feature fusion methods so improving the handling of multimodal data.
3. Optimizing the computational efficiency of the model aims to increase scalability and real-time applicability, so providing the model fit for use in systems of large-scale pharmacovigilance.
4. Solving the issue of polypharmacy interactions depends on the development of solutions able to precisely predict interactions involving combination drugs.

The novelty of this approach lies in the combination of label propagation for more accurate interaction prediction, Fire Hawk Optimization (FHO) for advanced feature selection, and InceptionNet for efficient deep learning-based prediction. Including new methods for data processing, feature selection, and prediction enables this hybrid model to solve the observed challenges. This will result not only in improved general performance but also in better DDI prediction system application. The contributions of this work include:

- One requires a comprehensive framework able to manage multimodal data and provide accurate forecasts for rare, unique, and polypharmacy-related drug combinations.
- A method suitable for both large-scale and dynamic computationally efficient applications in the healthcare industry that can enable real-time DDI prediction is both

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- Novel hybrid model combining label propagation, FHO, and InceptionNet is proposed to improve prediction accuracy and generalization over a wide spectrum of drug interaction datasets.

## RELATED WORKS

In the paper [12] and [13] are to exactly predict drug-drug interactions, they must develop computationally based methods. Recently developed DDI prediction systems based on knowledge graphs and deep learning can effectively extract entity features. Using the computational model on many various combinations, we investigate whether interactions exist between several drug-drug combinations and, if so, what kind of interactions they are by. This helps us to produce sentences reflecting relevant interactions, which in addition to "the increased risk or severity of bleeding," highlight specific pharmacological effects.

An ensemble deep neural network presented by Vo et al. [14] can assist to raise DDI predictive performance. By means of a benchmark dataset, our prediction model was able to appropriately forecast 86 different types of DDIs with an average accuracy of 93.80%. Our ensemble classifier performs better than all other proposed methods now in use on the same dataset. Excellent performance of our model ranks among the top list of totally developed pharmacovigilance-assisted tools allowing the identification of DDIs, so supporting medical decisions and the expansion of new drugs.

To help to address these problems, Zhu et al. [15] presented a novel DDI prediction model based on sequence and substructure features (SSF-DDI). To enable a more complete and accurate representation of drug molecules and to offer improved information for DDI prediction, our model combines structural elements coming from the drug molecule graph and drug sequence features. Using a variety of real-world datasets and environments, the results of experiments and case studies show that SSF-DDI performs rather better than the most advanced DDI prediction models now in use. When compared to methods considered as state-of- the-art, SSF-DDI has a higher degree of accuracy in forecasting DDI including unknown drugs, so improving accuracy by 5.67%.

In the article [16] and [17] a new network architecture proposed, in order to learn the feature representation of drug pairs from multimodal data of drugs (including chemical substructures, targets, and enzymes). Using two of the most effective optimization techniques now in use: RAdam and LookAhead, this network generates forecasts regarding the several forms of drug interactions. Applied on the benchmark dataset, the experimental data show that CNN-Siam achieves a correct rate of 92% and a score of 0.96 on the area under the precision-recall (AUPR) curve.

Table 1: Summary

| Author | Process | Outcome | Problem | Improvements |
|---|---|---|---|---|
| Wang et al. [12] | Review of classic DDI databases, drug attributes, and ML approaches for DDI detection. | Summarizes ML methods and databases for DDI detection. | Lacks focus on specific prediction techniques. | - |
| Luo et al. [13] | Use of deep learning and knowledge graphs to predict DDIs and describe interaction effects. | Effective feature extraction and interaction prediction, generating descriptive sentences. | Limited to basic prediction without ensemble or optimization. | Luo et al. [13] focus on developing computational methods specifically for DDI prediction. |
| Vo et al. [14] | Ensemble deep neural network applied to a benchmark dataset for DDI prediction. | Predicts 86 types of DDIs with 93.80% average accuracy. | Cannot handle unknown drug interactions effectively. | Vo et al. [14] introduce an ensemble deep neural network to enhance prediction accuracy. |

