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Implementation of Machine Learning (ML) in Biomedical Engineering

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Abstract

The subfields within AI have been discussed throughout the article and the findings of the article have provided a positive outcome. ML has a huge potential through ML methodologies such as supervised and unsupervised learning as discussed in the article. However, supervised learning requires only labeled data while unsupervised learning has the potential to identify the hidden characteristics of the data. The clinical predictors that have been provided through "NN model" and "DT model" have the potential through determining the small datasets within biomedical engineering that further helps medical practitioners or healthcare professionals to decide on the medicine and treatment required for a patient.

Index Terms

Biomedical Engineering, Machine Learning, ML Model, Nanoscale

INTRODUCTION

The research article encompasses two most important terms that are machine learning (ML) and also biomedical engineering where ML is a subfield within artificial intelligence (AI technology) where a machine is assumed to possess the capability of imitating human behaviour. As AI has already been incorporated within the healthcare industry and biomedical engineering revolves around applying the principles and also problem-solving techniques associated with engineering to medicine thus, there is a connection between ML and biomedical engineering. The main aim of the research is to implement ML within the field of biomedical engineering. Algorithms within ML have been trained to figure out different patterns along with correlations within datasets [1]. The datasets help in considering decisions and making predictions based on the results. The methods of deep learning have been utilised in medical imaging where algorithms in deep learning aim to run the data in several layers within algorithms of neural networks where each data passes through simple representation towards the next layer.

Deep networks have helped in achieving best results as per recognition, prediction and classification of medical data where healthcare professionals have been able to cope with diverse complex problems that have been considered to be time-consuming, and difficult to resolve in reality. It is seen that biomedical signals have been utilised for designing and developing human interfaces, which is an evolving branch of biomedical engineering. There is a system that has been developed for people with disabilities that is a "***hands-free head-gesture-controlled interface***" [2]. This machine helps send messages and helps visually impaired people to manage travel aids. Two methods are used in the system where signals have been recorded through a "***three-axis accelerometer***" while a "***three-axis gyroscope***" is used for calculating statistical parameters. The second technique revolves around analysing the signal samples that have been recorded through the "***Inertial Measurement Unit***" (IMU), which is an essential device for measuring and reporting gravity and also angular rate of a particular object. Pitch, immobility, yaw, and others can be evaluated thus, IMU sensors can be used within biomedical engineering.

Medical imaging that includes "***biomedical signal acquisition***" is important not only within diagnostics yet in therapy as well to monitor the impacts [1]. The huge amount of datasets that have been generated through diagnostic devices has certain difficulties for exploration and in terms of analysing the data. The creation of "***automatic data analysis systems***" have been detected with various problems, which is the reason that the system has been implemented with different methods of ML. Thus, an automatic system cannot work alone unless it is supported by ML to further identify the complex patterns in large datasets. However, there are some issues with ML where sometimes ML fails to provide quality and quantity of data. Faulty programming through ML results in offering incorrect data where the accuracy of the results may get affected.

There is another difficulty with ML as per generalising the data, which is a complex problem. The most important challenge for deploying ML is about understanding the ML systems and their related performance tasks as part of the inputs [3]. There is a requirement for using a sample of training data that represents new cases to generalise it. However, usage of non-representative training data may provide inaccurate predictions. Tendency of ML to capture noisy and also inaccurate data within the training dataset is a problem that requires an understanding of ML systems for deriving the results. The problem of overfitting within ML takes place because of utilising non-linear models utilised in algorithms of ML. However, this issue is resolved through linear and parametric algorithms.

