How to Cite:
Dubey, A., Mujoo, S., Hannan, S. A., Satpathy, G., Arshad, M. W., & Manikandan, E. (2022). Cancer prediction using RNA sequencing and deep learning. *International Journal of Health Sciences*, *6*(S8), 4925–4939. https://doi.org/10.53730/ijhs.v6nS8.13318

Cancer prediction using RNA sequencing and deep learning

Dr. Alok Dubey
Associate professor, Department of Preventive Dental Sciences, College of Dentistry, Jazan University, Jazan, Saudi Arabia
Corresponding author email: dentaalok@yahoo.com

Dr. Sheetal Mujoo
Assistant professor, Division of Oral medicine & Radiology, College of Dentistry, Jazan University, Jazan, Saudi Arabia
Email: sheetalmujoo@yahoo.co.uk

Shaikh Abdul Hannan
Assistant Professor, Department of Computer Science and Information Technology, Albaha University, Albaha, Kingdom of Saudi Arabia
Email id: abdulhannan05@gmail.com

Gargibala Satpathy
Central Research Laboratory, Sree Balaji Medical College & Hospital (SBMCH), Bharath Institute for Higher Education & Research (BIHER), Bharath University, Chennai, Tamil Nadu, India
Email: gargi.immt@gmail.com

Muhammad Waqas Arshad
Research Scholar, Dept of Creative Technologies, Air University, Islamabad, Pakistan
Email: Muhammad.waqas.arshad.1@gmail.com

E. Manikandan
Central Research Laboratory, Sree Balaji Medical College & Hospital (SBMCH), Bharath Institute for Higher Education & Research (BIHER), Bharath University, Chennai, Tamil Nadu, India & Solid-State Nanoscale Laboratory, Dept. of Physics, Thiruvalluvar University, Vellore, India
Email: manicsir@gmail.com

***Abstract*---**Numerous areas of medical services, including as imaging diagnostics, advanced pathology, emergency clinic confirmation prediction, drug plan, grouping of cancer and stromal cells, specialist help, and so forth, have profited from the utilization of deep learning. Cancer prognosis involves predicting the course of the disease, the

International Journal of Health Sciences ISSN 2550-6978 E-ISSN 2550-696X © 2022.
Manuscript submitted: 9 June 2022, Manuscript revised: 18 August 2022, Accepted for publication: 27 Sept 2022

likelihood that it will spread and recur, and the likelihood that patients will survive. The clinical management of cancer patients will considerably benefit from the precision of cancer prognosis prediction. To better forecast cancer prognosis, modern statistical analysis and Deep learning techniques are being applied, as well as biomedical translational research being improved. In recent years, the processing capacity has significantly increased and the innovation of artificial insight, especially deep learning, has advanced quickly. Cancer is the leading reason for death in people. As a result, cancer detection is essential for early diagnosis and provides the best chance for treating cancer patients in a secure and efficient manner. It is, however, the trickiest way to increase the likelihood of the person surviving. RNA sequencing has significantly advanced in the last few decades and is now a crucial method for transcriptome profiling. The progress from mass RNA sequencing to single-atomic, single-cell, and spatial transcriptome methods has made it conceivable to determine individual cells with ever-more noteworthy precision while additionally including spatial information. Researching and treating cancer, a serious diverse, malignant disease, continues to be very difficult. In numerous areas of cancer exploration and treatment, including biomarker revelation, depiction of cancer heterogeneity and progression, drug deterrent, cancer safe microenvironment and immunotherapy, cancer neoantigens, and others, RNA sequencing has demonstrated a fundamental apparatus. This study has highlighted how RNA sequencing technologies and deep learning techniques can be used to predict cancer. The information used in this study was gathered from secondary sources.

***Keywords*---**cancer, RNA sequencing, deep learning, prediction, prognosis, artificial neural network.

Introduction

In the cutting edge time, cancer has arisen as one of the main sources of death and, in reality (WHO 2012). Oncologists might utilize divided cancers to affirm changes in growth size. The patient's response to treatment can then be gauged using this result, and if necessary, medical aid can be given. One of the urgent components in numerous uses of a clinical picture recuperation framework is the characterization of clinical pictures. When data from highly varied medical images is possible, precise classification methods are needed. Using the CT paradigm, radiologists can accurately recognise and monitor physiological changes during clinical diagnosis. Multiple tissues that are in line with various grey scales on a CT picture may be distinguished, providing information for a medical diagnosis. Cancer is the main source of death in various industrialized nations. Cancer analysis overall practice depends on logical and histological information that might add to loose or wrong ends (Ahmad, 2019).

