A Graph Neural Network Enhanced by Squirrel Search and Deer Hunting Strategies for PAN-Cancer Survival Prediction

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***Abstract*—This paper introduces PAN-cancer, a novel system that uses a Graph Neural Network (GNN) in conjunction with two nature-inspired optimisation strategies, such as Squirrel Search and Deer Hunting strategies, to predict patient survival across multiple cancer types. Because different cancers are so diverse and complex, predicting survival is extremely difficult. The suggested approach makes use of GNNs to identify connections between patients by comparing their genetic and clinical information. The model is fine-tuned and the most crucial features are chosen using the Squirrel Search and Deer Hunting algorithms to enhance performance. PAN-cancer datasets from The Cancer Genome Atlas (TCGA), which contain actual patient records, are used to train and evaluate the system. When compared to other models currently in use, this one achieved an accuracy of 98.68.**

***Keywords*—PAN-Cancer Analysis, Graph Neural Networks, Squirrel Search Algorithm, Deer Hunting Optimization, Survival Prediction, The Cancer Genome Atlas**

I. Introduction

This paper introduces a hybrid deep learning architecture that uses pan cancer gene expression data to predict survival across various cancer types. The combination of Biolith Search (SSDH) and Graph Neural Networks (GNN) in Squirrel Search (SSDH) improves biological interpretability and prediction accuracy [1] [2]. The SSDH algorithm uses natural feed and hunting tactics to choose favorable genes from high-dimensional RNAseq data, reduce noise, and prioritize features with high prognostic values [3].

Genes selected for expression-based similarity with the patient's sample are used to create graphs. [4] [5]. To simulate complex patient connections and survival outcomes, the GNN is trained using this diagram [6]. This model outperforms traditional machine learning models in survival classification, risk stratification, and generalization across cancer types. It has been verified using data from the Cancer Genome Atlas. This SSDH GNN technique improves survival forecasts and provides interpretable information on the biological origins of cancer.[7] [8].

This research presents a unique bioinspired strategy that blends squirrel search deer hunting (SSDH) algorithms with graph neural networks (GNNS) to improve cancer survival prediction. Predicting survival rates for various cancer kinds is a major difficulty in oncology. This framework focuses on processing high-dimensional gene expression data, a critical part of precision medicine [9]. The SSDH algorithm improves model output by focusing on relevant genes and facilitating effective functional selection. The GNN model identifies complicated correlations between patient 1 samples, leading to more accurate and understandable survival forecasts [10].

This paper is significant because it applies to all types of cancer and offers an interpretable tool for identifying crucial gene and molecular interactions that impact survival outcomes. The general goal of this project is to develop a robust, bio-inspired, deep learning frame to predict cancer survival outcomes through several types of tumors using pancancer gene expression data[11] [12]. This project integrates the SSDH algorithm (Horne Search Dear Hunt) to select efficient features so that biologically relevant genes are identified from the high-dimensional dataset. These selected genes are used to construct GNN models (graph neural networks) that record complex relationships between patient samples and allow prediction of survival outcomes[13] [14]. The scope of this project includes the application of this hybrid SSDH GNN model, in particular Cancer Icons (TCGA) to multicancer data records to assess performance related to accuracy, interpretability and generalization. The purpose of this study is to contribute to further development of personalized cancer predictions and to provide

a more reliable and interpretable tool for clinical decisions and treatment planning[15]. The organization of the paper is as follows: Section II provides a literature survey on PAN-cancer survival prediction and graph neural networks. Section III covers the theoretical background relevant to the study. Section IV describes the data preparation and pre-processing steps. Section V explains the proposed methodology, including the integration of Graph Neural Networks with Squirrel Search and Deer Hunting strategies. Section VI presents the results and discussion. Finally, Section VII concludes the study and outlines the future scope of the work.