REVIEW OF LITERATURE

ML and biomedical engineering

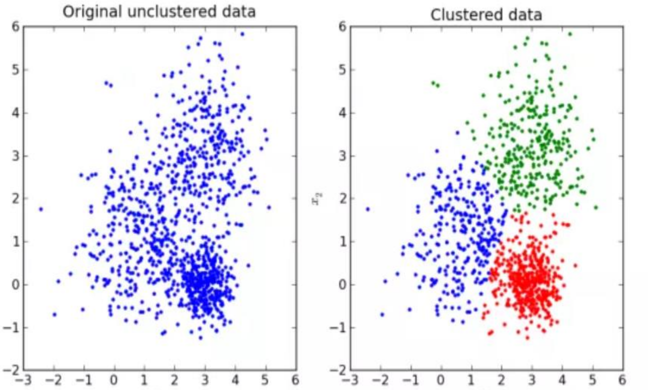

Figure 1: Clustered data [4]

ML is an essential subset within AI that has certain steps for the prediction of data that includes "***data collection***", "***feature engineering***", "***data preparation and exploration***", "***model selection***", "***model evaluation***", "***model training***" and others. [4] opined that the selection of the appropriate ML model is most important for figuring out the solution that also depends on the ML problem type that can be classified as "***unsupervised learning***", "***reinforcement learning***", "***association rules***" and others". "***Unsupervised learning***" can be categorised into two different types such as clustering and also association rules where clustering revolves around an arrangement of unlabeled data into similar groups according to the similarity and dissimilarities. Association rules figure out certain relationships among the essential points within the datasets where these points occur together within a dataset.

Biomedical engineering is a subset within the field of bioengineering that makes use of different practices within engineering for different healthcare practices through the help of designing various medical devices. [5] argued that engineered materials that have been used are biomaterials for therapeutic and diagnostic purposes. As biomedical engineering is a multidisciplinary field that uses concepts and design standards of engineering in medical biology for making advancement in human health. Therefore, the areas have been highly dependent on possessing knowledge regarding human anatomy and also physiology to provide solutions through biomaterial designs, which have been manufactured and integrated within the body to enhance tissue repair and tissue replacement.

ML in nanoscale biomedical engineering

ML has empowered biomedical engineering by optimising performance by modeling the data without much dependence on strong assumptions. [6] stated that datasets within nanoscale biosystems have been huge and complex for mentally parsing. ML has helped analyse as well as extract insights through enhancing the discoveries on the structures and materials for further supporting the communications and networks within nanoscale. There have been certain challenges identified in nanoscale biosystems that have been resolved through ML, especially through important categories. "***SOTA ML methodologies***" have been utilised in nanoscale biomedical engineering that further have been reviewed. One of the important challenges ("***Structure and Material Design and Simulation***") within material science is about understanding the structural properties. The complexities even become worse in terms of nanomaterials as these nanomaterials embrace various properties from bulk components. These nanomaterials are assumed to be heterogeneous structures that consist of various materials.

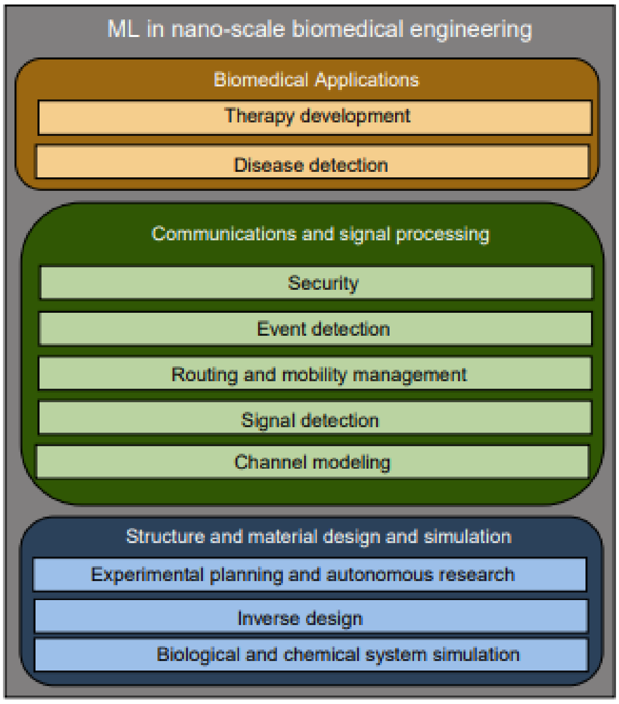

Figure 2: “ML within nanoscale biomedical engineering” [6]

