The Evolution and Reliability of Machine Learning Techniques for Oncology

https://doi.org/10.3991/ijoe.v19i08.39433

Hamza Abu Owida[1], Bashar Al-haj Moh'd[1], Nidal Turab[2(✉)], Jamal Al-Nabulsi[1], Suhaila Abuowaida[3]
[1]Medical Engineering Department, Faculty of Engineering, Al-Ahliyya Amman University, Amman, Jordan
[2]Department of Networks and Cyber Security, Faculty of Information Technology, Al-Ahliyya Amman University, Amman, Jordan
[3]Department of Computer Science, Prince Hussein Bin Abdullah Faculty of Information Technology, Alal-Bayt University, Mafraq, Jordan
n.turab@ammanu.edu.jo

Abstract—It is no secret that the rise of the Internet and other digital technologies has sparked renewed interest in AI-based techniques, especially those that fall under the umbrella of the subset of algorithms known as "Machine Learning" (ML). Electronic innovations have enabled us to comprehend the universe beyond the limits of human cognition. The difficult nature of a high-dimensional dataset. Although these techniques have been regularly employed by the medical sciences, their adoption to enhance patient care has been a bit slow. The availability of curated diverse data sets for model development is all examples of the substantial hurdles that have delayed these efforts. The future clinical acceptance of each of these characteristics may be affected by a number of limiting conditions, such as the time and resources spent on data collection and model development, the cost of integration relative to the time and resources spent on translation, and the potential for patient damage. In order to preserve value and enhance medical care, the goal of this article is to evaluate all facets of the issue in light of the validity of using ML methods in cancer, to serve as a template for further research and the subfield of oncology that serves as a model for other parts of the discipline.

Keywords—Machine Learning, oncology, cancer classification

1 Introduction

Machine learning (ML) methods and their accompanying use cases have been steadily expanding over the past two decades. There are many examples of ML's subtle but pervasive presence in our daily lives, from shopping suggestion software to advanced image and speech recognition systems. The presence of ML techniques is also felt in the workplace by scientists and doctors, in the form of a plethora of algorithms and ML-based tools that assist and, in some cases, have come to replace human practice in the biomedical sciences [1, 2].

The term "machine learning" (ML) is used to describe a wide range of computational methods that help computers "learn," or improve their proficiency at a given activity, over time. The ML method relies on a large amount of data that the computer system iteratively examines in an effort to minimize the difference between its forecast and the expected result [3, 4].

The breakthroughs in computing and digital technology that made machine learning approaches possible also greatly increased data-acquisition and data-storage capabilities in a variety of scientific study disciplines, thereby ushering in the so-called 'Big Data' movement. In turn, the enormous quantity of data made it possible for ML methods to be effectively applied in various fields. ML is becoming increasingly prevalent in the medical practice, and oncology is no exception. This is true across the board, from approaches that aid in diagnosis by uncovering complicated patterns in screening data to expert systems that decide treatment recommendations [5, 6]. Figure 1 shows the block diagram of Machine Learning algorithm.

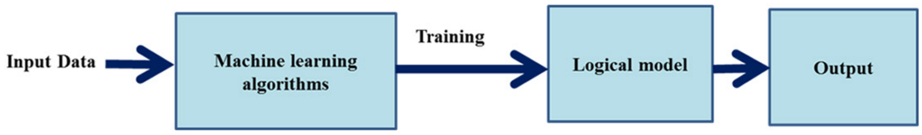

Fig. 1. The block diagram explains the working of Machine Learning algorithm

Since a few decades ago, the fields of medical radiology and oncology have followed the customary practice of gathering data in separate silos, where it is then kept in a variety of formats. On the other hand, drawing conclusions from such a massive resource has proven to be difficult. Despite this, there were a few noteworthy achievements in the sector that had taken use of the data repositories [7, 8]. In recent years, the tide of deep learning has been hastened by unrelenting efforts made by the information technology industry to incorporate open-source tool innovations [9, 10]. The pioneering open-source efforts by leaders in both industry and academia were unheard of in recent history [11, 12].

To be more specific, recent progress in the convolutional deep neural community has included the demonstration that machine intelligence is on par with or exceeds human perception by identifying image groupings [13]. The present-day success of deep neural networks indicates a paradigm shift from old machine learning methods, which relied on features extracted by humans

Although deep learning networks now contain convolutional layers, the entire learning process can be deemed entirely automated. Fully connected layers were formerly used in regular detection or classification layers. Adaptive learning has greatly benefited the improvement of network-based learning [14, 15]. These ML techniques provide the possibility of tackling difficult problems, but their implementation has a checkered history. Among these were the system's complicated implementation, the need for more contextual information, and the negative connotation of the backbox. As a result of these setbacks, unanticipated outcomes have occurred, often referred to as "AI winters" [16].

In this study, we discuss the development of ML approaches, the difficulties inherent in their application to the medical field, and the elements that contribute to their trustworthy use in oncological research. To boost trustworthiness, reproducibility, and user confidence in clinical research and care acceptance, we conclude with suggestions for future AI/ML model development.

2 Potential implications of machine learning in oncology

In the field of cancer research, an early diagnosis and accurate prognosis of a specific cancer type have become essential requirements since they can improve the subsequent clinical management of patients. Because of how critical it is to accurately categories cancer patients into high or low risk groups, a significant number of research teams in the biomedical and bioinformatics fields are focusing their attention on the application of ML approaches. As a result, these methods have been applied with the purpose of modelling the development of malignant disorders as well as the therapy of those conditions. In addition, the capacity of machine learning techniques to extract significant features from complicated datasets demonstrates the significance of these features [17–19].

There is significant potential for ML in the field of oncology. It can also be utilized to help with diagnosis and early intervention, as well as to derive risk cohorts, forecast prognosis, inform treatment strategies, and aid in prognosis prediction [20]. Approaches that are driven by the data that are collected from patients can help us gain a better knowledge of cancer and how it affects individuals, given the growing number of patient records that are now available. It is a laudable project that will be altered how cancer care is delivered, even though ML poses several difficult technological and organizational hurdles [21–23]. Figure 2 shows the potential applications of machine learning in oncology.

3 Diagnosis and early detection

It is impossible to make an accurate diagnosis of cancer without analyzing large amounts of clinical data, such as gene expression, radiological imaging, histology, or a combination of these. Cancer biomarkers in gene expression profiles have been analyzed using ML since the early 2000s. Recent developments in computer vision have allowed for raw images to be analyzed and diagnosed. [24, 25]. Because mammograms are so useful in detecting breast cancer, it has served as a natural forerunner in this field. There has been a lot of development in mammography-based diagnosis recently, but related work dates to 1995 [26, 27]. Analogous methods have been used to detect lung cancer using CT scans. The many uses of imaging in diagnostics, and the potential of image-based diagnostics in the field of histology have also been investigated [21, 28, 29].

