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A State-of-the-Art Survey of Deep Learning Techniques in Medical Pattern Analysis and IoT Intelligent Systems

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Article Info

Extended Abstract

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*Corresponding Author's Email Address: safari.aref@gmail.com Deep learning techniques have been concentrated on medical applications in recent years. The proposed methodologies are inadequate while medical applications' evolutionary and complex nature is changing quickly and becoming harder to recognize. This paper presents a systematic and detailed survey of the deep learning techniques in medical pattern analysis applications. In addition, it classifies deep learning techniques into two main categories: advanced machine learning and deep learning techniques. The main contributions of this paper are presenting a systematic and categorized overview of the current approaches to machine learning methodologies and exploring the structure of the effective methods in the medical pattern analysis based on deep learning techniques. At last, the advantages and disadvantages of deep learning techniques and their proficiency were discussed. This stateof-the-art survey helps researchers comprehend the deep learning field and allows specialists in intelligent medical research to do consequent examinations.

Introduction

The applications of the modern A.I. sub-domain, such as machine learning (ML) and deep learning (DL), have been growing fast in recent years. ML covers a broad area of research. Many methods have been developed like Bayesian, clustering, decision tree, and deep learning [1]. Artificial neural networks and the DL methods are specific ML tools that simulate the functionality of the neurons in the human brain cells. The numerous deep learning methods benefit the big data available and accomplish tasks including classification, clustering, prediction, segmentation, and anomaly detection. Various deep learning techniques have been beneficial in medical imaging and image analysis for the diagnosis and prognosis of life-threatening illnesses such as lung cancer, breast cancer, and brain tumor, which stand as a tedious task and error-prone for specialists and doctors when performed manually [2]. Medical images are processed using these DL methods to resolve tasks like segmentation, prediction, and classification with accuracy bypassing experts' capabilities. According to the size of the data, it has been revealed that for the small size of the

datasets, traditional ML algorithms achieved extraordinarily as compared to the neural network models. However, the outcome has been drastically changed for large amounts of data where DL techniques perform much more reliable and outstanding. The traditional healthcare decision-making system is fully dependent on experts' experience. It is time-consuming, leading to a high error rate in such a model. The overall performance of ML tools for a small dataset is outstanding. However, ML algorithms and their related models do not perform well for big data and large datasets. Hence, the era of ML is further explored, and DL makes a paradigm shift with many reliable consequences for big data, especially in medical applications and pattern analysis. Table1 shows a summary of the application and research area of ML and DL in medical pattern analysis, respectively.

Research Area	Applications	Methodology
Medical Imaging and Processing	Neural cell classification Brain tissue classification AD/MCI classification Tissue classification Cell clustering Hemorrhage detection Organ segmentation Tumor detection	CNN DBN Deep Neural Network Deep auto- encoder GAN DBM LSTM DCIGN
Bioinformatic Systems	Hand gesture recognition Obstacle detection Bioinformatics Gene selection Gene classification Gene variants detection/prediction Cancer Diagnosis R.N.A. binding D.N.A. methylation Compound protein interaction	DBN Deep Neural Network Deep auto- encoder GAN DBM LSTM DBN CNN
Pervasive Sensing Systems	Anomaly detection Biological parameter monitoring Human activity recognition by videos	Deep Neural Network CNN DBN
Medical Informatics	Data mining and pattern analysis Human behavior monitoring Disease prediction	Deep auto- encoder DBN RNN
Health Monitoring	Lifestyle disease prediction Air pollutant prediction Infectious disease detection Demographic information prediction	DBN LSTM CNN/ DBN Deep auto- encoder

