Machine Learning based Assessment of Preclinical Health Questionnaires

Calin Avram[1*+], Adrian Gligor[1*+], Dumitru Roman[2,3], Ahmet Soylu[3], Victoria Nyulas[1], Laura Avram[4]

1. George Emil Palade University of Medicine, Pharmacy, Science and Technology of Targu Mures, Romania; calin.avram@umfst.ro; adrian.gligor@umfst.ro, victoria.rus@umfst.ro
2. SINTEF AS, Norway; dumitru.roman@sintef.no
3. OsloMet – Oslo Metropolitan University, Norway; ahmet.soylu@oslomet.no; dumitrur@oslomet.no
4. "Dimitrie Cantemir" University of Târgu-Mureș, Romania; laura.avram@cantemir.ro

* Correspondence: calin.avram@umfst.ro; adrian.gligor@umfst.ro
+authors with equal rights

Abstract

Background: Within modern health systems, the possibility of accessing a large amount and a variety of data related to patients' health has increased significantly over the years. The source of this data could be mobile and wearable electronic systems used in everyday life, and specialized medical devices. In this study we aim to investigate the use of modern Machine Learning (ML) techniques for preclinical health assessment based on data collected from questionnaires filled out by patients.

Method: To identify the health conditions of pregnant women, we developed a questionnaire that was distributed in three maternity hospitals in the Mureș County, Romania. In this work we proposed and developed an ML model for pattern detection in common risk assessment based on data extracted from questionnaires.

Results: Out of the 1278 women who answered the questionnaire, 381 smoked before pregnancy and only 216 quit smoking during the period in which they became pregnant. The performance of the model indicates the feasibility of the solution, with an accuracy of 98% confirmed for the considered case study.

Conclusion: The proposed solution offers a simple and efficient way to digitize questionnaire data and to analyze the data through a reduced computational effort, both in terms of memory and computing power used.

Keywords: public health; big data; feature extraction; machine learning; Hopfield neural network

1. Introduction

The use of modern health systems has brought up the possibility of accessing a significant amount and a variety of data related to patients' health. The source of this data could be mobile and wearable electronic systems used in everyday life, and specialized medical devices. These devices with access to communication networks and implicitly to the Internet enable storing collected data in traditional databases or more complex storage solutions offered by the cloud. This paves the way for long-term and real-time patient monitoring. Additionally, the

Author accepted manuscript version of the publication by
C. Avram, A. Gligor, D. Roman, A. Soylu, V. Nyulas & L. Avram.
In International Journal of Medical Informatics, 180, 105248, December 2023.
Published version: https://doi.org/10.1016/j.ijmedinf.2023.105248

availability of medical data that could be collected through current solutions allows faster tracking of changes and evolutions in many fields of medicine [1,2]. The realization of international standards by which a set of data related to a medical condition or intervention are identically collected, even if they are taken from different places, would lead to a better understanding of the diseases and even to faster treatments [3].

A very large part of medical data is in unstructured or even undefined formats. With the help of natural language processing (NLP), this problem could be alleviated by using methods such as semantic analysis and text mining [4-6]. In a broader sense, the processing and interpretation of medical data with the help of Artificial Intelligence (AI) and Machine Learning (ML) has become a topic of great interest in the literature. This direction of research is due to the progress achieved in the area of Big Data analysis and developments in storing and accessing structured and unstructured data, data mining, natural language processing, as well as to emerging technologies in the field of Internet of Things (IoT) [7]. Several studies in medicine have been carried out with the help of ML and Big Data technologies, examples including [8,9] for the control of colorectal cancer and nicotine, respectively. Supervised and unsupervised ML are well known ML subsets. The former requires labeled data to infer test data, while the latter looks for patterns and trends within unlabeled data [10]. Neural networks are another subset of ML and are at the heart of deep learning algorithms. Hopfield networks are neural networks which are associative memory networks. These networks were created to store and process samples [11]. Modern Hopfield networks can exponentially store the data they process, and these data can be retrieved only through a single access [12]. These networks have been successfully applied to various models [13], however, their usage is focused on retrieving the expected results, for example predictions, the correct interpretation of obtained results being nowadays still a challenge [14]. The use of ML enables processing of large volumes of data for identification of several important characteristics that the human specialist can omit. Using ML enables the rapid identification of complex patterns that result from training data and thus can make predictions for newly collected data [15]. The initialization and exploitation of the models represented by means of neural networks are based on ML methods that use the neuron as the fundamental processing unit, principally through the connections made imitating the functioning of the human brain. This approach has been used successfully in medical image processing [16].