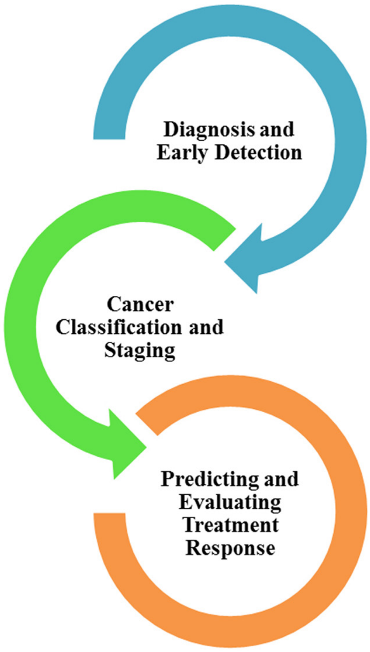

Fig. 2. Applications of machine learning in oncology

By integrating trends among patients across a potentially long-time horizon, ML may also be useful for early cancer identification. Although the importance of early cancer detection is well acknowledged, it is difficult to achieve due to the subtlety and individual variability of the variables that are indicative of cancer onset. Breast densities in mammography and computed tomography (CT) scans of the lungs have both been utilized in conjunction with computer vision techniques to provide predictions about the likelihood of a future diagnosis of cancer [21, 30]. While other researchers have used EMR data to predict pancreatic cancer risk in a high-risk cohort, others have concentrated on identifying cancer susceptibility using gene expression data. Cancer screening practices and policies might be improved with the help of these early warning systems. Most importantly, they may allow for quicker treatment and better health results for patients [21, 22].

4 Cancer classification and staging

Cancers are often classified according to the stage at which they are detected. It has far-reaching ramifications for treatment guidelines and patient care because it often determines eligibility criteria for clinical trials and prognostic estimations. Since they were created in 1977, the American Joint Committee on Cancer (AJCC) guidelines have been seen as the best way to stage cancer in clinical settings Particularly, the TNM classification permits stage categorization based on a small number of parameters, including primary tumor size (T), affected lymph nodes (N), and the existence of metastases (M). This ease of use is especially useful for cancer classification schemes, which can then function with minimum data collection in order to establish a consistent and widely acknowledged set of features. Clinically generated cut-off values are used in these methods, despite the fact that they may be missing key clinical aspects. Recognition of the system's limitations has stimulated exploration of new avenues of inquiry [21, 31, 32].

Staging cancer is a method used to divide patients into distinct risk groups. AI provides a chance to designate staging criteria directly from data, which could lead to more accurate prognostic difference between stages. Patients can be divided into prognostic groups, for instance, with the help of a model that forecasts disease-free survival. And so, in a way, this becomes the de facto way to categorize cancer [21].

This method has been used to study a variety of cancers, including pancreatic cancer and intrahepatic cholangiocarcinoma. Patient stratification is improved over the AJCC technique in all of the methods, despite their differences, because of the use of large-scale data to discover new predictors. These works make use of the possibility to analyze possibly thousands of patients at once, parsing a large number of features simultaneously, which was not possible when the AJCC was first established [33, 34].

The standard method for cancer staging involves using a supervised learning framework to predict survival, and then using an analysis of the predictors to establish staging criteria. Separate cohorts within cancer types can be identified with the help of unsupervised learning as well. Even though the algorithm does not take survival directly into account, it has been applied to lung cancer and breast cancer with similar results: the resulting subgroups had distinct prognoses [21]. Subgroups can be derived without an explicit outcome, which is useful because assessing survival is notoriously noisy and complex. To divide cancer patients more broadly into clinical groupings, clustering provides a fresh perspective. It has also proven possible to employ unsupervised learning to find cancer-related gene signatures. Scientists have used this to get insight into the many different types of cancer profiles. The discovery of such groups opens the door to enhanced disease knowledge and individualized approaches to therapy planning [35, 36].

5 Predicting and evaluating treatment response

Prescriptive insights are another benefit of ML. Alternative treatment selections and patient monitoring can be improved with the help of individual predictions of response and harmful effects. The increasing availability of cell line data has allowed for widespread drug sensitivity prediction based on genetic profiles, and genomic data have played a key part in this effort. Pan cancer analysis and more specific interactions, such as the response to leucovorin, fluorouracil, and oxaliplatin in patients with colorectal cancer, have both made use of genomic information to predict clinical response measures [21, 37, 38].

Patients undergoing neoadjuvant chemotherapy have had their response predicted using ML, radiomics has been utilized to treat NSCLC, and breast cancer patients have been treated using a mix of clinical and imaging data. There has been additional work to identify treatment-related side effects, both at the medication level and at the patient level [39, 40].

When evaluating tumor response, ML can be utilized instead of the standard two-dimensional tumor assessments based on RECIST. As a result of practical considerations, such as utilizing features that could be reasonably measured by radiologists, it was necessary to rely on two-dimensional measures. Some researchers have discovered that RECIST may not properly track progress in patient outcomes; hence this method is not without its flaws. In the same way that ML has been used to improve diagnostic imaging, it has also been utilized to automatically detect RECIST criteria in patients with NSCLC. Response assessment sequences of CT scans for non-small cell lung cancer (NSCLC) and volumetric measurements of magnetic resonance imaging (MRI) for brain tumors are two examples of RECIST alternatives introduced in other publications [21, 41].

6 Evolution of machine learning methods in oncology

For a long time now, data mining and the identification of recurring patterns and dependencies have been essential parts of ML approaches to AI. Quantitative methods have proven useful in the last decade, but clinical science [22, 23]. The rule-based system MYCIN, developed in the 1970s at Stanford University, was the first significant application of AI in medicine. Using patient data and laboratory measurements, the system would identify the presence of germs and provide treatment recommendations. In the 1980s and 1990s, radiologists used computer-aided diagnosis and detection based on image analysis, thanks to the initial success of AI technologies in the medical field. With the advent of the computer and the information era, however, this optimism faded, giving way to the prospect of progress in most people and cynicism in a few others. Revitalized enthusiasm can be attributed to the recent development of AI techniques and their application in medicine, particularly through the use of machine intelligence [23, 42].

There is apprehension about the benefits of ML in healthcare settings because of the unknowns that come with new technologies. Concern about being replaced by machines is a major source of anxiety for medical professionals. Even though most healthcare decisions are reached through consensus in general, tumor boards in oncology are a classic working example of this. The role of ML will be to assist the practitioner in making decisions, much like having a personal smart assistant that can quickly sift through vast amounts of data, make instantaneous comparisons, and offer immediate advice [22].

To compensate for incorrect judgments brought on by variations in the test population or other sources of bias in training [43, 44]. There is also the argument that people's knowledge is biased because it is based on their experiences and the characteristics that they can see in the data. To get the most out of an AI system, it is best to completely automate the decision-making process, as machines learn to follow a set of rules [23]. Most neural architecture-based AI systems still in use today rely heavily on a corporate-developed codebase, which ideally needs to be trained, tested, and validated across medical centers to reduce overtreatment (false negatives); until then, It's possible that keeping human specialists in the process is inevitable.

When architectures first became available, the image-centric sciences (radiology/pathology) were among the first to exploit them [45]. One translational use of deep learning convolutional neural network (CNN) is in the detection of skin lesions (melanoma) using images. These programs are promoted as a screening and diagnostic assistance that can be used right at the front lines. AI has also been put to use in the detection of diabetic retinopathy using retinal fundus photographs, an application that has proven useful for expansion into areas with fewer medical facilities [22, 46].

