Machine Learning in Oncology: Techniques, Applications, and Challenges

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Abstract
Machine learning (ML) is the subpart of artificial intelligence that duplicated of intelligence human behavior. Its ability to detect critical features from complex datasets reveals their significance. Cancer is a group of aberrant cells that are classified as a heterogeneous illness with subtypes of cancer. Primary identification of cancer is needed in cancer research to facilitate the clinical management of patients. Machine learning applications in cancer research acknowledges in the biomedical and bioinformatics fields. ML techniques such as Support Vector Machines (SVM), Decision Tree Models (DTM), Neural Networks (NN'S), and Naive Bayes (NB) have been extensively used in cancer research for the appropriate predictive models which lead to transformation in accurate and precisely to construct a decision. Diagnosis and treatment of cancer components are critical for indicative management. ML is an effective tool that asses the course and influence of these indicators which have prospectively assisted the clinician in diagnosing and treating cancer patients efficiently and intervening timelier. From literature revealed that the precision of cancer types and their related stress prediction results upgraded by 20% per annum with the applicability of the ML Method.

Keywords: Artificial Intelligence, Machine learning, Cancer

1. Introduction
Computer based artificial intelligence is a machine program that plays a role to pretend human intelligence. The artificial intelligence subdivides part is machine learning (ML), its important feature is to detect and predict the stress level of a cancer patient. [1]. In ancient times, continuous fruition has been accomplished in cancer research. The researcher used knowledge to identify different methods, to find types of cancer before showing symptoms and screened in a primitive stage of cancer [2]. However, clinical researchers and scientists are involved in the development of novel techniques for the prediction of cancer treatment in early-stage outcomes. The novel technologies are advent in the arena of medicine to composed a large data of cancer and provide to the community of medical research [3]. Still, the accuracy in the predictability of cancer diseases is the most challenging chore to the researcher. Nowadays, medical researchers use ML methods as a popular screening tool. The machine learning methods could ascertain and pinpoint patterns and inter relate the complex datasets to forecast the prosperous outcome of neoplasm [4]. ML methods are assimilated and actively involved in effective guidance therapy and cancer treatment. ML methods include integration and selectively compilation of complex data such as genomics and clinical. Further, the use of ML methods improved the correctness of neoplasm liability, relapse, and existence prediction [5]. The literature study suggested that various strategies apply for the primary finding of neoplasm prognosis and analysis approach. Precisely, profiling of circulatory mRNAs which have proofing for the primary prediction and inferences of cancer. Though, all methods were low compassion to screening at early-stage detection which differentiates benign from malignant tumors. The numerous aspects discussed on gene expression which was fruitful for primary finding and predicting of neoplasm outcome [6].

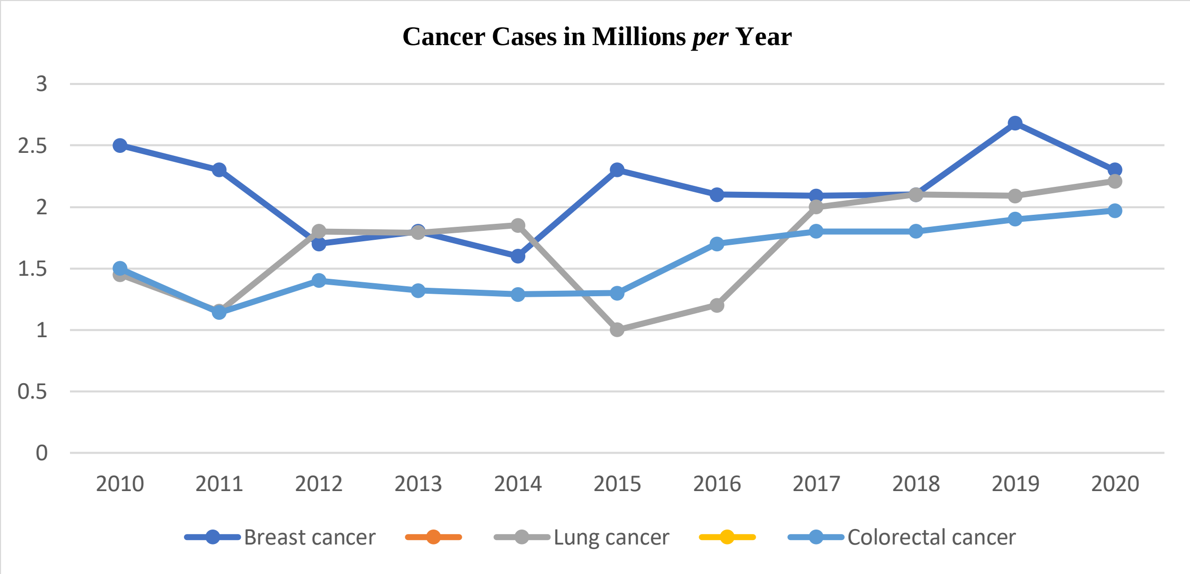

Figure 1: Worldwide Survey of Three Types of Cancer Cases in Millions *per* Ten Years [7]

