

Review

Comparative analysis of machine learning and deep learning models for improved cancer detection: A comprehensive review of recent advancements in diagnostic techniques

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ARTICLE INFO

Keywords:

Machine learning
Cancer detection
Deep learning
Feature extraction
Preprocessing techniques

ABSTRACT

Cancer remains a leading reason of mortality, with the current global death toll estimated at 10 million and projected to surpass 16 million by 2040 as reported by the World Health Organization (WHO). In addition to the devastating loss of lives, incorrect cancer diagnoses and medical errors further contribute to the mortality rate. To address these challenges, there is an urgent need for automated and computerized diagnostic techniques that can reduce errors and improve the treatment of cancer patients. In the recent decades, extensive investigation has centred on developing automatic and accurate detection techniques for various categories of cancer. This article exhibits a thorough review of five categories of cancers: pancreatic, esophageal, prostate, colorectal, and leukemia, utilizing both classical machine learning (ML) and deep learning (DL) methods. Notably, the selection of these cancers arises from both their lethal impact and the observed scarcity of consolidated literature surveys

Abbreviation: ABDNN, Attention-Based Deep Neural Networks; ACLD, Amreek Clinical Lab Database; ADBRF, AdaBoost Based Random Forest; AFM, Atomic Force Microscopy; AML, Acute Myeloid Leukemia; AML-C-LMU, Acute Myeloid Leukemia Cytomorphology by Ludwig Maximilian University of Munich; ASH, American Society of Hematology; ASODTL-ECC, Atom Search Optimization with a Deep Transfer Learning-Driven EC Classification; BCCD, Blood Cell Count Detection; BES, Bald Eagle Search; BiT-M, Big Transfer Model; BmzP, Binning of m/z Points; CAD-WLI, Computer-Assisted Diagnosis under Conventional Endoscopic White-Light Imaging; CEUS, Conventional Endoscopic Ultrasound; CHFSPW, Color Histogram Features Based on Sub-patch Weight; CIWO-FS, Chaotic Invasive Weed Optimization based Feature Selection; CJT-DEO-EDNN, Condorcet's Jury Theorem and Differential Evolution Optimization based Ensemble of Deep Neural Networks; CLACHE, Contrast Limited Adaptive Histogram Equalization; CRAG, Colorectal Adenocarcinoma Gland; CSQ, Color Space Quantization; CS-SVM, Cuckoo Search Algorithm-Support Vector Machine; DCGAN, Deep Convolutional Generative Adversarial Networks; DCNN_DBN, Deep Convolutional Neural Network with Deep Belief Network; DL-CS, Deep Learning Models for the Classification between Clinically Significant and Non-Clinically Significant Prostate Cancer; DL-FCN, Double-Labeling Fully Convolutional Network; DNN, Deep Neural Network; DOST, Discrete Orthonormal S-Transform; DRS, Diffuse Reflectance Spectroscopy; DWI, Diffusion Weighted Imaging; EAI, Explainable Artificial Intelligence; EGB, Extreme Gradient Boosting; EGD, Esophagogastroduodenoscopy; EHLL, Extended Healthy Lifestyle Index; EL-SVM, Ensemble Learning-Support Vector Machine; EUS, Endoscopic Ultrasonography; EUS, Endoscopic Ultrasound; FEE-DL, Fully End-to-End Deep learning; FS-GA, Feature Selection Based on Genetic Algorithm; GCN-MIL, Graph Convolution Network with Multiple-Instance Learning; GGMRF, Generalized Gaussian Markov Random Field; GHF, Gradient-Based Histogram Features; GLDMs, Gray-Level Dependence Matrices; HCCA, Hierarchical Cluster and Correlation Assessment; HFB-SVM-RF, Hybrid Feedback-Support Vector Machine-Random Forest; HOS, Higher Order Statistics; Hosc, Proprietary Dataset Hospital Colon; HRF, Handcrafted Radiomics Features; HSV, Hue-Saturation-Value; HU-Net, Hybrid U-Net; IAOA, Improved Archimedes Optimization Algorithm; ICC, Intraclass Correlation Coefficient; JDPCA, Joint Diagonalisation Principal Component Analysis; LASSO, Least Absolute Shrinkage and Selection Operator; LDP, Local Directional Pattern; LSSVM, Least-Squares Support Vector Machine; MDA, Mean Decrease Accuracy; MDG, Mean Decrease Gini; MGED, Microarray Gene Expression Dataset; MICCAI, Medical Image Computing and Computer-Assisted Intervention; MILLIE, Multiple Instance Learning for Leukocyte Identification; MIP, Maximum Intensity Projection; MMSD, Moroccan Multicenter Study Database; mpMRI, Multi-Parametric MRI; mpMRI-IF, mpMRI Derived Imaging Features; MRMR, Minimum Redundancy and Maximum Relevancy; MSLF, Major Structure and Location Information based Features; MSTA, Multiresolution-Statistical Texture Analysis; NBI, Narrow-Band Imaging; nCLE, Needle-Based Confocal Laser Endomicroscopy; NGDM, Neighborhood Gray-Level Dependence Matrix; ODL-PTNTC, Optimal Deep Learning Based Pancreatic Tumor and Nontumor Classification; PAS, Photoacoustic Spectroscopy; PCCD, Pancreatic Cell Images Dataset; PHDA, Population Health Data Archive; QDA, Quadratic Discriminant Analysis; QIF, Quantitative Image Features; QRF, Quantitative Radiomics Features; SCAD, Smoothly Clipped Absolute Deviation; SE-CNN, Squeeze and Excitation based CNN; SE-KNN, Subspace Ensemble K Nearest Neighbor; SOM, Self-Organizing Competitive Maps; SVD, Singular Value Decomposition; TCIA, The Cancer Imaging Archive; TCLDAASCA, Two-class LDA-based Automated Sequential Classification Algorithm; URF, Untuned Random Forest; ViT, Vision Transformer; WBC, White Blood Cells; WSI, Whole-Slide Images; YCNN, You Only Look Once Model-Based CNN.

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<https://doi.org/10.1016/j.eswa.2024.124838>

Received 26 June 2023; Received in revised form 15 June 2024; Accepted 19 July 2024

Available online 23 July 2024

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encompassing these specific types. A total of 191 peer-reviewed publications are considered which were published spanning the years 2018 to 2023. The analysis and review of cancer detection techniques were conducted separately for ML and DL models, with 87 articles focusing on ML-based techniques and 104 articles focusing on DL-based techniques. The study, a synthesis of diverse research endeavors, offers a comparative dissection of the best and worst performing classifiers. Additionally, it illuminates overarching findings and confronts challenges, encapsulating a compendium of insights crucial for the trajectory of future research. We put emphasis on the magnitude of advancements in diagnostic methods and the choice of appropriate classification models. Additionally, we highlight the significance of feature engineering techniques in advancing cancer detection performance. By consolidating the findings of numerous research articles and analyzing the advantages and limitations of distinctive methodologies, this study contributes to the ongoing efforts to improve cancer detection methods. The results underscore the pressing need for reducing medical errors and advancing the field of cancer diagnosis and treatment.