Table -1: Application and research area of ML and DL in medical pattern analysis

I. Packages, Datasets, and Development of the CAD Systems based on DL

In the medical field, accurate prognosis or diagnosis of illness or anomalies are challenging tasks. Thus, ML tools with automated or semi-automated computer-aided diagnosis (CAD) systems play an excellent role in diagnosing illnesses or anomalies for medical experts to prepare accurate treatment scheduling or make decisions. [3,4]. With the improvement of A.I. technologies, CAD systems based on ML and DL perform better than manual procedures, and the system's outcome is helpful for experts to make good decisions. The working framework of three different health monitoring models [5-8] is shown in Fig. 1. From the detailed study of literature, it has been analyzed that there are so many study areas in medical and health monitoring where ML algorithms and DL techniques are appropriate. From the study of literature associated with ML algorithms and DL techniques in medical pattern analysis, it has been found that most of the research was confirmed on a self-collected dataset. Table 2 shows a summarized list of the famous software packages that implement DL-based methods. Collecting datasets from hospitals and laboratories is a time-taking process and extensive work. Therefore, the list of open-access datasets for medical study and research is presented in Table 3.



Fig.1: Comparison of Traditional CAD System (a), ML CAD System (b) and DL CAD System (3).

Table-2: Software packages that provide DL-based	methods
implementation	

Package	License	Interfac e	Platfo rm	Creator
Neon [9]	Apache 2.0	Python	Linux, O.S.X.	Nervan a System s
Keras [10]	M.I.T	Python	Linux, Win, O.S.X.	Franois Chollet

Torch [11]	BSD	Lua, LuaJIT, C	Linux, Win, O.S.X., Andro id, iOS	Ronan Collobe rt et al.
Theano [12]	BSD	Python	Cross- platfo rm	Universi t'e de Montr'e al
TensorFlow [13]	Apache 2.0	Python	Linux, O.S.X.	Google Inc
Wolfram Math [14]	Propriet ary	Java, C++	Linux, Win, O.S.X., Cloud	Wolfra m Researc h
Deeplearnin g4jK [15]	Apache 2.0	Java, Scala, Clojure	Linux, Win, O.S.X., Andro id	Skymin d
CNTK [16]	M.I.T	Comma nd line	Linux, Win	Microso ft
Caffe [17] FreeBSD		C++, Python, MATLA B	Linux, Win, O.S.X., Andro id	Berkele y Center

Table 3:Open access datasets and libraries for medical research

Dataset	Descriptio n	Source	
TCGA	The cancer genome atlas has genomic, transcripto mic, epigenomi c, and proteomic data	https ://www.porta l.gdc.cance r.gov/	
NLST	It has S.C.T. screening images and a lung cancer progressio n dataset	https ://www.biome try.nci.nih.gov/cdas/learn /nlst/image s/	
LIDC	Lung images database Consortiu m contains lung screening thoracic C.T. scan	https ://www.wiki.cance rimag ingar chive .net/displ ay/Publi c/LIDC-IDRI	
LUNA	Lots of C.T. images are in this	https ://www.luna1 6gran d- chall enge.org/data/	

	dataset	
ALL-IDB	It is a new and public dataset of microscopi c images of blood samples	https ://www.homes .di.unimi .it/scott i/all/
DRIVE	Digital Retinal images for extraction. It contains 40 images of the retina	https ://www.isi.uu.nl/Resea rch/Datab ases/DRIVE /downl oad.php
LIDC	Lung image database consortiu m. C.T. scan images of the lung for detection of lung cancer	https ://www.wiki.cance rimag ingar chive .net/displ ay/Publi c/LIDC-IDRI#
ADNI	ADNI dataset contains data of Alzheimer' s disease patients	https ://www.adni.loni.usc.edu/dat a-sampl es/acces s-data/
INbreas t	115 cases with 410 images, 90 cases are from women with both breasts, and 25 cases from mastecto my patients	https ://www.medic alres earch .inesc porto .pt/breas trese arch/ index .php/Get_INbre ast_Datab ase
DDSM- BCRP	2620 scanned film contain normal, benign, and malignant cases with verified pathology informatio n	https ://www.eng.usf.edu/cvprg /Mammo graph y/DDSM/ BCRP/bcrp_mass_01.html