In worldwide, WHO had reported 2.3 million new cases of breast cancer in 2020; 20% increased incidence over the past period [7]. Progression in oncology research leads to a change in the focus from simply surviving to quality living after cancer. The stress of cancer may affect other parameters such as body thermostat, breathing, pulse rate, fluctuation in blood pressure, and ache [8]. The pandemic infection covid-19 also expressed moderate to high-level stress associated with uncertainty, life change, and communication in cancer patients. Commonly, the treatment of cancer significantly decreases their quality of life [9]. The relation between quality of life and cancer prognosis are opposite to each other. Some researchers found that the quality of life may uplift cancer patient survival. Other studies suggested that the quality of life is not reliable to predict illness outcome at primitive diagnosis [10]. The relapse of cancer is significantly stronger than the later. The association of illness and quality of life outcome were more advanced than the cancer patient's illness perception. Generally, survival outcomes, treatment, and severity of symptoms associated with breast cancer and predictable more negative consequences related to their illness with high mortality rate and poor quality of life [11]. Thus, the correlation between illness perception and mortality rates in cancer patients is through the body's stress response. Another study reported that breast cancer patients suffered from irregularity in the flow of neurochemicals in the endocrine and sympathetic system and stressful life events that occurred through physiological changes. Both the endocrine and sympathetic systems are responsible for the stress in the human body's which may affect the normal physiology of the body such as reproduction, digestion, and growth is prohibited [12]. Other chemical constituents in the body like glucose and free fatty acid are elevated and stress hormones adrenaline and cortisol cease to make the person combat the threats. Mainly, the stress responses are dependable on the pituitary-adrenal hypothalamic axis. During the stressful condition, the hypothalamus subpart periventricular nucleus release corticotrophin-releasing hormone which stimulates the pituitary gland to release an adrenocorticotropic hormone, thus regulating the release of cortisol in the adrenal gland. However, to avoid hyper-system usable condition detached to discharge of cortisol releasing hormone by the cortisol [13]. These momentary system reactions are essential and helpful. Although, the body comes to its normal response once over the danger. However, breast cancer is noted as a chronic stressor, and the patient's suffered for a longer period. In chronic stress, fluctuation is observed in the production of stress hormone which leads to imbalance and the response of body unable to come in normal phase [14]. Several studies suggested that chronic stress dysregularized both hyper and hypo cortisol regulation. The cortisol is steroidal anti-inflammatory which preventing nerve impairment due to inflammation. Long-lasting chronic stress is influenced by deregulation of cortisol with inflammatory response and psychological stress and this may affect the prognosis of cancer and survival outcome. However, the hypothalamic-pituitary-adrenal axis is crucial for the biological system as associated with psychosocial factors and survival outcomes in breast cancer patients [15].
The colon-related malicious tumor is a colorectal neoplasm with enormous illness and may cause death. Every year approximately 1.4 million people may get to diagnose with colorectal cancer [16]. Nowadays, surgical treatment is carried with multiple methods like radiotherapy, chemotherapy, and targeted

therapy. Therefore, improvement in survival rate has to de did at the initial finding of colon neoplasm in patients. But, as initial indications are unrecognized and ignored by the patients, further leads to development to the mid, late stages and lastly, the patients have to be admitted to hospitals. It may cause constraint treatment and the survival rate of patients [17]. Machine learning methods have a novel technique for the accurate predictive and increment in the analysis and forecasting of health diseases and disorders. Machine learning methods are a compiled data analysis that has assimilates predictive algorithms for various risk factors. Most of the ML methods have algorithms based includes support vector and decision tree machine which has value to the early prognosis condition of the patient and pattern of illness started later medication with various medical data and individual health information. For now, ML methods are designed with gender, stage of age, and data of blood cell count to observe the initial detection of colorectal cancer [18]. It has a non-metastatic model suitable for forecasting the existence rate of colon-related cancer.

Lung carcinoma is a worldwide disease; the foremost cause of neoplastic demise in a few decades. Lung carcinoma patients' survival rate in 5 years is decreased by 18% due to late prediction and diagnosis. Therefore, to increase the survival rate of patients' needs to be the early diagnosis. If the patients get proper treatment at an early stage who have an existing rate of 5 years up to 40-50 %. Awkwardly, patients (70%) are diagnosed with tumors at the tolerant stages, and ultimately, they are abandoned from operation [19]. This may be partly related to the initial diagnosis yet not sensitive and specific so far. Therefore, it is necessary to look at the most superior and logical indicative biomarkers of lung cancer which will diagnose cancer at an early stage. The researcher studied metabolomics which focuses on physiological function and tumor development [20]. The study of cell metabolism revealed the data of cells involved in the progression and generation of tumors. The metabolites also characterized the stage of the tumor, the nature of histology, and drug responses. The alteration pattern of metabolites helps evaluate clinical properties of pancreatic tumor, ovarian tumor, colorectal tumor, renal tumor, and oral tumor. Even though to evaluate cell metabolism in tumors of lung cancer more precise and sensitized biomarker is required [21].

Artificial intelligence submerges machine learning to forecast and duplicate human behaviour and handling an extensive amount of data. ML is a computer system that analyses automatically from experience without explicit programmed [22]. However, ML learns the data using algorithms and making the prediction of the upcoming condition of newly incorporated data. It also seemed to the system of design model on the base of experience and improve its enactment. The model aims to find out effective variables and relations amongst them. In forthcoming years, artificial intelligence is most suitable to study as a real-world application. ML method is generously involved in the study of lung cancer metabolomics and is superior to predict and diagnose lung cancer at an early stage [23]. Still, the treatment remains a challenge even after a diagnosis of cancer. Managing cancer patients is complicated as comorbidities exist which collectively increase risk factors in cancer patients. [24]. Around 30% - 50% of all types of cancer survivors grieve with other complications as per the U.S. survey. Another major factor involves in cancer patients is psychological disturbances, as one-third of all cancer patients clinically shows increases level of stress and anxiety along with depression. The forgoing study revealed a strong association between psychological distress and medical challenges in the common population but it is uncertain as to whether other medical challenges may influence the mental distress of cancer patients [25]. Further studies revealed that the aging factor has shown adversative physical symptoms and impaired functional status which serves as the basis of prognosis for psychological distress. Also, the other medical complication may increase financial load which may result in psychological stress. Besides that, cancer itself influences psychological agony in cancer patients that leads to anxiety. The purpose of the study is to explore anxiety in cancer patients which primarily account for physical distress. Specifically, machine learning methods approach to collect data from the large survey.