The purpose of this study is to demonstrate the possibility of processing data collected through a questionnaire using ML techniques with conventional processing and memory resources. With the help of Hopfield networks, we classify health data collected through a questionnaire. The questions from the questionnaire are transposed into images that are then analyzed to allow predictions of patients' health conditions. The proposed network HopDetect (Hopfield detect) allows the identification of the life-style health index of pregnant women who are smokers based only on questions from a questionnaire. The unique feature of the present proposal consists in the way of encoding the answers based on the questionnaire and the possibility of automatic processing with a Hopfield type structure. The main advantage of this method is its suitability for direct analysis of the collected data. This, combined with one of the easiest ways to obtain data, in this case through questionnaires, leads to a new tool that provides fast and efficient support in medical decision-making. The area of collecting data through a questionnaire can be either restricted by specific requirements (certain areas of interest, population, etc.) or can be considered for a large geographical area, or for certain purposes, worldwide, easily accessible via social networks that have an important role in the distribution and data collection. The proposal presented in this article allows making predictions, useful for identifying health conditions at a specific group level or a population, based on the data collected through a questionnaire. The disadvantages of this model are closely related to the collected data that in certain situations may not be very accurate, the answers to the questions in a questionnaire can be subjective compared, for example, to the data that are collected from medical equipment characterized by high accuracy.

The rest of the article is structured as follows. Section 2 presents materials and methods, while Section 3 presents the results. Section 4 provides a discussion, and finally Section 5 concludes the article.

2. Materials and methods

Data collection

To identify the health conditions of pregnant women, we developed a questionnaire that was distributed in three maternity hospitals in Mureș County, Romania. This questionnaire was applied between March 2015 and March 2016 to all women who were admitted to maternity hospitals to give birth. The questionnaire included questions related to the condition of the pregnant woman as well as socio-demographic questions. A section of the questionnaire included questions related to patient's smoking, but also questions about passive smoking to which the patient is subject to. In the county there are around 2,500 births per year for a population of 130,000 inhabitants.

In this cross-sectional study, data were collected from 1278 pregnant women who were admitted to the hospital to give birth, the questionnaire was validated and contained 109 questions, of which 50 questions were meant to identify the attitude related to smoking.

Measurements

In the questionnaire, pregnant women were grouped into three categories, all closely related to smoking: women who did not smoke, women who quit during pregnancy, and women who continued to smoke throughout pregnancy. In the first part of the questionnaire, the questions were related to the personal socio-economic situation of the patient, the health status of the pregnant woman, and the pregnancy.

The goal of the questionnaire was to highlight the potential life-style risk in the studied group. The measurement of this risk is proposed to be evaluated through a three-state life-style health index:

$$i_R \in \{a_1, a_2, a_3\}$$

where i_R gets values from the set $\in \{a_1, a_2, a_3\}$, where a_1 has the meaning of *"No risk of smoking"*, the subject didn't belong to the existing risk group; a_2 is associated with a *"Lowered risk of smoking"*, subjects that belong to the risk group (smoked) but they quit smoking; and, a_3 has the associated meaning of *"Risk of smoking"*, representing subjects with high potential of continuing or adopting the risks factor life-style.

Methodologically, we excluded all the patients who did not answer all the questions related to smoking, since these questions were considered essential for the study. The research protocol was approved by the ethics committee at the "George Emil Palade'' University of Medicine, Pharmacy, Science and Technology of Târgu Mureş, Romania, and the study was conducted in accordance with the Helsinki Declaration.

Machine learning

The developed solution based on Hopfield networks and proposed data representation, namely Code-map model, with parameters correlated with the socio-demographic status of pregnant women, allows the identification of the patient's status related to smoking. The algorithm was implemented in MatLab 2022A update 5. Considering the number of questions and the number of possible associated answers, a Hopfield-type associative memory is adopted with several units per elementary layer that is multiplied by the number of questions of the matrix expressed through neural networks.

The model was trained to identify women who smoke during pregnancy on a data set of 70% of those collected. These were randomly selected from the people who were included in the study and the testing was performed on the remaining 30% of the patients. The list of parameters included in the learning process is presented in Table 1. Since the selected data were not numerical data, we used data encoding. The tests carried out led to results that can be implemented in other fields as well.

Encoding data

Encoding was performed according to the number of variables that will determine the space and the number of neurons. Encoding using the binary representation was done to obtain a two-level mapping array. Such encoding allowed the use of more questions from the questionnaire and thus enabled a better accuracy of the results. The number of neurons that were needed to perform the tests was identified depending on the number of questions used and the number of variables that were found in the answers to the questions in the questionnaire.