Mini- MIAS	3369 mammogr ams of 967 patients. It is classified based on lesion type, morpholog y, breast tissue and pathology type	https ://www.mammo image .org/datab ases/
EPILEPS IAE	More than 200 patients with epilepsy	https ://www.epile psy.uni- freib urg.de/datab ase
lmage CLEF	CT images and biomedical images	https ://www.image clef.org
NLM's MedPix	A free online Medical Image Database with over 59,000 indexed and curated images from over 12,000 patients	https://medpix.nlm.nih.gov/h ome
TCIA	TCIA is a service that de- identifies and hosts an extensive archive of medical images of cancers.	https://www.cancerimaginga rchive.net/
Re3Dat a	Re3data is a global registry of research data repositorie s covering research data from different academic disciplines.	https://www.re3data.org/

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II. Research Background

This section briefly reviews some essential and significant Deep learning methods in pattern analysis, including DNN, CNN, RNN, DBN, DSN, LSTM, and DAN. Also, Table 2 summarizes research done in the past for the medical fraternity using ML and DL techniques in medical image pattern analysis. Depending on whether labels of the training dataset are present, deep learning can be roughly divided into supervised, unsupervised, and semisupervised learning. In supervised learning, all training images are labeled, and the model is optimized using the image-label pairs. The optimized model will generate a likelihood score for each testing image to predict its class label. The model will analyze and learn the underlying patterns or hidden data structures without labels for unsupervised learning. Suppose only a small portion of training data is labeled. In that case, the model learns the input-output relationship from the labeled data. The model will be strengthened by learning semantic and finegrained features from the unlabeled data. This type of learning approach is defined as semi-supervised learning. Also, we summarize some DL-based methods that can be combined with different learning paradigms for medical pattern analysis in Table 4.

A. Deep neural network (DNN)

In this architecture, at least two layers allow nonlinear complexities. Classification and regression can be carried out here. The advantage of this model is generally used because of its extraordinary accuracy. The drawback is that the training method will not be easy since the error is transmitted back to the past layer and becomes low. Also, the model's learning behavior is too late.

B. Convolutional neural network (CNN)

This model could be best suited for 2D data. This network consists of a convolutional filter for transforming 2D to 3D, which is quite strong in performance and is a rapid learning model. For classification process, it needs a lot of labeled data. However, CNN faces issues, such as local minima, slow rate of convergence, and intense interference by humans.

C. Recurrent neural network (RNN)

RNN.s can recognize sequences. The weights of the neurons are spread through all measures. There are many variants such as LSTM, BLSTM, MDLSTM, and HLSTM. The RNN-based methods include state-of-the-art accuracies in character recognition, speech recognition, and other natural language processing-related problems. Learning sequential events can model time conditions. The disadvantage is that this method has more issues because of gradient vanishing, and this architecture requires big datasets.

D. Deep belief network (DBN)

Deep Belief Networks are a graphical, generative portrayal; all the possible qualities that can be produced for the current situation are created. It is a combination of likelihood and measurements with neural organizations, and A.I. Deep belief networks comprise a few layers with values, where the layers have a relationship but not qualities. The essential target is to assist the machine with characterizing the information into different classifications. The drawback of this architecture is that the initialization process makes the training expensive.

E. Long short-term memory Network (LSTM)

The LSTM was pulled out from ordinary neuron-based neural association models and introduced the possibility of a memory cell. In 2014, an improvement of the LSTM was introduced with the gated recurrent unit. This model has two entryways, discarding the yield entrance present in the LSTM model.

F. Deep autoencoder (DAN)

Applicable in the unsupervised learning process, this could be helpful for dimensionality reduction and feature extraction. Here the number of inputs is equal to the number of outputs. The advantage of the model is that it does not need labeled data. Various kinds of autoencoders, such as denoising autoencoder, sparse autoencoder, and Conventional autoencoder, are needed for robustness. Here it needs to give pre-training steps, but training could have vanished.