Amongst the diseases, Cancer is one of the most dangerous and expensive diseases in the world [26]. Various antitumor therapies are available to treat tumors liked targeted drug therapy, radiation treatment, molecular therapy, surgery, immunotherapy, and endocrine therapy which cast off-centered effectiveness of tumor cells. In the treatment of cancer, majorly the side effects are faced to the patients along with that an important challenge is drug resistance which leads to tolerances for the anti-cancer therapy. Traditional chemotherapeutic agent abolishes cancer cell by damaging DNA strand and are not specific; also gives wider side effects. Therefore, the need to develop novel anticancer drugs to treat cancer cells is on the base of the target [27]. The drug resistance occurred due to the mechanism of cancer cell-specific or non-specific like drug effluxes. Hence the challenges to the researcher to look at drug resistance parameters. The researcher has differentiated the drug resistance mechanism of neoplasm by drug responses like inactivation, alteration, effluxes, repairing of deoxyribonucleic acid [28]. Thus, therapeutic drug resistance can be predicted as a certain failure of activity and drug unwanted effects in antineoplastic therapy. Various methods are performed to predict drug resistance

such as cellular mechanisms chemosensitivity test, deoxyribonucleic acid, ribonucleic acid, and enzyme-dependent chemical sensitive test and now developed computer-based techniques [29]. These techniques are time-consuming and have some technical weaknesses except computational methods. Therefore, chemotherapeutic responses are forecast with the help of interdisciplinary methods, statically and computationally are used for predicting chemotherapy responses. These computational methods are based on mechanistic modelling methods and data-driven prediction methods [30]. Computational methods analysed and generated of algorithms are utilized for forecasting cancerous cell growth responses based on scoring. ML methods correlate the cancer-associated datasets and predict the result which is less economic and time-saving with an instant evaluation of biological information of cancerous cells [31].
A case study on the resistance of cisplatin as an anticancer drug. Some cancer cell line produces resistance against cisplatin. ML methods used a variety of algorithms which used to differentiate anticancer drug cisplatin sensitivity and confrontation toward cancer cell lines. DIANA mirPath v.3, UniProt, and Enrichr are databases of ML methods to predict cancer [32].
Bone cancer is the most malicious neoplasm which causes to damage the cell and their growth in the body. The survival rate of bone cancer suffered patients are very low, so far, as early detection may increase the survival rate. The abnormal growth of cells evacuated the surrounding tissue and it's dangerous to the patients. This type of tumor may damage the function of another system such as the digestive system, nervous system and may also affect the hormonal functions [33]. If this abnormal cell is not refurbished at an early stage may cause damage to DNA structure, leads to the generation of unwanted neo cells. [34]. The researcher observed initial symptoms in cancer patients like abnormal bleeding, prolongation in cough secretions, indigestion, frequent weight loss, etc. cancer or tumors are classified into two parts i.e., benign, and malignant [35]. Benign tumors are easily removable using surgical operation but malignant tumors are difficult to remove because they feast in large cell nuclei of the body. Bone cancer is related to sarcoma term which starts up in muscle, fibrous tissue, bones in which affect displacement and growth and affected other body parts. There is numerous bone cancer such as chondrosarcoma, osteosarcoma, pleomorphic sarcoma, Ewing's sarcoma, fibrosarcoma, etc. [36].

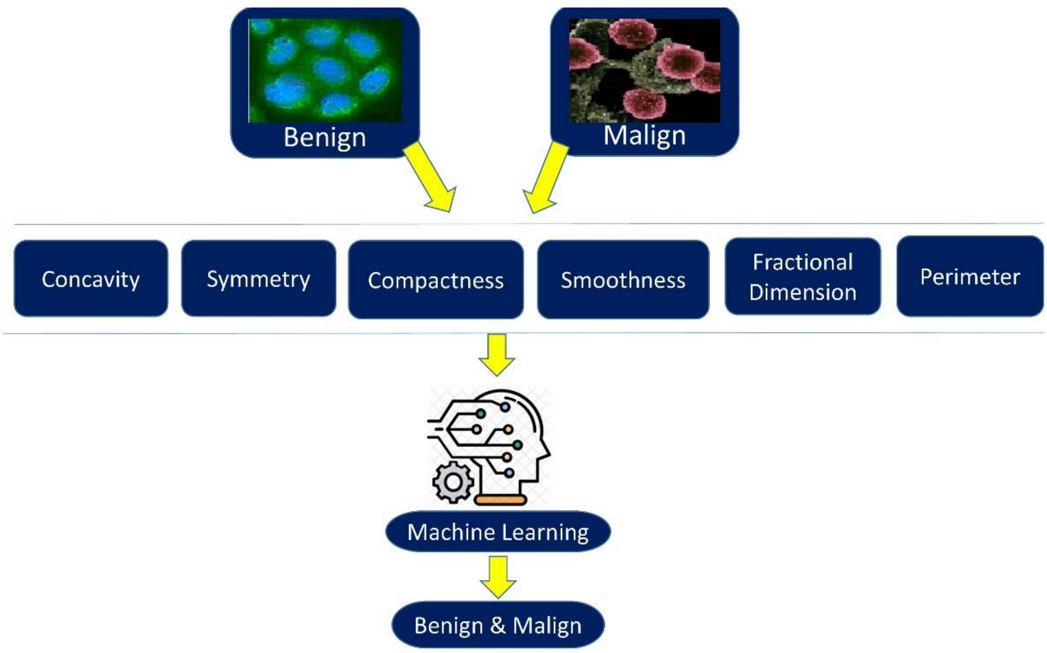

Fig 2: Machine Learning predict Cancer [37]