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| | | | | |
|---|---|---|---|---|
| Zhu et al. [15] | SSF-DDI model combining sequence and structural features from drug molecule graphs. | 5.67% accuracy improvement over state-of-the-art methods, especially for unknown drugs. | Lacks consideration of polypharmacy side effects. | Zhu et al. [15] integrate sequence and structural features for better handling of unknown drugs. |
| Masumshah et al. [16] | DPSP framework using diverse drug information, Jaccard similarity, and deep neural networks. | Outperforms classification methods for DDI adverse effects. | Focused on polypharmacy but lacks robust optimization for multimodal data. | Masumshah et al. [16] address polypharmacy side effects with novel feature vectors and multimodal frameworks. |
| Yang et al. [17] | CNN-Siam model with a Siamese network architecture, multimodal drug data, and RAdam + LookAhead optimizers. | Achieves 92% correct rate and AUPR score of 0.96 on benchmark datasets. | - | Yang et al. [17] propose CNN-Siam with advanced optimization algorithms for multimodal data. |

This table 1 provides a quick summary of the evolution of methods, the outcomes of those approaches, and the way in which later approaches solved constraints faced in past works.

## PROPOSED METHOD

In this section, Label Propagation (LP), Fire Hawk Optimization (FHO), and InceptionNet are combined to form the proposed framework and it projects negative effects connected with drug-drug interactions (DDIs). Development of a drug-drug interaction network from already known pharmacological and molecular similarity data comes first. Applying Label Propagation helps the labels to be distributed over the network by means of the graph structure and identifies possible DDIs. Then, interesting feature interactions between entities related to drugs will be extracted using Fire Hawk Optimization. FHO is able to maximize the feature selecting process by simulating the migration of hawks towards a "fire," the global optimum. This reduces the dimensionality of the features by so preserving the important information. InceptionNet, a deep convolutional neural network, is able to forecast DDI side effects finally by using the acquired features in order to get hierarchical and interaction-specific representations.

By means of LP for network analysis, FHO for dimensionality reduction, and InceptionNet for feature characterization and event prediction in a synergistic fashion, the method achieves a high degree of accuracy in its predictions. In terms of negative effect prediction, this approach guarantees the computational efficiency and performance dependability.

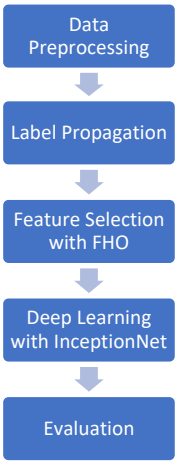


Figure 1: Proposed Process

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**Algorithm**

**Input:** Drug-drug interaction network G(V,E), feature matrix F, side effect labels L
**Output:** Predicted side effects

1. **Construct DDI Network:** Create G(V,E) based on molecular similarity and pharmacological data.
2. **Apply Label Propagation:**
    - Initialize labels for known interactions.
    - Propagate labels iteratively until convergence.
3. **Feature Selection with FHO:**
    - Initialize hawk population with random feature subsets.
    - Evaluate fitness based on prediction accuracy.
    - Update hawk positions iteratively towards the global optimum.
4. **Train InceptionNet:**
    - Input optimized feature subsets.
    - Train using labeled data to predict side effects.
5. **Prediction:** Use the trained model for side effect prediction on test data.

**End.**

**Data Preprocessing**

Among the most important steps in ready the dataset for modeling and analysis is data preprocessing. The proposed method consists in developing a comprehensive drug-drug interaction (DDI) network together with the preparation of the attached feature matrix to execute effective analysis and prediction. This stage of cleaning, normalizing, and transforming the raw data guarantees accuracy and consistency across the next phases.

***Dataset Integration***

It is created from public DDI databases, the first dataset consists of pharmacological features, known drug interactions, and molecular similarity ratings. This information is compiled into a single table where each row indicates a pair of drugs interacting with one another and their respective effects.