The optimisation of structures and also materials after discovering the properties and behaviours through simulations and experiments have led to multi-parameters and multi objective issues that can be resolved through ML. ML aims to create associate configurations of atomic and molecular systems that will be performed through acquiring knowledge of experimental data. [6] argued that “***communications and Signal Processing***” is another challenging area where nano-sensors have been used for monitoring and detecting tasks. Size of those nanosensors has been around “***1−100***” nm, which has been referred to as macro-molecules and also bio-cells. Choosing the size and material is difficult in respect of system performance as constrained by target area, safety concerns and others. These nano-networks have been incorporated within the human body for communication with biological processes to collect information.

“***Molecular communications***” (MC) systems may support those nano-networks through communications by ***terahertz*** (THz) band however, there is a need for a model for THz communication among the nana-sensors for simulation and also for performance assessments. [7] opined that these nano-networks have a limitation in communication ranges and in processing power which can be resolved through ML where ML will offer tools for modeling space-time trajectories within nanosensors even within the complex environment of a human body. ML methodologies used in biomedical engineering are "***supervised***" and also "***unsupervised***" learning. The methodologies of "supervised learning" need labeled data for training.

The objective revolves around mapping out the input data for output labels. A mapping function “(x)” that can be increased through scoring function is “$f(x_n, y_n)$” where $n \in [1, N]$ (n is the sample within the input data and yn represents label within xn, N is the size within that training data). “***Unsupervised learning***” methodologies figure out the hidden characteristics and also structures within the data without dependency on the training sets. [7] argued that these methodologies have been extensively utilised in discovering chemical and also biological properties within the nano-scale structures and nan-scale materials. However, there is a disadvantage of the methodologies as it is impossible to obtain standard accuracy of the output in the wake of absence of training datasets.

ML in wearable devices within biomedical engineering

Collection of biological data through wearable sensors which includes “***ExG signals***”, “***electroencephalography***” (EEG), “***photopletysmography***” (PPG), “***speech signals***”, “***surface electromyography***” (sEMG) and others have gradually resulted in the processing of complex and heterogeneous data. [8] opined that detection through human activity along with diagnosis and prognosis of various patients on account of manual investigation of those chosen data that has been obtained through sensors have been complex and also time-consuming. In such a scenario, there is a requirement for an intelligent system for decision-making whereas neuroimaging techniques that include "***structural magnetic resonance***" (sMRI), and "functional MRI" are a productive diagnosis of the disease. "***Magnetic Resonance Imaging***" (MRI) is an imaging technology that helps in the production of three-dimensional anatomical images in biomedical engineering.

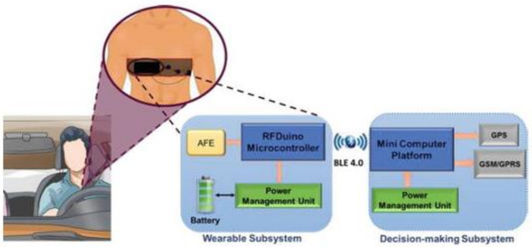

Figure 3: Wearable device [9]

Wearable devices have been prepared for various applications that include "***real-time detection of heart attack***", monitoring of blood pressure and others. ML algorithm diagnoses the patient's condition wearing those wearable devices. [9] argued that there are certain steps for understanding the condition that involves hardware designing that includes selection of sensors followed by characterisation, and communication with the subsystem on decision-making. The other steps emphasises on usage of algorithm design in ML that involves feature extraction, training, testing and others.

The use of wearable devices can be better understood through an example where a “***wearable prototype system***” has been developed for monitoring the “***real-time heart attack***” through the help of two different subsystems. [9] mentioned that the two subsystems have been considered wearable subsystems and also decision-making subsystems according to the above image. "***Wearable sensor subsystem***" is found responsible for getting the signal acquisition, wireless transmission, digitisation and others of ***Electrocardiogram*** (ECG). In this aspect, ML algorithms have been trained according to the classification of ECG real-time where "***MIT-BIH ST Change Database***" has helped in identifying both the normal and the abnormal subjects.