2. ML techniques used in Cancer prediction

Continuous progress in the field of cancer studies took placed in the past few years. Different methods are developed by scientists for detection of early-stage screening, to detect cancers before they cause symptoms [37]. The availability of a huge amount of cancer data and the progression of novel technological skills in the area of medication science helps the medical researcher to study the field of cancer. But accurately predicting the outcome of the disease is so far difficult and stimulating work for medical professionals. Due to difficulties in result prediction, nowadays artificial intelligence techniques are used as a widespread means for the medical practitioner. ML helps in detection of pattern and correlation between composite data sets, and help efficiently to forecast future perspective of the form of cancer [38]. The implementation of ML techniques supports refining the result accurateness of cancer sensitivity, repetitions, and existence prognosis. The success rate of correct prognosis of cancer is increased by 15%–20% from past times with the assistance of ML techniques [39]. But with the benefits of ML, several complications are there while adopting ML techniques in medicine. The accomplishment of several techniques is based on the accessibility of a wide range of designed data. Due to large differences in data detection among the health division increases the challenge of collecting a defined data set for investigation [40].

ML includes a wide variety of cancer prediction tasks and methods. The main methods used are i) supervised learning ii) unsupervised learning and iii) reinforcement learning. Supervised learning technique depending on the defined labelled data set. These data sets are designed liked wise, they accurately classify the statistics or forecast results using algorithms over time. Unsupervised learning methods identify patterns and subgroups in the statistics which is not clear in their predictable outcome. The outcome is depending on machine learning techniques to examine and group unlabelled data sets. These algorithms help to find hidden designs in the statistics without physical interference. Usually, it is used for more investigative analysis [40, 41]. Reinforcement learning is machine learning used for consecutive decision-making, these are used where the algorithm and its function are conclusive. The reinforcement agents can decide what to perform in the given task. In the case of the absence of a training dataset, the reinforcement agent learns from its previous experiences [42].

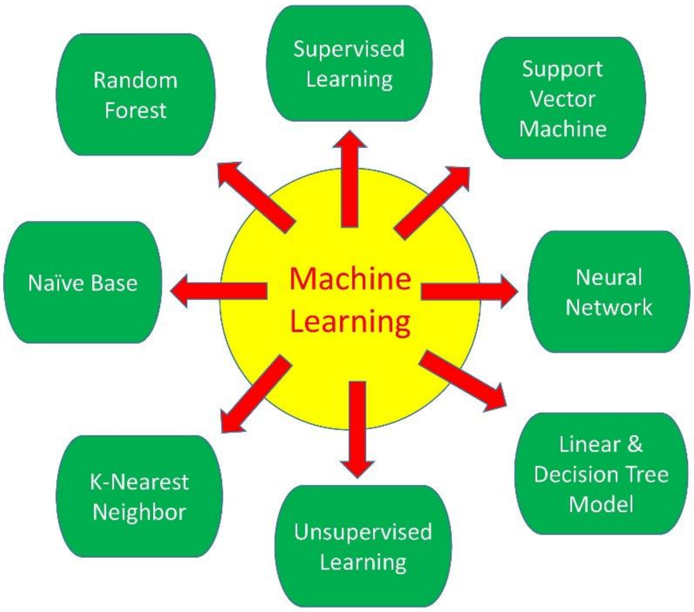

Figure 3: Types of Machine Learning Method [41]

2.1 Supervised learning

Supervised learning algorithms are majorly divided into two kinds of problems, classification, and regression. Supervised learning algorithms help in the forecast of a selected outcome, which could be either regression (continuous) or classification (discrete). Classification uses to precisely assign test data into precise categories while Regression uses an algorithm to understand the relationship between dependent and independent variables.

2.1.1 Linear models

In this model, the results of interest of autonomous variables are maps through linear equations. The model discovers the β coefficient for each feature and the experiential forecasting is given by a subjective grouping of these structures. Assuming, linear regression result is linearly related to the value of the feature and the additive affiliation between the characteristics. For binary classification, logistic regression, and survival analysis the Cox regression are the additional alternatives of regression models and have additional relation between the structures but it involves linear function conversion which depends on the forecasting task. Due to easy and simple interpretation, the linear model is a common choice in the healthcare system. The Linear models are enabled to capture the interaction between variables naturally as the results are often normally non-linear in characteristics. For example, the tumor size of different age groups can have different effects on the risk of cancer recurrence [40]

2.1.2 Support vector machines (SVMs)

Among all techniques of machine learning, SVM is one of the extremely powerful methods of forecasting cancer. It works by identifying understated patterns in multifaceted datasets. With the help of nonlinear kernels, the SVM is applicable to perform nonlinear classification. The data from linear feature space to nonlinear space is transfer with the help of these nonlinear kernels. With the help of these diversified kernels, the presentation of the SVM classifier is intensely advanced [39]. The objective of SVM is to produce a decision boundary (Hyperplane) among the two classes that allow forecasting of labels from feature vectors. For better results, the hyperplane is positioned in a way that, it is located as near as every class of data point (support vector) [43]. A significant feature of SVM is to circumvent degradation of computational performance that always occurs in high dimensions [44].

2.1.3 Decision tree models.

CARTs (Dimitris Bertsimas) are a type of classification and regression tree that can be used instead of linear models. In this model, feature splits divide data into subsections, and the leaves contain the final subsections of observations in a decision tree. The final tree divides the population based on the feature splits and each observation is allotted to a single leaf. In the case of classification, the prediction is a probability, which is computed as the occurrence of the typical result in the leaf, and a number value for unceasing results that is calculated as the average value of the outcomes in the leaf. The model's tree-based structure permits it to hold nonlinear feature interactions. CARTs help to determine to knock off criteria for patients over and under age group to characteristic risk levels. Decision tree algorithms give the most correct data when we compare with other similar algorithms [45].