The data prior to the training and further the analysis were transformed using the function from equation (4) and then provided as input to the parameterized Hopfield network, which learns and analyzes it as a binary data map.

Statistical analysis

Descriptive statistics were performed to highlight smoking during pregnancy but also to highlight the factors that are considered for the developed model. For the data containing nominal variables, we applied the Chi-square test and for the data containing nominal variables we applied the Kruskal-Wallis test. To verify the normality of the data, the Shapiro-Wilk normality test [17] was applied to the nominal variables.

Two multivariable logistic regression models were used to assess the odds of continuing smoking versus never smoking and the odds of continuing smoking versus never smoking. Analyzes were performed using SPSS v22.0 statistical software and the statistical significance threshold was set to 0.05.

3. Results

Out of the 1278 women who answered the questionnaire, 381 smoked before pregnancy and only 216 quit smoking during the period in which they became pregnant. The age of the questioned subjects is between 14 and 47 years with an average of 29.46 years. Most pregnant women have university degrees (660, i.e., 51.64%) and reside in urban areas (752, i.e., 58.84%) (Table 1).

Table 1. Basic characteristics used in the model

Variable	Total (N=1278)	Non-smoker (n=894)	Smokers who quit smoking during pregnancy (n=216)	Smokers who continued to smoke during pregnancy (n=165)	p
Residence					
• Urban	752	499	144	109	0.0016*
• Rural	526	398	72	56	
Number of weeks the mother gave birth					
• Min	25	27	31	25	0.4365**
• Max	42	42	41	41	
• Mean/SD	38.26/2.57	38.27/2.56	38.57/1.80	37.84/3.30	
Mother's age					
• Min	14	14	20	16	0.0003**
• Max	47	44	50	52	
• Mean/SD	29.46/5.49	29.69/5.47	29.90/4.91	28.44/7.54	
Marital status					
• Married	1056	780	177	99	<0.0001*
• Concubinage	204	102	39	63	
• Divorce	3	-	-	3	
• Living separately	12	12	-	-	
Studied					
• Eight classes	218	102	36	69	<0.0001*
• High school	169	111	24	30	
• Professional	78	48	21	9	
• Post high school	153	111	30	12	
• University	660	513	105	42	
Social status					
• Employee	843	627	147	69	<0.0001*
• Housewife	183	99	30	54	
• Unemployed	90	57	6	27	
• Parental leave	81	66	9	6	

*Chi-square test, **Kruskal-Wallis test

Table 1 shows the number of women who are pregnant and continue to smoke (n=165) and the number of women who quit smoking when they found out they were pregnant (n=216). According to the calculations performed, it can be observed that there is statistical significance between the studied categories ($p<0.0003$), but also an association between residence ($p=0.0016$), marital status ($p<0.0001$), level of education ($p<0.0001$) and social status ($p<0.0001$).

Table 2. Identification of factors that facilitate smoking during pregnancy

	Smokers who quit smoking during pregnancy (n=216) vs non-smokes (n=897)		Smokers who continued to smoke during pregnancy (n=165) vs non-smokes (n=897)	
	OR	95%CI	OR	95%CI
Residence (rural)	0.56*	0.40 – 0.79	0.51*	0.34 – 0.75
The number of weeks at which the mother gave birth (<37 weeks)	0.61	0.37 – 1.03	0.61	0.35 – 1.07

Marital status (single mother)	1.70*	1.06 – 2.72	2.42*	1.52 - 3.84
Studies (below university level)	1.76*	1.22 - 2.53	2.66*	1.67 - 4.25
Salary level (less than 100 Euro)	0.79	0.51 - 1.21	1.67*	1.07 - 2.58

* statistical significance

According to the data, 381 of the surveyed women were smoking when they found out they were pregnant, of which 165 continued to smoke throughout their pregnancy. According to Table 2, single mothers (OR=2.42, 95% CI: 1.52–3.84) and those with a high level of education (OR=2.66, 95% CI: 1.67 -4.25) are more likely to smoke during pregnancy compared to non-smokers.

Code-map model

Human's natural way of data and knowledge representation are difficult to be directly used in machines processing. In this work, we proposed and developed a methodology of data obtained from questionnaires encoding for fast pattern detection in common risk assessment.

