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Study of Deep and Convolutional Neural Networks for Personalized Chemotherapy Drug Response Prediction

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Abstract: Due to the significant differences between cancer patients, traditional chemotherapy regimens often vary in efficacy and side effects, making it difficult to meet the needs of precision treatment. The rise of deep learning has provided new ideas for drug response prediction and has gradually become a hot topic in personalized treatment research. This review focuses on the application progress of deep neural networks and convolutional neural networks in personalized cancer chemotherapy drug prediction and systematically sorts out the data types, modeling methods, and prediction performances involved in existing studies. This article evaluates the application results of Deep Neural Network (DNN), Convolutional Neural Network (CNN), and their fusion models in cancer drug sensitivity prediction from the perspectives of multi-omics data integration, gene expression image conversion, and time series modeling. By comparing the advantages and disadvantages of various models in processing high-dimensional data, feature extraction capabilities, and generalization performance, this article summarizes the applicable scenarios and limitations of current methods. Studies have shown that DNN has outstanding advantages in multi-omics fusion and complex relationship modeling, CNN is suitable for local feature extraction and image-based gene data analysis, and the Recurrent Neural Network - Convolutional Neural Network (RNN-CNN) model improves the accuracy of time series data modeling. Finally, this article discusses the challenges of model interpretability, data standardization, and clinical transformation and proposes future development directions.

Keywords: Deep neural networks, Convolutional neural networks, Chemotherapy drug response, Personalized cancer treatment, Cancer pharmacogenomics

1. Introduction

Cancer is a leading cause of mortality worldwide, with chemotherapy serving as a primary treatment. Despite being a standard therapy, chemotherapy has inconsistent effectiveness across different cancers. For instance, chemotherapy success rates are 40%-50% for breast cancer and 20%-30% for non-small cell lung cancer (NSCLC), while pancreatic cancer has a response rate below 20% [1, 2]. Notably, NSCLC patients with EGFR mutations respond better to targeted therapies, with success rates exceeding 70% [3]. Additionally, chemotherapy is often accompanied by severe side effects, such as immune suppression, nausea, and organ toxicity, which can significantly impact patients' quality of life. These findings underscore the limitations of standardized chemotherapy and highlight the need for personalized treatment in optimizing cancer care. Advances in deep learning have

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improved cancer prognosis and drug response prediction, enabling more precise, personalized treatments [2].

Deep learning techniques, particularly deep neural networks (DNNs) and convolutional neural networks (CNNs), have emerged as powerful tools for personalized chemotherapy drug response prediction [3,4]. DNNs have shown great promise in integrating multi-omics data, including genomic, transcriptomic, and proteomic data, to identify complex patterns that traditional methods often miss. Liu et al. applied DNNs to the Genomics of Drug Sensitivity in Cancer (GDSC) dataset, achieving a Pearson correlation of 0.912 and an R^2 of 0.831 for drug response predictions, surpassing earlier models [1]. Zuo et al. developed the SWnet model, which combines gene expression, genetic mutations, and cheminformatics features to predict drug responses [3]. Their model, tested on datasets like CCLE and GDSC, achieved 85% accuracy, outperforming previous methods in predicting drug responses across various cancer types. Pang et al. further enhanced drug response prediction accuracy with their DrugGene model, which integrates genomic and chemical structure data [4]. Tested on GDSC, their model reached a 91% accuracy rate. Elwahsh et al. extended this work by applying deep neural learning to cancer prediction, achieving an impressive 93% accuracy across five cancer datasets, showing the model's strong generalizability [5]. Mostavi et al. contributed with CNN-based models, predicting cancer types with high accuracy [6]. Using a combined dataset of 10,340 samples from 33 cancer types in the Cancer Genome Atlas (TCGA), their CNN models achieved accuracy rates between 93.9% and 95.0%, demonstrating their effectiveness in handling high-dimensional gene expression data. Their model also provided valuable insights into cancer marker genes, helping to identify biomarkers for specific cancer types. Despite these advances, challenges remain in ensuring the interpretability and clinical applicability of these models in real-world settings, particularly in terms of data integration and model transparency.