1. Introduction

Since the beginning of recorded history, cancer has been a problem for humans. However, in the past few eras, the prevalence of cancer has risen dramatically because of various reasons, including accelerated population aging, an increase in potentially harmful health habits among citizens in general, and an enhancement in the presence of carcinogens in the atmosphere and in food and beverage products (Faguet, 2015). The mere mention of cancer evokes fear, given its perilous nature as a disease. Until recent years, its treatment posed formidable challenges, bordering on the realm of near impossibility. However, contemporary times have witnessed a notable paradigm shift, with a considerable cohort successfully undergoing treatment. Yet, what precisely defines cancer? It manifests as an aberrant and hazardous physiological state wherein the body experiences anomalous cellular proliferation, detrimentally affecting normal physiological processes (NCI, 2021). While cellular division is an inherent facet of our organism's functioning, typically regulated with precision, cancer ensues when a specific bodily locus loses control over its cellular governance. Unrestrained and proliferative, if left unchecked, cancer burgeons exponentially, culminating in the manifestation of a neoplasm, colloquially referred to as a tumor. Upon the occurrence of an abnormal proliferation of cells beyond the regulatory purview of the body, two discernible types of manifests: one that encroaches upon and influences neighboring cells, and the other, less ominous, in which the cellular deviation is confined to its origin (Saxena et al., 2019). The former, termed malignant cancer or tumor, poses a profound peril due to its capacity to extensively affect the adjoining cellular milieu. Conversely, the latter, characterized by a limited impact on surrounding cells and an incipient developmental stage, exhibits a lesser degree of severity, rendering its treatment more tractable. Timely medical intervention is imperative, necessitating prompt attention from a medical professional to curtail progression at its nascent phase. The identification of symptoms and underlying causes assumes paramount importance. Common manifestations include abrupt fluctuations in body weight, cutaneous nodules, alterations in complexion, gastrointestinal irregularities, voice modulation, muscular and joint discomfort, protracted wound healing, diminished appetite, and conspicuous edema. The recognition of these symptoms, coupled with a multitude of potential additional indicators, underscores the urgency of seeking immediate medical counsel for a comprehensive evaluation and intervention (Du et al., 2023).

Numerous etiological factors contribute to the genesis of cancer, with a preeminent role attributed to carcinogenic agents known as carcinogens. This class of substances represents a pivotal and formidable instigator, significantly augmenting the proclivity towards cancer onset (Esgiar et al., 1998; Fiste et al., 2022). Furthermore, the adoption of deleterious dietary habits, a lack of regularity in lifestyle patterns, and an aberration in dietary comportment collectively constitute significant determinants fostering an environment conducive to cancer initiation. Beyond these lifestyle-oriented influences, a spectrum of viral agents, encompassing hepatitis B and papillomavirus, serves as insidious catalysts in the oncogenic process. Genetic predisposition, an intrinsic facet

of our biological makeup, also assumes a salient role in the genesis of cancer. Excessive alcohol consumption emerges as a discernible causative factor, notably linked to the inception of liver cancer. Habits such as the consumption of tobacco, cigarette smoking, and exposure to ultra-violet rays impart a heightened susceptibility to various forms of cancer. Additionally, seemingly unrelated phenomena, including constipation and specific sexual relations, have been implicated in the pathogenesis of select cancer types, underscoring the intricate web of multifactorial influences that contribute to the intricate tapestry of cancer causation. Cancer, typically characterized by a nuanced progression, unfolds across four discernible stages, with stage zero denoting an incipient state wherein cancerous cells exist, albeit not constituting a full-fledged malignancy. Any factors heightening the vulnerability to cancer are encapsulated within this preliminary stage. Stage one heralds the presence of a minuscule tumor devoid of metastasis, confined to a singular area without encroachment upon neighboring cellular domains, rendering its treatment relatively facile. However, as the disease advances to stage two and subsequently to stage three, the magnitude of cellular aberration burgeons, and cells extend their reach into adjacent territories. The expeditious initiation of treatment at these junctures becomes imperative, as malignancy acquires an augmented degree of peril and recalcitrance. The nomenclature "Mita static cancer" underscores the metastatic potential inherent in these later stages. It is incumbent upon medical counsel to mitigate the pronounced danger posed, as at this juncture, the cancer may have disseminated to other vital organs, and failure to procure prompt and specialized attention augurs a perilous trajectory, carrying a substantive risk of mortality. The global landscape of cancer encompasses over 200 distinct types, with a subset of approximately 10 to 12 types manifesting with the highest prevalence (Bray et al., 2018). Presently, the arena of cancer care has advanced to a point where treatment modalities are not only feasible but also preventative measures have become attainable. The World Health Organization records a staggering annual incidence of approximately 10 million new cancer cases worldwide, with recent data indicating that one in 10 individuals in India will grapple with this affliction. The ubiquity of cancer across the lifespan is emphasized by the statistic that one in 15 individuals may succumb to its deleterious consequences. Alarming statistics pertaining to India's cancer landscape further underscore the gravity of the situation, with an annual reportage of 16 million cancer cases in both rural and urban settings. Six predominant types, encompassing lung, oral, stomach, breast, and cervical cancers, dominate the Indian oncological profile. In a global context, however, the spectrum widens to include approximately 15 types, such as colorectal, leukemia, lung cancers, and stomach cancers. Given the pervasive nature of cancer, particularly as the most prevalent malignancy worldwide, the timely and efficacious treatment of these varied types assumes paramount significance (Faguet, 2015).

The omnipresent specter of cancer, a malady of profound gravity, unveils a disquieting narrative underscored by staggering statistics emblematic of its far-reaching global resonance. In contemporary epochs, a discernible surge in cancer incidence has cast a formidable shadow across the world stage. Projections unfurl a disconcerting

trajectory, with over 19 million novel cancer diagnoses documented in the annus horribilis of 2020 alone, a numerical crescendo poised to crescendo further, breaching the ominous threshold of 30 million by the temporal juncture of 2040. This precipitous uptick in cases begets a corresponding elevation in the grim toll exacted by cancer, with the year 2020 witnessing an approximate culmination of 9.9 million cancer-related demises, a macabre tableau set to unfold into an even direr crescendo, eclipsing 16 million by the daunting threshold of 2040. The orchestration of these numerical symphonies reflects not merely a statistical surge but a somber testament to the pressing imperative for heightened global efforts and innovations to confront, ameliorate, and ultimately curtail the relentless encroachment of this insidious and pervasive adversary (World Health Organization, 2019; World Health Organization International Agency for Research on Cancer, 2020). These risk factors have become more prevalent, particularly in developing regions, highlighting the need for targeted interventions and public health initiatives. Access to affordable and quality healthcare remains a significant challenge, particularly in underserved areas. Disparities in cancer care and treatment options persist, hindering the ability of many individuals to receive timely and appropriate care. However, advancements in medical research and technology offer hope for improved outcomes. Early detection, combined with prompt and targeted therapies, has been shown to enhance survival rates and improve the overall prognosis for cancer patients.