Table 4: Summary of most practical ML and DL techniques in medical image pattern analysis

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ML/DL Models	Architecture	Description
Recurrent Neural Network (RNN)		RNN remembers its input due to an internal memory, which makes it ideally suited for machine learning problems that involve sequential data
Long Short- Term Memory (LSTM)		An extension of RNN.s extends the memory. LSTM is well suited to learn from essential experiences with long- term lags and remember inputs over a long time.
Deep Auto Encoder Network		A deep autoencode r is composed of two symmetrica I deep- belief networks. The layers are restricted

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III. Medical Imaging Pattern Analysis

Medical imaging in health informatics brings many ML, DL and AI-based techniques to medical pattern analysis to provide healthcare systems. A broad spectrum of multidisciplinary medical pattern analysis systems has grown over the last decades from routine clinical practice to advanced human physiology and pathophysiology. The objective of medical imaging informatics is thus to improve the reliability, efficiency, accuracy, and of services within the medical enterprise concerning medical image applications procedures and exchange throughout complex healthcare systems. In that context, linked with the associated technological advances in big-data image processing and electronic health records (EHR) analytics, context-awareness, and visualization, a novel era is emerging for medical imaging in pattern analysis based on DL-based techniques prescribing the way through the

precise medicine. Table 5 shows the summary of imaging modalities characteristics

Table-5.	ummary of imaging modalities characteristics				
Tech nolo gy	Visualiza tion	Ana tom ies	Dimensi on	Suita ble DL	
X- Ray	No.	Wid e rang e of org ans	2D and 2D+t	DDN CNN GAN DBM RNN	Al1 Osteo Detect
CT- Scan		Wid e rang e of org ans	2D, 3D and 4D	DNN CNN GAN	Al1 Head CT Lung Al Liver Al AmCA D-UT
Ultra soun d		Wid e rang e of org ans	2D, 2D+t, 3D and 4D	LSTM CNN DNN	iCAD DiA Cepha sonics
MRI		Wid e rang e of org ans	3D and 4D	DDN CNN GAN DCIG N	IcoBrai n Lung AI Liver AI AI1
Nucl ear		All ora ns with radi oact ivat e trac er upt ake	2D, 3D and 4D	DDN CNN GAN	Al1 MiE IBC
Micr osco py		Pri mar ily biop sies and surg ical spe cim ens	2D, 3D and 4D	DDN CNN GAN DBM	Paige Al NMMI Exalta LAS X

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Review of Recent DL Techniques in Medical Pattern Analysis

IV.

In [18], a Deep Embeddings (D.E.) architecture has been proposed for medical image processing. The authors work on histopathology digital scans with large-size images containing valuable information at the pixel level. As they described, the content-based comparison of these images is a very challenging task. Their study proposes a content-based similarity measure for highresolution gigapixel histopathology images with an expansion of cosine vector similarity to a matrix. Each image is divided into same-size patches with a meaningful amount of information in their work. Its similarity is measured by extracting patch-level deep embeddings of the last pooling layer of a pre-trained deep model at four different magnification levels, namely, 1x, 2.5x, 5x, and 10x magnifications. Another important work in medical imaging with deep CNNs, is proposed in [19]. Their primary focus is finding a solution to minimize the gap between semantic information in an image and numerical features. Their study was performed on C.T. images which are usually considerably smaller than digital pathology images. Although they achieved high accuracy in retrieval, their method is limited to small-size images. On the other side, some researchers presented a self-supervised deep learning method of image similarity learning that employs ResNet-50. However, it does not offer any finite valued measure for images as a comparison [20].

In [21], they presented the Fine-Tuning and training of densenet for histopathology image representation using TCGA diagnostic slides. In their study, they propose a new network, namely KimiaNet, that employs the topology of the DenseNet with four dense blocks, fine-tuned and trained with histopathology images in different configurations. They used more than 240,000 image patches with 1000 ×1000 pixels acquired at 20 ×magnification through the proposed "high- cellularity mosaic" approach to use weak labels of 7126 whole slide images of formalin-fixed paraffin-embedded human pathology samples publicly available through The Cancer Genome Atlas (TCGA) repository. Also, they tested KimiaNet using three public datasets, namely TCGA, endometrial cancer images, and colorectal cancer images, by evaluating the performance of search and classification when corresponding features of different networks are used for image representation. Besides these steps, they designed and trained multiple convolutional batch-normalized ReLU (C.B.R.) networks, showing that KimiaNet provides superior results compared to the original DenseNet and smaller C.B.R. networks used as a feature extractor to represent histopathology images.