This review explores the application of deep learning, especially Deep Neural networks (DNN) and Convolutional Neural networks (CNN), in predicting chemotherapy drug response to enhance personalized treatment. This study aims to highlight the potential of deep learning in improving personalized chemotherapy treatment.

2. Theoretical background

2.1. Traditional drug response prediction

Traditional drug response prediction methods mainly include statistical models and machine learning methods, which have improved prediction accuracy to a certain extent but also have limitations in data adaptability and interpretability.

Statistical models were widely used in drug response prediction in the early days. For example, the Cox regression model is used to analyze the relationship between gene features and chemotherapy effects, but it is difficult to analyze complex biological mechanisms because it assumes that the effects of all variables are constant [2]. Kaplan-Meier estimation is suitable for survival analysis, but it has limitations in dealing with multi-factor interaction effects. In addition, linear regression and logistic regression are often used to predict drug IC50 values and patient responses to drugs and have been used in cancer drug sensitivity studies, but their ability to handle nonlinear data is limited [7].

As the data dimension increases, machine learning methods are gradually applied to drug response prediction. For example, support vector machines (SVMs) perform well in small-sample genomic data analysis [8]. Random forests (RFs) improve prediction accuracy by integrating multiple decision trees, but the model has low interpretability [9]. In addition, Bayesian networks are suitable for probabilistic modeling, but their high computational cost limits their application in large-scale datasets [2].

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2.2. Deep learning in biomedical applications

Deep learning has gradually become a new trend in drug response prediction with its powerful feature extraction capabilities. A deep neural network is an artificial neural network composed of multiple layers of neurons that can simulate the learning mode of the human brain and extract complex relationships in the data through hierarchical feature learning. Its basic structure includes an input layer, multiple hidden layers, and an output layer, in which the hidden layer uses nonlinear activation functions (such as ReLU) to learn the deep features of the data. Zhu et al. showed that DNN combined with clinical and genomic data can effectively improve the accuracy of cancer prognosis prediction [2].

The convolutional neural network is a deep learning model specifically designed for processing structured data (such as images and gene expression data). Its core components include convolutional layers, pooling layers, and fully connected layers. The convolutional layer extracts key features through filters, and the pooling layer reduces the amount of calculation by reducing the dimension, thereby improving the generalization ability of the model. Yanagisawa et al. showed that CNN can analyze single-cell images to identify chemotherapy resistance and improve the accuracy of personalized treatment [10]. In addition, CNN also performs well in pathological image classification. Mathema et al. found that CNN showed significant advantages in tissue section analysis and cancer classification prediction [11].

At the same time, personalized chemotherapy has shown potential in multi-drug combination optimization, which can accurately evaluate drug synergy and formulate more effective treatment plans for patients [12]. A deep neural network is one of the commonly used deep learning models in personalized cancer treatment. It can effectively integrate structured data such as gene expression and drug sensitivity and mine potential gene-drug interaction patterns. In the study of Liu et al., the Pearson correlation coefficient (Rp) of DNN on the GDSC dataset reached 0.912, and the R^2 value was 0.831, which was significantly better than traditional machine learning methods [1]. Baptista et al. showed that DNN still has high predictive ability on small sample data, especially in drug sensitivity analysis [7]. Zhu et al. further found that DNN combined with genomic and clinical data can improve the accuracy of survival prediction for cancer patients, providing strong support for precision medicine [2].

Convolutional neural networks are widely used in image analysis and genetic data processing due to their powerful feature extraction capabilities. For example, Mostavi et al. trained CNN on the TCGA dataset (containing 33 cancer types and a total of 10,340 samples), and the cancer type prediction accuracy reached 93.9%-95.0%, showing the advantages of CNN in high-dimensional genetic data analysis [6]. In addition, Wang et al. showed that CNN can also be used for multi-omics data fusion to improve the accuracy of drug sensitivity prediction [8]. The deep learning method proposed by Elwahsh et al. achieved a classification accuracy of 93% in five different cancer datasets, further demonstrating the potential of CNN in cancer biomarker identification [5].

In summary, DNN is suitable for integrating multi-omics data, while CNN has advantages in gene expression image conversion and drug response prediction. Combining the characteristics of the two may further improve the accuracy of personalized cancer treatment in the future.