METHODOLOGY

ML algorithms possess a “***degree of randomness***” within the training and also initiation routines. “***Random starting point***” has been assumed to be significant for enhancing convergence of the algorithms; however, there is a negative aspect of the algorithm stability and also on the generalisation that becomes pronounced with the availability of small training samples. The ML algorithm that has been trained for a small dataset will provide mismatched output patterns based on a random initial condition. The ML model also encounters erratic fluctuations according to performance [10]. Introduction of multiple run methods has the potential to offer means for comparisons between ML models enabling subsequent optimisation. Certain instances have been trained with the initial conditions. The ML model performance has been evaluated through different instances and not through a specific instance.

The optimal design has been evaluated through the comparison of the average performances of those runs within the ML models where individual instances are not able to be compared [10]. An optimal model has been chosen therefore, the performing instances of that design have been used in the form of a final model. ***Neural Network*** (NN) (subset within ML) have been used for predicting the “***Compressive Strength***” (CS) within the trabecular bone of the human body in terms of severe osteoarthritis through regression model while ***Decision Trees*** (DT) (supervised learning algorithm) have been used for predicting “***acute antibody-mediated rejection***” (ABMR) within the kidney transplants according to the pre-operative indicators through classification model. Application of both NNs and DTs shows that the strategy of selecting optimal models to obtain the best performance has been differing as the best performing instance of NN/DT has been chosen to be the predictive model. The comparison between various ML models through the utilisation of multiple runs provides a different result from using NN/DTs.

The size of the model run or the number of NN/DT model instances is influenced by the required balance between computational efficiency and expected performance precision. More time and memory are required for the simulation of a larger run. It has been identified that the maintained performance consists of the "minimum size" of runs up to three decimal points and the values are 600 for "DTs" and 2000 for "NNs" [10].

It is impractical to validate an ML model to operate regression tasks with a small dataset and concerning random effects. It has been observed that conventional methods including the "cross-validation approach" can be unreliable when there are limited samples of the independent test [10]. Therefore, it becomes crucial to go for an alternative approach to validate regression tasks through the ML models by considering the random effects of small data.

Based on the success of the surrogate data in nonlinear and biomedical applications it has been proposed to use surrogate data as a small dataset for the validation of ML models in regression tasks. These surrogates generate from random numerals to interpret the distribution of the actual dataset for individual components of the "***input vector***". In reality, the surrogate does not maintain the intricate interconnection between the variables of the original dataset when resembling real data according to standard deviation, mean and range [10]. Thus, effective "***real-data models***" are preferred to ensure significant performance compared to "***surrogate data models***".

In this ML framework, the validation related to the "***surrogate data***" is assumed in terms of multiple runs. It is used for comparing the actual data of the "NN model" related to the "optimal design" with the NN model of the same design related to surrogate data co considering a run of "***2000 NN instances***". The above experiment is replicated with 10 runs which involves a total "of 2000 NNs" for improving robustness [10]. This ML "regression model" can be tested and trained based on the surrogate data to create a benchmark to validate the "real data model". If the "surrogate model" achieves the highest performance then a lower performance can be expected from the "real data model".

"Biomedical engineering" has developed significantly over the years due to the innovation and application of advanced technologies in the biomedical field. As a result, the study of neuroscience becomes much improved in terms of benchmarking and predictions. "Machine learning" (ML) technology has brought revolutionary improvements in neuroscience and neural coding which are going to be illustrated in the below section.

Neural decoding: Several standard ML approaches are used for "neural decoding" including the "linear Wiener filter", Kalman filter, Wiener cascade (no online), and different neural networks [11]. However, the use of modern "neural networks" in biomedical science and neural coding has become the most effective ML approach in recent times.

Neural encoding: It helps in understanding how signals from the brain or neurons react to the external variables with the tuning of curve analysis. "***Generalised linear model***" (GLM) of ML technology is widely used in successful "neural encoding" [11].