In [22], the authors work on the histogram of cell types with an automated deep learning approach for bone marrow cytology. They have developed an end-toend deep learning-based technology for automated bone marrow cytology. Their work automatically detects suitable regions for cytology and subsequently identifies and classifies all bone marrow cells in each region. This collective cytomorphological information is captured in a novel representation called Histogram of Cell Types (H.C.T.), quantifying bone marrow cell class probability distribution and acting as a cytological and patient fingerprint. Their work achieves high accuracy in region detection, cell detection, and cell classification. H.C.T. has the potential to revolutionize hematopathology diagnostic workflows and probably lead to more costeffective, accurate diagnoses in precision medicine. In [23], the authors proposed an unsupervised detection of lung nodules in chest radiography using GAN. They devolved and evaluated P-AnoGAN, an unsupervised anomaly detection method for lung nodules in radiographs. Their proposed model modifies the fast anomaly detection GAN (f-AnoGAN) by operating an advanced GAN and a convolutional encoder-decoderencoder pipeline. The training of their model uses just unlabeled healthy lung patches extracted from the Indiana University chest x-ray collection. Their model robustly identifies patches covering lung nodules in external validation and test data with ROC-AUC of 91.17% and 87.89%, respectively.

In [24], the authors present a deep-evolutionary computation of hyperdimensional deep embedding spaces of gigapixel pathology images. They developed a new evolutionary method for whole slide images (WSI) representation based on large-scale multi-objective optimization (LSMOP) of deep embeddings. They used a patch-based sampling to feed KimiaNet a histopathologyspecialized deep network and extract many feature vectors. Then they applied the Coarse multi-objective feature selection to reduce search space strategy guided by the classification accuracy and the number of features. They validate the proposed systems based on The Cancer Genome Atlas (TCGA) images regarding WSI representation, classification accuracy, and feature quality. Also, their work presents a novel decision space for multicriteria decision-making in the LSMOP field for optimal patch-level visualization and increasing the interpretability of in-depth features. On the other hand, the authors developed an evolutionary deep feature selection for compact representation of gigapixel images in digital pathology [25]. They presented a hybrid model to characterize histopathology images, compactly representing a gigapixel whole-slide image (WSI) via salient features to enable computational pathology is still an urgent need and a significant challenge. They proposed an original WSI characterization method to signify, search and classify biopsy specimens using a compact feature vector (C.F.V.) extracted from many deep feature vectors. Also, they presented a low-cost stochastic technique to optimize the output of pre-trained deep networks using evolutionary algorithms to generate a very small set of features to represent each tissue/biopsy accurately. They envaulted the performance of their proposed model using WSIs from the publicly available TCGA image data. Figure 2 and Figure 3 shows the architecture of the proposed model in [24] and the procedure of creating the M.F.V. and C.F.V. in the proposed model of [25].

In [26,27], the authors present a Deep Interval Type-2 Fuzzy LSTM (DIT2FLSTM) model for predicting COVID-19 incidence, including new cases, recovery cases, and mortality rates in both short and long time series. Their proposed model was evaluated on real datasets produced by the world health organization (WHO) on top highly risked countries for both short-term and long-term. The proposed model in [26] was applied to a well-known standard benchmark, the Mackey-Glass time series, to show the robustness and proficiency of the proposed model in uncertain and chaotic time series problems. Their results were evaluated using a 10-fold crossvalidation technique and statistically validated through the t-test method. Another work in Covid-19 pattern analysis was introduced in [28]. They proposed DL-based solutions for COVID-19 diagnosis using computerized tomography (CT) images and 12 cutting-edge DL pretrained. Their proposed model is trained on 9,000 COVID-19 samples and 5,000 standard images, which is higher than the COVID-19 images used in most studies.