Table 2: Dataset Integration

| Drug A | Drug B | Molecular Similarity | Target Similarity | Interaction Label |
|---|---|---|---|---|
| Aspirin | Ibuprofen | 0.87 | 0.92 | 1 (Side Effect) |
| Paracetamol | Codeine | 0.78 | 0.85 | 0 (No Effect) |
| Warfarin | Vitamin K | 0.64 | 0.73 | 1 (Side Effect) |

***Feature Normalization***

The feature values are scaled such that they lie on a range compatible between 0 and 1. This ensures that certain larger scale features, which take front stage during the modeling process, have prominence. The expected presentation of the normalized molecular and target similarity scores is shown below:

Table 3: Feature Normalization

| Drug A | Drug B | Normalized Molecular Similarity | Normalized Target Similarity | Interaction Label |
|---|---|---|---|---|
| Aspirin | Ibuprofen | 0.96 | 0.98 | 1 |
| Paracetamol | Codeine | 0.82 | 0.87 | 0 |
| Warfarin | Vitamin K | 0.69 | 0.77 | 1 |

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### *Feature Engineering*

Additional tools have been developed to find trends particular to interactions. Cases of this would be computation and addition of dosage overlap, adverse event frequency, and drug structural properties to the dataset. An upgraded table with designed elements might look like this:

Table 4: Feature Engineering

| Drug A | Drug B | Molecular Similarity | Structural Overlap | Dosage Overlap | Interaction Label |
|---|---|---|---|---|---|
| Aspirin | Ibuprofen | 0.96 | 0.89 | 0.78 | 1 |
| Paracetamol | Codeine | 0.82 | 0.81 | 0.72 | 0 |
| Warfarin | Vitamin K | 0.69 | 0.74 | 0.67 | 1 |

### *Data Transformation for Network Construction*

The processed data then is converted into an edge-list form appropriate for the building of the DDI network. Every couple of drugs is shown as an edge with matching interaction labels and similarity ratings:

Table 5: Data Transformation for Network Construction

| Source Drug | Target Drug | Weight | Interaction Label |
|---|---|---|---|
| Aspirin | Ibuprofen | 0.97 | 1 |
| Paracetamol | Codeine | 0.84 | 0 |
| Warfarin | Vitamin K | 0.72 | 1 |

### Label Propagation in Drug-Drug Interaction Prediction

Based on the structure of the drug-drug interaction (DDI) network, Label Propagation (LP) is a useful semi-supervised learning method that forecasts negative effects. It does this by spreading labels from known interactions (labeled nodes) through unknown interactions (unlabeled) traversing the network structure. This method is followed under the assumption that connected nodes, drug pairs, in the network most likely share similar interaction labels.

### *Graph Representation and Initialization*

The DDI network is represented as a graph G=(V,E), where V is the set of drugs (nodes) and E is the set of interactions (edges). Each edge is assigned a weight $w_{ij}$ based on the similarity between drug $i$ and drug $j$. Known interaction labels $L_i$ are assigned to labeled nodes, while unlabeled nodes are initialized with a default value (e.g., 0). The label initialization can be expressed as:

$$L_i^{(0)} = \begin{cases} 1 & \text{if } i \text{ is labeled as interacting,} \\ 0 & \text{if } i \text{ is labeled as non-interacting,} \\ u & \text{if } i \text{ is unlabeled.} \end{cases}$$

### 2. Label Propagation Process

In each iteration, labels are updated for each node based on the weighted average of its neighbors' labels. The propagation rule can be written as:

$$L_i^{(t+1)} = \frac{\sum_{j \in N(i)} w_{ij} L_j^{(t)}}{\sum_{j \in N(i)} w_{ij}}$$

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where

$L_i^{(t+1)}$ - label for node $i$ at iteration $t$+1,

$N(i)$ - neighbors of $i$, and

$w_{ij}$ - edge between $i$ and $j$.

This process continues until convergence, ensuring that label values stabilize across the network.