The detection of polyps in colonoscopy images using deep networks has been demonstrated to be effective [46]. In pathology, there are a number of uses; for example, in a recent study, researchers demonstrated the ability to detect tumor-infiltrating lymphocytes (TIL) in a variety of cancer types on whole slides [23]. The AI methods like HistoQC and DeepFocus are being used in the real world to standardize and improve the quality of whole slide imaging, which has the potential to enhance detection abilities [47]. Numerous radiological applications have been found to be helpful [48], with one recent study demonstrating the ability to spot malignant nodules in screening CT scans. Despite the potential of these methods to enhance detection and care for patients, they have been hampered by a lack of "high quality" curated datasets [23].

Methods in machine learning: ensuring their validity and repeatability.

Even while recent advances in deep learning analyses have shown promise in clinical research, the actual impacts on ordinary clinical care may still remain speculative. Although many studies have claimed clinical translation, most of these are based on historical data that presumably pertains to older technologies, and medical research is always progressing [49]. Internal and external validation of ML approaches may be required for ML-related clinical applications to increase the likelihood of being beneficial for routine patient care with some degree of prospective (or live) training. Several guidelines have been proposed that detail the most effective ways to advance AI for use in healthcare [50].

Transparency in reporting multivariate prediction models for prognosis or diagnosis (TRIPOD) [51] is one such relevant guideline that offers a reliability score for multivariate analysis. There have been more nuanced proposals for radiological application, such as the Checklist for Artificial Intelligence in Medical Imaging (CLAIM) [52]. MI-CLAIM (Minimum information about clinical artificial intelligence modeling) [53] proposes additional guidelines specific to oncological applications. Radiation oncology/medical physics, among others, are just two examples of the many proposed domain-specific uses by numerous societies [54]. The use of AI and ML in cancer care is likely to become standard once these guidelines are implemented [22]. Figure 3 demonstrates the validation and repeatability of ML methods.

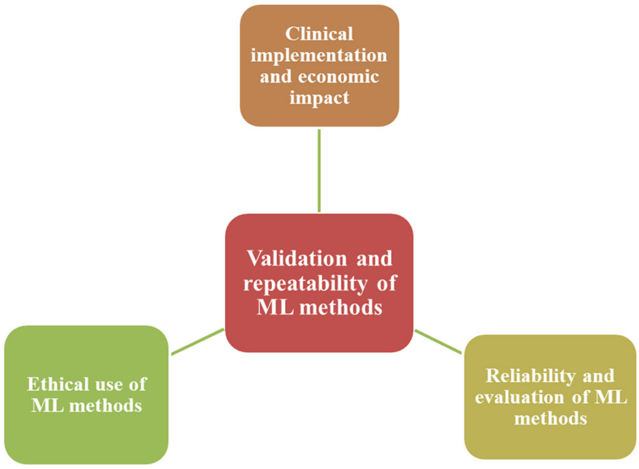

Fig. 3. Validation and repeatability of ML methods

7 Clinical implementation and economic impact

For ML methods to be validated in the clinic, doctors must work closely with the researchers to ensure that they have a thorough understanding of the system and a non-perspective experts on the method's functionality, which will help them notice and identify possible erroneous results. Most published work lacks inclusion criteria or consistency that allows comparison between research, and a recent analysis of AI-related articles reveals no or minimal economic clinical assessment [55]. Initial investment, operational cost for an AI system, and a tangible return in terms of patient care, which may comprise a decrease in medical errors, etc., will form the backbone of the deployment process in a clinical setting. Examination of these features is important since they affect clinical uptake. More detailed genetic analysis at the cellular level and other similar methodologies [22, 23].

Adopting AI technologies to existing treatment in a clinical setting will require tight integration with the existing Electronic Medical Record (EMR) process. Clinical cost-benefit analyses are often necessary at the institutional level whenever even a minor change to the present workflow needs a clinician's time for system evaluation or more staff time. Many targeted biopsies are taken during a single office visit in breast and genitourinary oncology clinics, to provide just two examples. Adaptive learning-based clinical judgments will play a part in the treatment and management of diseases, and AI systems will bring with them the promise of increased optimism in healthcare [22, 23].

It may still be necessary for the clinical expert to engage with the human patient, learn about the patient's unique circumstances, and decide in tandem with the patient; taking into account the latter's unique psychological make-up, cultural background, and social preferences. Machines will make decisions that are supplementary to those made by humans, with humans typically making the final clinical call [43]. Some familiarity studies have analyzed the ways in which these tools are being used in healthcare generally and oncology in particular, placing special emphasis on the reliable (ethical) application of AI approaches [44]. Although it is likely that new technologies will benefit from having a human expert in the loop, it is important to ensure that they are being used in the right context [23, 44].

8 Reliability and evaluation of ML methods

There has been resurgence in discussion on the governance of AI models in the medical sciences as well as their interpretability; these issues have been aggravated using models that cannot be explained by utilizing deep neural networks [56]. On the other hand, it is not required of the majority of practitioners that they grasp the workings of the system. As a point of comparison, driver must be capable of driving a vehicle safely and effectively based solely on past knowledge. Whereas it's true that a mechanic is an expert who is well-versed in the nuances of the system, they're not the only one. It is not uncommon for consumers to control a vehicle (whether it is mechanically driven or driven by AI) without being required to have any expertise about the technology [22, 23].

In order to save lives, it is essential that the models we use improve clinical decision-making and minimize unintended negative outcomes. Below is a list of generally regarded competitors TRIPOD, CLAIM, MI-CLAIM, which were developed by a broad survey of academic and industry professionals' perspectives and are cited in the latest consensus statements that give criteria to evaluate multivariate statistical approaches [52, 53]. A recent review of ML approaches in oncology gives insights and recommended practices [34], although ML methods have yet to catch up. New restrictions from the Food and Drug Administration (FDA) on AI systems underline the importance of performance accuracy and additional clinical value if the method is to be trusted [57, 58].

It is generally agreed that models should be created with a large and varied population, and that methods should be tested on a separate dataset to ensure they produce accurate and reliable results. Model transparency in cancer may be hindered by the incomprehensible complexity of ML models, especially deep learning networks. Typically, a model that functions within the scope of a disease or molecular subtype is developed through the tried-and-true processes of training and validation. The emerging set of AI-based methods challenge this common sense. Pre-trained deep network models have been used to effectively claim to provide disease risk assessment in oncology [59], and these models are being trained on photos of everyday objects (cats, dogs, toilets, etc.) from mixed contexts. Previously, the most effective deep networks, which contained over 650,000 neurons and nearly 60 million parameters, require a tremendous amount of data to train. Since there aren't many carefully managed public datasets for oncology, researchers have resorted to transfer learning to train their networks to discriminate between different diseases. It's possible that these methods have a solid technical foundation for training massive deep networks, but they're definitely going against the grain [21, 23].

The greatest level (level 4) as assessed by the TRIPOD statement would be met if clinical models could be reproduced by an independent research group, either by re-implementing the approach or by using the same code base to generate (near to) equivalent findings [60].

The first step in assessing variability to acquire confidence in the employment of a method may be to test the approach's repeatability in a technically repeated variations in extracted metrics can be expected when scanning the same patient multiple times using most methodologies, such as imaging, due to differences in patient position, as determined by reconstruction operations and delineations procedure. To assess the volume metrics [61] and other quantitative imaging aspects [62], it was crucial to be able to estimate reliable metrics in repeated patient scans. Quantitative characteristics may be impacted by patient-related factors (motion, respiration, etc.), which are widely known to be a potential source of variation. Features collected at the lesion level must be robust enough to resist some change without impacting the clinical judgment, detection, or risk assessment. The experimental variability of an omics-based biomarker is comparable to that of a biomarker produced in the basic sciences. The greater amount of time spent on development has enabled for the assay refining that has reduced variability to a more manageable percentage [63]. Therefore, ML techniques must undergo a progression in order to achieve sufficient reproducibility and repeatability [64, 65].