II. LITERATURE SURVEY

A. A. Review of Prior Research

Over the years, substantial research has been conducted in the domain of cancer survival prediction using machine learning and deep learning approaches applied to high-dimensional biomedical data. Initial studies largely focused on classical survival models and shallow learning techniques, which often struggled with the complexity and heterogeneity of PAN-cancer datasets [16]. Traditional statistical methods, while interpretable, frequently underperform when applied to large-scale multi-omics data [17], [18]. With the rise of deep learning, models such as Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs) have been increasingly employed for feature extraction and survival prediction tasks due to their ability to capture complex patterns in data [19], [20], [21]. For example, CNNs have shown promise in extracting spatial features from histopathology images, while RNNs, including Long Short-Term Memory (LSTM) networks, effectively model temporal dependencies in sequential omics data [22], [23]. Recently, Graph Neural Networks (GNNs) have gained attention for their capability to integrate relational biological data, such as gene interaction networks, improving the prediction accuracy of survival outcomes in oncology studies [24], [25]. Despite these advances, the training and optimization of GNNs remain challenging due to the high dimensionality and noise inherent in biomedical datasets. To address these challenges, metaheuristic optimization techniques like the Squirrel Search Algorithm (SSA) and Deer Hunting Optimization (DHO) have been proposed to enhance feature selection and model parameter tuning [26], [27]. These bio-inspired methods help avoid local optima and improve the overall generalization ability of predictive models. Although several works have integrated metaheuristic strategies with deep learning frameworks, the combination of SSA and DHO with GNNs for PAN-cancer survival prediction is still an emerging area of research with significant potential to improve clinical prognostic models. Table I shows Summary of Prior Research on Survival Prediction using GNNs and Optimization Techniques.

TABLE I
SUMMARY OF PRIOR RESEARCH ON SURVIVAL PREDICTION USING GNNS AND OPTIMIZATION TECHNIQUES

Paper	Key Findings	Methodology	Limitations	Accuracy
[16]	Classical models show limited accuracy on PAN-cancer data	Cox regression, Kaplan-Meier	Struggles with high-dimensional omics data	65%
[20]	CNNs effective in extracting spatial features from histopathology	CNN-based feature extraction	Ignores temporal data dependencies	72%
[23]	LSTM models capture temporal gene patterns well	LSTM, RNN-based modeling	Poor performance on noisy data	74%
[25]	GNNs outperform traditional models in modeling biological relations	Graph Convolution Networks (GCN)	Optimization difficulty with high-dimensional inputs	78%
[27]	Metaheuristics improve feature selection	Genetic Algorithm, Particle Swarm Optimization	Tendency to converge to local minima	76%

B. Identified Research Gaps

Survival prediction in cancer research is a critical task that demands accurate interpretation of complex and high-dimensional biomedical data, such as gene expression profiles. While Graph Neural Networks (GNNs) have demonstrated strong capabilities in modeling biological structures and relationships, they often struggle with optimization in large-scale, noisy, and heterogeneous datasets[28]. Traditional optimization methods fail to provide global solutions in such contexts, limiting the GNN's predictive potential. Advanced metaheuristic strategies such as Squirrel Search and Deer Hunting algorithms have been underutilized in this domain, even though they have proven effective in other optimization tasks.

Current models are also hindered by a lack of generalizability across PAN-cancer datasets, which include a wide range of cancer types with varied genetic and clinical characteristics. Most survival models are tailored to specific cancer types, making them less effective when applied to diverse or unseen datasets. This heterogeneity is not sufficiently addressed by conventional feature selection or learning strategies. Furthermore, existing models often lack robust mechanisms to integrate multi-omics data—such as gene expression, methylation, and copy number variations resulting in suboptimal performance and reduced biological insight.

Interpretability and clinical applicability remain significant barriers to deploying these models in real-world medical environments. Despite high predictive performance, many GNN-based approaches operate as black boxes, offering limited transparency into their decision-making process. There is a

clear gap in developing explainable GNN models that can identify key biomarkers and pathways relevant to patient outcomes. Moreover, few studies incorporate survival-specific loss functions like Cox loss or consider temporal aspects of cancer progression, which are essential for accurate time-to-event predictions.

In summary, the key research gaps include limited use of nature-inspired metaheuristic algorithms for optimizing GNNs, insufficient generalizability across PAN-cancer datasets, lack of effective multi-omics integration, minimal focus on model interpretability, and underexplored survival-specific modeling techniques. Addressing these issues can significantly enhance the reliability, explainability, and clinical relevance of AI systems in cancer prognosis, paving the way for more robust and patient-specific survival prediction frameworks.