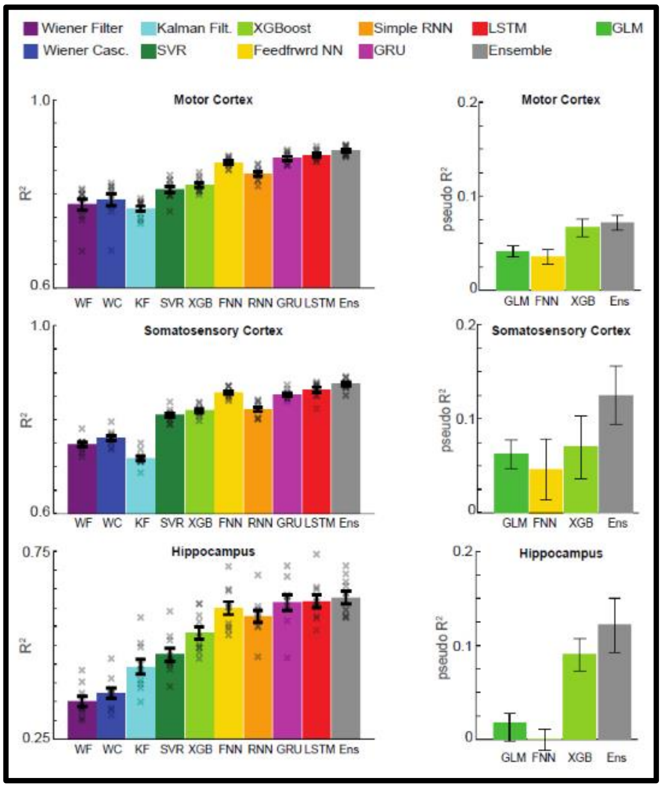

Figure 4: "Neutral decoding" (left), and "neural encoding" (right)[11]

RESULTS AND DISCUSSION

Result

The small dataset has been possessing the features of the domain of biomedical engineering where complexity along with high expenses have restrained the availability of samples. It has been proclaimed that ML has the potential to provide an indispensable tool for biomedical problems containing heterogeneous data. The "NN model" has been designed to make predictions of CS within an "***osteoarthritic trabecular bone***" that has been obtained from "***micro–CT indications***" in respect of morphology, interconnectivity, patient's gender, age and others [10]. The dataset has been composed of "35 human femora" whereas the samples have been segregated as training samples consisting of 22 samples and validation based on 6 samples that have been utilising random permutation whereas the rest of samples have been considered for testing out 7 samples.

The size and nature of the data have been considered where the NN model has been considered to be the base of the CS model possessing 5 input and 1 output features. 1*5 is the input vector where x has been stacked in a way that x_1 = "***Structure Model Index***" (SMI), x_2= "***trabecular thickness***" considered as Tb, Th, x_3= "***bone volume densit***y" considered as “BV, TV”, x_4= “***age***” while $x_{5=}$ ***“gender***" [10]. NNs have been trained by utilising "***Leverberg-Marquardt backpropagation algorithm***”, the result in the form of NN model has been formulated mapping output as y in “MPa” towards the input vector “x” as follows:

$$y = \tanh\left[\bar{x} \cdot IW + \overline{b_{(1)}}\ \right] \cdot \overline{lw'} + b_{(2)} \qquad (1)$$

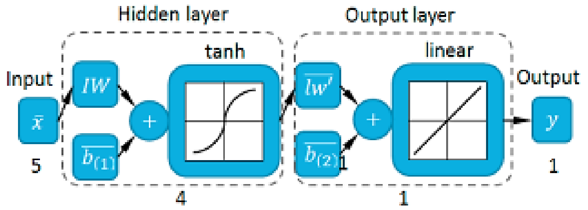

Figure 5: “NN model topology and configuration of layer of a 5D input vector”[10]

The above typology and layer configuration show that there is a hidden layer containing 4 neurons and also a single output as a neuron. Optimal NN has made a prediction of CS having "***root-mean-square error***” (rmse) as ***0.85 MPa***. However, factors on linear regression as R is present among “***actual and predicted CS***" have been around 99.9% within the dataset and also around 98.3% on those regression and classification tests. Real data on NNs have outperformed comparison with surrogate NNs in terms of a correspondence increase as presented as $\mu(R_{\text{all}})$ [10].