9 Ethical use of AI methods

The rise of AI and the popularity of its approaches have prompted a wider discussion on the ethics of applying AI in general. According to a recent evaluation by UNESCO [66], it has been stated that AI approaches can produce biased results that are erroneous and discriminatory. Artificial intelligence algorithms are used frequently to locate sought individuals and spot possible societal disruptions individuals in the context of population surveillance. It is common for some groups to be singled out as possible matches, especially in countries like the United States. False positives in identity verification have led to widespread scepticism about the reliability of modern technologies [67].

The capacity to explain how a clinical model works, defines its structure and parameters, and articulate its underlying assumptions are all prerequisites for its acceptance. Transparency can be achieved through clear model definition and subsequent model validation, as described in a recent consensus statement that outlines the requirements of a decision-making model in healthcare [23, 69]. There is a concerted attempt to uncover aspects and attributes that may be accountable for a machine decision [67], sometimes known as the "black box method," which is commonly connected with ML model techniques. Models may have to record the deficiency, quantify the risk of false detection or uncertainty. The term "explainable artificial intelligence" (XAI) refers to a group of techniques that go beyond mere interpretability and transparency. Some of these strategies have concentrated on visualization, such as saliency or activation maps [68], while others have employed approximations like LIME (Local Interpretable Model- Agnostic Explanations) to get closer to the truth. Using SHAP values, a concept borrowed from game theory that tends to assign an importance value for a feature, in a particular forecast, is an interesting strategy that finds traction to reduce bias. Although it may be necessary for an ideal clinical decision support system, it must be stressed that interpretability is only a first step toward better explaining the model. Moreover, interpretability does not indicate causality [22, 23].

10 Discussion and conclusion

Most research projects employ some form of learning strategy, and those strategies can be roughly classified as either supervised or unsupervised [70]. Thanks to recent developments in deep networks [71], artificial intelligence may soon surpass human cognition. These techniques have expanded from their initial use in radiological sciences [23] to other oncological-omics datasets [72]. Many deep learning networks have been primed for the context of interest using a smaller cohort and trained on smaller data sets or random iterations of training data. Recent developments in Few-Shot learning methods have raised hopes for the potential of these AI approaches in low-volume contexts [73].

Users and clinical practitioners face a huge issue when trying to evaluate the trustworthiness of these network techniques for therapeutic use. Recent retinopathy detection system had various ground level concerns, including failed expectations owing to quality and user level issues. These problems highlight the fact that there are real obstacles to the successful implementation of AI technology [23].

Certainly, typical of all technological implementations, to date automobile recalls are recognized as adequate repair method and other technologies improve any shortcoming [74]. Future adoption hinges on how the technology is perceived by people, but it also requires decisive action to address existing and emerging issues for it to be reliable.

In this decade, the high-tech industry has led the way in implementing new methodologies, such as the usage of massive code bases that have been painstakingly adapted for oncological data, with an unknown extent of reprocessing, all in an effort to discern and go beyond human levels of perception. The results of these methods are consistent across hitherto unexplored data types. The necessity for open disclosure of codebase, datasets used for training, and reprocessing processes to reach desired output has been cited to increase transparency and dependability of these deep network discoveries in recent work [75]. Permitting an open and unbiased evaluation of the validity and reproducibility of these methods may be important.

We have reached a crossroads in cancer due to the use of ML techniques, and this has led to several arguments among oncologists about how the AI systems are either a) inexplicable, or b) a threat to their livelihood since they believe machines can do a better job than people. While it's possible that these networks can't be explained, once we give them enough data to learn from, they'll be put to good use. Examples of useful recommendations include recommending further product support after a customer has made a purchase and using facial recognition software to reunite lost family members. Clinical systems must be either transparent or interpretable to allow for flexible multi-expert input to be considered in AI judgments. As it has been clear that AI technologies will have far-reaching effects on human civilization in a variety of ways, it has also become clear that ethical use of technology with some oversight is important for adaptation. Because of the potential for AI technology to have far-reaching consequences, UNESCO commissioned a paper on the ethical use of AI technologies [23].

In medicine, a federated model that updates the model utilizing data from many silos has shown promising results. There is much promise in the recent application of distributed learning across numerous centers located on three continents to construct a strong clinical model. Due to the complexity of medicine and oncology in particular, robots may not be able to totally replace human involvement in diagnosis and treatment, necessitating a multi-stage process beginning with creation and ending with widespread adoption of the resulting technologies. Artificial intelligence (AI) systems will play an increasingly important role in oncology, assisting doctors with diagnostics and treatment decisions and raising hopes for the development of new therapies and the discovery of effective treatments for previously incurable diseases. Figure 4 shows advantages and disadvantages of ML method [76, 77].

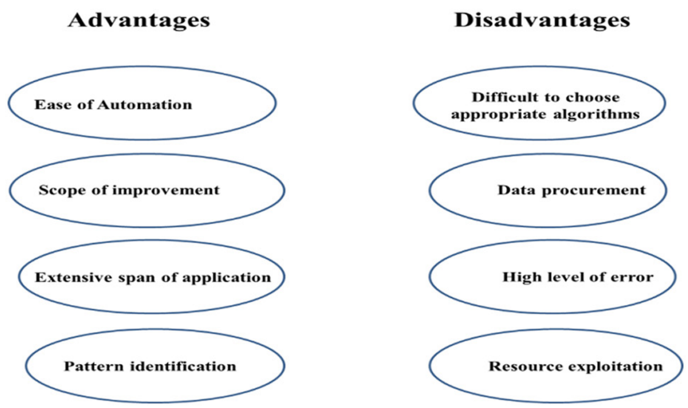

Fig. 4. Advantages and disadvantages of ML method

Final thoughts we anticipate that the use of AI techniques will provide a significant chance to overcome the current limitation of our ability to understand the complexities of the human mind and to automate previously manual tasks. Due to the intricacy of cancer, these methodologies, together with ML methods, are going to remain and will be of great use to the professional medical sector. In order to increase the openness and trustworthiness of ML and deep approaches in the medical sciences, we have developed the following based on a review of the relevant literature and actual research findings. Both centralized and federated/distributed learning models, which draw from a wide variety of data silos, have the capacity to deliver a varied cohort of patient records for the purpose of model training. The difference between the two types of models is in how they access those data silos. Putting together a group of people who have nothing in common with each other and testing it on a large number of patients in a remote place. In addition to having the ability to observe the structure of a model that contains a deep neural network; one must also have the ability to trust the model's outputs, at least to some extent, also the installation of a wide range of AI components in a responsible manner and with some kind of oversight. Testing artificial intelligence models multiple times to determine whether or not they can be depended on to provide the same results each time. A model that is open and honest about its structure, the data sets it uses, and the training weights it uses is transparent and frank. a quality assurance program that is possible to be put into action and whose results can be tracked in real time.

Lung cancer diagnosis, skin cancer diagnosis, and breast cancer brain tumor detection are only some of the pathology-based diagnostic tasks that have benefited from the use of convolutional neural networks. Table 1 demonstrated recent studies in machine learning algorithms are used in cancer detection and diagnosis.