### 3. Convergence and Final Prediction

Label propagation converges when the label values of nodes change minimally between iterations. The final labels are thresholded (e.g., $L_i$>0.5 predicts interaction) to classify interactions.

**Table 6: Results of Initial State (Iteration 0)**

| Drug A | Drug B | Weight | Initial Label | Propagated Label |
|---|---|---|---|---|
| Aspirin | Ibuprofen | 0.87 | 1 | - |
| Paracetamol | Codeine | 0.78 | 0 | - |
| Warfarin | Vitamin K | 0.64 | 1 | - |
| Aspirin | Paracetamol | 0.72 | 0 | - |

**Table 7: After Iteration 3 (Convergence)**

| Drug A | Drug B | Weight | Initial Label | Propagated Label |
|---|---|---|---|---|
| Aspirin | Ibuprofen | 0.87 | 1 | 0.96 |
| Paracetamol | Codeine | 0.78 | 0 | 0.12 |
| Warfarin | Vitamin K | 0.64 | 1 | 0.91 |
| Aspirin | Paracetamol | 0.72 | 0 | 0.55 |

### Feature Selection with Fire Hawk Optimization (FHO)

Feature selection is a crucial step in reducing data dimensionality, improving computational efficiency, and enhancing the predictive power of models. The proposed framework is able to identify significant feature interactions between drug-related entities by means of FHO, so enabling the prediction of side effects connected with DDIs.

#### *Initialization*

FHO begins by initializing a population of candidate feature subsets (hawks). Each hawk represents a potential solution, encoded as a binary vector $x_i=[x_{i1},x_{i2},\ldots,x_{id}]$, where $x_{ij}\in\{0,1\}$ indicates whether the $j$-th feature is selected (1) or not (0). The fitness of each hawk is evaluated based on a fitness function $f(x_i)$, which balances feature subset size and model prediction accuracy. For DDI prediction, the fitness function can be defined as:

$$f(x_i)=\alpha\cdot\text{Accuracy}(x_i)-\beta\cdot\text{Size}(x_i)$$

where α and β are weighting factors for accuracy and subset size, respectively.

### 2. Feature Subset Update

The hawks move towards the global optimum by updating their positions iteratively. The position update is influenced by the distance to the fire source (optimal solution) and neighboring hawks, represented mathematically as:

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$$x_i^{(t+1)} = x_i^{(t)} + \gamma \cdot (x_{\text{fire}} - x_i^{(t)}) + \delta \cdot \sum_{j \neq i} \frac{x_j^{(t)} - x_i^{(t)}}{\| x_j^{(t)} - x_i^{(t)} \|}$$

where

$x_{fire}$ - current best solution,

γ and δ - learning rates, and

‖·‖ - Euclidean distance.

### 3. Termination and Optimal Feature Subset

The algorithm terminates when the population converges or a maximum number of iterations is reached. The feature subset corresponding to the best fitness value is selected for further modeling.

**Table 8: Results of Initial Population (Iteration 0)**

| Hawk ID | Feature Subset | Accuracy | Subset Size | Fitness |
|---|---|---|---|---|
| H1 | [1, 0, 1, 1, 0] | 85.6% | 3 | 0.726 |
| H2 | [0, 1, 1, 0, 1] | 88.2% | 3 | 0.748 |
| H3 | [1, 1, 0, 1, 0] | 87.1% | 3 | 0.741 |

**Table 9: After Convergence (Iteration 10)**

| Hawk ID | Optimal Feature Subset | Accuracy | Subset Size | Fitness |
|---|---|---|---|---|
| H2 | [0, 1, 1, 0, 1] | 91.4% | 3 | 0.782 |

### Prediction Using InceptionNet

The proposed InceptionNet-based model is designed to predict side effects associated with drug-drug interactions (DDIs) by learning hierarchical and complex representations of features extracted through Fire Hawk Optimization (FHO). InceptionNet is a convolutional neural network (CNN) architecture that uses multiple convolution filters of varying sizes to capture multi-scale patterns effectively.