2.1.4 Random forests

Random forests are also synonym as random decision forests. The model helps in creating a huge quantity of trees which gain results via collective learning for regression and classification. For the construction of those trees, special characteristics like Catching and feature randomness are used. The random forest method is more suitable than the decision tree because it does not overfit the data [46, 47].

In random forest, work practice is as follows

1. K data point is randomly selected from the training set, the
2. K data point is used to create a decision tree.
3. The number of N trees is selected from the generated tree and repeat steps a and b
4. N forecast the data point-related categories of the new data point, and map the new data point to the category with the highest probability.

2.1.5 Neural networks

Through a layered link of mathematical changes, neural networks relate features to projected outcomes. A nonlinear activation function is then used to map these nodes to a result. Neural networks can capture intricate connections between attributes and outcomes thanks to these network dynamics [48]. Deep learning, an area of machine learning based on neural networks, is built on these methodologies. Neural networks have gain popularity because of their capability to synthesis raw images and free text. Neural networks can handle unstructured data and increase to a greater level [41]

2.1.6 K nearest neighbours

From many supervised learning algorithms, KNN (K- Nearest Neighbours) method is helpful in data handling and machine learning. In this algorithm, results are depending on prediction with similar data from other data. The working principle of KNN is used to find the gap among a point in the data and select the number of examples (K) which is nearest to the point [46].

2.1.7 The Naive Bayes

It is taken into consideration, a semi-supervised technique due to the fact it can be used for grouping or type tasks. The set of rules is well-known for its qualifications withinside the Bayesian probability theorem. When applied as a method to create clusters, Naive Bayes does now no longer wants to specify the result. It makes use of conditional chance for facts values, they are assigned to classes, so it's far a shape of unsupervised learning. However, while used to categorize facts, Naive Bayes calls for entering variables and goal variables, so it's far a method of supervised learning. The set of rules creates Bayesian networks as a classifier, which is timber generated and primarily based totally on the conditional possibilities of the consequences of the possibilities imposed at the enter variables [45].

Table 1: Advantages, disadvantages, uses and limitations of machine learning methods

Model type	**advantages**	**disadvantages**	**uses**	**limitations**	**Ref**
Neural network	Extremely nonlinear: captures intricate relationships high-dimensional unstructured data is possible (eg. images)	Black box: hard to interpret approach Training complexity: creating models requires fine-tuning numerous parameters	With just one neural network pass, it can identify items in an image.	Only a small number of functions may be represented by this neural network. Only hyperplanes may be used as the decision boundaries that correspond to the threshold boundaries. Only data that can be separated linearly can be used in this approach.	[1,5,68]
Support vector machine	The optimization issue is converted into dual convex quadratic algorithms so that the challenges of employing linear functions in the high-dimensional feature space can be avoided.	When the target classes overlap and the data set has more sound, it does not operate very well. The support vector machine will perform poorly when there are more attributes for each data point than there are training data specimens.	The method offers effective solutions to classification issues without making any assumptions about the distribution and interdependence of the data, is model-free.	Large data sets are not appropriate for it. When the target classes are overlapping and the data set includes more noise, SVM does not perform very well.	[40,42]
Decision tree	Nonlinear: able to represent variable interactions. Highly interpretable: decision paths explicitly characterize high-/lowrisk feature combinations	Noncontinuous: does not naturally capture continuous relationships between variables and outcomes	Creating profiles of oncogene mutations for cancer cell lines, calculating drug molecule chemical-descriptor fingerprints, determining the oncogenes with the highest prognostic value for cancer cells' sensitivity to treatment	Ignores qualitative components of decisions and simply uses quantitative facts.	[5,70]
Random forests	It is capable of both classification and regression tasks. A random forest generates accurate predictions that	Accessing a list of a bigger population can be difficult and expensive, and prejudice can still exist in some situations.	Analyze patient medical records to determine a patient's condition and	A huge number of trees may slow down the process and	[5,66]

	are simple to comprehend. Large datasets can be handled effectively. The random forest method offers a greater level of prognostic accuracy.		determine a drug's sensitivity to it.	render it useless for making predictions in real time.	
Linear model	It simplifies the estimation process and, more significantly, the modular level understanding of these linear equations is straightforward.	Linear communication is susceptible to noise interference, which can alter the initial message. Linear communication is not dynamic since it sometimes prevents recipients from responding at all.	Utilized to make predictions about the value of one variable based on the value of another.	It is unable to correctly fit complicated datasets. As the relationships between the dataset's variables are rarely linear in real-world situations, a straight line cannot accurately represent the data.	[1,5]
K nearest neighbours	It is very intuitive, adaptable to various proximity calculations, and memory-based in nature.	• The level of data quality affects accuracy. • The prediction stage may take a while if there is a lot of data. • sensitive to both irrelevant features and the size of the data. • High memory is needed since all of the training data must be stored	To offer important insights into the interaction between clinical parameters such age, mutated genes, and mutations and how this affects the duration that cancer patients survive after diagnosis.	Does not function well when there are several dimensions, and it is necessary to constantly determine the value of K, which can occasionally be difficult.	[31,67]
The Naive Bayes	There is less training data needed. It manages data that is continuous and discrete. Regarding the quantity of predictors and data points, it is quite scalable.	If the test data set contains a categorical variable of a category that was not present in the training data set, the Naive Bayes model will give it zero probability and be unable to produce any predictions in this regard.	used to conduct sentimental analysis and separate patients' positive and negative reviews. The medical institute can choose the drug that will benefit them the most and cause the fewest negative effects with the help of this framework.	Naive Bayes implicitly assumes that all the attributes are independent of one another. In actual life, it is uncommon to encounter a set of predictors that are completely unconnected to one another.	[63]

