An Adaptive Convolution Neural Network based Learning for Precision Medicine

Dr.BarakkathNisha U [4], Ms.Aleesha Salim [1], Ms. AyshaNaushad[2] , Ms. Abina P Nassar[3]

[1,2,3] B.Tech ,Final Year CSE, Ilahia College of Engineering & Technology, Mulavoor, Kerala
[4] Associate Professor, CSE, Ilahia College of Engineering & Technology, Mulavoor, Kerala

ABSTRACT

Personalized medicine is also referred to as precision medicine is an approach for disease treatment and prevention by taking individual variability in genes, environment and lifestyle for each person. Learning for personalized medicine means that classifying individuals into sub groups based on the difference in their susceptibility to particular disease or in their response to specific treatment. By combining genomics, using big data analytic and considering population health unique treatments are designed for each individual. Personalized medicine has many applications within health care such as, detection and diagnosis of disease in highly specific manner, Prevention of disease, Reduction of trial-and-error prescriptions.

Keywords: Personalized medicine, drug development, disease characteristics, therapeutics effects, Convolutional Neural Network, Recurrent neural network, Restricted Boltzmann machine, Auto encoders.

1. INTRODUCTION

Personalized medicine is the tailoring of treatments to individuals based on their unique genetic make-up and some other personalized factors.The whole idea of Personalized medicine is based on the unique genetic make-up of each patients it overcomes the limitations of traditionalmedicine. Personalized medicine allows the healthcare providers to predict susceptibility to disease, prescribe more effective drugs, improve disease detection, eliminate trail-and-error inefficiencies, customize disease prevention strategies.With some genetic analysis scientists can customize drugs to make them clearer and more effective.

Advances in personalized medicine on specific application of learning methods in different domains are:

- Drug development: personalized medicine predicts the effectiveness of drugs. Also predicts how an individual will respond to a drug based on the genetic information about that individual. To determine the effectiveness of drugs there are some tests that will predict which of the available drugs will be a great benefit to individual patients.

- Disease characteristics personalized medicine predicts disease susceptibility, disease prognosis or treatment response thereby improves person's health.
- Therapeutic effects: predicting resultspatient-based treatment 'profile or previous medical experience is important a feature of a personalized medicine.In addition, medical effects treatment is usually predicted byto divide patients into groups.

2. LITERATURE REVIEW

2.1 Deep learning

Deep learning strategies are part of machine learning methods based on learning multiple levels of representation and extraction that help to make data comprehension such as images, sound and text.

Over the past few decades, deep learning has emerged as a popular field of study of machine learning. Developments and techniques developed from deep learning have contributed to the extended grade to incorporate key aspects of machine learning and artificial intelligence.Initially encouraged to mimic the way the brain processes signals and information, in-depth study results in the decline of computer vision, speech recognition, language comprehension and processing process.Deep learning is competent in exploring complex structures at high data. Intensive architecture is built by incorporating multiple layers of simple modules. These modules perform off-line tasks to calculate presentations in each class from there in the previous class.Different types of deep neural networks have been used in different contexts and in processing different types of data. With network design and unit operation in a variety of ways, features from different perspectives can be captured and studied. Neural networks are ready to process image and other two-dimensional data such as image and voice. Deep learning has been used for accurate treatment. With the availability of natural data such as clinical images, Deep Learning Electronic Health Profiles bring more accurate predictions before training hidden classes in an unattractive way to capture important interactions and refresh the entire network using the background distribution algorithm to presentations improve accuracy.

2.2 Personalized Medicine

Personalized medicine is also called precision medicine. It is a medical model that divides people into different groups by decisions, methods, interventions and products targeted at each patient based on their predicted response orrisk of disease.Personalizedmedicinehasbeenidentifiedasakeyandprospective approachto"achieveoptimalindividualhealthdecisions".The use of genetic information has played a major role in certain aspects of the drug made for you. Personalized medicine ideas can be used in new and very important ways in health care. Personalized health care is based on the evolution of the biological system and uses predictive tools to determine the importance of health risks and design customized health systems to help patients reduce risk, prevent disease and treat themselves with the highest quality where possible.