3. Case studies

3.1. Case study 1: multi-omics deep learning models for drug response prediction

Personalized cancer treatment relies on accurately predicting patients' responses to chemotherapy drugs. Ahmed et al. proposed the Enhanced Deep-DR model to integrate multi-omics data and predict cancer drug responses [13]. The researchers collected information from CCLE, TCGA, and GDSC

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databases, including gene expression, mutation, and drug response data, and used principal component analysis (PCA) and autoencoders for dimensionality reduction to reduce redundancy and optimize feature extraction [13].

The model uses a multi-layer, fully connected neural network for training, combined with the ReLU activation function to improve nonlinear expression ability, uses the mean square error (MSE) as the loss function, and introduces batch normalization to accelerate convergence and improve stability. Finally, the model evaluates drug sensitivity through IC50 values (half-inhibitory concentration) and uses five-fold cross-validation to ensure generalization ability.

Experimental results show that Enhanced Deep-DR outperforms traditional deep learning models in terms of Pearson correlation coefficient (PCC) and mean square error (MSE). On different data sets, the model's PCC increased by 5%-12%, MSE decreased by 25%, and generalization ability was stronger. In addition, the integration of multi-omics information significantly improved the accuracy of drug recommendations, especially on breast cancer, lung cancer, and colorectal cancer data sets. Further analysis found that gene mutations such as TP53 and EGFR were significantly correlated with drug response, providing new ideas for future biomarker research.

3.2. Case study 2: CNN-based approaches for chemotherapy drug response prediction

Traditional cancer chemotherapy drug response prediction relies on statistical models and machine learning methods, but the effect is limited due to the complexity of genomic data. CNN can automatically extract features and adapt to high-dimensional data and performs well in cancer drug prediction.

Ahmed et al. used the DeepInsight method to convert gene expression data into 2D images to adapt to CNN processing [14]. The researchers used InceptionV3, Xception, and EfficientNetB7 pre-trained models and combined them with transfer learning for optimization. The data was reduced in dimension by t-SNE to reduce noise interference, and then CNN was used to predict drug response, and the model performance was evaluated by IC50 value. During the training process, the Adam optimizer was used to adjust the learning rate, and data enhancement was combined to improve the generalization ability.

Experimental results show that the Xception model performed best in all test data sets, with a 14%-22% decrease in MSE and a significant reduction in prediction error. In addition, CNN is superior to traditional methods such as random forests and support vector machines in high-dimensional data processing and feature extraction, and is particularly suitable for gene-drug interaction analysis. Further analysis found that KRAS and TP53 mutations have a significant effect on chemotherapy drug response. The model's prediction accuracy on lung cancer and breast cancer datasets is higher than that on colorectal cancer, indicating that CNN is more adaptable to certain cancer types.

3.3. Case study 3: RNN-CNN hybrid model for cancer gene expression analysis

Gene expression data is crucial in cancer research, and CNN is good at extracting local patterns. Thakur et al. extracted gene expression data of breast cancer, lung cancer, kidney cancer, colorectal cancer, prostate cancer, and other cancers based on TCGA and CCLE datasets and constructed a Recurrent Neural Network - Convolutional Neural Network (RNN-CNN) combination model for training [15]. The data was standardized, and redundant features were removed to improve quality and consistency. The study used VGG16 and VGG19 pre-trained CNN to extract spatial features and performed dimensionality reduction optimization before inputting into the Recurrent Neural Network (RNN). RNN uses Bi-LSTM (bidirectional long short-term memory network) for time series modeling and combines it with a fully connected layer for cancer classification. In terms of model optimization, the cross-entropy loss function (Cross-Entropy Loss) is used to calculate the error, the

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Adam optimizer is used for gradient update, and the generalization ability is ensured by five-fold cross-validation.

Experimental results show that the RNN-CNN combination model performs best on multiple cancer datasets, with a classification accuracy of 97.8% for Dataset 1 and 99.4% for Dataset 2, and better stability than ResNet50, InceptionV3, and MobileNet. The study found that CNN is responsible for extracting spatial features, and RNN processes temporal information, which improves the overall prediction accuracy.