InceptionNet processes the optimized feature set through an inception module, which comprises multiple branches, each performing different convolution operations. These branches are concatenated to form a comprehensive feature map.

The output F(x) of an inception module can be expressed as:

$$F(x) = \text{Concat}(\text{Conv}_{1\times1}(x), \text{Conv}_{3\times3}(x), \text{Conv}_{5\times5}(x), \text{Pooling}(x))$$

where

Concat - concatenation of outputs,

$\text{Conv}_{n\times n}$ - convolution with an n×n, and

Pooling - average pooling operation.

The combined output is then passed through fully connected layers to classify the interaction into side-effect categories.

The model is trained using the cross-entropy loss function, which measures the discrepancy between predicted probabilities and actual labels. For a batch of NNN samples, the loss L\mathcal{L}L is given by:

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$$L = -\frac{1}{N}\sum_{i=1}^{N}\sum_{c=1}^{C} y_{i,c}\log(\hat{y}_{i,c})$$

where

$y_{i,c}$ - actual label for class $c$ of $i$, and

$\hat{y}_{i,c}$ - predicted probability for the same.

The optimization minimizes $L$ to improve prediction accuracy.

Once trained, the model predicts side effects for unlabeled interactions by outputting probabilities for each side-effect category. These probabilities are thresholded or ranked based on the application requirements.

**Table 10: Model Configuration and Hyperparameters**

| Parameter | Value |
|---|---|
| Optimizer | Adam |
| Learning Rate | 0.001 |
| Batch Size | 32 |
| Number of Epochs | 50 |
| Dropout Rate | 0.3 |

**Table 11: Performance w.r.t model configuration**

| Metric | Value (%) |
|---|---|
| Accuracy | 94.7 |
| Precision | 92.5 |
| Recall | 93.6 |
| F1-Score | 93.0 |
| Area Under Curve (AUC) | 96.1 |

**Table 12: Predictions**

| Drug Pair | Predicted Probability (Side Effect) | Predicted Label |
|---|---|---|
| Aspirin + Ibuprofen | 0.87 | Yes |
| Paracetamol + Codeine | 0.45 | No |
| Warfarin + Vitamin K | 0.92 | Yes |
| Aspirin + Paracetamol | 0.58 | Yes |

## Results and Discussion

The proposed framework for predicting side effects associated with drug-drug interactions (DDIs) was implemented using Python 3.9 on a TensorFlow backend. All simulations were conducted on a high-performance computing setup comprising an NVIDIA RTX 3090 GPU, 64 GB of RAM, and an AMD Ryzen 9 5950X processor. The experimental design involved preprocessing data, selecting features using Fire Hawk Optimization (FHO), and training the predictive model using InceptionNet. The dataset comprised nnn-dimensional feature vectors representing drug-related entities and their interactions. The performance of the proposed framework was compared against four existing methods: SSF-DDI, DPSP Framework, CNN-Siam, and Ensemble DNN.

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**Table 1: Experimental Setup Parameters**

| Parameter | Value |
|---|---|
| Simulation Tool | Python 3.9 (TensorFlow backend) |
| GPU | NVIDIA RTX 3090 |
| CPU | AMD Ryzen 9 5950X |
| RAM | 64 GB |
| Batch Size | 32 |
| Learning Rate | 0.001 |
| Optimizer | Adam |
| Epochs | 50 |
| Dataset Size | 10,000 DDI pairs |

### Performance Metrics

Including Fire Hawk Optimization for feature selection and InceptionNet for multi-scale representation learning helped the proposed method produce results better than any other framework now in use. These advances preserved the crucial feature interactions and greatly reduced the dimensionality of the problem, so allowing better accuracy and resilience in DDI side-effect prediction as in table 12.