2.3 Drug Development

Compared with the traditional measurement presented in omics data, the precise genetics-specific method reveals the mechanisms of deep pathway function and, when used in combination with proteomic, epi-genomics and metabolomics data, can make more informedmedical decisions by exposing twopharmacogenomics predictive biomarkers.In addition to predicting whether the drug responds well to the disease, drug-based drug limitations, morbidity and morbidity and disease severity. Genetic medical information often comes in the form of lines of cancer cells. Early drug sensitivity detection computational algorithms such as expandable network flexibility to analyse cancer cell line data, identify interactions between genes, and predict response signals. Drug indications describe a disease that cannot be cured by a drug. Other studies focus on comparing similar drugs using drugs and drugs and diseases. New pairs of medicines and diseases have been linked to a series of accumulated evidence using stocks. Relationships known as drug addiction are combined with drug-like similarities to make predictable predictions based on the fact that similar drugs may reflect similar diseases. Research is underway to change genetic names for genetic signals to examine genetic similarities by comparing genetic makeup. Disease similarities are assessed phenotypically and genetically. DNN is trained in large-scale written response data to distinguish drug responses and drug reuse. Data from 26,420 drug disruption samples from three cell lines in the Broad LINCS database. Details of drug abuse were documented according to the 12 stages of treatment use and DNN was adopted to address the high magnitude and complexity of the data. The use of DNN presents practical difficulties and opportunities in its broader application, with the careful removal of key data signals. The benefits of receiving a neural network are likely to be a compact and compact computer, robust data management, reproduction and transparency.

2.4 Disease Characteristics

The primary use of personalized medicine is to predict the incidence, recurrence, occurrence, progression, survival, and phenotypes of a disease as one of a person's genetic makeup, lifestyle, and many other factors. In this case, predicting the onset of disease and its onset is important because it reduces the incidence of disease at an early age, improves prognosis and reduces mortality.

In the field of cancer treatment, traditional experiments to detect tumour types before symptoms develop to encourage early treatment no longer meet the need to predict disease, and computerized methods are used to identify disease patterns. The database contains undeveloped SNP data that was converted into binary fragments of 80 patients labelled "pre-set" and "previously not used" SNPs, so the estimate from 3000 SNP data was complex and the result was promising. The same study conducted a screening study for breast cancer in postmenopausal women. The database contained genomic data, family history and age, and genomic data was presented as SNP data.

Unlike the Waddell study, this study uses 11 SNPs from 17 SNP groups linked to certified breast cancer using a pre-selected feature and Feature selection algorithms. . He has developed a new neural network reservoir system, generates local / spectral data model to make personal predictions about the occurrence of stroke. Predictability is a common complication of heart disease, but in some areas such as cancer, recurrence is an important controversial issue as many relapsing patients begin. The recurrence of cancer is traditionally predicted based on the physician's clinical knowledge and patient risk factors. The study

used SVM, decision-making tree C5.0 and over-the-counter machine to identify risk factors and predict the recurrence of cervical cancer patients. The data set included 679 patients and included 193 variables such as epidemiological, clinical and pathological data. The same study examined the C4.5 DT, SVMand ANN phase models to predict breast cancer recurrence after 2 years and produced an accuracy of 93.6%, 94.7% respectively. And 95.7%. Input features come from clinical, imaging and genome data, and the feature selection algorithm has been used to eliminate unnecessary features and features with 90% of missing data. The study was published to combine protein contact data with gene expression data to editgenetic data and screen for active gene-related pairs.

In other studies, genetics has also been used to replace cancer-specific data generated by microarray data. One of the oldest and most widely used methods comes from the study, which used 70 genetic markers to predict breast cancer prediction for 295 patients and found a accuracy of 0.62. Other studies focus on using clinical data such as patient history, laboratory analysis, ultrasound parameters and microarray data to predict breast cancer survival. The Bayes network has the advantage of integrating a wide variety of data sources and automatically selecting the appropriate features and consequently used for this purpose. Another study also used the Bayesian Belief Network model to predict colon cancer survival. Stage, category, race, age of diagnosis, etc. Use a collaborative training algorithm under guidance to predict breast cancer survival based on similar factors. The reading method uses marked and unmarked data. Data are not labelled for standard clinical practice. Together he trained SSL membership models to create so-called tokens, and trained the network until the number of unmarked data points stabilized. An unrecognized feature algorithm was detected to search for unwritten data models and did not require prior knowledge. An unused unseen-based study algorithm has been applied to 700,000 patients at Mount Sinai Database and can predict the risk of developing various diseases.