2.2 Unsupervised Learning

In unsupervised learning, the machine is enforced to instruct an unlabelled data set and then distinguish it based on certain properties, and allow the algorithm to act on that information that lacks external supervision [49]. Unsupervised data learning involves pattern recognition, not target attributes. That is, all variables used in the analysis are used as input, and because of this method, the technique is suitable for clustering and association mining techniques. That is, the unsupervised clustering set of rules identifies inherent clusters in unlabelled information, after which assigns a label to every information value. On the contradictory, unsupervised affiliation removal algorithms generally tend to perceive policies that correctly constitute the connection among attributes [45]. Although the above techniques can be expecting unique outcomes, unsupervised mastering is much less instructive; seeking to perceive the underlying shape withinside the information. The outcomes of those techniques are not task-unique (that is, they're now no longer primarily based totally on unique anticipated outcomes, along with survival) and offer popular information [40]. For maximizing similarity inside clusters and separation among clusters, the clustering algorithms partition the records into K-clusters [50].

3. Machine Learning Application in Cancer Prediction

As per literature, machine learning techniques in malignancy were conducted for susceptibility, recurrence, and liability prediction. Electronic databases were accessed namely Springer, Science Direct, Web of Science, PubMed, Scopus. To maintain appropriate commentary further scrutinization was needed [51]. AI has mainly been used for differentiating between normal and malignant conditions. It helps to classify breast tumors. Breast cells (BC) are healthy cells that begin to produce abnormally which divide more rapidly than healthy cells and are malignant tumors and hence to save the lives of this type of patient's early findings as well as identification can be carried out. Digital mammography technique is utilized for consistent image quality than screen-film techniques. Various novel methods of machine learning are used to identify breast cancer namely; Support Vector Machine (SVM), Classifier, Naive Bayes Classifier, Decision tree, Computer-Aided Detection (CADe) and Diagnosis (CADx), R-CNN (Convolutional Neural Networks) Classifier, Bidirectional Recurrent Neural Networks (HA-BiRNN). To detect features of mammograms, Hough transform is used and it is classified using SVM. For reduction of painful surgeries for diagnosis and prognosis of breast cancer merger of AI and ML is utilized which helps in confirmation of disease. Various algorithms such as logistic regression (LG) which is a classifier that classifies the target, supervised ML algorithm is support vector machine (SVM), K-nearest neighbor (KNN), and Decision tree (DT) both useful for classification and regression problems, nowadays in data mining tools, Neural network (NN) is most powerful and also useful for training a big amount of data. It is also useful for constructing a breast cancer-detecting system. The best model for cancer detection is constructed through NN with very little FP and FNAA, NN was implemented by Gated Recurrent Unit (GRU). The accuracy of GRU SVM was highest and by using a tool like Waikato Environment for Knowledge Analysis (WEKA) best results with SVM were obtained [52, 53, 54].

Springer Linkage (http://www.springerlink.com), Science Direct (Elsevier) (http://www.sciencedirect.com), IEEE Xplore (http://www.ieeexplore.ieee.org, and (https://www.ncbi.nlm.nih.gov/pubmed/) these are all different electronic databases that were searched for maximum data. The computer creates Electronic Health Record (EHR) to check symptoms for treatment of cancer and advanced computational methods are used for extraction of data such as normal language processing [55].

In a patient with a thyroid tumor, computed tomography (CT) for [cervical lymph node metastasis (LNM)] and deep learning-based computer-aided diagnosis (CAD) system is used. Preoperative CT in accumulation to ultrasonography (US) for patients with a clinical doubt of multiple or bulky lymph nodes was also checked. This model has 90.4% accuracy in thyroid cancer detection and radiologist used these images for diagnosis and risk stratification. Advanced technologies for the finding of thyroid lumps are color Doppler ultrasonography, 3D imaging procedures like ultrasonography elasticity imaging technique which aid doctors to distinguish between benign nodes from malicious nodes [56, 57].

Cervical cancer is the fourth prevalent type of cancer affecting worldwide in women. With the use of automated Pap smear analysis, which containing stages like Image attainment; pre-processing; division; feature extraction; and organization, both normal as well as abnormal cells can be classified. Diagnosis of cervical malignancy using a Support Vector Machine (SVM) classifier can be used, KNN method used to classify, multiscale convolutional network (MSCN) and graph-partitioning-based technique used for division of cervical cytoplasm and nuclei, Fuzzy C-Means (FCM) System for cervical cell subdivision and classification study. For nucleus and cytoplasm from single-cell extract, Radiating