One of the most dangerous malignant illnesses to human life and health, cancer still involves intricate biological processes that need correct and thorough investigation. Starting from the presentation of high-throughput sequencing in 2005, it has become ready to act top to bottom exploration to explain the genome and transcriptome and to grasp natural exercises at the sub-atomic level. RNA sequencing, particularly single-cell RNA sequencing, is a pivotal part of high-throughput sequencing and gives organic insights regarding a solitary growth cell. It likewise examinations the elements that impact intratumor articulation heterogeneity and pinpoints the sub-atomic reasons for the development of numerous ontological sicknesses. As a result, RNA sequencing provides essential information for the study and treatment of cancer. RNA sequencing will be widely used for research on various kinds of cancer with the beginning of the time of accuracy medication.

The key objectives of cancer prognosis and prediction differ somewhat from those of cancer detection and localization. In terms of cancer prognosis and prediction, three prophetic focuses are important: 1) cancer vulnerability prediction (risk assessment); 2) cancer repeat prediction; and 3) cancer endurance prediction. In the primary occasion, one is endeavoring to predict the probability of having a particular sort of cancer before the sickness shows itself (Bangyal, Hameed, Alosaimi, & Alyami, 2021). In the subsequent occasion, one is endeavoring to gauge the gamble of cancer returning following the sickness' obvious goal. In third instance, after a diagnosis of the illness, one attempts to forecast a result (life expectancy, survival, progression, tumour-drug sensitivity). Within the final two scenarios, the prognostic prediction's effectiveness is obviously influenced by the accuracy or efficacy of the diagnosis. A prognosis for a disease, nonetheless, must be made after a clinical finding, and it should think about additional variables than essentially the determination alone.

Cancer and Its Types

It is a potentially fatal and life-altering condition to have cancer. Fundamentally, the term "cancer" (or "malignancy") refers to a group of more than 200 serious diseases that are characterised by uncontrolled and abnormal cell proliferation. There is a significant lag between the beginning of cancer and the appearance of its symptoms, and it has the potential to metastasis. The spread of cancer to distant body organs and regions is known as metastasis. This makes it a very deadly illness that can damage various body sections of a person. The type, extent, and stage of the cancer, as well as the patient's (victim's) age 121, all affect symptoms, survival rates, medical care provided to the patient, and long-term outlook. To greatly improve survival rates and the likelihood of recovery, cancer must be diagnosed in its early stages. The two primary classifications of cancer are based on the type of cells they develop from and the organ in which they first appear (Chatterjee A, 2018). They are divided into five categories based on the type of cell they originate from: carcinoma, which creates from epithelial cells; sarcoma, which creates from non-hematopoietic mesenchymal cells; lymphoma, which originates from lymphocytes; germ-cell tumours, which develop from germ cells; blastoma, which results from malignancies in precursor cells; leukaemia, which originates from leukocytes or white blood cells; and mal (arises from pigment-containing cells or melanocytes). It can also be categorised according to the area of the body from where they arise (e.g., thyroid cancer, pancreas cancer, brain cancer, breast cancer, and so on). While some malignancies cause cells to grow and divide slowly, others cause tumours to grow quickly.

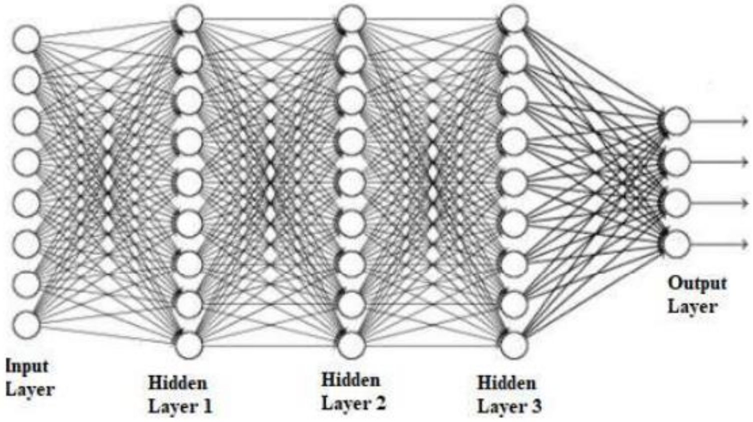
Overview of Deep Learning

Because of advances in model design, PC power, and the outstanding ascent of information obtained by cell and different gadgets, deep learning, otherwise called deep neural network (DNN), has accomplished a few huge advances lately. Regulated learning, solo learning, and support learning are the three principal Deep learning standards. A bunch of preparing information including highlights (data sources) and marks ought to be taken care of into directed learning calculations (yields). SVM, innocent bayes, angle supporting, grouping trees, arbitrary timberlands, and linear and logistic regression are a few well-known supervised learning methods. In classification and regression investigations, these techniques are frequently applied. Then again, unaided learning plans to recognize designs in view of the information appropriations and don't need prior result or marks. The most popular unsupervised learning technique is clustering (e.g., hierarchical clustering, K-means). Word2vec, PCA, and Latent Dirichlet Allocation (LDA) are some of the most modern and well-liked unsupervised learning techniques. The versatility of neural network (NN) learning suggests that it can be either supervised, unsupervised, or semi-supervised. Support learning might be summarized as a prize framework that permits a PC program to search out the ideal response by boosting the prizes.