Fig. 1 elucidates a bar graph, encapsulating estimates of new cancer incidences, fatalities, and survival trajectories across diverse cancer types spanning the temporal expanse from 2020 to 2040, denoting values in thousands ('k'). This intricate visual representation, tailored for a global demographic, succinctly communicates that the magnitudes for cancer incidence, fatalities, and survival are delineated in units of thousands. A meticulous dissection of the data reveals, for instance, that in 2020, the incidence of brain cancer was quantified at 308 thousand, precipitating 251 thousand fatalities and yielding 57 thousand survivors (Bray et al., 2018). Projections for 2040 envisage a surge in brain cancer incidences to 435 thousand, accompanied by 368 thousand fatalities and 67 thousand survivors. Lung cancer, an eminent concern, exhibited 2,210 thousand incidences in 2020, concomitant with 1,800 thousand fatalities and 410 thousand survivors. Anticipating 2040, lung cancer incidences are poised to elevate to 3,630 thousand, with fatalities surmounting 3,010 thousand and survivors numbering 620 thousand. Skin cancer, with 1,525 thousand incidences in 2020, recorded 120.7 thousand fatalities and yielded 1,404.3 thousand survivors. A foresight into 2040 prophesies an escalation in skin cancer incidences to 2,525 thousand, alongside 170 thousand fatalities and a resilient cohort of 2,355 thousand survivors. This meticulous dissection extends across various cancer types, unraveling intricate trajectories for pancreatic, esophageal, prostate, colorectal, and leukemia. The overarching tapestry

culminates in a synthesis for all cancer types combined, registering 19,300 thousand incidences in 2020, comprising 9,960 thousand fatalities and fostering 9,340 thousand survivors. A somber extrapolation into 2040 portends a surge in all cancer incidences to 30,200 thousand, accompanied by a daunting toll of 16,300 thousand fatalities and a persevering cohort of 13,900 thousand survivors. This elaborate visualization not only portrays the quantitative dimensions of the global cancer landscape but also underscores the exigency for comprehensive strategies to confront and mitigate the impending escalation of this formidable public health challenge.

In Fig. 2, a meticulous comparative analysis discerns the death rates attributable to various cancer types in the year 2020, drawing a juxtaposition between the global perspective and the Asian landscape. The discernible trend unfolds a disconcerting reality wherein Asia consistently registers elevated death rates vis-à-vis the world averages, positing the notion that the mortality rate associated with cancer surmounts to higher thresholds in the Asian demographic. This paradigm is notably evident across a spectrum of cancer types, including brain, pancreatic, esophageal, prostate, colorectal, and leukemia, lung, breast, skin, and the collective amalgam of all cancer types. Asia, in each instance, presents discernibly higher death rates, with disparities ranging from incremental increases to marked differentials. For instance, in the realm of brain cancer, the death rate stands at 82.63 % in Asia, marginally surpassing the global average of 81.49 %. Lung cancer manifests a similar trend, with an 84.09 % death rate in Asia compared to the 81.45 % global average. A particularly pronounced discrepancy is observed in the case of skin cancer, where Asia reports a staggering 35.92 % death rate, sharply contrasting the 7.91 % global average. This trend persists consistently across leukemia, colorectal cancer, prostate cancer, breast cancer, and the comprehensive amalgamation of all cancer types, collectively painting a sobering tableau that underscores the imperative for targeted interventions and region-specific healthcare strategies to ameliorate the disproportionate burden of cancer-related mortality prevalent in the Asian context. The data indicates that Asia has a higher overall death rate for cancer at 61.16 %, whereas the world average stands at 51.61 %. These statistics suggest that cancer-related mortality is more prevalent in Asia compared to the global scenario. These findings emphasize the need for focused efforts to improve cancer prevention, early detection, and treatment strategies in Asia. By addressing factors such as healthcare accessibility, awareness, and education about cancer, as well as promoting healthy lifestyles and screening programs, it may be possible to reduce the death rates and improve outcomes for individuals affected by cancer in Asia.

In the intricate dance of healthcare, the timely unraveling of life-threatening conditions, particularly the labyrinth of malignancies, holds the promise of charting transformative narratives for patients, potentially salvaging the very fabric of existence. The mortality tapestry

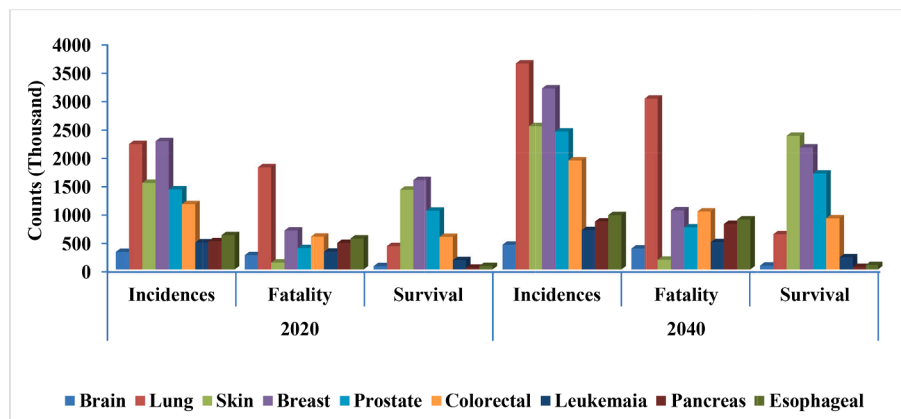


Fig. 1. Projected trends of cancer incidence, fatalities, and survival for various cancer types from 2020 to 2040 (In thousands).

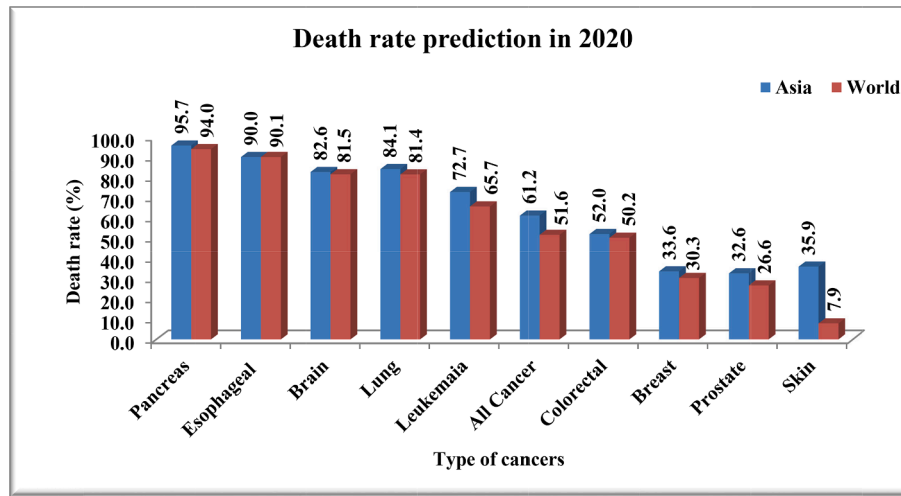


Fig. 2. Comparative analysis of cancer death rates: World vs. Asia for all cancer types in 2020.

woven by cancer, a haunting second in the dirge of causes, has witnessed a slow but sure ebbing since 1993 in the United States, a symphony orchestrated by the crescendo of refined early detection and cost-effective therapeutic interventions (Jiaquan et al., 2021). Yet, within this symphony, a discordant note emerges, resonating from manual missteps and diagnostic fumbles, casting a shadow that claims a substantial toll – 40–50 thousand lives annually, forming a stark composition in the litany of medical litigation (Harada et al., 2021). Amidst this dissonance, empirical musings from chart evaluations echo a more subdued melody, unveiling a mere 0.4 % error rate in a canvas of 7,926 cases and a slightly heightened 2.4 % in a narrative spun from 1,957 instances. However, these vignettes, drawn from the canvas of hospitals, paint a mere fraction of the broader tableau, with implications cascading over twelve million individuals annually within the realms of primary care. Extrapolating this narrative to the realms of emergency departments and non-primary care clinics, the specter of misdiagnosis looms large, reaching a crescendo that could potentially embrace 31 million lives (Newman-Toker et al., 2021). The global stage, fraught with financial and corporeal peril, bears witness to the colossal stakes woven into the fabric of diagnostic precision. These missteps, beyond squandering temporal, monetary, and emotional currencies, unfurl a perilous tapestry that places the very essence of patient well-being in the crucible of uncertainty. The imperative for an ever-evolving panorama of diagnostic precision becomes not just a call to arms but a resonating hymn to safeguard lives, forging a transformative journey through the intricate labyrinth of healthcare complexities.