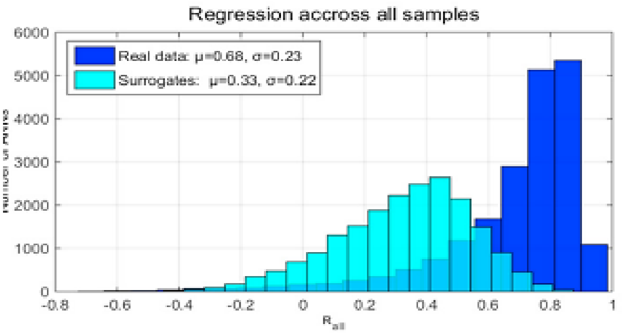

Figure 6: Performance of regression coefficients[10]

The outperformance shows a difference between NNs surrogate and “real data NNs” that is “from ***0.33 to 0.68***". p<0.000001 is statistical significance that has been achieved where the median value for $R_{\text{sur, all}}$ has been around 0.38 as per surrogate NNs while median value for $R_{\text{real, all}}$ is 0.78 according to real data NNs [10]. In this respect, surrogate threshold is assumed to be a surrogate model on high performance that has eventually exceeded the "optimal real-data NN model".

Model	Performance measure	performance on data subsets			
		training	*validation*	*test*	*all*
NN	regression, *R*	0.999	0.991	0.983	0.993
DT	classification, *C*	0.867	n/a	0.850	0.862

Table 1: Performance measurements from NN and DT (ML models) [10]

Conversely, “***optimal DT***" model has been achieved through classification accuracy where C has been assumed as 86.7% in the wake of training phase and accurately classified as 85% within test cases. The results show that DT model has recognised ***ABMR+ve patients*** with around 88.9% sensitivity along with ***ABMR-ve cases*** possessing 82.9% specificity [10]. HLA DSA antibodies where DSA stands for “Donor Specific antibodies” is an important concept associated with transplantation medicine and eventually describes antibodies in Donor's HLA-Molecules. These antibodies are a contraindication opposed to transplantation in several cases [12]. Furthermore, “***HLA DSA antibodies***” have an association with ABMR+ve/ABMR-ve classes. The DT model has identified that patients possessing an increasing level of “Mean fluorescence intensity (MFI) Donor Specific Antibodies”MFI DSA that is below 834 therefore, belong to “ABMR-ve group” however “***igg_hi ≥ 834***” and “***igg4 ≥ 36.5***” possessing a likelihood towards transplant reject at an early stage. Simultaneously patients possessing a mismatch of around 4 or 5 HLA molecules diagnosed with “ABMR+ve group”.

Discussion

The compressive strength within certain trabecular tissue within the femoral head indicates risk from bone fracture that has affected around 20% of cases in the orthopaedic hospital. The "NN model" has been related to biological as well as structural parameters that offer the output values for the specimen CS. The "NN model" has been successful to map out the 5-dimensional input in the wake of a continuous CS vector possessing an accuracy of around 99.3%. Regression coefficients among the actual and also predicted CS values have been determined through test samples that are 98.3%. Identified 5 biological and structural indicators (such as SMI, trabecular thickness, age, gender and others) have been evaluated from the scans of computer tomography providing an opportunity for nondestructive estimation of fracture risk of trabecular tissue [10]. This driven model on patient data for CS estimation can easily be utilised by engineers associated with hard tissue for designing "bioscaffolds" imitating trabecular bone.