The main principle of the solution resides on a bijective transformation of the input data through a code-map representation (CMR):

$$r_k = F(p_k) \tag{1}$$

with

$$F(p_k) = \Lambda_{i=1}^{n} f_i(p_{k,i}) \tag{2}$$

and

$$f_i : M_i \rightarrow N_i \tag{3}$$

where: i is the index of the question item from the questionnaire; M_i is the set of possible values for a question in the questionnaire; N_i is positive integer binary coded set of the possible values corresponding to the i-th question item in the questionnaire; n represents the numbers of question item in the questionnaire; k is the index of the k-th item acquired in the questionnaire; f is the linguistic to binary encoding function; and, Λ is the internal binary mapping function.

The aim is to obtain a representation that could be processed in frequency domain to easily reveal generic patterns. In this way, an image-like representation is obtained and thus established algorithms can be used in the process of achieving the intended goal.

Considering as input data results coming from a questionnaire, we first have to consider the inference transformation described by the f_i function in the form:

$$f_i(p_{k,i}) = sel\{M_i\} \tag{4}$$

with *sel* function mapping the input into binary apriori defined code.

The size of the obtained code-map model is related to the number of questions from the questionnaire and of their type. The following formula can be used to predetermine the required dimension for CMR for a particular application:

$$\dim_{CMR} = \sum_{j=1}^{n} n_{N_j}(\lfloor \log_2 v_{N_j} \rfloor + 1) \tag{4}$$

where: $\lfloor \cdot \rfloor$ denotes the round down function; n_{N_j} represents the occurrences number of a specific type of question in the questionnaire, e.g., Likert type, two options responses or a value with known maximum size; and, v_{N_j} represents the number of adopted point in Liker scale, the number of options or maximum allowed value in responses as required.

The encoding verification was performed using the ROC curve. In the case of verification, we obtained the following results: Sensitivity=69.77, Specificity=72.32, Youden index J = 0.4209, 95% CI= 0.710 - 0.845, p<0.001 and Area under the ROC curve (AUC)=0.783 (Fig. 1).

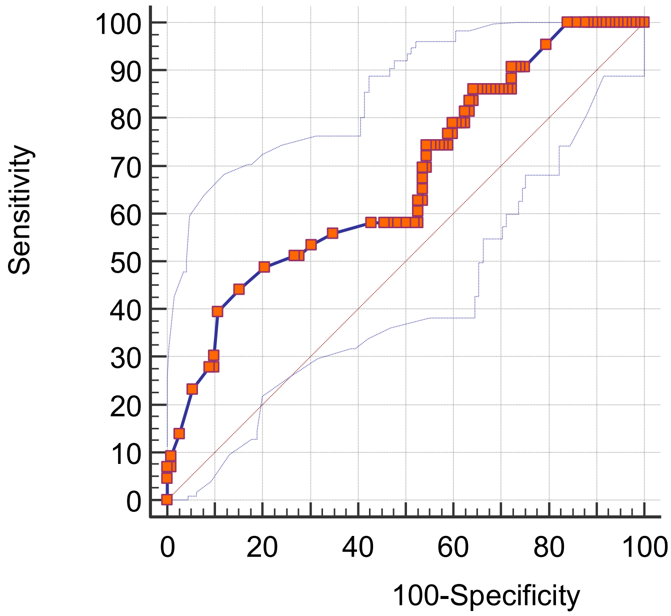

Figure 1. Verifying the encoding of the collected data

Feature extraction

Feature extraction could be considered as a classification problem. Given the obtained CMR encoding that resembles a similarity with images representation, corresponding processing approaches are adopted.

In this article, based on existing literature [18-22], a recurrent neural network (RNN) is proposed in the form of an associative memory, also known as Hopfield network. The main goal is to identify if a previously learned pattern is present in the analyzed response from the used questionnaire, see Fig. 2.

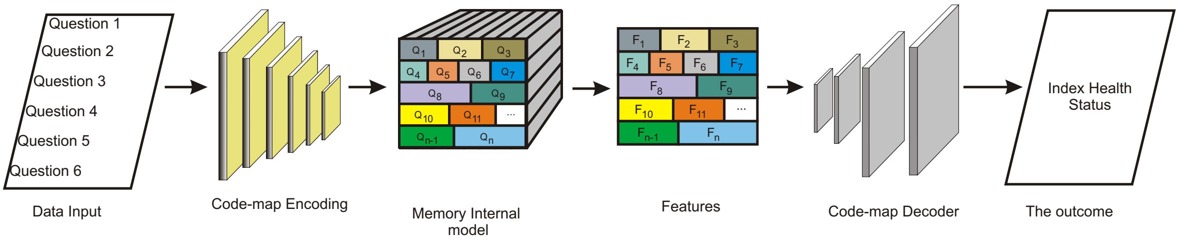

Figure 2. Feature extraction with RNN

As illustrated in Fig. 2 the process was developed in two stages: a learning phase and then the effective pattern detection phase. In the learning phase each available response of the questionnaire is encoded in CMR and used for training the RNN. At the end of this one-time stage any new available response can be evaluated.