Further analysis shows that the model has different effects on different cancer types. The accuracy of breast cancer and lung cancer datasets is the highest, while the prediction accuracy of renal cancer and colorectal cancer is slightly lower, which may be related to the complexity of gene regulation.

3.4. Comparative analysis of different deep learning models

Different models have different data processing methods. As shown in Table 1, DNN uses PCA and autoencoders for dimensionality reduction, CNN converts genetic data through the DeepInsight method, and RNN-CNN combines CNN to extract features and uses RNN for time series modeling.

Table 1: Comparison of different deep learning models in multi-omics data analysis

Model	Method	Feature extraction	Core Technology
DNN (3.1)	Multi-omics data fusion	Directly input gene expression and mutation data	PCA dimensionality reduction, autoencoder, fully connected network
CNN (3.2)	Converting genetic data into 2D images	DeepInsight generates image features	Convolutional layer local extraction, pooling dimensionality reduction
RNN-CNN (3.3)	CNN feature extraction + RNN time series modeling	CNN processes spatial information, and RNN processes temporal information	VGG16/VGG19 feature extraction, Bi-LSTM prediction

The data sources used by each model are different, which affects its scope of application. As shown in Table 2, DNN integrates TCGA, CCLE, and GDSC data, CNN mainly uses TCGA and GDSC, and RNN-CNN relies on TCGA and CCLE for time series data analysis.

Table 2: Comparison of different deep learning models in terms of data sources and processing methods

Model	Data Source	Data processing
DNN (3.1)	TCGA, CCLE, GDSC	Standardization, multi-omics integration
CNN (3.2)	TCGA, CCLE, GDSC	Converting genetic data to 2D images
RNN-CNN (3.3)	TCGA, CCLE	Standardization, time series modeling

Different models have different performances in prediction accuracy. As shown in Table 3, DNN improves PCC and MSE indicators, CNN reduces the MSE error by 14%-22%, and RNN-CNN has the highest classification accuracy of 99.4%, which is suitable for time series data modeling.

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Table 3: Comparison of different deep learning models in terms of predictive performance and applicability

Model	Prediction Accuracy	Advantage	Limitation
DNN (3.1)	PCC increased by 5%-12%, MSE decreased by 25%	Suitable for multi-omics integration and stable training	Reliance on large-scale data, low interpretability
CNN (3.2)	MSE error reduced by 14%-22%	Suitable for gene data conversion, strong local feature extraction	Requires DeepInsight conversion, complex preprocessing
RNN-CNN (3.3)	The highest classification accuracy reached 99.4%	Combining CNN and RNN for time series analysis	Computationally expensive and sensitive to small samples

Different models have their advantages. DNN is suitable for multi-omics data fusion, CNN is suitable for gene expression data conversion, and RNN-CNN is suitable for time series gene data modeling. The choice of method depends on the data type and computing requirements. For example, DNN is suitable for multi-omics integration, while CNN and RNN-CNN are more suitable for local feature extraction or time series data processing.

4. Discussion

Deep learning performs well in predicting personalized chemotherapy drug responses, especially in high-dimensional data integration, feature learning, and generalization capabilities. DNN can integrate multi-omics data to improve the accuracy of gene-drug interaction modeling, CNN structure optimizes gene expression analysis and improves drug sensitivity prediction, and RNN-CNN combined with time series modeling shows potential in cancer classification and progression monitoring [13-15].

4.1. Challenges and limitations

At present, deep learning still faces challenges in predicting personalized chemotherapy drug response, mainly including data quality, model interpretability, and clinical translation issues. These factors not only affect the model's predictive ability but also limit its promotion in actual clinical applications.

4.1.1. Data issues

Deep learning relies on large-scale, high-quality biological data, but cancer multi-omics data still has many limitations. In the DNN multi-omics data fusion model, data heterogeneity and standardization issues affect the stability and generalization ability of the model [13]. In addition, data sparsity and imbalance result in fewer samples of some cancer types, reducing prediction accuracy.

The complexity of data annotation is also a major challenge. In the CNN gene expression image conversion study, the conversion of gene expression data into 2D images may lead to the loss of key information [14]. At the same time, the high-dimensional characteristics of genomic data make the annotation process more complicated, affecting the interpretability and generalization ability of the model.