Gradient Vector Flow (RGVF) snake system was used. Combining KNN with the SVM algorithm act as an excellent classifier for cervical cancer [58].
The fifth most shared form of malignant cancer is gastric cancer. Convolutional neural networks (CNNs) are useful to medical arenas to investigative endoscopic images that automatically detect gastric cancer which simulates the human brain. CNN detects initial and progressive gastric malignancy. Endoscopists can easily identify small intramucosal gastric cancers and invasive gastric cancer by means of the narrow-band imaging (M-NBI) method. Further, it is used for evaluating early cancer, microvessels, and microstructure of the gastrointestinal mucosa. The main benefit of M-NBI with CNN is that M-NBI can progress the rapidity and correctness of the CNN diagnostic system matched with images provided by conventional endoscopy. AI-based omics analyses biomarker for early detection, (IEE) image-enhanced endoscopy and (BLI) blue-laser imaging for diagnosing image accurately than conventional imaging, Helicobacter pylori (HP) infection which may because of intestinal-type gastric cancer can be diagnosed by these techniques. These all are important techniques that are more effective as a hopeful approach for detection. An automatic capsule system for screening is a useful and new opportunity for gastric blood detection [59].
A life-frightening illness is an oral cancer also called Oral squamous cell carcinoma (OSCC) which having a survival rate of only 50-60%. Hence by using AI computer-assisted software and automated analysis of microscopic images for biopsy and for diagnosing cancerous cells automatically. Classifiers namely, SVM, used for greater accuracy, decision tree (DT) which is simple and commonly used that breakdown database into smaller ones, k-nearest neighbor (KNN) used for categorization of new data, to observe the results, linear discriminant analysis, and logistic regression are used. These all-classifier's results can be assessed depending upon sensitivity, precision, specificity, and overall accuracy. (Tongue) oral cancer or oral tongue squamous cell carcinoma which is a type of oral squamous carcinoma that has algorithms or classifiers like SVM useful for grouping and regression problems, to get a better result Boosted Decision tree, Decision Forest, Naive Bayes (NB) are used. Out of these all classifiers, those having the best performance in accuracy are boosted decision tree algorithm [60].
By using (SEER) e Surveillance, Epidemiology, and End Results type of algorithms and software tool as well as program databases to categorize different types in the lung cancer. Other databases like NCI60 which contain sixty cell lines can be used for lung cancer management. Datasets like Montgomery County (MC) and Shenzhen Hospital dataset (SH) both content regular and irregular chest X-rays. An example that has the largest publicity that is chestX-ray14 is available as it contains 14 different types of lung diseases. Techniques like tomography, imaging are useful for only the initial evaluation of lung cancer. Computer-aided automatic detection of tumor cells in lymph nodes is a useful technique and for getting more information by using computer-aided techniques like Computer-Aided Detection (CADe) systems for location of lesions and classification of malignancy Computer-Aided Diagnosis (CADx) systems are used. Due to the limitation of these two techniques advanced machine learning techniques like Fibered Confocal Fluorescence Microscopy (FCFM) are used which can classify both benign from malignant tumors. For histopathological identification two techniques like support vector machine (SVM) and decision tree combine useful for (NSCLC) Non-Small Cell Lung Cancer, by using immunohistochemistry (IHC) machine learning technique biopsy specimens are being established. 2D CXRs (chest X-ray images) by deep learning technique radiologist can identify different types of lesion and nodules of lung cancer. These all-ML techniques are useful to reduce the workload for the pathologist [61].
Among all cancers, most of the death occurs in bone cancer. The main cause of spread from the original site to the bone causes bone metastases. Various methods to generate models for diagnosis of bone cancer are XGBoost, support vector machine, and algorithms methods are used. As compared to CT and MRI, the Ultrasound method is more convenient in various cancers. But one disadvantage of the ultrasound technique is that in bone cancer it does not give good results because the ultrasound waves do not transmit well through bone in bone cancer. This cancer occurred with physiological and genetic disorders. To check the abnormalities like thinning of bones and their cancer, a CT scan is used in machine learning techniques [62]. For data and images for bone cancer, the bone shadow eliminated (BSE) version was also used. Bao H. Do and their co-author developed a model for a bone cancer diagnosis like the naive Bayes model (NBM), this model has comparative prospects which provide diagnosis predictions but, in this work, the clinical value was not tested [63]. Diagnosis is possible by deep learning using a convolutional neural network (CNN). Another technique for detecting bone cancer metastasis is bone scintigraphy (BS) this contains AI model 99mTc-MDP and assessment of cancer is cost-effective and efficient [64]. For the study of the anatomy of bone techniques like tomography and Magnetic image resonance (MRI) are used.
Colorectal cancer is malignant; its early detection can be done by convolutional neural networks (CNNs). Artificial intelligence-based software ANN is used for the prediction of the time of

surgery. With artificial intelligence cancer-on-a-chip technologies are useful for enhancing prognostic drug screening models in various types of cancer [65]

Table 2: Summary of Machine learning applications for the diagnosis of Cancer

Authors	**Type of cancer**	**Type of data**	**Methods**	**Analysis**
Petalidis L.P., et al. [71]	Breast cancer	Gene expression profile+copy number alteration profile+clinical data	Multimodal deep neural network	The suggested strategy performs better than existing methods and prediction algorithms using single-dimensional data.
Joshi R., et al. [72]	Malignant melanoma	Custom dataset	Nonlinear ANN model	The performance of ANN model better than Cox model
Shimizu H., et al. [73]	Breast cancer	TCGA	Random forest, neural network	Log-rank $p < 0{:}05$
Chi C.L., et al. [74]	Breast cancer	Nuclear morphometric features	ANN	Good (>5 years) and bad (<5 years) prognoses
Chi C.L., et al. [74]	Astrocytic tumour	Microarray gene dataset	ANN	96.15% accuracy
Al-Antari M.A. et al., [75]	Breast cancer	INbreast database	Different DL methods	Jaccard similarity coefficient of 86.37%, accuracy of 98.96%, MCC of 97.62%, F1-score of 99.24%
Huang Z., et al. [76]	Breast invasive carcinoma	Gene expression data	Multiomics neural	Improved performance using more omics data
Hao J., et al. [77]	Glioblastoma multiforme	TCGA	Pathway-associated sparse deep neural network	AUC = $0{:}6622 \pm 0{:}013$, $F1 = 0{:}3978 \pm 0{:}016$
Sun D., et al. [78]	Breast cancer	Gene expression profile+copy number alteration profile+clinical data	Multimodal deep neural network	The suggested strategy performs better than existing methods and prediction algorithms using single-dimensional data.
Chaudhary K., et al. [79]	Hepatocellular carcinoma	TCGA	DL-based model	p value = $7{:}13 \times 10{-}6$ Concordance index = $0{:}68$
Bychkov D., et al. [80]	Colorectal cancer	Images of tumor tissue samples	Combined convolutional and recurrent architectures	Prediction with only small tissue areas (hazard ratio 2.3), tissue microarray spot