These bioscaffolds or scaffolds have been assumed to certain substitutes for bones that have been prepared from "***poly(lactic acid)***" (PLA) that have been assumed as the substitute materials for bone [13]. Bioscaffolds have helped make clinical decisions especially for diagnosis and potential treatment for osteoarthritis patients. However, the "DT model" has acquired an accuracy of around 85% for predicting ABMR within renal transplantation. There have been around 92,844 patients who have been recorded as compared with availability of 80 samples for this "DT model" possessing high-performance in terms of short-term rejection. The "DT model" predictions have an indication that has been associated with patient-specific concerns [10]. The prediction is made based on the clinical indicators where those indicators are either known prior to the surgery or in the period of post-transplantation. The model is helpful as it offers predictions as per "ABMR risk stratification" moving towards individual transplantation.

In addition, it can be stated that within the domain of clinical and biomedical engineering, these predictive models of ML have helped map out the input and output patterns [14]. The techniques on multiple runs in the tasks of regression and classification conform to the fact that size of the dataset does not limit the use of ML-based methods within the biomedical domain. The accuracies that have been derived through NN and DT models on the 35 samples have been compared further with some high-performance models of ML that have been designed on huge datasets in correspondence with biomedical applications [15]. The high-performance models of ML may include "***Support Vector Machine" (SVM)*** or others that have helped predict hip fractures within n osteoporosis, risk patterns associated with genotype- phenotype in a patient suffering from diabetes and kidney disease.

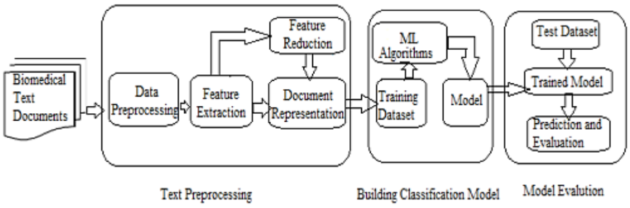

Figure 7: Classification process within the biomedical text [16])

AI technology is applied in both medicine and healthcare and has undergone a regulatory analysis along with clinical adoption. The data that have been used for training the algorithms have also undergone scrutiny [16]. The biases and pitfalls within the algorithms can easily be understood and determined where it has been further found that trained algorithms with biases typically possess biases and thus fail in case of deployment in a setting that is different from trained data that has been acquired [17]. However, extreme dependency of AI-driven diagnostic models on historical data has been assumed to be not capable of diagnosing the phenotypes where patients have earlier suffered from a stroke and have also shown coronavirus symptoms. The segregation of various biomedical literatures within biomedical engineering is a cumbersome process where automatic text of biomedical documents consists of modules such as text processing, model evaluation, and others [18]. Input within the module of text processing contains raw biomedical documents and valuable words and characteristics have been extracted to obtain an appropriate format with the help of well-defined methods of processing.

CONCLUSION AND RECOMMENDATION

The article is important as the article has emphasises a significant relationship between the adoption of ML models within biomedical engineering. The issues of using ML have been identified where it has been found that ML sometimes fails to offer quantity and also the quality of data. The requirement of training data is one of the most important aspects of ML implementation that has been identified within the article. Different significant aspects have been evaluated where it has been seen that nanoscale biosystems have been [prepared through nanomaterials that are found to have different properties. These nano-networks have been seen to be incorporated within the human body to collect important information. The result from utilising NN and DT models have been assumed to be accurate for curing bone diseases in osteoarthritis and also kidney transplantations

REFERENCES

[1] M. Strzelecki and P. Badura, Machine Learning for Biomedical Application. Applied Sciences, 12(4), p.2022, 2022

[2] N. U. Ahamed, K. T. Krajewski, C. C. Johnson, A. J. Sterczala, J. P. Greeves, S. L. Wardle, T. J. O'Leary, Q. Mi, S. D. Flanagan, B. C. Nindl, and C. Connaboy, "Using machine learning and wearable inertial sensor data for the classification of fractal gait patterns in women and men during Load Carriage," Procedia Computer Science, vol. 185, pp. 282–291, 2021.