Numerous artificial neuronal layers that closely resemble the neurons in the human brain make up deep learning (also known as DNN). Similar to linear regression, back propagation using the gradient descent algorithm updates each neuron's weight value to reduce the overall loss function. It was feasible to extricate additional theoretical numerical connections from the information to move to the result by applying nonlinearity using initiation capabilities, for example, sigmoid, tanh, or relu, to the various layers of every neuron (Chaudhary, Poirion, Lu, & Garmire, 2018). Consequently, new unlabeled information can be anticipated utilizing a thoroughly prepared model. Since deep learning is a subfield of Deep learning, it acquires a portion of the central ideas from Deep learning, like essential measurements and likelihood, the misfortune/cost capability, etc, yet it likewise has greater adaptability and can be created to have more complicated layers and various neurons in each layer for worked on prescient capacity. Completely associated NN (or just NN) for organized information, convolutional NN (CNN) for picture information, and repetitive NN (RNN) for text and grouping information are the three kinds of NN that are most often utilized in clinical exploration.

Deep learning has as of late been utilized in biomedical examination to improve protein folding prediction, annotate pathogenicity of genetic variants, and display cutting-edge performance in the process of calling genomic variants. Deep learning works better compared to many cutting edges draws near and is more adaptable and flexible to apply on discrete or ceaseless information than different methodologies. It also requires less feature engineering knowledge than Deep learning as a whole.

Figure: 1. Typical Deep Neural Network



Review of Literature

There are many deep learning and Deep learning methods accessible for cancer location and prediction. The absolute most utilized deep learning strategies are Convolutional Neural Network, Repetitive Neural Network and a few pre-prepared models, for example, Alex Net, Google Net, VGG16, VGG19, ResNet. Probably the most utilized dataset accessible for preparing and testing are Mammogram picture, Diviner, UCI, WBCD. Dongdong Sun et al. have proposed a deep learning (DL) strategy named D-SVM for the prediction of human bosom cancer prognosis. The calculation really gained various leveled and conceptual portrayal from crude information and effectively coordinated customary order technique

Another deep learning-based, multimodel outfit method that utilizes KNN, SVM, Dt's, Rf's, and inclination supporting choice trees has been proposed by Yawen Xiao et al (GBDT). Three distinct types of cancer — LUAD, stomach adenocarcinoma (STAD), and BRCA — were undeniably treated utilizing their proposed approach (Dey, 2014). This technique was executed to prepare every classifier exclusively utilizing the provided information to get predictions, and afterward apply those predictions to a multimodel gathering approach utilizing deep learning. When compared to data produced by a single classifier, this technique more accurately predicts cancer.

An extraordinary streamlined deep learning system in view of paired molecule swarm improvement choice tree (BPSO — DT) and CNN was proposed by Nour Eldeen M. Khalifa et al. The dataset was used in their research to categorise various cancer types, including uterine corpus endometrial carcinoma, lung squamous cell carcinoma, BRCA, kidney renal clear cell carcinoma, and lung adenocarci-noma (UCEC). There were three phases to this strategy. First, relevant features were extracted using BPSO for the feature extraction component. The second phase, which was known as the augmentation phase, sought to address the issue of overfitting data to provide correct findings. The third and final phase, known as deep CNN, uses the connected layer architecture of CNN to categorise different forms of cancer based on input data. Compared to the CNN method, this methodology gave more accurate findings.

Cancer

A wide definition of cancer is a condition in which the body's normal cells proliferate and spread abnormally without being controlled. In a strict sense, one should refer to a new development as a "neoplasm" rather than a "cancer." Neoplasms that solely exhibit limited growth are referred to as "benign" neoplasms. Malignant tumours are defined as those that also possess invasiveness and the ability to metastasize. The term "cancer" is often only used to describe certain types of growth. Even though a tumour is really just a local swelling, the term is frequently and increasingly used to refer to cancer.

Characteristics of benign and malignant tumours

Fibrous tissue frequently surrounds benign tumours, making surgical excision of the entire tumour with it. The cells of a benign tumour closely resemble the surrounding healthy cells at the point when inspected under a magnifying lens. In any case, harmless cancer cells commonly show a more prominent number of cells in the mitotic (jumping) phase of the cell cycle than do typical cells, which display a high level of cells in a development captured or calm stage in the cell cycle (ongdong Sun, 2017). While certain malignant tumours may be encapsulated in the early phases of their development, advanced malignant tumours typically show invasion into the nearby healthy tissues rather than having distinct boundaries. They can also be distinguished from both benign tumour cells and normal cells. They typically have an abnormal number of chromosomes in addition to being mostly in the mitotic phase of the cell cycle (aneuploidy).