[29] present a multimodal deep learning model for cardiac resynchronization therapy response prediction. Their deep learning framework has been applied to a cardiac resynchronization therapy (CRT) response prediction from 2D echocardiography and cardiac magnetic resonance (CMR) data. Their proposed method first uses the 'nnU-Net' segmentation model to extract segmentations of the heart over the full cardiac cycle from the two modalities. Then, a multimodal deep learning classifier is used for CRT response prediction, combining the two modalities' latent spaces of the segmentation models. For the test procedure, their framework used 2D echocardiography data. At the same time, they evaluated their pipeline on a cohort of 50 CRT patients for whom paired echocardiography/C.M.R. data. Similarly, in [30] the authors proposed a deepquantitative medical image analysis methods applied on brain tumor diagnosis. Their work presents a deep learning approach based on soft-max activation function to obtain more reliable medical image diagnosis results.



Fig.2: The architecture of the proposed model in [23]; The process of EMOFS is represented as a separate block.



Fig. 3: The procedure of creating the MFV. and CFV in the proposed model of [24].

Table 6: Summary of state-of-the-art research in medical
pattern analysis with DL-based methods

Method	Dataset	Research Area
Deep Embeddings (D.E.) [18]	KIMIA-NET	Digital pathology and digital histopathology scans
Deep CNN [19]	Private CT images	Digital pathology
Self-supervised deep learning [20]	ResNet-50 Dataset	CT Scan Image Processing
Fine-Tuning and training of deep densenet system [21]	KIMIA-NET and TCGA repository	Histopathology image representation
histogram of cell types with deep automated learning [22]	1247 bone marrow aspirate WSIs of the Hamilton Health Sciences.	H.C.T. and bone marrow cytology

P-AnoGAN unsupervised anomaly detection [23]	Indiana University chest x-ray collection	Lung nodules in radiographs
Deep- evolutionary computation of hyperdimension al embedding spaces of gigapixel pathology images with a WSI-LSMOP of deep embeddings [24]	The Cancer Genome Atlas (TCGA) images	Pathology image processing
Evolutionary- deep feature for compact representation of gigapixel images [25]	TCGA image dataset	Digital pathology
Deep Interval Type-2 Fuzzy LSTM (DIT2FLSTM) model [26]	Official world organization of health (WHO) covid-19 time series dataset	Prediction of the COVID-19 pattern of incidences, including new cases, recovery cases, and mortality rate
Deep Fuzzy LSTM model [27]	Short and long time series of covid-19 official dataset	COVID-19 patterns prediction and analysis for short and long term
DL-based solutions for COVID-19 [28]	diagnosis using computerized tomography (CT) images and 12 cutting-edge DL pre-trained	Chest X-Ray images for covid-19 pattern analysis
Multimodal deep learning model [29]	Response prediction from 2D echocardiograp hy and cardiac magnetic resonance (CMR) data	Cardiac resynchronizati on therapy response prediction.
Deep Quantitative Network [30]	Private CMR Dataset	Brain tumor analysis

Conclusion

Deep learning methods have grown an essential role in recent years in machine learning and pattern analysis, especially in medical applications. In this research, we have drawn how deep learning techniques have enabled the development of more capable solutions in medical

pattern analysis by allowing the automatic generation of features that reduce the amount of human intervention in this process. However, a significant amount of information is encoded in structured data such as E.H.R.s, which provide a detailed picture of the patient's past, pathology, treatment, diagnosis, outcome, and the like. In the case of medical imaging, the cytological notes of a tumor diagnosis may include compelling information like its stage and spread. This information is beneficial to acquiring a holistic view of a patient condition or disease and improving the quality of the obtained inference. Robust inference through deep learning combined with artificial intelligence could ameliorate the reliability of clinical decision support systems. However, several technical challenges remain to be solved. Patient and clinical data are costly, and healthy control individuals represent a significant fraction of a standard health dataset. Deep learning algorithms have mainly been employed in applications where the datasets were balanced or, as a workaround, in which synthetic data was added to achieve equity.

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