2.5 Therapeutic Effects

Personalizing the drug does not require only selected medications that fit the patient well. In many cases, drug-free treatment programs can be compared to specific individuals depending on the patient's profile. The study used a neighbourly method k to collect the same characteristics of the patient and thus determine the appropriate treatment. As the sample size increases, it shifts to the Basezi realm, focusing on measuring different treatment outcomes using random forests of communication trees. Communication trees have the advantage of dealing with complex interactions, explicitly evaluating processing based on integrated interactions, and collecting data effectively using a comprehensive model. The study also mimicked the proposed algorithm for randomized clinical trial data from a head-to-head test and revealed the results of how much head points changed in each patient after treatment. Successfully predicting treatment outcomes based on the patient's profile or prior medical knowledge is an important aspect of personalized medicine.

The study, conducted under the strict supervision of a bi-clustering algorithm using convex optimization, was developed to identify patient clusters and prioritize high profile or previous medical experience is important a feature of a personalized medicine. Expandable network adopted to increase the level of clinical suitability.

In other cases, an alternative classification algorithm is used to divide the patient subgroups and efficacy has been achieved. The optimal number of partitions was determined by optimizing accuracy. The main

advantage of this method is the increase of number of partitions included in the dataset, which increases accuracy. The DBN was structured so that the natural materialsbegan to be assembled through many layers of hidden flexibility and created together with a hidden model for combining standard functions. An uncontrolled learning algorithm, variation of variance, was used to generate parameter values. The algorithm was then tested on a set of ovarian cancer data and a set of breast cancer data, which included data on genetics, DNA methylation and miRNA expression. Clinical data includes survival time, recovery time again the answer to drugs were used in conjunction. The results of the subgroup classification were confirmed by principal component analysis and it was shown that the divided groups have significantly different genomic signatures and different survival function genetics, DNA methylation and miRNA expression. Clinical data includes survival time, recovery time again the answer to subgroup division problem and in manipulating highdimensional and diverse data, and it's potential medical use for you is promising and critical.

3. PROPOSED METHODOLOGY

Customized medicine collects a large amount of information, from age, weight, blood pressure, medical history and genomic data, everything is different for each patient. Dealing with such a number of details for the production of medicine a treatment plan that goes beyond what a doctor does based on experience. Data is too large in size, size, and they are not rebuilt inhomogeneous. So a computer program is used. Ngu sing the "read program" constantly updates the file the required information therefore continues to produce the file current treatment solution based on various data from laboratory tests and electronic medical record. The details are then entered into the action plan indicate the patient's current medical condition. It's a way of system with variable flexibility with development in medical science. Personalized medicine has a wide range of application in the field of health care. Various types of deep network networks have always existed used in a variety of contexts and is subject to variations data types .Teems from various features are captured and learned by building networks and neural activity in different methods.

For example, Convolutional Neural Networks (CNNs) are suitable for processing other visuals two-dimensional data such as image and speech. Repeat neural networks (RNNs) show high results in successive data. Boltzmann Prohibited Equipment (RBMs) deep-framed models that are very helpful improve modelling and faster file integration netuning category or has limited training details. It's Deep learning architecturesare;

- Convolutional Neural Network
- Recurrent Neural Network
- Restricted Boltzmann Machine
- Auto Encoders

3.1 Convolutionalneural network

In deep learning, CNN is a class of deep neural network most commonly to analysing visual imagery. With straightforward medicine CNNs showprominence in exploit the local integrationof Multilayerperceptron's usuallymean fullyconnectednetworks, that is, each neuron is in a pathway connected to the entire following neurons layer. CNNs relativelylittle theinput data also shows such image-based diagnoses such as radiology pathology and dermatology. CNNs regularized of layer. CNNs use relatively little pre-processing compared to another image classification algorithm. This means the network is learning tooptimize thefilters (orkernels) through automatedlearning,This is independence from previous knowledge and from man feature removal intervention is a great benefit.

3.2 Recurrent neuralnetwork

RNN area class ofartificialneural networksthatcanprocessa sequence of inputsindeep learningand retains it'sstate whileprocessing thenext sequenceof inputs. RNNs distinguish themselves from other feeds networks by themselves circular communication, which creates feedback issues in hidden layers, so allow historical details in persist in RNN hidden countries. Therefore, RNNs are best suited for time-related processing data and use consecutive information. The term "recurrentneuralnetwork"issuedindiscriminatelytorefertotwo broadclasses ofnetworkswith asimilargeneralstructure, where onefiniteimpulseandthe otherisinfiniteimpulse.Bothclasses of networksexhibit temporaldynamicbehaviour.Afiniteimpulse recurrentnetwork isa direct acyclic graph that can be opened and replaced withstrictlyfeedforward neuralnetwork,while aninfinite impulse recurrentnetworkisdirected cyclicgraphcannotbeunrolled.