4.1.2. Model problem

The complexity of deep learning models increases computational costs and reduces transparency in the biomedical field. In the study of RNN-CNN combination models, LSTM performed well in gene

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expression temporal modeling, but it has large computational complexity, long training time, and high hardware resource requirements [15]. In addition, RNN may have a gradient vanishing problem, which affects the ability to learn long sequences.

CNN is mainly suitable for structured data (such as images) but has weak adaptability to unstructured data (such as gene expression matrices). Although CNN solved some problems in case 3.2, it still cannot fully retain information about gene interactions. In addition, deep learning models are "black box" models for that are difficult to provide clear biological explanations for, affecting the trust of clinicians.

4.1.3. Clinical translation issues

Most deep learning models are still in the laboratory stage and lack support from large-scale clinical trials, which limits their ability to be clinically translated. In the study of DNN multi-omics data fusion models, the adaptability of DNN on real patient data remains to be verified. Similarly, CNN and RNN-CNN methods currently lack independent test sets, making it difficult to evaluate their clinical application value.

The application of deep learning in clinical settings is also limited by data privacy, regulatory compliance, and medical ethics. Personalized cancer treatment involves sensitive genomic data, and the balance between data sharing and privacy protection remains a core challenge in the field of precision medicine.

4.2. Future directions

4.2.1. Optimizing model interpretability

The "black box" nature of deep learning limits its application in precision medicine. In the future, explainable AI (XAI) can be introduced to improve prediction transparency. In the study of DNN multi-omics data fusion model, deep neural networks extract gene-drug interaction features, but lack biological interpretability [13]. Therefore, Shapley value, Grad-CAM or Attention mechanism can be used to identify key gene features to make the prediction results more biologically meaningful. In addition, combined with biological pathway analysis of KEGG, GO and other databases, the biomarkers discovered by the model can be further verified.

4.2.2. Multimodal data fusion

Deep learning has achieved good results on a single data modality (such as gene expression and mutation data), but cancer prediction involves a variety of biological data, and multimodal data fusion still needs to be strengthened. In the study of the CNN gene expression image conversion model, the model only relied on gene image conversion to improve feature extraction capabilities without combining other key biological information [14]. In the future, it can explore the integration of multi-source information such as imaging (CT/MRI), clinical data (blood markers), and genomic data to improve prediction accuracy. In addition, the cross-modal deep learning framework (Multi-modal DL) is expected to optimize the integration of multi-omics data and improve the generalization ability of the model.

4.2.3. Standardization and reproducibility

Deep learning faces challenges in data standardization and model reproducibility in biomedical research. Different cancer datasets have data heterogeneity, and models and training data lack unified standards, which affects research reproducibility. In the study of RNN-CNN combination models, the generalization ability of the model on different datasets still needs to be verified [15]. In the future, a

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unified deep learning framework should be established, and a shared data platform should be developed to ensure that different research institutions use the same standard datasets and evaluation methods. In addition, open model parameters, training codes, and pre-trained models will help improve research reproducibility and promote the application of deep learning in precision medicine.

4.2.4. Advancing deep learning models toward clinical trials

Most deep learning models are still in the laboratory stage and lack large-scale clinical trial validation. In the future, independent evaluation with real clinical data is needed to verify the applicability of the model in different populations. For example, in the study of the DNN multi-omics data fusion model, although the model was trained on a public dataset, its applicability in real patient data has not been verified [13]. Therefore, it is possible to cooperate with clinical institutions to collect patient genomic data and treatment response information and conduct cutting-edge research to evaluate the robustness of the model in a clinical setting.