Table 1. Several machine learning algorithms are used in cancer detection and diagnosis

References	Cancer Type	Algorithms	Performance Accuracy
Osman 2017 [78]	Breast	Two-Step-SVM	Accuracy: 99.1%
Latchoumi & Parthiban 2017 [79]	Breast	WPSO-SSVM	Accuracy: 95.2% Sensitivity: 97.57% Specificity: 93.45%
Kumar et al., 2017 [80]	Breast	Voting classifier and SVM-Naive Bayes-J48	Accuracy: 97.1%
Vijayarajeswari et al., 2019 [81]	Breast	SVM	Accuracy: 94%
Faisal et al., 2018 [82]	Lung	MLP, Decision Tree and SVM	Accuracy: 90%
Bhandary et al., 2020 [83]	Lung	MAN and EFT classifier	Accuracy: 97.2% Sensitivity: 98.1% Specificity: 95.3%
Makaju et al., 2018 [84]	Lung	Watershed segmentation and SVM	Accuracy: 92% Sensitivity: 100% Specificity: 50%
Singh and Gupta, 2019 [85]	Lung	k-nearest neighbours and SVM classifiers	88.5%
Lohman et al., 2020 [86]	Brain	GLSZM and SVM-RFE	Accuracy: 70% Sensitivity: 100% Specificity: 40%
Wang et al., 2020 [87]	Brain	Texture LASSO	Accuracy: 79.2% Sensitivity: 75.0% Specificity: 91.7%
Zhang et al., 2018 [88]	Brain	RUSBoost	Accuracy: 86.6% Sensitivity: 99.07% Specificity: 97.93%
Gao et al., 2020 [89]	Brain	GLCM, GLSZM and SVM	Accuracy: 93.33% Sensitivity: 100% Specificity: 90%
Murugan et al., 2019 [90]	Skin	SVM, Random Forest and kNN Classifiers	Accuracy: 89.4% Sensitivity: 91.1% Specificity: 87.7%
Banasode et al., 2021 [91]	Skin	SVM	Accuracy: 96.9% Sensitivity: 95.7% Specificity: 90.2%
Farooq et al., 2016 [92]	Skin	GLCM and HOG	Accuracy: 97.8% Sensitivity: 75% Specificity: 65%
Vaishnavi et al., 2016 [93]	Skin	GLCM	Accuracy: 98% Sensitivity: 96.3% Specificity: 95%

11 Acknowledgment

This work was supported and sponsored by Al-Ahliyya Amman University. The authors would like to express gratitude for their financial support.

12 References

[1] J. G. Greener, S. M. Kandathil, L. Moffat, and D. T. Jones, "A guide to machine learning for biologists," Nature Reviews Molecular Cell Biology, vol. 23, no. 1, pp. 40–55, 2021, https://doi.org/10.1038/s41580-021-00407-0

[2] E. Francy Irudaya Rani, T. L. Pushparaj, E. Fantin Irudaya Raj, and M. Appadurai, "New approaches in machine-based image analysis for medical oncology," Machine Learning and Deep Learning Techniques for Medical Science, pp. 333–359, 2022, https://doi.org/10.1201/9781003217497-17

[3] T. Oladipupo, "Types of machine learning algorithms," New Advances in Machine Learning, 2010, https://doi.org/10.5772/9385

[4] R. A. Rayan, "Machine learning for smart health care," Machine Learning Algorithms and Applications in Engineering, pp. 1–16, 2023, https://doi.org/10.1201/9781003104858-1

[5] B. J. Erickson, P. Korfiatis, Z. Akkus, and T. L. Kline, "Machine learning for medical imaging," RadioGraphics, vol. 37, no. 2, pp. 505–515, 2017, https://doi.org/10.1148/rg.2017160130

[6] K. Y. Ngiam and I. W. Khor, "Big data and machine learning algorithms for health-care delivery," The Lancet Oncology, vol. 20, no. 5, pp. e262–e273, 2019, https://doi.org/10.1016/S1470-2045(19)30149-4

[7] K. Bera, K. A. Schalper, D. L. Rimm, V. Velcheti, and A. Madabhushi, "Artificial intelligence in digital pathology—new tools for diagnosis and precision oncology," Nature Reviews Clinical Oncology, vol. 16, no. 11, pp. 703–715, 2019, https://doi.org/10.1038/s41571-019-0252-y

[8] I. El Naqa, M. A. Haider, M. L. Giger, and R. K. Ten Haken, "Artificial intelligence: Reshaping the practice of radiological sciences in the 21st century," The British Journal of Radiology, vol. 93, no. 1106, p. 20190855, 2020, https://doi.org/10.1259/bjr.20190855

[9] T. Munakata, "Thoughts on Deep Blue vs. Kasparov," Communications of the ACM, vol. 39, no. 7, pp. 91–92, 1996, https://doi.org/10.1145/233977.234001

[10] B. L. Lewis, "In the game: The interface between Watson and Jeopardy!," IBM Journal of Research and Development, vol. 56, no. 3.4, pp. 17:1–17:6, 2012, https://doi.org/10.1147/JRD.2012.2188932

[11] D. Mulfari, "A TensorFlow-based Assistive Technology System for Users with Visual Impairments," Proceedings of the 15th International Web for All Conference, Apr. 2018, https://doi.org/10.1145/3192714.3196314

[12] Y. Sun et al., "Identification of 12 cancer types through genome deep learning," Scientific Reports, vol. 9, no. 1, 2019, https://doi.org/10.1038/s41598-019-53989-3

[13] A. Krizhevsky, I. Sutskever, and G. E. Hinton, "ImageNet classification with deep convolutional neural networks," Communications of the ACM, vol. 60, no. 6, pp. 84–90, 2017, https://doi.org/10.1145/3065386

[14] S. E. Dreyfus, "Artificial neural networks, back propagation, and the Kelley-Bryson gradient procedure," Journal of Guidance, Control, and Dynamics, vol. 13, no. 5, pp. 926–928, 1990, https://doi.org/10.2514/3.25422

[15] Y. LeCun, Y. Bengio, and G. Hinton, "Deep learning," Nature, vol. 521, no. 7553, pp. 436–444, 2015, https://doi.org/10.1038/nature14539