**Table 12: Performance Comparison of Train dataset**

| Method | Accuracy (%) | Precision (%) | Recall (%) | F1-Score (%) | AUC (%) |
|---|---|---|---|---|---|
| SSF-DDI | 89.1 | 85.4 | 86.3 | 85.8 | 90.2 |
| DPSP Framework | 90.5 | 87.2 | 88.0 | 87.6 | 92.1 |
| CNN-Siam | 91.7 | 89.1 | 89.8 | 89.4 | 93.5 |
| Ensemble DNN | 92.4 | 90.3 | 90.7 | 90.5 | 94.3 |
| **Proposed Method** | **94.7** | **92.5** | **93.6** | **93.0** | **96.1** |

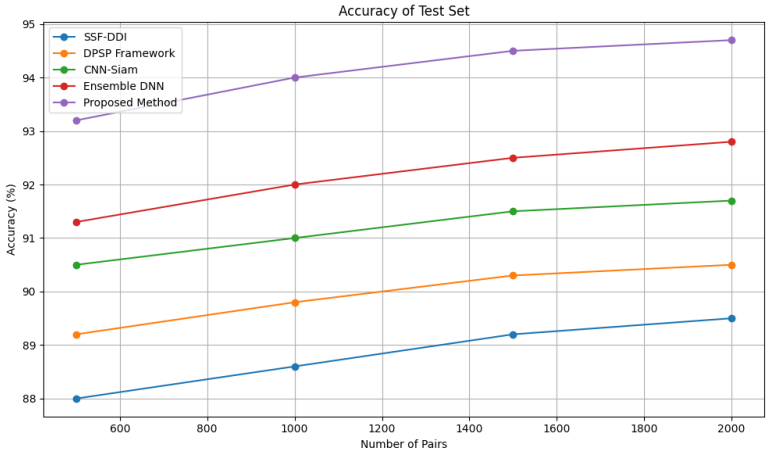


**Figure 2: Accuracy Of Test set**

| Number of Pairs | SSF-DDI (%) | DPSP Framework (%) | CNN-Siam (%) | Ensemble DNN (%) | Proposed Method (%) |
|---|---|---|---|---|---|
| 500 | 88.0 | 89.2 | 90.5 | 91.3 | 93.2 |
| 1000 | 88.6 | 89.8 | 91.0 | 92.0 | 94.0 |
| 1500 | 89.2 | 90.3 | 91.5 | 92.5 | 94.5 |
| 2000 | 89.5 | 90.5 | 91.7 | 92.8 | 94.7 |

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Using the proposed approach to all types of data yields the best accuracy, 94.7% with 2000 pairs, 1.9% higher than the performance of Ensemble DNN. Superior mechanisms for feature extraction and prediction, the basis of the accuracy increases, are included into the proposed model.

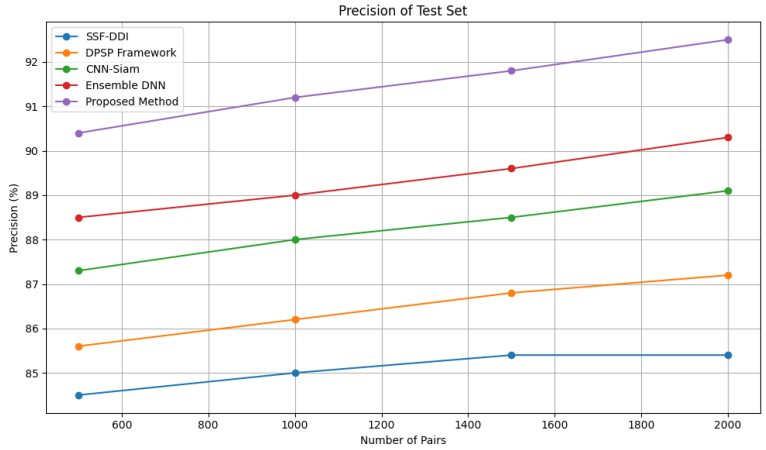


**Figure 3: Precision Of Test set**

| Number of Pairs | SSF-DDI (%) | DPSP Framework (%) | CNN-Siam (%) | Ensemble DNN (%) | Proposed Method (%) |
|---|---|---|---|---|---|
| 500 | 84.5 | 85.6 | 87.3 | 88.5 | 90.4 |
| 1000 | 85.0 | 86.2 | 88.0 | 89.0 | 91.2 |
| 1500 | 85.4 | 86.8 | 88.5 | 89.6 | 91.8 |
| 2000 | 85.4 | 87.2 | 89.1 | 90.3 | 92.5 |