In navigating the labyrinth of cancer prevention, the imperative emerges to transcend the current stage by obviating diagnostic pitfalls and ushering in a paradigm shift from manual diagnostics to automated, technologically sophisticated processes. The vanguard of this transformative endeavor lies in the integration of ML and DL, underpinned by cutting-edge reset technology. The envisioned system, meticulously crafted for efficiency, precision, and reliability, holds the potential to revolutionize cancer diagnosis, particularly in its nascent stages. A collective effort spearheaded by the relentless pursuit of Researchers, Academy Missions, Medical Professors, and Scientists has crystallized into a corpus of research and reviews, meticulously tackling the challenges and nuances inherent in deciphering fatal cancer types. This discourse, however, is not merely a retrospective gaze but a forward-looking endeavor, presenting a compendium of research employing ML and DL methodologies over recent years. Its focus transcends the present, delving into the realm of clinical diagnostics to envisage possibilities that hold the key to unveiling nuanced solutions. Through this exploration, we aspire not just to discern the current landscape but to delineate a trajectory toward an optimized, adaptive solution. The triad

of cancer detection, segmentation, and prevention emerges as the linchpin, weaving a narrative where cutting-edge technology converges with the relentless pursuit of a future where lives are saved from the clutches of this pernicious affliction.

2. Related work

This section encapsulates a comprehensive literature review focused on review articles delving into cancer classification and detection through the lens of artificial intelligence techniques. The purview extends to encompass articles published within the temporal span from 2015 to 2023, illuminating the landscape of multiple cancers (involving two or more cancer types) and their examination through the prism of artificial intelligence, employing methods such as DL, ML, or a hybrid of both. Table 1 serves as an informative repository, offering a succinct overview of the findings, limitations, and the spectrum of AI techniques employed in the selected review articles, contextualized by the specific cancer types scrutinized during the review process. This compilation seeks to empower scholars with a synthesized understanding, facilitating insights into the nuances of performance, identified limitations, and emergent trends within the realm of cancer classifications guided by AI techniques. (Kourou et al., 2015) delved into the intricate realms of cancer relapse identification and survival prognostication, orchestrating a narrative that, while steeped in methodological acumen, exhibited a judicious selection of literature references. Placing a poised emphasis on pivotal parameters encompassing publication dynamics, methodological intricacies, cancer typology nuances, patient cohort dimensions, data modalities, accuracy metrics, validation methodologies, and the crux of salient features, the review unfolded as an erudite symphony. However, it wielded a deliberate constraint, refraining from an exhaustive foray into the realms of cancer diagnosis or detection. Instead, its narrative danced intricately on the precipice of predictive modelling for cancer outcomes, refraining from plunging into the granular terrain of specific detection techniques. (Al-shamasneh & Obaidallah, 2017) explored the use of ML techniques for brain, breast, and lung cancer identification. The review included enough literature references and explored various performance parameters. However, it had limitations such as evaluating only three cancer types and not comparing DL models to ML-based classifiers. The focus was on ML algorithms and their performance in cancer detection.

(Levine et al., 2019) concentrated predominantly on the radiological and diagnostic medical procedural flow concerning neoplastic identification. The scrutiny delineated the intricacies of formulating and implementing a convolutional neural network (CNN) for the analysis of medical images. However, it had a limited number of literature

Table 1
Comparative study of review articles on cancer classifications: insights and constraints.

References	No. of Cancer Categories	Techniques (ML, DL)	Distinct ML & DL reviews	Findings	Limitations
(Kourou et al., 2015)	4	ML	NO	– Centered on neoplastic relapse and prognostication of viability.	– A limited corpus of literary references has been incorporated. – Examination of cancer identification or discernment was omitted.
(Al-shamasneh & Obaidallah, 2017)	3	ML	NO	– Explored ML-based classification methods for cancer.	– Only evaluated three types of cancer (Breast, Lung, Brain). – Focused solely on ML-based methods and did not compare with DL models.
(Levine et al., 2019)	3	DL	NO	– Highlighted radiological and diagnostic medical procedural flow.	– Reduced focus on the identification of cancer. – Incorporated a limited quantity of scholarly references. – Limited evaluation parameters considered.
(Huang et al., 2020)	4.	ML & DL	No	– Compared AI algorithms with human pathologists in prognosis and diagnosis.	– Restricted literary references per malignancy category, capped at a maximum of three sources. – Neglected the incorporation of ML and DL categorizers.
(Saba, 2020)	6	ML & DL	NO	– Evaluated performance metrics without separating ML and DL approaches.	– Relatively smaller review of literature. – Did not separate ML and DL approaches. – Did not compare DL with ML-based methods.
(Majumder & Sen, 2021)	4	ML & DL	NO	– – emphasizes AI's transformative role in cancer diagnostics, improving lesion detection through digital image analysis.	– A limited array of cancer categories and a sparse selection of scholarly references encompassed. – Metric parameters gauging performance displayed heterogeneity throughout the literature.
(Tufail et al., 2021)	4	DL	NO	– Outlined openly accessible databases, deliberated upon cancer identification, and delineated cancer segmentation.	– Concentrated exclusively on DL-driven cancer identification. – Abstained from scrutinizing each distinct cancer category autonomously.
(Murthy & Bethala, 2021)	5	ML & DL	NO	– Enumerated methodologies and computational strategies for the anticipation and prognosis of malignancies.	– Small number of literature sources included. – Did not validate classifier performances. – Parameters were enumerated sans an exhaustive review grounded in data scrutiny.
(He et al., 2022)	6	ML & DL	NO	– Analyzed preprocessing and feature abstraction methodologies concurrently along with various cancer review.	– Limited literature sources for each cancer type. – Only considered accuracy as an evaluation metric. – Did not discuss the dataset and its modality separately.
(Kumar & Alqahtani, 2022)	3	DL	NO	– Deliberated upon DL models and their structural frameworks, scrutinized literature predicated on image categorization.	– Only focused on DL methods, did not consider ML approaches. – Different literature sources used different performance metrics.
(Kumar et al., 2022)	4	DL & ML	NO	– Encompassed a diverse array of malignancies and incorporated an extensive body of scholarly works.	– Abstained from individual scrutiny of distinct cancer categories. – Failed to discriminate between DL & ML driven methodologies.
(Painuli et al., 2022)	6	ML & DL	Yes, only best model Compared	– Offered an intricate examination of open access databases and the utilization of ML/DL approaches.	– Reviewed DL and ML techniques together instead of separately.
(Manhas et al., 2022)	4	ML & DL	NO	– Conducted a complete review of literature for every categories of cancer.	– DL/ML methodologies were not evaluated distinctly.
(Ibrahim et al., 2022)	5	DL	NO	– Explored diverse imaging databases and illustrated architectures of DL classifiers.	– Assessed a restricted quantity of scholarly references. – Only included DL models.
(Maurya et al., 2023)	5	ML & DL	NO	– Encompassed various performance parameters, discussed benefits and drawbacks, and presented challenges of each cancer type.	– ML/DL methodologies were not autonomously appraised and juxtaposed. – The utilized dataset was not expounded upon.
(Mokoatle et al., 2023)	4	ML & DL	NO	– Examined methodologies for cancer identification, suggested proprietary techniques, and introduced cutting-edge approaches.	– Investigated only four types of cancer. – Did not include a study on datasets. – Provided only one type of assessment metric.
(Rai & Yoo, 2023)	4	ML & DL	Yes	– Explored a diverse range of literature, to assess the application of ML and DL techniques separately.	– Examined only four cancer categories (brain, breast, lung, and skin). – Did not present a novel methodology based on the review of articles.