				(hazard ratio 1.67), and whole-slide level (hazard ratio 1.65)
Wang S., et al. [81]	Ovarian cancer	CT images	Combined DL and Cox proportional hazards model	Concordance index was 0.713 and 0.694
Mobadersany P., et al. [82]	Lower-grade glioma and glioblastoma	TCGA	CNNs	Median concordance index = 0:754
Courtiol P., et al. [83]	Mesothelioma	TCGA+French source	CNNs	Concordance index of 0.656 on TCGA cohort
Liu. B., et al. [84]	Multiple	TCGA+Gene Expression Omnibus dataset	DL-based model	For both marker types, the specificity of normal whole blood was 100%
Jing. B., et al. [85]	Multiple	WHAS, SUPPORT, METABRIC, Rotterdam tumor bank	Deep feedforward neural network	Better prognostic accuracy than the clinical experts for the prognosis of nasopharyngeal carcinoma
Yap. M. H., et al. [86]	Breast cancer	Ultrasound images, 2 datasets (A & B)	LeNet, U-Net, AlexNet	*F*-measure = 0:91 (on dataset A) and *F*-measure = 0:89 (on dataset B)
Zeng Y., et al. [87]	Colon cancer	Custom dataset	CNN model	AUC = 0:998, specificity = 99:7%, sensitivity = 100%
Ca. D., et al. [88]	Breast cancer	ICPR 2014 mitosis dataset, TUPAC 2016 mitotic cell dataset	Modified regional CNN	Precision = 0:76, recall = 0:72, *F*1-score = 0:736 on TUPAC 2016 dataset
Zhou. J., et al. [89]	Breast cancer	Custom dynamic contrastenhanced MRI dataset	3D deep CNN architecture	83.7% accuracy, 90.8% sensitivity, 69.3% specificity, AUC of 0.859, overall dice distance of 0:501 ± 0:274
Nasrullah. N., et al. [90]	Lung nodules	LUNA16, LIDC-IDRI	Two deep 3D customized mixed link network encoder-decoder architectures	Accuracy of 94.17%
Das. A., et al. [91]	Liver cancer	225 CT scans of hemangioma, hepatocellular carcinoma, and	Watershed segmentation, Gaussian mixture model (GMM), and deep	Dice score of 0.9743, accuracy of 99.38%

		metastatic carcinoma	neural network	
Panic. J., et al. [92]	Colorectal cancer	Custom dataset of MRI images of 28 adenocarcinomas and 5 mucinous carcinomas	CNN architecture which is a combination of three CNN architectures	Dice score of 0.60, precision of 0.76, and recall of 0.55
Chen. X, Z., et al. [93-94]	Pancreatic cancer	Custom dataset of MRI images belonging to 73 patients	DL method using spiral transformation	Dice score of 0:656 ± 0:1021

4. Limitations

In the case of thyroid cancer by using AI non-ultrasound clinical information is largely neglected. Limitations to M-NBI with CNN for gastric cancer is that Japanese studies using this technique have considerably higher sensitivity and accuracy due to the diverse histological elucidation like Vienna classification. By revising the Vienna classification, Japanese pathologists used this for early gastric cancer diagnosis. The limitation of (CADe) Computer-Aided Detection is that it is valuable for noticing nodules, but it cannot characterize the type of nodule and on other hand (CADx) Computer-Aided Diagnosis system is valuable for characterization, however not for detection of cancer.

5. Challenges and Upcoming Forecasts

Despite the stated Machine Learning accomplishment for cancer imaging, several hurdles and restrictions should be overcome earlier than the clinical adoption. A maximum amount of content is generated because of the rising response for MRI and CT, by the care provider. Different standards include the SVM, CNN, DT CAD, etc. that have confirmed for fast admittance of records and recovery. A major challenge in various types of detection of cancers with machine learning contain in what way we can design models by using medical images and databases. An important role in diagnosing by imaging plays an important role in cancer. Day by day command in addition to the potential of Machine Learning is growing, but some directions are quite left behind in terms of clinical practice. Machine Learning techniques are efficiently meant for complex and big biological data analysis for solving bioinformatics problems. For calculating dimension, position, and step of bone cancer added improvement of a neural network can be finished. The best method concerning efficiency in breast cancer prediction is SVM. In relation to precision and error rate, the SVM method has attained the best method. Magnifying endoscopy through narrow-band imaging (M-NBI) combine with CNN is used to examine early gastric cancer but more progression in medical practice is required in association with artificial intelligence.

Conclusions

Machine learning is an effective tool that assesses the progression and influence of cancer symptoms, and there relate stress. In this chapter, we have attempted to explain and assess the performance of machine learning techniques and their application in cancer patients' stress prediction, and outcomes. Specially, we discussed various types of machine learning methods which used, integrated types of training data set, endpoint prediction outcome, and susceptibility of cancer concerning stress. All the methods are applied to predict the different types of cancer with their outcome. The machine learning method is suitable for the early prediction and prognosis of cancer as compared to conventional statics systems. ML method well-constructed and validated the quantitative and qualitative biological data. Overall, we proposed that the machine learning method become popular and easily handily to hospital administrators and clinicians.

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