[3] J. Wexler, M. Pushkarna, T, Bolukbasi, M. Wattenberg, F. Viégas, and J. Wilson,. The what-if tool: Interactive probing of machine learning models. IEEE transactions on visualization and computer graphics, 26(1), pp.56-65, 2019

[4] A. Mosavi,, , P. Ozturk and K.W. Chau. Flood prediction using machine learning models: Literature review. Water, 10(11), p.1536, 2018

[5] M.K. Egbo. A fundamental review on composite materials and some of their applications in biomedical engineering. Journal of King Saud University-Engineering Sciences, 33(8), pp.557-568, 2021

[6] A.A.A. Boulogeorgos, S.E. Trevlakis, S.A. Tegos, V.K. Papanikolaou and G.K., Karagiannidis. Machine learning in nano-scale biomedical engineering. IEEE Transactions on Molecular, Biological and Multi-Scale Communications, 7(1), pp.10-39, 2020

[7] C. Park,, C.C. Took, and J.K. Seong. Machine learning in biomedical engineering. Biomedical Engineering Letters, 8(1), pp.1-3, 2018

[8] C. Turchetti and L., Falaschetti. Machine Learning in Electronic and Biomedical Engineering. Electronics, 11(15), p.2438, 2022

[9] M.E. Chowdhury, A. Khandakar, Y. Qiblawey, M.B.I. Reaz, M.T. Islam, and F. Touati. Machine learning in wearable biomedical systems. In Sports Science and Human Health-Different Approaches, 2020

[10] D. T. Shaikhina, S. Lowe, D. Daga, Higgins. Briggs, R. and Khovanova. N. Machine learning for predictive modelling based on small data in biomedical engineering. IFAC-PapersOnLine, 48(20), pp.469-474, 2015

[11] P. K. KORDING, A. S. BENJAMIN, R. FARHOODI and J. I. GLASER. Frontiers of Engineering: Reports on Leading-Edge Engineering from the 2017 Symposium. National Library of Medicine [Internet]. 2018 [Cited 2022 Dec 15]. Available from: https://www.ncbi.nlm.nih.gov/books/NBK481619/

[12] J. Callemeyn, E. Lerut, H. de Loor, I. Arijs, O. Thaunat, A, Koenig, V. Meas-Yedid, J.C. Olivo-Marin, P. Halloran, J. Chang and L Thorrez. Transcriptional changes in kidney allografts with histology of antibody-mediated rejection

without anti-HLA donor-specific antibodies. *Journal of the American Society of Nephrology*, *31*(9), pp.2168-2183, 2020

[13] Z.B. Velioglu, D. Pulat, B. Demirbakan, B. Ozcan, E. Bayrak and C. Erisken. 3D-printed poly (lactic acid) scaffolds for trabecular bone repair and regeneration: scaffold and native bone characterization. *Connective tissue research*, *60*(3), pp.274-282, 2019

[14] K.D. Humbird, J.L. Peterson and R.G. McClarren. Deep neural network initialization with decision trees. *IEEE transactions on neural networks and learning systems*, *30*(5), pp.1286-1295, 2018

[15] T. Shaikhina, D. Lowe, S. Daga, D. Briggs, R. Higgins, and N., Khovanova. Decision tree and random forest models for outcome prediction in antibody incompatible kidney transplantation. *Biomedical Signal Processing and Control*, *52*, pp.456-462, 2019

[16] R.J. Chen, M.Y. Lu, T.Y. Chen, D.F. Williamson and F. Mahmood. Synthetic data in machine learning for medicine and healthcare. *Nature Biomedical Engineering*, *5*(6), pp.493-497, 2021

[17] B. Behera and G. Kumaravelan. Performance evaluation of machine learning algorithms in biomedical document classification. *Performance evaluation*, *29*(5), pp.5704-5716, 2020

[18] M. Alauthaman, N. Aslam, L. Zhang, R. Alasem and M.A. Hossain. A P2P Botnet detection scheme based on decision tree and adaptive multilayer neural networks. *Neural Computing and Applications*, *29*(11), pp.991-1004, 2018