references and did not emphasize cancer detection extensively. The review aimed to provide insights into the integration of CNNs into the radiology workflow rather than in-depth analysis of cancer detection algorithms. (Huang et al., 2020) presented a prognostication and diagnostic efficacy juxtaposition between AI's algorithms and human pathologists across 6 categories of malignancies. Despite encompassing a broad spectrum of cancer types, the review exhibited a scarcity of literary references per specific malignancy and overlooked the integration of ML/DL classifiers. The central theme revolved around appraising the comparative efficiency of AI algorithms and human pathologists in the realms of cancer diagnosis and prediction. (Saba, 2020) delivered a concise elucidation of benchmark datasets and scrutinized performance metrics across 6 varieties of malignancies. The examination encompassed a myriad of performance parameters and delineated a systematic structure for each category of cancer classification methodologies. Notably, it refrained from segregating ML & DL based classifications individually and abstained from contrasting DL and ML methodologies. The core emphasis rested on the validation of evaluation metrics within the realm of diverse cancer identification algorithms. (Majumder & Sen, 2021) exemplified the deployment of AI's transformative role in cancer diagnostics, improving lesion detection through digital image analysis. The review spanned breast, lung, solid, and brain cancers but presented constraints, such as a restricted number of cancer types and scholarly references, coupled with disparate performance parameter metrics throughout the literature. The central theme revolved around illustrating the practical application of AI in diverse facets of oncology, with a specific focus on cancer detection. (Tufail et al., 2021) wove the scholarly tapestry and the discourse unfolded as a meticulous exploration of publicly available datasets, casting an illuminating spotlight upon the expansive landscape of cancer research. The narrative, however, sculpted its contours predominantly around the intricate realm of DL-driven intricacies in cancer finding and segmentation. Amidst the abundance of performance metrics adorning the canvas, the review, like a selective maestro, chose to orchestrate its symphony exclusively within the harmonious corridors of DL, refraining from an autonomous ballet of scrutiny for each unique cancer type. Its thematic nucleus pulsed with a vibrant cadence, centering on the vibrant discussion of datasets and the nuanced deployment of DL-based methodologies in the ever-evolving panorama of cancer detection and segmentation. (Murthy & Bethala, 2021) presented an ensemble of vital metrics and a compendium of paramount metrics emerged, intricately harnessed for the prognostication of malignancies within the annals of literature. The discourse further unfurled an array of diverse algorithms curated for the dual purpose of predicting and prognosticating cancer trajectories. Yet, within this erudite opus, a discerning eye would discern the nuance of limitations, with a meager assortment of literary references adorning the narrative. The scrutiny, akin to a restrained virtuoso, abstained from the validation of performance in the scope of cancer classifications and refrained from the granular dissection or analysis of parameters grounded in empirical data. The thematic heartbeat reverberated with a singular focus – to showcase an eclectic array of algorithms and metrics employed in the profound arena of cancer classification and diagnosis.

(He et al., 2022) an examination of preprocessing methodologies and strategies for extracting features from histopathological images within the realm of neoplastic identification. The scrutiny encompassed a spectrum of malignancies, coupled with distinct analyses for conventional categorizers and DL categorizers. Nevertheless, it showcased a restrained quantity of scholarly citations corresponding to each specific cancer type, exclusively appraised accuracy as the sole evaluative metric, and refrained from a dedicated discourse on datasets and their modalities. The thematic essence gravitated towards the intricacies of preprocessing techniques and feature extraction in the domain of cancer discovery utilizing histopathological images. (Kumar & Alqahtani, 2022) provided an overview of ovarian, breast, lung, cervical, prostate, colorectal, and liver cancers and their detection using ML classifiers. The review covered different aspects such as feature extraction, classifiers,

performance metrics, and data modalities. However, it did not separately assess DL and ML techniques and did not finance a broad overview of the databases used. The focus was on discussing ML-based classifiers for cancer identification. (Kumar et al., 2022), in their scholarly exploration, navigated a comprehensive spectrum of neoplastic categories, meticulously from thyroid, stomach, skin, prostate, oral, lung, liver, kidney, colorectal, cervical, breast, to brain cancers. The exposition, adorned with a profusion of meticulously curated references, intricately delved into diverse performance metrics, simultaneously unraveling the intricate challenges inherent in each scrutinized literature. Despite its meticulousness, the review abstained from isolating the exploration of ML/DL approaches, opting against a segregated scrutiny for each distinct cancer type. The primary focus pivoted around presenting a panoramic perspective of diverse cancer types and their detection methodologies, intricately interwoven with the inherent challenges posed by each facet. (Painuli et al., 2022) embarked on an exhaustive analysis, scrutinizing benchmark datasets tailored for pancreatic, brain, skin, liver, lung, and breast cancers. Their investigation meticulously traversed the overall utilization shares of both ML & DL approaches within these intricate cancer domains, with a specific emphasis on identifying optimal classifiers based on accuracy. However, despite the depth of their exploration, the review opted not to autonomously assess and contrast DL and ML techniques, choosing instead to collectively examine their application. The focal point of this scholarly endeavor remained anchored to benchmark datasets and the nuanced exploration of ML/DL approaches across a diverse spectrum of cancer types. (Manhas et al., 2022), in their expansive literary inquiry, traversed a comprehensive landscape encompassing brain, breast, oral, cervical, and various other cancers. The scrutiny, adorned with a substantial number of references, meticulously covered all performance parameters. However, the evaluation refrained from a separate dissection of DL/ML approaches, and a detailed description of the dataset employed was not provided. The central focus of this scholarly endeavor revolved around the thorough review of diverse cancers and the array of methodologies employed for their detection. (Ibrahim et al., 2022), in their investigative journey, honed in on a spectrum of 5 categories of cancer. The review intricately dissected various image datasets, presenting a myriad of DL model architectures pivotal in the realm of identification of cancers. However, the assessment, confined to an inadequate collection of scholarly articles, singularly incorporated DL models, eschewing a comprehensive review of the broader literature and neglecting consideration for ML-based approaches. The primary emphasis of this scholarly endeavor orbited around the intricate exploration of diverse image datasets and the manifold DL model architectures instrumental in the pursuit of cancer identification. (Maurya et al., 2023), in their scholarly exploration, delved into the intricacies of brain, cervical, lung, breast, and skin cancers. Their comprehensive examination meticulously scrutinized performance parameters, benefits, drawbacks, and challenges inherent within these diverse cancer domains. Despite the breadth of their exploration, the review abstained from autonomously evaluating and contrasting ML/DL techniques. Additionally, a detailed exposition of the dataset employed remained conspicuously absent. The crux of their academic pursuit revolved around a meticulous discussion encompassing the intricacies of performance and challenges intrinsic to cancer detection techniques specifically tailored for distinct cancer types. (Mokoatle et al., 2023) in their scholarly review, meticulously scrutinized cancer detection approaches tailored for colorectal, prostate, breast, and lung cancers. The review not only proposed novel cancer detection techniques but also integrated cutting-edge sentence transformers and unsupervised SimCSE approaches. Despite the innovation showcased, the investigation was confined to only four cancer types, lacked an in-depth dataset study, and provided a singular assessment metric. The primary focus of this academic endeavor remained anchored in proposing innovative cancer detection techniques and scrutinizing their performance within the context of specific cancer types. (Rai & Yoo, 2023) extensively explored the applications of ML and DL in cancer