Objectives of the Study

The following is a list of the research's current goals:

- Researching and comprehending the use of deep learning in predicting cancer prognosis
- To investigate deep learning methods for cancer prediction.
- To research new RNA sequencing applications and technology.
- To investigate how RNA sequencing techniques can be used to predict cancer.

Problem Statement

Researchers are using Deep learning techniques in the medical area since these techniques have been successful in many other disciplines. In contrast to other fields, the science of medicine greatly benefits from computerised DSS. As a result, there is a growing need for an opportunity for research in the fields of medical DSS and predictive analysis. However, new and alternative scientific design procedures or approaches may be investigated in order to further improve diagnostic performance. Clearly, there is a growing need for an opportunity for study in this area. The approach to categorization that is currently most widely accepted is deep learning (Feng, 2018). The issue tended to here is giving a more modern choice emotionally supportive network for the precise prediction of bosom cancer from different kinds of information, for example, BI-RADS (Breast Imaging-Reporting and Data System) finding, microRNA profiling, FNA biopsy of the breast, etc. and by exploring advanced DL techniques in order to achieve notable improvements in accuracy.

Current Application of Deep Learning in Cancer Prognosis

We surveyed the application of deep learning in the field of cancer prognosis using key terms like "deep learning." In order to find relevant studies, I searched PubMed using the terms "neural networks" and "cancer prognosis." We have included research that developed straightforward NN models with 3-4 levels and studies that constructed DNNs with multiple layers to more readily grasp the advancement of the field and for better correlation. These studies and models were examined and summarised. The articles we looked at could be divided into three divisions depending on the different NN types and whether feature extraction was used: (1) NN models without highlight extraction, (2) Element extraction utilizing multi-omics information to fabricate completely associated NNs, and (3) CNN-based models. Here, we broke down and refined these models and studies (Grumett S, 2003).

NN Models with no Feature Extraction

The Cox corresponding dangers model (Cox-PH), which has lately come up for discussion, is a multivariate semi-parametric relapse model that has been extensively utilised in cancer studies to examine the characteristics of endurance across at least two treatment groups. Early attempts at predicting the prognosis of cancer either built the models using clinical tumour furthermore, patient information, cell highlights from tissue slides, or a few information on quality articulation. These examination assessed the exhibition of NN to that of Cox-PH and additionally Kaplan Meier strategies to show execution, and they showed that basic NN models had equivalent execution to that of these methodologies. Additionally, feature selection was not required in these investigations because the number of features was very low in the absence of omics data.

Feature Extraction from Gene Expression Data to build Fully Connected NNs

High-aspect, short example size, and muddled non-direct impacts between natural parts are signs of wellbeing information. The integrative investigation of multi-omics information is supported by aspect decrease. The experiments that follow have experimented with various strategies to minimise the dimension of sequencing data, extract fewer features, and develop an entirely connected NN.

CNN-Based Models

Lately, deep learning approach has been gained the main headway since cutting edge networks have been assembled utilizing convolutional NN (CNN) and intermittent NN (RNN). Numerous achievement have been displayed in the space of picture acknowledgment/characterization and PC vision by CNN, and normal language handling (NLP) and sequencing information examination by RNN. In particular, extraordinary execution has likewise been seen in numerous clinical regions, including characterization of skin cancer types, distinguishing proof of obsessive histological slides, ID of Aβ plague area in Alzheimer's patients, order of cancer cells from ordinary cells utilizing atomic morphometric measure, and extraction data from electronic wellbeing records (EHR) to foresee medical clinic readmission, mortality, and clinical result. CNN has been used in cancer prognosis reviews to group malignant tissue for endurance prediction or to extract elements for subsequent prognosis (Hsia TC, 2003).

Table: 1. an overview of the various deep learning approaches used for cancer cell segmentation and identification

Problem Areas	Technology used
Brain Tumour	Segmentation of images of brain tumours
Cancer cell and tumour detection	Dataset for CNN Architectures Specifications and Transfer Learning
Prostate cancer detection	Detection using targeted contrast-enhanced ultrasound
Breast cancer	Deep crowd sourcing learning
To identify morphologic chromatin organisation alterations	A decision-aid system
Breast cancer evaluation	Her2Net: A substantial framework for classification and semantic segmentation
Prostate cancer recurrence	Convolutional Neural Networks (CNN)
Histological pictures of colon cancer	Deep Learning with Locality Sensitivity