For the cases when it is known that the model of the analyzed process is changing, an “on-line” type approach can be adopted for dynamic learning as questionnaire acquires new responses and evolve. However, if rarely, new, unknown or unclassified entry becomes available the RNN, due to its generalization power, does not need to be retrained, as it has already been tested with noisy images but still good responses were obtained. The decision on the adopted version should be taken based on percentage rate change of the questionnaire responses.

Solution integration

The integrated solution links together the questionnaire response preprocessing and encoding, feature extraction and then transformation to end-user compliant results. Figure 3 illustrates the structure of the proposed ML-based solution where the main components and processes can be identified.

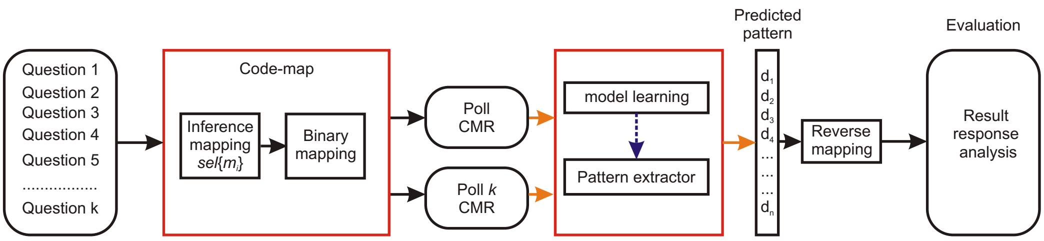

Figure 3. ML based poll responses analysis process flow.

The analysis flow is depicted in Fig. 3, identifying the classification for each new response set relying on the learnt model.

Testing the associative memory model allowed the identification of people who smoke based only on the information requested in the questionnaire. This model has a performance of 98% confirmed based on the tests carried out.

4. Discussions

The management and interpretation of medical data is facilitated by the use of new and emerging technologies such as AI and ML, e.g., drug synergy prediction [23], drug-target prediction [24], and drug discovery [25]. With the emergence of various AI-based solutions, such solutions can also be adapted to the automatic learning of prototypes by implementing neural networks [26]. The use of ML methods in the case of longitudinal medical data can provide better results than classical statistical models [27], however the learning techniques must use strong regularizations to be used for tabular data [28]. Medical databases offer many elements for understanding health conditions, but also many challenges related to data management and processing. The use of Big Data technologies is necessary to process large databases that grow in size but also in complexity [29]. A known case, reported in [30], includes the medical data of UK patients that were used to identify the incidence of cardiovascular disease using four ML approaches. The results encouraged the authors to make recommendations to benefit as many patients as possible.

Other studies have identified the fact that parallel processing can improve the learning process. Thus, the tasks are learned simultaneously, but by communicating information between them, more accurate models can be created than if the learning had been carried out separately. The first multitask Hopfield network for classification purposes that is capable of simultaneously learning multiple tasks was presented in [31]. The Hopfield model was also used in the case of dementia, for investigating the associated occurrence possibility of disruption in the neural network. In the situation of weak connectivity state, it was found a similar disruption behavior in case of the Hopfield network structure, as in the case of the neural network observed in dementia subjects [32]. In the case of Hopfield networks [33,34] with at least two neurons, we may find various other applications, valuable results being obtained in case of system engineering in adaptive control implementation. This network works by minimizing an energy function, in which the result is represented by the obtained extrema [35]. Prediction models can be found in the identification of viral diseases, fungal infections and even cancer. The treatments performed with pectites allow the use of prediction models that have a high degree of accuracy using algorithms such as pAVP_PSSMDWT-EnC [36], cACP-DeepGram [37], and iAFPs-EnC-GA [38].

Some researchers have created Deep Learning architectures that include modern Hopfield networks that allow the storage of two types of data: all the training data or the vectors of the original inputs [39]. The application of all these techniques for large databases brings benefits due to the complexity of the models used, and also contributes to the accuracy in which the results of a model are interpreted and put into medical practice. There are tested models that have the same utility, but there is still no explanation related to which model should be applied in special situations [40,41]. The formalization of the processes would allow an understanding of their limitations and how these models work, a fact that will lead to much more innovative solutions [42,43].

The results of the study presented in this paper complement the results of related works, and highlight the possibility of fast assessment of clinical states based on learnt features.