detection, focusing on brain, breast, lung, and skin cancers. They reviewed 130 pieces of literature and their study included descriptions of benchmarked datasets and commonly used features. Despite a comprehensive examination, the study did not introduce a new methodology based on the reviewed articles.

3. Research gap

- **Lack of Separate Survey on ML and DL Classifiers:** A significant research gap exists as there are very few separate surveys comparing traditional ML and DL classifiers for cancer detection, impeding comprehensive insights for optimal selection in specific cancer scenarios.
- **Limited Coverage of High Death Rate Cancers:** Another significant research gap is the limited coverage of cancers with high death rates, such as esophageal cancer and pancreatic cancer, in many reviewed studies. These types of cancers pose unique challenges due to their aggressive nature and limited treatment options. The lack of focus on developing accurate and effective detection techniques for these specific cancer types indicates a research gap that needs to be addressed. Further research is needed to improve early detection and prognosis prediction for esophageal and pancreatic cancers.
- **Lack of Consistent Review Parameters:** The variety of review parameters used by different researchers adds complexity to comparing and evaluating studies. This lack of consistency makes it challenging to identify the most effective approaches and benchmarks for cancer detection. Establishing a standardized set of review parameters would enable better comparison and analysis, facilitating the identification of trends and advancements in the field.
- **Heterogeneity of Performance Evaluation Metrics:** Another research gap is the heterogeneity of performance evaluation metrics used in different studies. Diverse evaluation metrics are commonly utilized, lacking a consistent preference, creating challenges in comparing and benchmarking the performance of various cancer detection techniques. A standardized set of commonly used and accepted evaluation metrics would allow for more meaningful comparisons and reliable assessment of the performance of various methods.
- **Research Gaps and Challenges:** Through the review of numerous research articles, several additional research gaps and challenges have been identified in the field of cancer detection. These include addressing data imbalance issues in medical datasets, exploring the use of hybrid and ensemble classifiers that combine multiple techniques, developing adaptive classifiers capable of handling evolving data and new cancer subtypes, and optimizing the performance of cancer detection models in terms of accuracy, speed, and interpretability. These research gaps and challenges represent opportunities for further investigation and advancements in cancer detection methodologies.

By methodically tackling these research lacunae and herculean obstacles, scholars and professionals have the potential to produce substantive research to the advancement of the detection of cancer classifications, fostering enhanced accuracy, resilience, and efficiency. Such advancements hold the promise of exerting a considerable influence on critical aspects like early diagnosis and treatment strategizing, yet, even in this ongoing battle, patients forge new paths towards better outcomes.

3.1. Contribution and highlights

This scholarly endeavor provides an intricate and comprehensive examination of the present status and prospective trajectories in the realm of diagnosing and detecting diverse cancer types, employing both classical ML and DL classifiers. The elucidation of main contributions in this review article unfolds as follows:

- **Comprehensive Review of Five Types of Cancers:** This study meticulously scrutinizes five specific cancers – pancreatic, esophageal, prostate, colorectal, and leukemia – chosen for their elevated mortality rates, underscoring their pivotal role in cancer research.
- **Inclusion of a Large Number of Recent Peer-Reviewed Articles:** The review assimilates a significant corpus of current information, encompassing 191 peer-reviewed articles on cancer research utilizing AI within the last five years (2018 to 2023). This extensive coverage ensures a comprehensive analysis of the current literature in the field.
- **Separate Review of ML/DL Approaches:** The investigation undertakes distinct assessments for cancer classifications methodologies employing both classical ML and DL approaches. This meticulous approach facilitates an intricate scrutiny and comparison of the respective strengths and limitations inherent in each methodology.
- **Analysis of ML and DL Research Articles:** The review analyzes and reviews 87 research articles that focus on identifications of cancers using classical ML algorithms and 104 articles that utilize DL techniques. This enables a comprehensive understanding of the advancements and progress made in each area.
- **Examination of Various Parameters:** The review adopts a nuanced approach, considering diverse parameters for the analysis of included articles. These parameters encompass intricate aspects such as databases utilized for classifications, feature extraction methods, best classifiers employed, and the consequential performance metrics, notably accuracy. This comprehensive evaluation provides a nuanced and in-depth overview of the intricate research landscape in the realm of cancer detection.
- **Comparative Analysis of Review Articles:** The research encompasses a meticulous juxtaposition of recently issued critical appraisals, spanning diverse facets of cancer detection within the timeline of 2015 to 2023. This discerning scrutiny elucidates the discoveries and constraints inherent in these evaluations, furnishing researchers with invaluable insights to discern and redress extant lacunae in the research landscape.
- **Descriptive review on benchmarked and open Access Databases:** An intricate examination of benchmark and open access datasets linked to the five cancer types scrutinized in this investigation is delineated. The scrutiny includes hyperlinks for dataset retrieval, easing accessibility for subsequent research and experimentation.
- **Commonly Utilized Features and Preprocessing Techniques:** The research identifies and deliberates upon the prevailing features frequently employed in the realm of cancer identification, furnishing succinct portrayals for each. Additionally, a concise analysis of commonly employed preprocessing techniques, along with a generalized formula, is presented, enhancing the understanding of the pre-processing stage.
- **Principal findings and Hindrances:** The analysis unveils principal discoveries and obstacles linked with both ML and DL methodologies for each category of cancer scrutinized. This imparts valuable perspectives into the capabilities, limitations, and domains necessitating enhancement within each methodology.
- **Evaluation of Optimal and Suboptimal Performing Models:** The research performs a comparative examination of the most effective and least effective models concerning each cancer type, focusing on detection accuracy. This scrutiny contributes to comprehending the efficacy of diverse models and illuminates areas amenable to enhancement.
- **General Description and Analysis of Commonly Utilized ML and DL Models:** The review article includes a comprehensive analysis and description of the most utilized ML/DL algorithms in cancer classifications. Furthermore, it features schematic representations of the suggested and refined methodology for cancer identification.
- **Unified structural diagram for ML/DL-based cancer classification:** To facilitate a clear understanding of the cancer detection

process using ML/DL approaches, this review article presents a generalized and sequential flow diagram. This diagram outlines the step-by-step process involved in detecting cancer, starting from the initial data acquisition or input, followed by preprocessing, feature extraction, model training, and finally, the prediction or diagnosis phase.