[16] J. V. Tu, "Advantages and disadvantages of using artificial neural networks versus logistic regression for predicting medical outcomes," Journal of Clinical Epidemiology, vol. 49, no. 11, pp. 1225–1231, 1996, https://doi.org/10.1016/S0895-4356(96)00002-9
[17] D. Bertsimas and H. Wiberg, "Machine learning in oncology: Methods, applications, and challenges," JCO Clinical Cancer Informatics, no. 4, pp. 885–894, 2020, https://doi.org/10.1200/CCI.20.00072
[18] P. Istasy et al., "The impact of artificial intelligence on health equity in oncology: Scoping review," Journal of Medical Internet Research, vol. 24, no. 11, p. e39748, 2022, https://doi.org/10.2196/39748
[19] M. Field, N. Hardcastle, M. Jameson, N. Aherne, and L. Holloway, "Machine learning applications in radiation oncology," Physics and Imaging in Radiation Oncology, vol. 19, pp. 13–24, 2021, https://doi.org/10.1016/j.phro.2021.05.007
[20] E. W. Sayers et al., "Database resources of the national center for biotechnology information," Nucleic Acids Research, vol. 49, no. D1, pp. D10–D17, 2020, https://doi.org/10.1093/nar/gkaa892
[21] E. Strickland, "IBM Watson, heal thyself: How IBM overpromised and underdelivered on AI health care," IEEE Spectrum, vol. 56, no. 4, pp. 24–31, 2019, https://doi.org/10.1109/MSPEC.2019.8678513
[22] J. Kirby et al., "Introduction to special issue on datasets hosted in The Cancer Imaging Archive (TCIA)," Medical Physics, vol. 47, no. 12, pp. 6026–6028, 2020, https://doi.org/10.1002/mp.14595
[23] C. Nardini, "Machine learning in oncology: A review," ecancermedicalscience, vol. 14, 2020, https://doi.org/10.3332/ecancer.2020.1065
[24] Y. Balagurunathan, R. Mitchell, and I. El Naqa, "Requirements and reliability of AI in the medical context," Physica Medica, vol. 83, pp. 72–78, 2021, https://doi.org/10.1016/j.ejmp.2021.02.024
[25] H.-J. Lu, C.-L. An, X.-P. Ma, E.-H. Zheng, and X.-B. Yang, "Disagreement measure based ensemble of extreme learning machine for gene expression data classification," Chinese Journal of Computers, vol. 36, no. 2, pp. 341–348, 2014, https://doi.org/10.3724/SP.J.1016.2013.00341
[26] K.-B. Hwang, D.-Y. Cho, S.-W. Park, S.-D. Kim, and B.-T. Zhang, "Applying machine learning techniques to analysis of gene expression data: Cancer diagnosis," Methods of Microarray Data Analysis, pp. 167–182, 2002, https://doi.org/10.1007/978-1-4615-0873-1_13
[27] W. H. Wolberg, W. N. Street, and O. L. Mangasarian, "Machine learning techniques to diagnose breast cancer from image-processed nuclear features of fine needle aspirates," Cancer Letters, vol. 77, no. 2–3, pp. 163–171, 1994, https://doi.org/10.1016/0304-3835(94)90099-X
[28] R. Ramos-Pollán et al., "Discovering mammography-based machine learning classifiers for breast cancer diagnosis," Journal of Medical Systems, vol. 36, no. 4, pp. 2259–2269, 2011, https://doi.org/10.1007/s10916-011-9693-2
[29] A. Madabhushi, "Digital pathology image analysis: Opportunities and challenges," Imaging in Medicine, vol. 1, no. 1, pp. 7–10, 2009, https://doi.org/10.2217/iim.09.9
[30] R. Etzioni et al., "The case for early detection," Nature Reviews Cancer, vol. 3, no. 4, pp. 243–252, 2003, https://doi.org/10.1038/nrc1041
[31] B.-J. Kim and S.-H. Kim, "Prediction of inherited genomic susceptibility to 20 common cancer types by a supervised machine-learning method," Proceedings of the National Academy of Sciences, vol. 115, no. 6, pp. 1322–1327, 2018, https://doi.org/10.1073/pnas.1717960115
[32] "AJCC cancer staging manual," 2002, http://doi.org/10.1007/978-1-4757-3656-4
[33] M. B. Amin et al., "The eighth edition AJCC cancer staging manual: Continuing to build a bridge from a population-based to a more 'personalized' approach to cancer staging," CA: A Cancer Journal for Clinicians, vol. 67, no. 2, pp. 93–99, 2017, https://doi.org/10.3322/caac.21388

[34] A. Das and S. Ngamruengphong, "81 machine learning based predictive models are more accurate than TNM staging in predicting survival in patients with pancreatic cancer," American Journal of Gastroenterology, vol. 114, no. 1, pp. S48–S48, 2019, https://doi.org/10.14309/01.ajg.0000589856.45106.e0
[35] D. I. Tsilimigras et al., "A machine-based approach to preoperatively identify patients with the most and least benefit associated with resection for intrahepatic cholangiocarcinoma: An international multi-institutional analysis of 1146 patients," Annals of Surgical Oncology, vol. 27, no. 4, pp. 1110–1119, 2019, https://doi.org/10.1245/s10434-019-08067-3
[36] C. M. Lynch, V. H. van Berkel, and H. B. Frieboes, "Application of unsupervised analysis techniques to lung cancer patient data," PLOS ONE, vol. 12, no. 9, p. e0184370, 2017, https://doi.org/10.1371/journal.pone.0184370
[37] Z. Kakushadze and W. Yu, "*K-means and cluster models for cancer signatures," Biomolecular Detection and Quantification, vol. 13, pp. 7–31, 2017, https://doi.org/10.1016/j.bdq.2017.07.001
[38] M. Q. Ding, L. Chen, G. F. Cooper, J. D. Young, and X. Lu, "Precision oncology beyond targeted therapy: Combining omics data with machine learning matches the majority of cancer cells to effective therapeutics," Molecular Cancer Research, vol. 16, no. 2, pp. 269–278, 2018, https://doi.org/10.1158/1541-7786.MCR-17-0378
[39] C. Huang et al., "Machine learning predicts individual cancer patient responses to therapeutic drugs with high accuracy," Scientific Reports, vol. 8, no. 1, 2018, https://doi.org/10.1038/s41598-018-34753-5
[40] P. Bloomingdale and D. E. Mager, "Machine learning models for the prediction of chemotherapy-induced peripheral neuropathy," Pharmaceutical Research, vol. 36, no. 2, 2019, https://doi.org/10.1007/s11095-018-2562-7
[41] A. Abajian et al., "Predicting treatment response to intra-arterial therapies for hepatocellular carcinoma with the use of supervised machine learning—an artificial intelligence concept," Journal of Vascular and Interventional Radiology, vol. 29, no. 6, pp. 850–857.e1, 2018, https://doi.org/10.1016/j.jvir.2018.01.769
[42] L. C. Villaruz and M. A. Socinski, "The clinical viewpoint: Definitions, limitations of RECIST, practical considerations of measurement," Clinical Cancer Research, vol. 19, no. 10, pp. 2629–2636, 2013, https://doi.org/10.1158/1078-0432.CCR-12-2935
[43] E. H. Shortliffe, R. Davis, S. G. Axline, B. G. Buchanan, C. C. Green, and S. N. Cohen, "Computer-based consultations in clinical therapeutics: Explanation and rule acquisition capabilities of the MYCIN system," Computers and Biomedical Research, vol. 8, no. 4, pp. 303–320, 1975, https://doi.org/10.1016/0010-4809(75)90009-9
[44] J. Goldhahn, V. Rampton, and G. A. Spinas, "Could artificial intelligence make doctors obsolete?," BMJ, p. k4563, 2018, https://doi.org/10.1136/bmj.k4563
[45] J. R. Geis et al., "Ethics of artificial intelligence in radiology: Summary of the joint european and north american multisociety statement," Radiology, vol. 293, no. 2, pp. 436–440, 2019, https://doi.org/10.1148/radiol.2019191586
[46] T. Rai et al., "Can ImageNet feature maps be applied to small histopathological datasets for the classification of breast cancer metastatic tissue in whole slide images?," Medical Imaging 2019: Digital Pathology, 2019, https://doi.org/10.1117/12.2512853
[47] V. Gulshan et al., "Development and validation of a deep learning algorithm for detection of diabetic retinopathy in retinal fundus photographs," JAMA, vol. 316, no. 22, p. 2402, 2016, https://doi.org/10.1001/jama.2016.17216
[48] C. Senaras, M. K. K. Niazi, G. Lozanski, and M. N. Gurcan, "DeepFocus: Detection of out-of-focus regions in whole slide digital images using deep learning," PLOS ONE, vol. 13, no. 10, p. e0205387, 2018, https://doi.org/10.1371/journal.pone.0205387