5. Conclusion

This article reviews the research progress of deep neural networks and convolutional neural networks in the prediction of personalized cancer chemotherapy drug response. This article analyzes the data integration method, feature extraction method, and model structure and systematically explores the application performance and scope of DNN and CNN in different types of biomedical data. DNN has good modeling ability in processing multi-omics data and can explore the complex relationship between potential genes and drugs; CNN is more suitable for modeling structured or image data and has advantages in extracting key local features. From the overall effect, these two types of models show high accuracy and stability in drug sensitivity prediction, providing effective support for more accurate drug recommendations and helping to promote the development of cancer treatment strategies towards individualization. At the same time, current research has also exposed some challenges, such as uneven data quality, weak model interpretability, imperfect standardized processes, and insufficient clinical verification, which still need further breakthroughs. Future research can start from improving model transparency, integrating multimodal data, strengthening research reproducibility, and conducting real-world data validation so as to gradually improve the clinical adaptability of the model. With the development of algorithms and the accumulation of data resources, DNN and CNN are expected to play a greater role in personalized cancer treatment and provide more reliable technical support for the implementation of precision medicine.

References

[1] *Liu, P., Li, H., Li, S., & Leung, K. S. (2019). Improving prediction of phenotypic drug response on cancer cell lines using deep convolutional network. BMC bioinformatics, 20, 1-14.*

[2] *Zhu, W., Xie, L., Han, J., & Guo, X. (2020). The application of deep learning in cancer prognosis prediction. Cancers, 12(3), 603.*

[3] *Zuo, Z., Wang, P., Chen, X., Tian, L., Ge, H., & Qian, D. (2021). SWnet: a deep learning model for drug response prediction from cancer genomic signatures and compound chemical structures. BMC bioinformatics, 22, 1-16.*

[4] *Pang, W., Chen, M., & Qin, Y. (2024). Prediction of anticancer drug sensitivity using an interpretable model guided by deep learning. BMC bioinformatics, 25(1), 182.*

[5] *Elwahsh, H., Tawfeek, M. A., Abd El-Aziz, A. A., Mahmood, M. A., Alsabaan, M., & El-shafeiy, E. (2023). A new approach for cancer prediction based on deep neural learning. Journal of King Saud University-Computer and Information Sciences, 35(6), 101565.*

[6] *Mostavi, M., Chiu, Y. C., Huang, Y., & Chen, Y. (2020). Convolutional neural network models for cancer type prediction based on gene expression. BMC medical genomics, 13, 1-13.*

[7] *Baptista, D., Ferreira, P. G., & Rocha, M. (2021). Deep learning for drug response prediction in cancer. Briefings in bioinformatics, 22(1), 360-379.*

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[8] *Wang, C., Lye, X., Kaalia, R., Kumar, P., & Rajapakse, J. C. (2021). Deep learning and multi-omics approach to predict drug responses in cancer. BMC bioinformatics, 22(Suppl 10), 632.*

[9] *Shen, B., Feng, F., Li, K., Lin, P., Ma, L., & Li, H. (2023). A systematic assessment of deep learning methods for drug response prediction: from in vitro to clinical applications. Briefings in Bioinformatics, 24(1), bbac605.*

[10] *Yanagisawa, K., Toratani, M., Asai, A., Konno, M., Niioka, H., Mizushima, T., ... & Ishii, H. (2020). Convolutional neural networks can recognize the drug resistance of single cancer cells. International Journal of Molecular Sciences, 21(9), 3166.*

[11] *Mathema, V. B., Sen, P., Lamichhane, S., Orešič, M., & Khoomrung, S. (2023). Deep learning facilitates multi-data type analysis and predictive biomarker discovery in cancer precision medicine. Computational and Structural Biotechnology Journal, 21, 1372-1382.*

[12] *Partin, A., Brettin, T. S., Zhu, Y., Narykov, O., Clyde, A., Overbeek, J., & Stevens, R. L. (2023). Deep learning methods for drug response prediction in cancer: Predominant and emerging trends. Frontiers in MEDICine, 10, 1086097.*

[13] *Ahmed, H., Hamad, S., Shedeed, H. A., & Hussein, A. S. (2022). Enhanced deep learning model for personalized cancer treatment. IEEE Access, 10, 106050-106058.*

[14] *Ahmed, H., Shedeed, H., Hamad, S., & Saad, A. (2023). Convolutional neural network models for cancer treatment response prediction. International Journal of Intelligent Computing and Information Sciences, 23(1), 98-105.*

[15] *Thakur, T., Batra, I., Malik, A., Ghimire, D., Kim, S. H., & Hosen, A. S. (2023). RNN-CNN based cancer prediction model for gene expression. IEEE Access, 11, 131024-131044.*