The limitation of the study is related to the quality of input data, more specifically related to the questionnaires designs and the accuracy of the obtained responses. Another limitation of the study is related to the relatively limited number of answers collected through this method, that of the questionnaire. The number of questions included in this model was relatively small for practical considerations.

5. Conclusion

In the medical field, patient anamnesis and the study of health in various communities have standardized questionnaires as a basic tool. Automatic processing solutions could come to the aid of practitioners in the field. In this work, we proposed, developed and tested such a solution, which is based on ML techniques. The proposed solution uses a "recurrent neural network" with associative memory functionality. In order to ensure a low computation effort, an encoding solution was proposed, and subsequently, a tuned parametrized machine learning model. The integration of encoding, machine learning and decoding parts lead to the proposed solution.-The performance of the model indicates the feasibility of the solution for the proposed study. Overall, the proposed solution offers a simple and efficient way to digitalize questionnaire answers, and to analyze it through a reduced computational effort, both in terms of the amount of memory and the computing power used.

6. Summary points

What we already knew:

- AI is used to make medical predictions.
- The applied questionnaires are easy to implement and can be used for various medical investigations.

What this study added to our knowledge:

- Quick identification of vulnerable patients or those who have harmful health habits based on answers to the questions in a questionnaire.
- The use of encoding of questionnaire data helps to quickly find answers to the medical needs of patients.
- Application of ML in medicine for fast data processing and accurate predictions.

Authorship contribution statement

Calin Avram: Conception and design, methodology and design, data collection, analysis, software development, drafting, revising, writing, review and editing, and overall project leadership and supervision. **Adrian Gligor**: Conceptualization, methodology and design, software writing, review and editing, supervision. **Dumitru Roman**: Study design, validation of the study, writing, review and editing, co-supervision. **Ahmet Soylu**: Methodology and design, writing, review and editing. **Victoria Nyulas**: Methodology and design, writing, review and editing. **Laura Avram**: Methodology and design, writing, review and editing.

Funding: This work was realized with the EEA Financial Mechanism 2014–2021's financial support. Its content (text, figures, tables) does not reflect the official opinion of the Program Operator, the National Contact Point, or the Financial Mechanism Office. The responsibility for the information and views expressed herein lies entirely with the authors.

Acknowledgments: This article was elaborated under the EEA Financial Mechanism 2014–2021, project 21-COP-0038, implemented by the George Emil Palade University of Medicine, Pharmacy, Science and Technology of Targu Mures, Romania, in partnership with SINTEF AS, Norway.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. S. Schneeweiss, Learning from big health care data. The New England Journal of Medicine, 370(23), (2014), 2161–2163. Doi:10.1056/NEJMp1401111

2. Y. Jung, R. Agulto, A public platform for virtual IOT-based monitoring and tracking of COVID-19, Electronics, 10(1), (2020), 12. Doi:10.3390/electronics10010012

3. I.D. Dinov, Methodological challenges and analytic opportunities for modeling and interpreting Big Healthcare Data, GigaScience, 5 (2016). Doi:10.1186/s13742-016-0117-6

4. É. Arnaud, M. Elbattah, M. Gignon, G. Dequen, NLP-Based Prediction of Medical Specialties at Hospital Admission Using Triage Notes, 2021 IEEE 9th International Conference on Healthcare Informatics (ICHI), 2021, 548-553. Doi: 10.1109/ichi52183.2021.00103

5. A. Wulff, M. Mast, M. Hassler, S. Montag, M. Marschollek, T. Jack, Designing an openEHR-Based Pipeline for Extracting and Standardizing Unstructured Clinical Data Using Natural Language Processing, Methods of Information in Medicine, 59(S 02), (2020), e64 - e78. Doi: 10.1055/s-0040-1716403

6. R. Chen, J. Ho, J.S. Lin, Extracting medication information from unstructured public health data: a demonstration on data from population-based and tertiary-based samples, BMC Medical Research Methodology, 20(1), (2020). Doi: 10.1186/s12874-020-01131-7

7. S.T. Leatherdale, J. Lee, Artificial intelligence (AI) and cancer prevention: the potential application of AI in cancer control programming needs to be explored in population laboratories such as COMPASS, Cancer causes & control: CCC, 30(7), (2019), 671–675. Doi:10.1007/s10552-019-01182-2

8. R. Goshen, E. Choman, A. Ran, E. Muller, R. Kariv, G. Chodick, et al., Computer-assisted flagging of individuals at high risk of colorectal cancer in a large Health Maintenance Organization using the Colon-Flag test, JCO Clin Cancer Inform, 2, (2018), 1–8.