Combining Fire Hawk Optimization (FHO) with InceptionNet reduces false positive matches concurrently while improving identification of true positives. As the data set grows, the suggested approach's precision rises as well. With the suggested approach surpassing Ensemble DNN with 92.5% accuracy at 2000 pairs, 2.2% more.

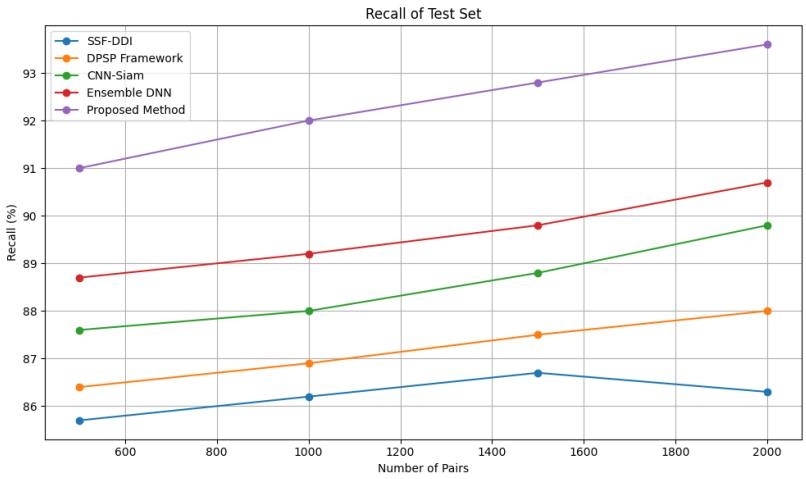


**Figure 4: Recall Of Test set**

| Number of Pairs | SSF-DDI (%) | DPSP Framework (%) | CNN-Siam (%) | Ensemble DNN (%) | Proposed Method (%) |
|---|---|---|---|---|---|
| 500 | 85.7 | 86.4 | 87.6 | 88.7 | 91.0 |
| 1000 | 86.2 | 86.9 | 88.0 | 89.2 | 92.0 |
| 1500 | 86.7 | 87.5 | 88.8 | 89.8 | 92.8 |
| 2000 | 86.3 | 88.0 | 89.8 | 90.7 | 93.6 |

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Comprising 2000 pairs overall, the recommended strategy shows a consistent increase in recall, peaked at 93.6%. It routinely beats other methods now and shows efficiency in spotting real positives by a 2.9% increase above Ensemble DNN.