III. THEORETICAL BACKGROUND

Cancer predicts the likelihood of clinical outcomes in patients following diagnosis. Accurate predictions provide decisions regarding the strength of the treatment, treatment strategies, and justification of clinical research. Traditionally, predictions of clinical parameters such as tumor stage, histological degrees, and molecular markers are based[29]. However, these factors alone often allow us to grasp the complete complexity of cancer biology.

1.GNN:Graph Neural Network GNN can directly model complex relationships in biological systems such as gene coexpression networks, protein protein interactions, and multiomics associations, making it highly suitable for cancer research. In survival analysis, GNNS offers a unique ability to include both individual traits and topological contexts. Researchers have developed a variety of architectures. These models can identify biomarkers, stratify patient subgroups, and even discover new ways to engage in cancer progression. This overall view allows the model to capture smarter interactions, leading to more robust and clinically relevant predictions

2.SSDH:Squirrel Search and Deer Hunting Strategies The SSDH algorithm is used for feature selection to identify the most informative genes that significantly contribute to cancer survival prediction. SSDH is a nature-inspired optimization technique that mimics hunting behaviors in nature.The best genes that can forecast survival outcomes are iteratively chosen using this algorithm according to their contribution and relevance. This is how the SSDH algorithm operates:

1) Initialization: Initialisation is done for a population of potential solutions (genes). A subset of the genes chosen for analysis is represented by each solution.
2) Evaluation: Using a predetermined fitness function, the SSDH algorithm assesses each gene subset's fitness in terms of its ability to predict survival outcomes.
3) Search Process: Finding the best gene subsets is done by SSDH through an iterative search process that refines the population until the top-performing subset is found.
4) Selection: For model training, the last subset of genes judged to have the best predictive ability for cancer survival is chosen.

IV. DATA PREPARATION AND PREPROCESSING

A. Data Pre-processing

Preprocessing gene expression data is essential for ensuring clarity, consistency, and analysis readiness. Gene expression data is typically obtained from publically available cancer datasets such as GEO (Gene Expression Omnibus) and TCGA (The Cancer Genome Atlas). Among the preprocessing actions are:

1) Data Cleaning: The process of eliminating inaccurate, outlier, or missing values from a dataset to ensure accuracy.
2) Normalization: Gene expression values are scaled using Min-Max or Z-score normalization to ensure data consistency across genes.
3) Log Transformation: To stabilize and normalize gene expression levels, a log transformation is used.
4) Dimensionality Reduction: Using approaches like as t-SNE or PCA (Principal Component Analysis), you can help minimize the curse of dimensionality while preserving the dataset's most important features.

B. Feature Selection with SSDH

The SSDH algorithm is used to pick the most informative genes for cancer survival prediction. SSDH is an optimization strategy that mimics natural hunting behaviors. This algorithm selects the most effective genes for predicting survival outcomes based on their relevance and contribution. Here's how the SSDH algorithm works:

1) Initialization: involves creating a population of potential fixes or genes. Each answer represents a subset of the chosen genes for analysis.
2) Evaluation: The SSDH algorithm uses a specified fitness function to evaluate each gene subset's ability to predict survival outcomes.
3) SSDH employs an iterative search approach to identify the optimal gene subsets.
4) Selection: To train the model, only the genes with the highest predictive potential for cancer survival are picked.

V. PROPOSED METHODOLOGY

The Squirrel Search Deer Hunting (SSDH)-Optimized Graph Neural Network (GNN)[30] model combines the SSDH feature selection algorithm with a Graph Neural Network (GNN) to predict cancer survival outcomes using pan-cancer gene expression data. This methodology includes data preparation, feature selection with SSDH, graph creation, GNN model development, and evaluation. A detailed explanation of each stage in the process is provided below. Fig. 1 displays the recommended methodology.