9. J.W. Ayers, M. Dredze, E.C. Leas, T.L. Caputi, J.P. Allem, J.E. Cohen, Next generation media monitoring: Global coverage of electronic nicotine delivery systems (electronic cigarettes) on Bing, Google and Twitter, 2013-2018. PLoS ONE, 13(11), (2018), e0205822. Doi:10.1371/journal.pone.0205822

10. R. Caruana, A. Niculescu-Mizil, An empirical comparison of supervised learning algorithms. Proceedings 23rd International Conference on Machine Learning, 2006.

11. E. Gardner, Multiconnected neural network models. Journal of Physics A: Mathematical and General 20(11), (1987), 3453–64. Doi: 10.1088/0305-4470/20/11/046

12. H. Ramsauer, B. Schafl, J. Lehner, P. Seidl, M. Widrich, L. Gruber, et al., Hopfield networks is all you need, Proc. Int. Conf. Learn. Representations, 2021.

13. Y. Xu, W. Yu, P. Ghamisi, M. Kopp, S. Hochreiter, Txt2Img-MHN: Remote sensing image generation from text using modern Hopfield networks. arXiv:2208.04441, 2022.

14. S.M. Lundberg, S.I. Lee, A unified approach to interpreting model predictions, Advances in neural information processing systems, 30, 2017. Doi: 10.48550/arXiv.1705.07874

15. J. Meng, Z. Liu, X. Xu, Applications of neural networks in liver transplantation, iLIVER, 1(2), (2022), 101–10. Doi:10.1016/j.iliver.2022.07.002

16. T.H. Su, C.H. Wu, J.H. Kao, Artificial intelligence in precision medicine in hepatology, J Gastroenterol Hepatol, 36, (2021), 569-580. Doi: 10.1111/jgh.15415

17. C. Avram, M. Mărușteri, Normality assessment, few paradigms and use cases, Revista Romana de Medicina de Laborator, 30(3), (2022), 251-260. Doi:10.2478/rrlm-2022-0030

18. S. Coulibaly, B. Kamsu-Foguem, D. Kamissoko, D. Traore, Deep convolution neural network sharing for the multi-label images classification, Machine Learning with Applications, 10, (2022), 100422. Doi:10.1016/j.mlwa.2022.100422

19. Y.M. Ren, M.S. Alhajeri, J. Luo, S. Chen, F. Abdullah, Z. Wu, et al., A tutorial review of neural network modeling approaches for model predictive control, Computers & Chemical Engineering, 165, (2022), 107956. Doi:10.1016/j.compchemeng.2022.107956
20. L. Hao, Optimal selection of control parameters for automatic machining based on BP neural network, Energy Reports, 8, (2022), 7016-7024. Doi:10.1016/j.egyr.2022.05.038
21. S. Tomassini, N. Falcionelli, P. Sernani, L. Burattini, A.F. Dragoni, Lung nodule diagnosis and cancer histology classification from computed tomography data by Convolutional Neural Networks: A survey, Computers in Biology and Medicine, 146, 105691, (2022). Doi:10.1016/j.compbiomed.2022.105691
22. Md. I. Milon, S. Nooruddin, F. Karray, G. Muhammad, Human activity recognition using tools of convolutional neural networks: A state of the art review, data sets, challenges, and future prospects, Computers in Biology and Medicine, 149, (2022). Doi: 10.1016/j.compbiomed.2022.106060
23. F. Rafiei, H. Zeraati, K. Abbasi, J. B. Ghasemi, M. Parsaeian, A. Masoudi-Nejad, DeepTraSynergy: drug combinations using multimodal deep learning with transformers, Bioinformatics, 39(8), (2023), Doi: 10.1093/bioinformatics/btad438
24. A. Dehghan, P. Razzaghi, K. Abbasi, S. Gharaghani, TripletMultiDTI: Multimodal representation learning in drug-target interaction prediction with triplet loss function, Expert Systems with Applications, 232, (2023), Doi: 10.1016/j.eswa.2023.120754.
25. K. Abbasi, P. Razzaghi, Incorporating part-whole hierarchies into fully convolutional network for scene parsing, Expert Systems with Applications, 160, (2020), Doi: 10.1016/j.eswa.2020.113662.
26. G. Li, V. Jampani, L. Sevilla-Lara, D. Sun, J. Kim, J. Kim, Adaptive prototype learning and allocation for few-shot segmentation, Proc. IEEE Conf. Comput. Vis. Pattern Recognit, 2021, 8334–8343
27. W. Engchuan, A.C. Dimopoulos, S. Tyrovolas, F.F. Caballero, A. Sanchez-Niubo, H. Arndt, et al., Sociodemographic indicators of health status using a machine learning approach and data from the English Longitudinal Study of Aging (ELSA), Med Sci Monit., 15, (2019), 1994-2001. doi: 10.12659/MSM.913283
28. A. Kadra, M. Lindauer, F. Hutter, J. Grabocka, Regularization is all you need: Simple neural nets can excel on tabular data, ArXiv, 2106.11189, 2021. Doi: 10.48550/arXiv.2106.11189
29. I.D. Dinov, P. Pestroyan, Z. Liu, P. Eggert, S. Hobel, et al., High-Throughput Neuroimaging-Genetics Computational Infrastructure, Frontiers in Neuroinformatics, 8(41), (2014),1–11. Doi: 10.3389/fninf.2014.00041
30. O. Taylan, A.S. Alkabaa, H.S. Alqabbaa, E. Pamukçu, V. Leiva, Early Prediction in Classification of Cardiovascular Diseases with Machine Learning, Neuro-Fuzzy and Statistical Methods, Biology, 12(117), (2023). Doi:10.3390/biology12010117
31. M. Frasca, G. Grossi, G. Valentini, Multitask Hopfield Networks. Machine Learning and Knowledge Discovery in Databases, ECML PKDD. Lecture Notes in Computer Science, 11907. Springer, Cham., 2019. Doi: 10.1007/978-3-030-46147-8_21.
32. R.A. Thuraisingham, Dementia and Hopfield model, J Neural Transm, 122, (2015), 773–777. Doi:10.1007/s00702-014-1339-3
33. J.J. Hopfield, Neurons with graded response have collective computational properties like those of two-state neurons, Proc. Nac. Acad. Sci. U.S.A., 81, (1984), 3088-3092. Doi: 10.1073/pnas.81.10.3088