[49] D. Ueda, A. Shimazaki, and Y. Miki, "Technical and clinical overview of deep learning in radiology," Japanese Journal of Radiology, vol. 37, no. 1, pp. 15–33, 2018, https://doi.org/10.1007/s11604-018-0795-3
[50] M. Nagendran et al., "Artificial intelligence versus clinicians: Systematic review of design, reporting standards, and claims of deep learning studies," BMJ, p. m689, 2020, https://doi.org/10.1136/bmj.m689
[51] M. Nagy, N. Radakovich, and A. Nazha, "Machine learning in oncology: What should clinicians know?," JCO Clinical Cancer Informatics, no. 4, pp. 799–810, 2020, https://doi.org/10.1200/CCI.20.00049
[52] G. S. Collins, J. B. Reitsma, D. G. Altman, and K. G. M. Moons, "Transparent reporting of a multivariable prediction model for individual prognosis or diagnosis (TRIPOD): The TRIPOD statement," British Journal of Surgery, vol. 102, no. 3, pp. 148–158, 2015, https://doi.org/10.1002/bjs.9736
[53] J. Mongan, L. Moy, and C. E. Kahn, "Checklist for artificial intelligence in medical imaging (CLAIM): A guide for authors and reviewers," Radiology: Artificial Intelligence, vol. 2, no. 2, p. e200029, 2020, https://doi.org/10.1148/ryai.2020200029
[54] B. Norgeot et al., "Minimum information about clinical artificial intelligence modeling: The MI-CLAIM checklist," Nature Medicine, vol. 26, no. 9, pp. 1320–1324, 2020, https://doi.org/10.1038/s41591-020-1041-y
[55] E. Huynh et al., "Artificial intelligence in radiation oncology," Nature Reviews Clinical Oncology, vol. 17, no. 12, pp. 771–781, 2020, https://doi.org/10.1038/s41571-020-0417-8
[56] J. Wolff, J. Pauling, A. Keck, and J. Baumbach, "Systematic review of economic impact studies of artificial intelligence in health care," Journal of Medical Internet Research, vol. 22, no. 2, p. e16866, 2020, https://doi.org/10.2196/16866
[57] S. Reddy, S. Allan, S. Coghlan, and P. Cooper, "A governance model for the application of AI in health care," Journal of the American Medical Informatics Association, vol. 27, no. 3, pp. 491–497, 2019, https://doi.org/10.1093/jamia/ocz192
[58] S. Benjamens, P. Dhunnoo, and B. Meskó, "The state of artificial intelligence-based FDA-approved medical devices and algorithms: An online database," NPJ Digital Medicine, vol. 3, no. 1, 2020, https://doi.org/10.1038/s41746-020-00324-0
[59] S. Zhu, M. Gilbert, I. Chetty, and F. Siddiqui, "The 2021 landscape of FDA-approved artificial intelligence/machine learning-enabled medical devices: An analysis of the characteristics and intended use," International Journal of Medical Informatics, vol. 165, p. 104828, 2022, https://doi.org/10.1016/j.ijmedinf.2022.104828
[60] D. Bychkov et al., "Deep learning based tissue analysis predicts outcome in colorectal cancer," Scientific Reports, vol. 8, no. 1, 2018, https://doi.org/10.1038/s41598-018-21758-3
[61] D. R. Boulbes et al., "A survey on data reproducibility and the effect of publication process on the ethical reporting of laboratory research," Clinical Cancer Research, vol. 24, no. 14, pp. 3447–3455, 2018, https://doi.org/10.1158/1078-0432.CCR-18-0227
[62] B. Zhao et al., "Evaluating variability in tumor measurements from same-day repeat CT scans of patients with non–small cell lung cancer," Radiology, vol. 252, no. 1, pp. 263–272, 2009, https://doi.org/10.1148/radiol.2522081593
[63] B. Zhao et al., "Reproducibility of radiomics for deciphering tumor phenotype with imaging," Scientific Reports, vol. 6, no. 1, 2016, https://doi.org/10.1038/srep23428
[64] C. R. Marshall et al., "Best practices for the analytical validation of clinical whole-genome sequencing intended for the diagnosis of germline disease," NPJ Genomic Medicine, vol. 5, no. 1, 2020, https://doi.org/10.1038/s41525-020-00154-9
[65] S. Kanwal, F. Z. Khan, A. Lonie, and R. O. Sinnott, "Investigating reproducibility and tracking provenance—A genomic workflow case study," BMC Bioinformatics, vol. 18, no. 1, 2017, https://doi.org/10.1186/s12859-017-1747-0

[66] M. Ryan, "In AI we trust: Ethics, artificial intelligence, and reliability," Science and Engineering Ethics, vol. 26, no. 5, pp. 2749–2767, 2020, https://doi.org/10.1007/s11948-020-00228-y
[67] A. Lunkov, "The problem of standardizing the ethics of artificial intelligence," Artificial Societies, vol. 15, no. 2, p. 0, 2020, https://doi.org/10.18254/S207751800009044-7
[68] A. L.-H. McArthur, "The debate over sensory processing disorder," American Journal of Psychiatry Residents' Journal, vol. 17, no. 4, pp. 14–15, 2022, https://doi.org/10.1176/appi.ajp-rj.2022.170405
[69] M. Ribeiro, S. Singh, and C. Guestrin, "'Why Should I Trust You?': Explaining the Predictions of Any Classifier," Proceedings of the 2016 Conference of the North American Chapter of the Association for Computational Linguistics: Demonstrations, 2016, https://doi.org/10.18653/v1/N16-3020
[70] A. Barredo Arrieta et al., "Explainable artificial intelligence (XAI): Concepts, taxonomies, opportunities and challenges toward responsible AI," Information Fusion, vol. 58, pp. 82–115, 2020, https://doi.org/10.1016/j.inffus.2019.12.012
[71] N. Rappoport and R. Shamir, "Multi-omic and multi-view clustering algorithms: Review and cancer benchmark," Nucleic Acids Research, vol. 46, no. 20, pp. 10546–10562, 2018, https://doi.org/10.1093/nar/gky889
[72] A. B. Levine, C. Schlosser, J. Grewal, R. Coope, S. J. M. Jones, and S. Yip, "Rise of the machines: Advances in deep learning for cancer diagnosis," Trends in Cancer, vol. 5, no. 3, pp. 157–169, 2019, https://doi.org/10.1016/j.trecan.2019.02.002
[73] Y. Li, W. Shi, and W. W. Wasserman, "Genome-wide prediction of cis-regulatory regions using supervised deep learning methods," BMC Bioinformatics, vol. 19, no. 1, 2018, https://doi.org/10.1186/s12859-018-2187-1
[74] J. Lu, S. Jin, J. Liang, and C. Zhang, "Robust few-shot learning for user-provided data," IEEE Transactions on Neural Networks and Learning Systems, vol. 32, no. 4, pp. 1433–1447, 2021, https://doi.org/10.1109/TNNLS.2020.2984710
[75] T. Gauthier, "Exploring employer perspectives of community college career and technical programs," Career and Technical Education Research, vol. 45, no. 1, pp. 63–76, 2020, https://doi.org/10.5328/cter45.1.63
[76] B. Haibe-Kains et al., "Transparency and reproducibility in artificial intelligence," Nature, vol. 586, no. 7829, pp. E14–E16, 2020, https://doi.org/10.1038/s41586-020-2766-y
[77] T. S. S. Fernando and G. A. T. R. Perera, "Achieving competitive advantage through dynamic capabilities: A study of ICT industry in Sri Lanka," Sri Lanka Journal of Marketing, vol. 7, no. 3, pp. 212–242, 2021, https://doi.org/10.4038/sljmuok.v7i3.80
[78] A. Hamza, "An enhanced breast cancer diagnosis scheme based on two-step-SVM technique," International Journal of Advanced Computer Science and Applications, vol. 8, no. 4, 2017, https://doi.org/10.14569/IJACSA.2017.080423
[79] T. P. Latchoumi, T. P. Ezhilarasi, and K. Balamurugan, "Bio-inspired weighed quantum particle swarm optimization and smooth support vector machine ensembles for identification of abnormalities in medical data," SN Applied Sciences, vol. 1, no. 10, 2019, https://doi.org/10.1007/s42452-019-1179-8
[80] U. K. Kumar, M. B. S. Nikhil, and K. Sumangali, "Prediction of breast cancer using voting classifier technique," 2017 IEEE International Conference on Smart Technologies and Management for Computing, Communication, Controls, Energy and Materials (ICSTM), 2017, https://doi.org/10.1109/ICSTM.2017.8089135