A. Models

The proposed model uses a Graph Neural Network (GNN) and a hybrid optimization approach, including the Squirrel Search Algorithm (SSA) and Deer Hunting Optimization

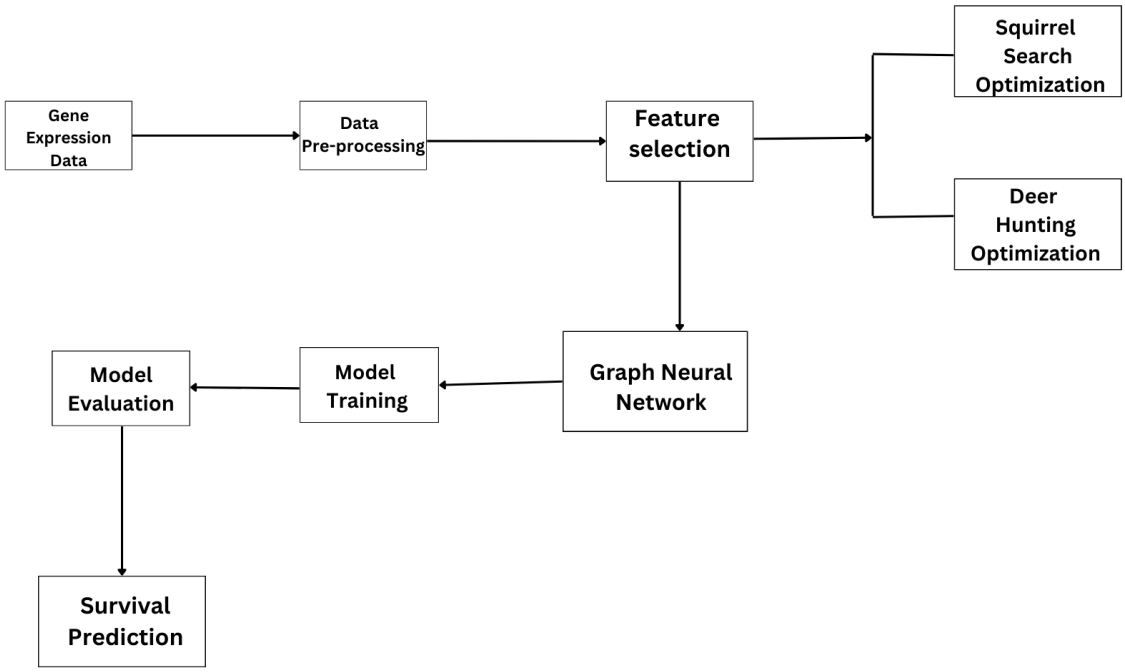

Fig. 1. Flow Diagram of Proposed Approach

TABLE II
MODEL PERFORMANCE METRICS FOR BREAST CANCER

Cancer Type	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
Breast Cancer	98.68	98.76	98.68	98.67

TABLE III
TOP SELECTED GENES AND CLUSTERING PERFORMANCE

Gene	Clustering Accuracy (%)	Number of Clusters	Gene Importance (%)
Gene1	92.3	4	17.4
Gene2	89.7	3	15.8
Gene3	87.5	3	13.3
Gene4	85.9	2	11.6

(DHO), to predict survival using PAN-cancer gene expression data.

B. Equations

To extract meaningful embeddings from the graph, we apply Graph Convolutional Networks. The operation for a single GCN layer is defined as in:

$$H^{(l+1)} = \sigma\left(\tilde{D}^{-1/2}\tilde{A}\tilde{D}^{-1/2}H^{(l)}W^{(l)}\right) \tag{1}$$

SSA-DHO-Based Feature and Hyperparameter Optimization.

$$\min_{F,\theta} \ \mathcal{L}_{\text{Cox}}(Z(F,\theta)) + \lambda \cdot \Omega(F) \tag{2}$$

VI. RESULTS AND DISCUSSION

The SSDH-GNN model exhibited strong accuracy of 98.68%, precision of 98.76%, recall of 98.68%, and an f1-score of 98.67%.

The gene selection process identified key genes crucial for survival prediction. Gene1, which had the highest clustering accuracy (92.3%) and an importance score of 17.4%, played a critical role in survival prediction across the cancer types. Gene2 and Gene3 also showed significant performance with clustering accuracy of 89.7% and 87.5%, respectively. These findings demonstrate the efficacy of the Squirrel Search Deer Hunting-inspired approach in selecting influential features from complex gene expression data.