34. K.J. Åström, B. Wittenmark, Adaptive Control. Reading, MA: Addison-Wesley, 1995
35. S.Y. Cavalcanti Catunda, J.H. Feitosa Cavalcanti, Adaptive Hopfield Neural Controller, ISIE '97 Proceeding of the IEEE International Symposium on Industrial Electronics, 3, 1997, 1206–10. Doi: 10.1109/ISIE.1997.648913.
36. A. Shahid, A. Farman, H. Maqsood, A. Ashfaq, K. Salman, G. Sarah, Prediction of Antiviral peptides using transform evolutionary & SHAP analysis based descriptors by incorporation with ensemble learning strategy. Chemometrics and Intelligent Laboratory Systems, 230, (2022). Doi: 10.1016/j.chemolab.2022.104682
37. A. Shahid, H. Maqsood, T. Muhammad, K. Salman, K.A. Fawaz, cACP-DeepGram: Classification of anticancer peptides via deep neural network and skip-gram-based word embedding model. Artificial Intelligence in Medicine, 131, (2022). Doi: 10.1016/j.artmed.2022.102349
38. A. Ashfaq, A. Shahid, T. Muhammad, H. Maqsood, A. Farman, iAFPs-EnC-GA: Identifying antifungal peptides using sequential and evolutionary descriptors based multi-information fusion and ensemble learning approach. Chemometrics and Intelligent Laboratory Systems, 222, (2022). Doi: 10.1016/j.chemolab.2022.104516
39. B. Schäfl, L. Gruber, A. Bitto-Nemling, S. Hochreiter, Hopular: Modern Hopfield Networks for Tabular Data. arXiv, (2022), 2206.00664. Doi: 10.48550/arXiv.2206.00664
40. M.T. Ribeiro, S. Singh, C. Guestrin, Why should i trust you? Explaining the predictions of any classifier, In: Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining. ACM., 2016, 1135–1144. Doi: 10.18653/v1/N16-3020
41. E. Štrumbelj, I. Kononenko, Explaining prediction models and individual predictions with feature contributions, Knowledge and information systems, 41, (2014), 647–665. Doi: 10.1007/s10115-013-0679-x
42. C. Avram, E.L. Avram, A. Gligor, Formal Models for Describing Mathematical Programming Problem, Procedia Economics and Finance, 15, (2014), 1501–1506. Doi: 10.1016/S2212-5671(14)00617-0
43. H. Arshad, A. Jantan, G.K. Hoon, I.O. Abiodun, Formal knowledge model for online social network forensics, Computers Security, 89, (2020) 101675. Doi: 10.1016/j.cose.2019.101675