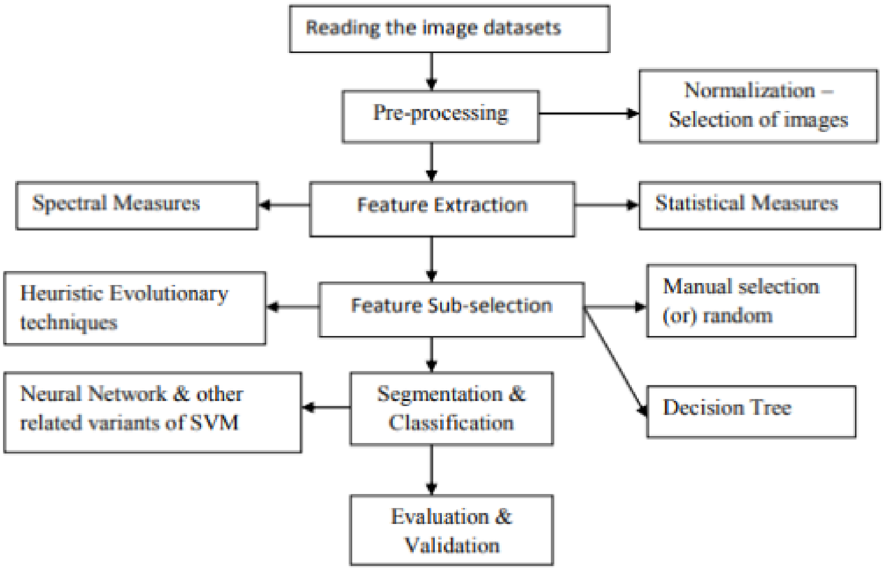
Medical Image Processing

Over the years, the growth in medical image processing has been \sincreasing in a considerable pace. The advancement of biomedical research is made possible by the speed at which diseases associated to different types of cancer and other related human issues are spreading. An expert opinion based on artificial intelligence can help with the decision even though human specialists are accessible to diagnose and anticipate the types of diseases and cancer cells. The applicability of various tools used for determining the pathology of human diseases is relevant in this context. The doctor typically advises the patient to undergo an X-ray, a CT scan, an MRI, and other biomedical signal diagnostic modalities like Echo Cardio Gram (ECG), Electro Encephalo Gram (EEG), and so on in order to receive a professional opinion on the presence of diseases. The usefulness of these diagnostic modalities in achieving an integrated analysis for treatment planning is increasing. At this stage, different medical images are gathered using the aforementioned medical imaging techniques (X-ray, CT, and MRI), and a diagnosis must now be made using these images. For clinical diagnosis, processing and analysis of these medical images are therefore crucial.

Medical image processing performs numerous segmentation and classification processes that are essential for diagnostic and medically related instructional purposes. As a result, the disorders that can be recognised using these processing techniques are appropriately determined. Different imaging modalities are used in conjunction with correct surgeries to address these needs. Medical imaging creates visual representations of a body's interior for clinical analysis, revealing information that would otherwise be hidden by the skin and bones.

In order to recognise problems, medical image processing fundamentally builds a database of normal anatomy and physiology. It should be noted that both grayscale and colour images are used in medical imagery. The number of digital photos taken in recent years has greatly increased thanks to research in digital imaging technology. There are many internet collections of medical photos thanks to the recent trend of picture archival and communication systems in all hospitals (Ismail Saritas, 2011). There are many internet images available for the medical fields of radiology, cytopathology, ophthalmology, gastroenterology, and others. A vital part of every patient's health record is the developed medical images created utilising imaging techniques, which are linked to the necessary computer processing and modification. The many phases of medical image processing are depicted in Figure 2.

Figure: 2. Steps involved in medical image processing



Methodology

Several deep learning algorithms have been utilised in this work to diagnose breast cancer. Pre-processing the data and developing prediction models make up the paper's two main sections. The Wisconsin Breast Cancer Dataset, which is openly accessible to researchers, has been used in this paper. Information investigation and pre-handling, which incorporates strategies like Name Encoder and standardization, are the initial steps. A successful device for changing over the degrees of classification highlights into mathematical qualities is the Name Encoder (Kather, et al., 2019). There is encoding for each classified characteristic. Malignant and benign values have been categorised as 0 and 1 in this study. The values of all the attributes are rescaled in the Normalizer Method to lie between 0 and 1. For this, the following formula is employed.

$$\frac{\boldsymbol{X_i}}{\sqrt{\boldsymbol{X_i}^2 + \boldsymbol{Y_i}^2 + \boldsymbol{Z}^2}}$$