[81] R. Vijayarajeswari, P. Parthasarathy, S. Vivekanandan, and A. A. Basha, "Classification of mammogram for early detection of breast cancer using SVM classifier and Hough transform," Measurement, vol. 146, pp. 800–805, 2019, https://doi.org/10.1016/j.measurement.2019.05.083
[82] M. I. Faisal, S. Bashir, Z. S. Khan, and F. Hassan Khan, "An Evaluation of Machine Learning Classifiers and Ensembles for Early Stage Prediction of Lung Cancer," 2018 3rd International Conference on Emerging Trends in Engineering, Sciences and Technology (ICEEST), Dec. 2018, https://doi.org/10.1109/ICEEST.2018.8643311
[83] A. Bhandary et al., "Deep-learning framework to detect lung abnormality—A study with chest X-Ray and lung CT scan images," Pattern Recognition Letters, vol. 129, pp. 271–278, 2020, https://doi.org/10.1016/j.patrec.2019.11.013
[84] S. Makaju, P. W. C. Prasad, A. Alsadoon, A. K. Singh, and A. Elchouemi, "Lung cancer detection using CT scan images," Procedia Computer Science, vol. 125, pp. 107–114, 2018, https://doi.org/10.1016/j.procs.2017.12.016
[85] G. A. P. Singh and P. K. Gupta, "Performance analysis of various machine learning-based approaches for detection and classification of lung cancer in humans," Neural Computing and Applications, vol. 31, no. 10, pp. 6863–6877, 2018, https://doi.org/10.1007/s00521-018-3518-x
[86] P. Lohmann et al., "FET PET radiomics for differentiating pseudoprogression from early tumor progression in glioma patients post-chemoradiation," Cancers, vol. 12, no. 12, p. 3835, 2020, https://doi.org/10.3390/cancers12123835
[87] K. Wang et al., "Individualized discrimination of tumor recurrence from radiation necrosis in glioma patients using an integrated radiomics-based model," European Journal of Nuclear Medicine and Molecular Imaging, vol. 47, no. 6, pp. 1400–1411, 2019, https://doi.org/10.1007/s00259-019-04604-0
[88] Z. Zhang et al., "A predictive model for distinguishing radiation necrosis from tumour progression after gamma knife radiosurgery based on radiomic features from MR images," European Radiology, vol. 28, no. 6, pp. 2255–2263, 2017, https://doi.org/10.1007/s00330-017-5154-8
[89] X.-Y. Gao et al., "Differentiation of treatment-related effects from glioma recurrence using machine learning classifiers based upon pre-and post-contrast T1WI and T2 FLAIR subtraction features: A two-center study," Cancer Management and Research, vol. 12, pp. 3191–3201, 2020, https://doi.org/10.2147/CMAR.S244262
[90] A. Murugan, S. A. H. Nair, and K. P. S. Kumar, "Detection of skin cancer using SVM, random forest and kNN classifiers," Journal of Medical Systems, vol. 43, no. 8, 2019, https://doi.org/10.1007/s10916-019-1400-8
[91] P. Banasode, M. Patil, and N. Ammanagi, "A melanoma skin cancer detection using machine learning technique: Support vector machine," IOP Conference Series: Materials Science and Engineering, vol. 1065, no. 1, p. 012039, Feb. 2021, https://doi.org/10.1088/1757-899X/1065/1/012039
[92] M. A. Farooq, M. A. M. Azhar, and R. H. Raza, "Automatic Lesion Detection System (ALDS) for Skin Cancer Classification Using SVM and Neural Classifiers," 2016 IEEE 16th International Conference on Bioinformatics and Bioengineering (BIBE), Oct. 2016, https://doi.org/10.1109/BIBE.2016.53
[93] K. R. Vaishnavi, "Detecting melanoma cancer using image processing," International Journal for Research in Applied Science and Engineering Technology, vol. 6, no. 5, pp. 6–13, 2018, https://doi.org/10.22214/ijraset.2018.5002

13 Authors

Hamza Abu Owida: Ph.D. in Biomedical Engineering, Assistant Professor at the Medical Engineering Department, Al-Ahliyya Amman University, Jordan. Research interests focused on biomedical sensors, nanotechnology, and tissue engineering (email: h.abuowida@ammanu.edu.jo).

Bashar Al-haj Moh'd: M.Sc. degree in Digital Communication Systems (DCS) from Loughborough University, United Kingdom, in 2006. Now, he works as a lecturer at Al-Ahliyya Amman University, Medical Engineering department since 2007. His research interests include digital communication systems, ultra-wide band, wireless systems, embedded systems, and power electronics (email: Bashar105@ammanu.edu.jo).

Nidal Turab: Ph.D. in computer science Professor at the Networks and Cyber Security Department, Al-Ahliyya Amman University, Jordan. His research interests include WLAN security, computer networks security and cloud computing security, eLearning and Internet of Things (email: N.turab@ammanu.edu.jo).

Jamal Al-Nabulsi: Ph.D. in Biomedical Engineering, Professor at the Medical Engineering Department, Al-Ahliyya Amman University, Jordan. His research interests are biomedical sensors, digital signal processing, and image processing (email: j.nabulsi@amm.edu.jo).

Suhaila Abuowaida: PhD from USM University, Malaysia. received the B. Sc degrees in computer information system and M.Sc. degrees in computer science from AL al-Bayt University, Jordan, in 2012 and 2015, respectively. Her research interests include Deep Learning and Computer vision (email: suhila@aabu.edu.jo).

Article submitted 2023-03-08. Resubmitted 2023-04-23. Final acceptance 2023-04-25. Final version published as submitted by the authors.