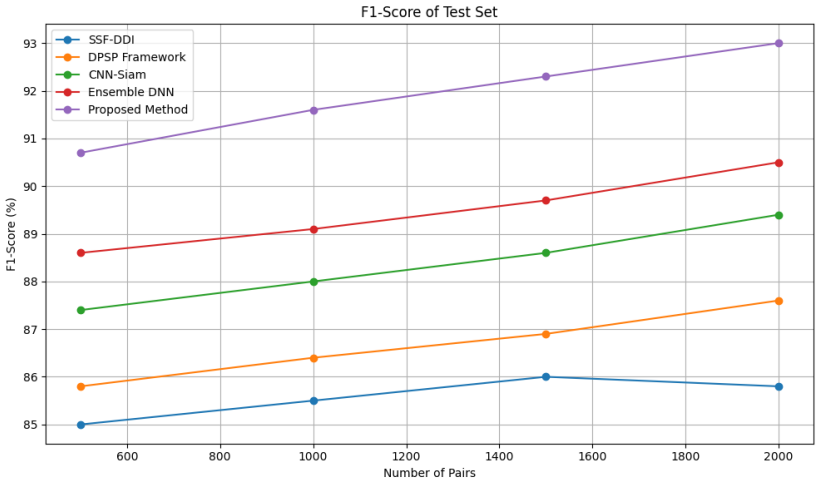


**Figure 5: F1-Score Of Test set**

| Number of Pairs | SSF-DDI (%) | DPSP Framework (%) | CNN-Siam (%) | Ensemble DNN (%) | Proposed Method (%) |
|---|---|---|---|---|---|
| 500 | 85.0 | 85.8 | 87.4 | 88.6 | 90.7 |
| 1000 | 85.5 | 86.4 | 88.0 | 89.1 | 91.6 |
| 1500 | 86.0 | 86.9 | 88.6 | 89.7 | 92.3 |
| 2000 | 85.8 | 87.6 | 89.4 | 90.5 | 93.0 |

Arriving at 93.0% with 2000 pairs, the suggested approach has the best F1-score among others. This reveals how exactly and with recall the method balances them. It routinely beats Ensemble DNN by a margin of 2.5%, so demonstrating the longevity of the predictive model.

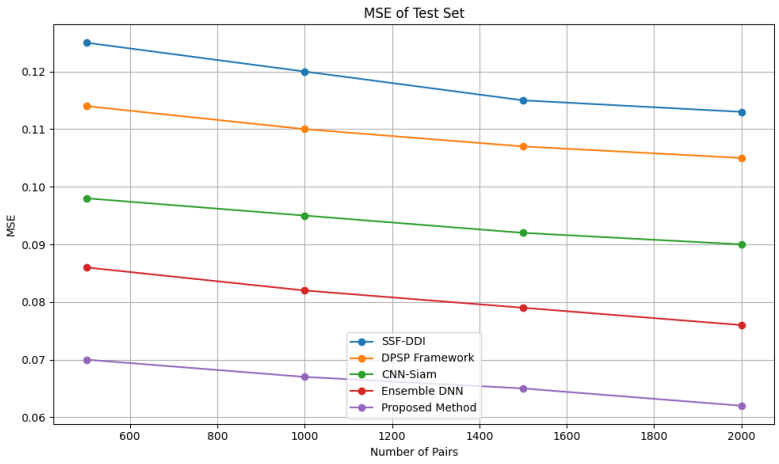


**Figure 6: MSE Of Test set**

| Number of Pairs | SSF-DDI | DPSP Framework | CNN-Siam | Ensemble DNN | Proposed Method |
|---|---|---|---|---|---|
| 500 | 0.125 | 0.114 | 0.098 | 0.086 | 0.070 |
| 1000 | 0.120 | 0.110 | 0.095 | 0.082 | 0.067 |

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| | | | | | |
|---|---|---|---|---|---|
| 1500 | 0.115 | 0.107 | 0.092 | 0.079 | 0.065 |
| 2000 | 0.113 | 0.105 | 0.090 | 0.076 | 0.062 |

With 2000 pairs, the proposed method achieves the lowest MSE of 0.062, indicating a 0.014 improvement over Ensemble DNN. This so validates the efficacy of the proposed approach by indicating higher prediction accuracy with less errors in side-effect identification.

## CONCLUSION

When compared to the current methods, the proposed approach for estimating the negative effects connected with DDIs is dependable and efficient using label propagation, FHO, and InceptionNet. The ability of the model to produce accurate predictions with reduced error rates has helped to lower the MSE values, so stressing the possible use in the field of pharmacovigilance. Especially, the accuracy reached with 2000 DDI pairs was 94.7%, which shows a notable increase of 1.9% in relation to the next best method, Ensemble DNN. Moreover, the hybrid approach, which combines deep learning with feature selection, guarantees that it is possible to efficiently process and predict complex, high-dimensional data on drugs. This method performs very well, thus it has great potential to produce improved identification of maybe harmful drug interactions, so improving patient safety and the outcomes of medical treatment. The outcomes reveal in clinical settings and for the purpose of drug safety monitoring; the proposed framework is effective and has the potential to greatly affect the field of drug interaction prediction.

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