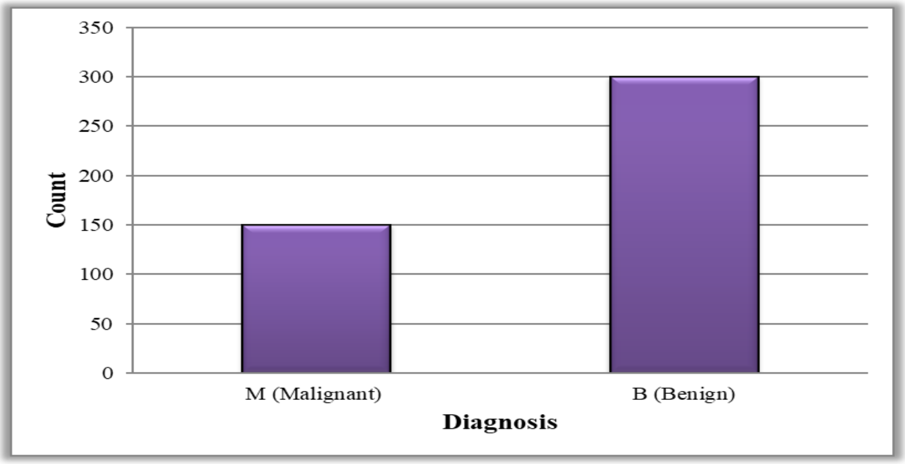
For the purpose of building models, pre-processing is trailed by the division of the information into train and test sets. The excess 25% of the information was utilized for testing, and the leftover 75% for preparing. The outcome of the dataset utilised for this project can be divided into two categories: M (malignant) or B. (benign).

The use of CNN and ANN algorithms is an example of deep learning. A Convolution Neural Network can take in an info picture, give different qualities and items in the picture significance (learnable loads and predispositions), and have the option to recognize them. ANN is the last calculation utilized. Because of their critical attributes, like parallelism, disseminated capacity, and versatile self-learning ability, artificial neural networks are every now and again utilized in science and data innovation. They have also been used to address issues in biomedicine, particularly in the classification and prediction fields.

Data Interpretation

In order to carry out the project, current breast cancer articles prediction was looked at many machine learning approaches. There are learning techniques for cancer discovery and prediction. Pre-handling techniques like Mark Encoder, and the Normalizer Strategy were utilized to proficiently deal with the information. Figure 3's visual chart shows the general number in looking at typical and harmful cells in the dataset gathered in the wake of utilizing the Mark Encoder procedure.

Figure: 3. Number of malignant and benign



Artificial Neural Networks, Convolutional Neural Networks, and Recurrent Neural Networks are three Deep Learning methods that can be used to predict breast cancer. Deep learning models CNN and ANN have been used in this research. The table 2 and 3 make sense of the boundaries used for both CNN as well as ANN models. The numerous boundaries incorporate the quantity of neurons, the amount of information, the quantity of preparing ages, and the enactment capability.

Table: 2. Parameters used in CNN model

Number of Neurons	Con Layer1- 36 Con Layer2- 64
Number of Input 30	20
Number of epochs 50	40
Activation Function	ReLU, Sigmoid

Table: 3. Parameters used in ANN model

Number of Neurons	10
Number of Input	20
Number of epochs	40
Activation Function	ReLU, Sigmoid

Implementation of DeepLNC

Coding transcript sequences and calibrated lncRNA k-mer frequencies are used by DeepLNC as its computational characteristics. To enable performance evaluation on additional large datasets for organisms including Drosophila melanogaster, Escherichia coli, Candida elegans, and Homo sapiens, the algorithm DNN was also evaluated on other biological processes, such as protein-protein interaction. DNN was therefore discovered to be a reliable, quick tool with a better accuracy rate. It is also appropriate for other ncRNAs that lack accurate genome sequences and annotation data. With less boundaries and unrivaled progressive layer-wise capability pressure, the proposed DNN calculation successfully handles non-linearity in information. With the utilization of a sped up gradient learning strategy, it enables global error correction across numerous weight layers (Kumar, 2017). Further, it was noted that the incorporation of cutting-edge optimization methods like Adaptive Learning - ADADELTA, Dropout, and Nesterov's Accelerated Gradient allowed for fast error minimization, excellent predictive accuracy, and minimum overfitting throughout the layers of DNN. Equations below define the standard performance measures that were used to evaluate the prediction performance of our classifier DNN (1, 2, and 3).

A few quantitative characteristics that were determined for the testing information were used to further assess the classifier's effectiveness: True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN). Actual lncRNAs that are accurately predicted are represented by TP, coding RNAs other than lncRNAs are represented by TN, false positives that fall into the lncRNA category are represented by FP, and true non-lncRNA classification errors are represented by FN.

Equations (1, 2, 3, and 4) were used to calculate the metrics Accuracy (ACC), Sensitivity (SN), Precision or Positive Prediction Value (PPV), and Specificity (SP), which show how accurately a classifier can categorise lncRNAs. The Receiver Operating Characteristic curve (ROC) was then plotted for the metrics. The following equations (5, 6, 7 and 8) show how to calculate the false discovery rate (FDR), false negative rate (FNR), fall-out or false positive rate (FPR), and negative predictive value (NPV) in order to improve our results.