In essence, this review thoroughly explores the diagnosis of diverse cancer categories through ML and DL methodologies. Through meticulous analysis of numerous research articles, it presents pivotal findings and challenges, contributing significantly to the progression of cancer detection approaches and steering future research endeavors.

4. Research methodology

In this section, we elucidate the intricacies of our model design and the methodologies employed for the detection of various categories of cancers. Given the plethora of approaches available for cancer detection, segmentation, and prediction, our focus narrows down to five fundamental approaches, which we categorize into two main groups. Fig. 3 visually outlines the architectural flow of these approaches, encompassing cancer detection and classification. The categories comprise (a) ML models, (b) DL approaches, (c) ML with deep features, (d) DL with

deep features, (e) ML-based transfer learning, and (f) DL-based transfer learning. Our study particularly hones in on two primary approaches: ML and Deep Neural Network (DNN). Consequently, we classify these approaches into two groups based on the type of classifier employed. Specifically, (a), (c), and (e) are deemed as ML approaches, utilizing ML classifiers for predictions, while (b), (d), and (f) fall under the DNN (DL) approach. Diverse researchers, stemming from various disciplines, have delved into numerous strategies aimed at augmenting cancer screening and diagnosis. In our comprehensive examination of cancer identification, we consider seven distinct types: brain, lung, skin, breast, prostate, colorectal, and leukemia. Throughout our review, we meticulously analyze a multitude of research articles employing two primary approaches—ML and DNN—for predicting various cancer types. Pre-processing techniques play a pivotal role in almost all cancer detection approaches, serving to filter and prepare raw databases. Notably, feature extraction techniques are not universally employed, especially in DNN-based methods. A prevalent approach involves using deep features extracted by diverse DNN models, subsequently fed into either ML or DNN classifiers. Transfer learning stands out as a popular strategy, where DNN models are pretrained on extensive image datasets, subsequently utilized for detection with DNN or ML classifiers. Dataset acquisition emerges as a fundamental prerequisite for all these approaches, with subsequent preprocessing tailored to the specific dataset

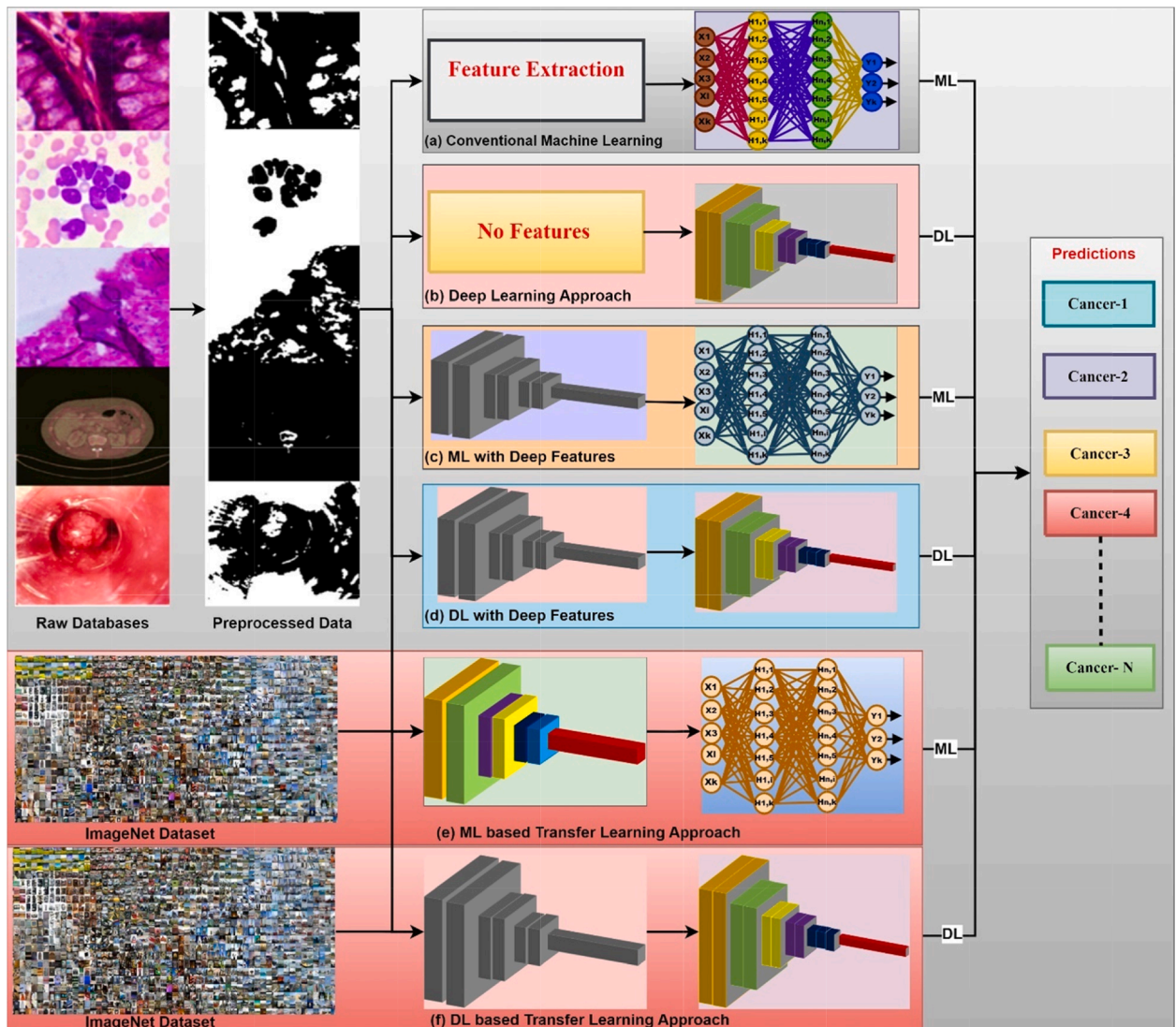


Fig. 3. Taxonomic exploration of cancer classification approaches using DL and ML Driven algorithms.

types and their sources. Researchers commonly explore pre-processing methods such as denoising, filtering, resizing, RGB to grayscale conversion, cropping, normalization, scaling, Region of Interest (ROI) acquisition, and image enhancement. Additionally, several other pre-processing techniques have undergone scrutiny by researchers. Feature engineering processes span diverse categories, including feature selection, reduction, optimization, fusion, and enhancement. While ML-based classifiers are prevalent for categorizing malignancies into binary or multi-class categories, processes in ML-based classification for cancer detection mirror those in DL-based models. Feature engineering is sometimes even employed in DL-based detection to further refine accuracy.