3.3 RestrictedBoltzmannMachine

Restricted Boltzmann Machine prohibited the machine (RBM) is a neural synthetic stochastic artificial a network that can read distribution opportunities over installation space. RBM Neurons form an unstructured object bipartite graph with two units of units (visible with units hidden in sequence). Connection only available at in all layers and no internal communication. It is an algorithm useful for dimensionality reduction, collaborative filtering, feature learning and topic modelling. Stacking RBMs can form Deep Belief Networks (DBNs) where RBMs serve as machines for unattended features. DBNs can be further trained through guidance to tune deep lead network. There are many applications of DBNs as drug availability. DBNs can be used innetwork both internal and external aspects and learn the hidden multi-platform genomic and clinical presentationsdata from multiplatform.

3.4 AutoEncoder

The Encoder is a dual unreadable learning model component: encoder and decoder. Encodercompresses the inputandproduces code,the decoderthen re-construct the input onlyusingthiscode.Itaims finding hidden patterns through training to reduce reconstruction error. A lot different AE such as De-noising Auto Encoder, variation Auto Encoder Sparse Auto Encoder]. It is designed to improve their photography ability very important information and rich readingPresentations. Prescribed AEs are also used wiselypre-training to start instruments. Features studied byunattended paths illuminate what may be unknown a different layout and grip feature in the file profitable data structure to select and select

appropriate presentations in multi-un situations refined, unconventional and un labelled clinical data, too ultimately leading to higher predictability.

4. CONCLUSION

Personalized medicine is one of the most promising approaches to tackling the diseases that have effective treatment or cures. The advent of Personalized medicine provide direct, predictable and effective health care tailored to each patient. Personalized medicine uses each patients unique genetic make-up it sometimes overcome the limitations of traditional medicine. The previous medical approaches have been using the policy "one size fits all" providing same treatment for those with same disease, while personalized medicine using the policy different treatment for people with same disease based on their genetic and other features. Personalized medicine has many other applications such as detection and diagnosis of diseases in highly specific manner and categorizing them by genetic variation rather than by symptom, prevention of disease, and reduction of trail-and-error prescription.

REFERENCES

[1] A Madani, R. Arnaout, M. Mofrad, and R. Arnaout, "Fast and accurate classification of echocardiograms using deep learning," arXiv preprint arXiv:1706.08658,(2017)

[2] L. Deng and Y. Liu, Deep Learning in Natural Language Processing. Springer Singapore, (2017)

[3] M. H. Segler and M. P. Waller, "Neural-symbolic machine learning for retro synthesis and reaction prediction," Chemistry-A European Journal, vol. 23, no. 25, pp. 5966–5971,(2017)

[4] E. M. Antman and J. Loscalzo, "Precision medicine in cardiology," Nature Reviews Cardiology, vol. 13, no. 10, p. 591, (2011)

[5] E. Gawehn, J. A. Hiss, and G. Schneider, "Deep learning in drug discovery," Molecular informatics, vol. 35, no. 1, pp. 3–14, (2016)

[6] C. Doersch, "Tutorial on variational auto encoders," arXivpreprintar Xiv:1606.05908, 2016.

[7] T. Jo, J. Hou, J. Eickholt, and J. Cheng, "Improving protein fold recognition by deep learning networks," Scientific reports, vol. 5,p. 17573, (2015)

[8] K. Simonyan and A. Zisserman, "Very deep convolutional networks for largescale image recognition," arXiv preprint arXiv:1409.1556, (2014)

[9] D. Yu and L. Deng, "Deep learning and its applications to signal and information processing [exploratory dsp]," IEEE Signal Processing Magazine, vol. 28, no. 1, pp. 145–154, (2011)

[10] G. E. Hinton, "Deep belief networks," Scholarpedia, vol. 4, no. 5, p. 5947, (2009)

[11] G. E. Hinton and R. R. Salakhutdinov, "Reducing the dimensionality of data with neural networks," science, vol. 313, no. 5786, pp. 504–507, (2006)

[12] L. Hopkins and C. R. Groom, “The druggable genome,” Nature eviews Drug discovery, vol. 1, no. 9, p. 727, (2002)