Accuracy (ACC) = $\frac{TP+TN}{TP+TN+FP+FN}$ **(1)**
Sensitivity (SN) or True Positive Rate = $\frac{TP}{TP+FN}$ **(2)**
Precision or Positive Prediction Value (PPV) = $\frac{TP}{TP+FP}$ **(3)**
Specificity (SP) = $\frac{TN}{TN+FP}$ **(4)**
False Discovery Rate (FDR) = 1- Positive Prediction Value (5)
False Negative Rate (FNR) = 1-True Positive Rate (6)
Fall-out or False Positive Rate (FPR) = $\frac{FP}{FP+TN}$ **(7)**
Negative Predictive Value (NPV) = $\frac{TN}{TN+FN}$ **(8)**

Result and Discussion

Deep learning methods like Convolutional Neural Networks (CNN) and Artificial Neural Networks (ANN) were used to boost prediction accuracy. The accuracy attained using the CNN model and ANN model, respectively, was 97.3% and 99.3%, which was very successful. Because of the use of enactment capabilities like ReLu and sigmoid, deep learning has proven to be quite effective. Using various high throughput approaches, IncRNAs have been discovered in numerous researches. The characteristics of IncRNA, however, have not yet been accurately framed. Accordingly, it is presently more significant than any other time to make a calculation that is autonomous of highlights that have previously been anticipated and that is easy to use on enormous datasets (López-García, 2020). We sought to apply the traditional k-mer feature in our experiments because it is crucial to have appropriate computational features for classification. The proposed k-mer usage frequencies and entropy estimation were ultimately discovered to be comparatively better elements for identifying IncRNAs. In comparison to shorter ones, a longer k-mer string contains more data. One could argue that DNN is more precise than different classifiers in light of AI.

Conclusion

The research on machine learning has advanced significantly, and it has started to alter our daily activities. Numerous studies using machine learning in the medical field have demonstrated many outstanding successes. Machine learning can keep preparing a model even after additional information opens up, which is one advantage. Additionally, because health care data come in a variety of formats, including text and picture (unstructured) data, clinical (structured) data, genetic data, and expression data, using various NN architectures to address various data challenges is becoming more and more common and beneficial (Mr. Madhan S, 2019).

Various deep learning techniques, CNN, and ANN were used in this work. The accuracy reported by CNN and ANN is 97.3% and 99.3%, respectively. Deep learning models provide good accuracy, according to the paper's conclusion. Additionally the result is unsurprising as far as likelihood in deep learning utilizing Actuation capabilities. In future, comparable methodologies might be conveyed on datasets that comprise of photos. The system might also be connected to a programme or webpage. To make better forecasts, the developed model's accuracy may be raised.

High-throughput RNA- sequence innovation has been a vital device to investigate the transcriptome. The fast progression of RNA- sequence innovation opens up various new fields for research while likewise setting aside time and cash. Nonetheless, RNA- sequence strategy actually has disadvantages that require improvement. An amazingly expansive scope of cancer studies has utilized RNA-sequence (Sarwinda, Paradisa, Bustamam, & Anggia, 2021) . All applications in cancer research rely upon the headway of RNA- sequence advancements, especially the mix of scRNA-sequence and spatial transcriptomics as well as data from various omics, which will bring RNA- sequence advances into single-cell goal and tissue-level transcriptomics and offer new information about cancer conclusion, therapy, and avoidance.

References

1. Ahmad, M, Ding, Y, Qadri, SF & Yang, J 2019, 'Convolutional-neuralnetwork-based feature extraction for liver segmentation from CT images', Eleventh International Conference on Digital Image Processing (ICDIP), P. 1117934.
2. Bangyal, W.H.; Hameed, A.; Alosaimi, W.; Alyami, H. A New Initialization Approach in Particle Swarm Optimization for GlobalOptimization Problems. Comput. Intell. Neurosci. 2021,2021, 6628889.
3. Chatterjee A, Ahn A, Rodger EJ, Stockwell PA, Eccles MR. A guide for designing and analyzing RNA-seq data. Methods Mol Biol. 2018;1783:35–80.
4. Chaudhary, K.; Poirion, O.B.; Lu, L.; Garmire, L.X. Deep learning–based multi-omics integration robustly predicts survival in liver cancer. Clin. Cancer Res. 2018, 24, 1248–1259.
5. Dey, B.K., Mueller, A.C. & Dutta, A. (2014). Long non-coding RNAs as emerging regulators of differentiation, development, and disease. Transcription, 5(4):e944014.
6. Dongdong Sun, M.Wang, H. Feng and Ao Li , "Prognosis prediction of human breast cancer by integrating deep neural network and support vector machine: Supervised feature extraction and classification for breast cancer prognosis prediction", 2017 10th International Congress on Image and Signal Processing, BioMedical Engineering and Informatics (CISP-BMEI)
7. Feng, Y., Yang, F., Zhou, X., Guo, Y., Tang, F., Ren, F., ... & Ji, S. (2018). A Deep Learning Approach for Targeted Contrast-Enhanced Ultrasound Based Prostate Cancer Detection. IEEE/ACM Transactions on Computational Biology and Bioinformatics.
8. Grumett S, Snow P, Kerr D. 2003. Neural networks in the prediction of survival in patients with colorectal cancer. Clin Colorectal Cancer, 2:239-44.
9. Gutschner, T. & Diederichs, S. (2012). The hallmarks of cancer: a long non-coding RNA point of view. RNA biology, 9(6):703-719.