Overall, the SDH-GNN model demonstrated a solid performance, highlighting the potential of combining graph neural network techniques with heuristic methods inspired by nature to improve survival prediction in PAN-cancer datasets [31], [32]. The results indicate that the SSDH-GNN model can be an effective tool in the clinical domain, providing more accurate survival predictions based on gene expression data. Future improvements may focus on refining feature selection, further optimizing hyperparameters, and extending the model to handle additional cancer types or datasets. Table II shows model performance metrics for breast cancer.

In this section, comparative analysis of SSDH GNN models

further discusses basic methods and attention-based GNN. Visualizations such as Kaplan-Meier survival curves, T-SNE diagrams embed the quality and importance of importance, highlighting the interpretability and robustness of the model. Table III shows top selected genes and clustering performance

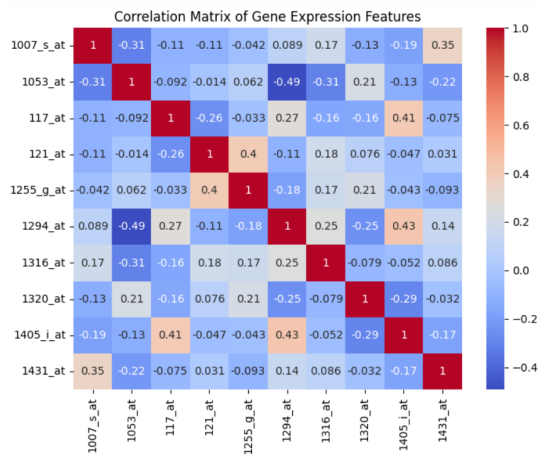

Fig. 2. Correlation Matrix of Gene Expression Data

These results confirm that biologically informed architectural design, coupled with advanced metashoulistic optimization, can significantly improve prediction accuracy and provide wise clinical insights into cancer prediction. Predicting patient survival outcomes using high-dimensional gene expression data has become an increasingly important field of study in arithmetic oncology. The proposed framework, Squirrel Search Brain Hunting Based Diagram Neural. Fig.3 shows Correlation Matrix of Gene Expression Data. Fig.4 shows Ratio of Principal Component Analysis

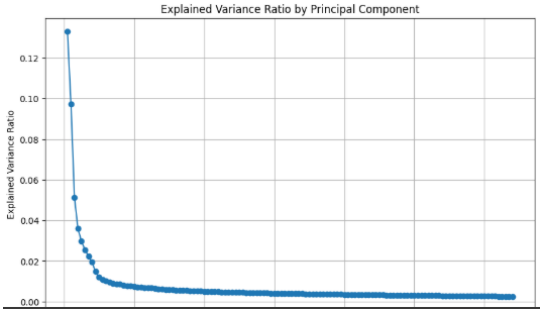

Fig. 3. Ratio of Principal Component Analysis

VII. Conclusion and Future Scope

This paper introduces the Hybrides Deep Learning Framework Search Deer Hunting-Based Graph Network (SSDH-GNN) to use pan-oncogene expression data to predict survival outcomes in cancer patients. This model integrates biologically inspired optimization techniques into GNN's structural learning capabilities and improves the accuracy, relevance and efficiency of survival prediction in several types of cancer. First, we effectively deal with the challenges of high-dimensional gene expression data using deer hunting algorithms for squirrel search and trait selection. These algorithms allow the model to concentrate on biologically important gene subgroups, reducing noise and redundancy, and at the same time improving interpretability. Second, using graph neuronal networks allows models to capture complex gene genres and spatial dependencies that are essential for modeling the heterogeneous nature of cancer. The development of a deer search search brain hunting-based graphics network (SSDH-GNN) for survival prediction using data from deer oncogene survival data shows significant advances in the fields of arithmetic oncology and personalized medicine. Nevertheless, several areas offer further research and improvement possibilities to improve the robustness, interpretability, and clinical benefits of the model. An important future direction is the integration of multi-amic records such as proteomic, epigenomics, metabolomics and gene expression data to convey a more comprehensive understanding of cancer biology and improve the accuracy of survival predictions

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