10. Hsia TC, Chiang HC, Chiang D. 2003. Prediction of survival in surgical unresectable lung cancer by artifi cial neural networks including genetic polymorphisms and clinical parameters. J Clin Lab Anal, 17:229-34.
11. Huang Z, Tgavalekos K, Zhao C. 221: AI-driven forecasting of mean pulmonary artery pressure for the management of cardiac patients. Crit Care Med. 2020;48(1):93.
12. Ismail Saritas, “Prediction of Breast Cancer Using Artificial Neural Networks”, Article in Journal of Medical Systems 36(5):2901-7, August 2011
13. Jiang, Q., Wang, J., Wang, Y., Ma, R., Wu, X. & Li, Y. (2014). TF2LncRNA: identifying common transcription factors for a list of lncRNA genes from ChIP-seq data. BioMed Res Int, 2014:317642.
14. Kather, J.N.; Krisam, J.; Charoentong, P.; Luedde, T.; Herpel, E.; Weis, C.-A.; Gaiser, T.; Marx, A.; Valous, N.A.; Ferber, D. Predicting survival from colorectal cancer histology slides using deep learning: A retrospective multicenter study. PLoS Med. 2019, 16, doi:10.1371/journal.pmed.1002730.
15. Kumar, N., Verma, R., Arora, A., Kumar, A., Gupta, S., Sethi, A., & Gann, P. H. (2017, March). Convolutional neural networks for prostate cancer recurrence prediction. In Medical Imaging 2017: Digital Pathology (Vol. 10140, p. 101400H). International Society for Optics and Photonics.
16. López-García, G., Jerez, J. M., Franco, L., and Veredas, F. J. (2020). Transfer Learning with Convolutional Neural Networks for Cancer Survival Prediction Using Gene-Expression Data. PloS one 15, e0230536. doi:10.1371/journal.pone.0230536
17. Mr. Madhan S, Priyadarshini P, Brindha C, Bairavi B, “Predicting Breast Cancer using Convolutional Neural Network”, SSRG International Journal of Computer Science and Engineering (SSRG – IJCSE) – Special Issue ICMR Mar 2019
18. Oh, J. H., Choi, W., Ko, E., Kang, M., Tannenbaum, A., and Deasy, J. O. (2021). PathCNN: Interpretable Convolutional Neural Networks for Survival Prediction and Pathway Analysis Applied to Glioblastoma. Bioinformatics 37 (Supplement_1), i443–i450. doi:10.1093/bioinformatics/btab285
19. Patel, D, Shah, Y, Thakkar, N, Shah, K & Shah, M 2020, ‘Implementation of artificial intelligence techniques for cancer detection’, Augmented Human Research, vol. 5, no. 1, P. 6.
20. Sarwinda, D.; Paradisa, R.H.; Bustamam, A.; Anggia, P. Deep Learning in Image Classification using Residual Network (ResNet)Variants for Detection of Colorectal Cancer. Procedia Comput. Sci. 2021,179, 423–431.
21. Shao W, Wang T, Huang Z, Cheng J, Han Z, Zhang D, Huang K. DiagnosisGuided Multi-modal Feature Selection for Prognosis Prediction of Lung Squamous Cell Carcinoma. In: International Conference on Medical Image Computing and Computer-Assisted Intervention: 13-17 October 2019. Shenzhen: Springer; 2019. p. 113–21.
22. Suvà ML, Tirosh I. Single-cell RNA sequencing in cancer: lessons learned and emerging challenges. Mol Cell. 2019;75:7–12.
23. Veeranki S. R, Varshney M. (2022). Intelligent Techniques and Comparative Performance Analysis of Liver Disease Prediction, International Journal of Mechanical Engineering, 7(1), 489-503. https://kalaharijournals.com/ijme-vol7-issue-jan2022part2.php,

24. Wang, J., Ding, H., Bidgoli, F. A., Zhou, B., Iribarren, C., Molloi, S., & Baldi, P. (2017). Detecting Cardiovascular Disease from Mammograms With Deep Learning. IEEE Trans. Med. Imaging, 36(5), 1172-1181.
25. World Health Organization. Accessed on: Feb 13, 2020. Available: https://www.who.int/news-room/fact-sheets/detail/cancer
26. Zhang, J, Xie, Y, Wu, Q & Xia, Y 2020, 'Medical image classification using deep learning', in Deep Learning in Healthcare, Springer, pp. 33-51.