4.1. Cancer types

4.1.1. Pancreatic cancer

Pancreatic cancer is a type of cancer illustrated by the unrestrained expansion of cancerous cells in the pancreas. The pancreas, a vital organ situated in the abdominal region posterior to the stomach, serves a dual role as both an endocrine and exocrine gland. In its exocrine capacity, the pancreas generates digestive enzymes facilitating the decomposition of ingested food within the small intestine. These enzymes are discharged into the pancreatic ducts, facilitating their transport to the digestive system. Moreover, the pancreas, functioning as an endocrine gland, synthesizes hormones like insulin and glucagon. These hormones intricately govern the concentrations of sugar in the bloodstream, thereby exerting a pivotal influence on metabolic processes. Pancreatic cancer can manifest in different forms, but the most common type is pancreatic ductal adenocarcinoma (PDAC) (Qiu et al., 2021). PDAC reports for roughly ninety percent of all pancreatic cancer cases. It originates in the cells lining the pancreatic ducts, which are responsible for carrying the digestive enzymes produced by the pancreas. Alternative variety of pancreatic cancer is Neuroendocrine Tumors (NETs), displaying diminished frequency in contrast to PDAC. NETs can be segmented into non-functional and functional tumors, contingent on their proficiency to generate hormones. Operational NETs discharge hormones that elicit distinct symptoms, whereas non-functional NETs are devoid of producing noteworthy hormonal effects. Compared to PDAC, NETs generally have a better prognosis, meaning they tend to have a more favorable outcome and response to treatment. It is critical to discern between these categories of pancreatic cancer as they may require unique treatment approaches. PDAC, being the most prevalent type, has been extensively studied, but ongoing research is aimed at understanding and developing effective treatments for both PDAC and NETs.

Pancreatic cancer poses a significant challenge to global health, as indicated by the following statistics. It assumes the twelfth position in the global cancer hierarchy, marking its presence with an estimated 495,773 freshly diagnosed cases in the sole year of 2020. This highlights the widespread incidence of pancreatic cancer and its impact on populations across the globe. Tragically, pancreatic cancer is highly lethal and on a global scale, it holds the position as the seventh principal cause of cancer-related fatalities. In 2020, it claimed approximately 466,003

lives, underscoring its devastating consequences. The elevated fatality rate coupled with pancreatic cancer is a pressing concern that demands increased attention and research efforts to improve patient outcomes (Jung et al., 2022; Lv et al., 2017). Fig. 4 shows the images of Atrial Phase CT scans of the pancreas, featuring (a) Pancreatic Cancer at tail/body, (b) Pancreatic Cancer at Head/Neck, (c) Normal Pancreas Tail/Body, and (d) Normal Pancreas Head/Neck from the dataset used by (Ma et al., 2020). These images depict different conditions and regions of the pancreas, allowing for a visual comparison between cancerous and healthy tissues.

4.1.2. Esophageal cancer

Esophageal cancer, a malevolent cellular expansion in the esophagus, unfurls as a sinister proliferation within the intricate passage connecting the ethereal realm of the throat to the corporeal sanctuary of the stomach. This ominous ailment diverges into two distinct archetypes: the esoteric esophageal adenocarcinoma and the formidable esophageal squamous cell carcinoma. Esophageal adenocarcinoma is associated with chronic acid reflux and often develops from glandular tissue in the lower esophagus. Contrastingly, Esophageal squamous cell carcinoma emerges from the planar cells coating the esophagus, typically within its upper and middle domains. Frequent indications encompass challenges in swallowing, unintentional weight reduction, chest discomfort, persistent cough, huskiness, and indigestion. Diagnosis encompasses a blend of scrutinizing medical history, physical examination, imaging assessments, and biopsy. Esophageal cancer, constituting around 5 % of global cancer cases, stands as the eighth most prevalent cancer and ranks as the sixth leading contributor to cancer-related fatalities, responsible for about 6 % of such deaths. Incidence is higher in Eastern Asia, Eastern and Southern Africa, and parts of Central Asia. Risk factors include tobacco and alcohol use, obesity, poor diet, GERD, and exposure to certain chemicals. The overall 5-year life expectancy is around 20 %, however it can reach up to 90 % for early-stage cancers. Esophageal cancer is more common in men, showcasing a gender disparity, esophageal cancer unfolds with a proportion of about 3 males to every 1 female. It typically affects older individuals, with the highest incidence rates in people over the age of 60. Early detection and timely intervention are crucial for better prognosis. Regular screening and surveillance for individuals at risk may be recommended. Ongoing medical care is essential for managing esophageal cancer effectively. Fig. 5 displays sample images of positive-to-adenocarcinoma cases from two esophageal cancer datasets (de Souza et al., 2021): the Augsburg dataset and the MICCAI dataset. The Augsburg dataset image represents a specific instance of esophageal cancer classified as positive-to-adenocarcinoma, providing a glimpse into the characteristics and visual features associated with this type of cancer. Similarly, the MICCAI dataset image showcases another example of positive-to-adenocarcinoma in esophageal cancer, contributing to the overall understanding and analysis of this particular cancer subtype.

4.1.3. Prostate cancer

Prostate cancer, an artistic intruder, ensnares the prostate gland, unveiling its dual nature – a languorous drift within the confines of the

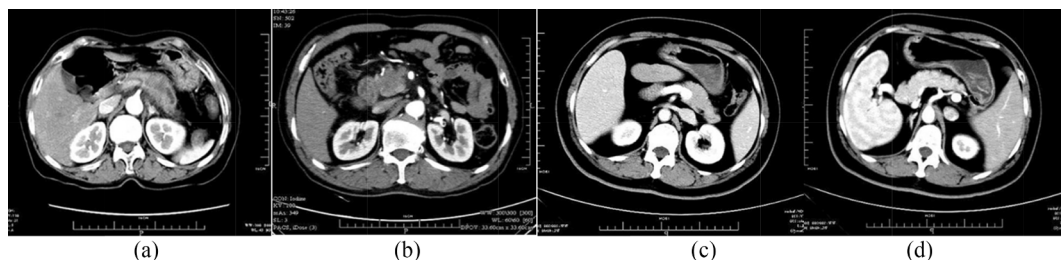


Fig. 4. Atrial phase CT images of (a) Pancreatic cancer at tail/body (b) Pancreatic cancer at Head/Neck (c) Normal pancreas tail/body (d) Normal pancreas head/neck.

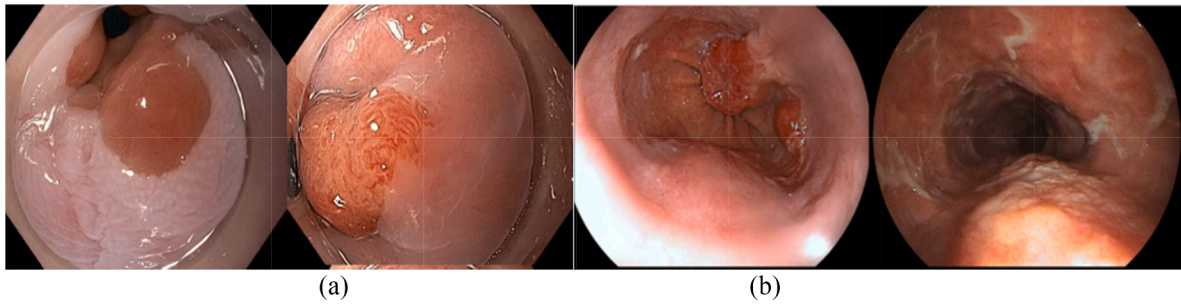


Fig. 5. Esophageal cancer datasets: sample images of positive-to-adenocarcinoma from Augsburg and MICCAI datasets.

prostate or a frenzied advance, swift and untamed. The quest to unveil this silent assailant involves the probing hands of a digital rectal exam (DRE) and the intricate insights whispered by the prostate-specific antigen (PSA) blood test. Abnormalities found in these tests may lead to further evaluations such as an ultrasound or a prostate biopsy. Ultrasound, a sonic artist, orchestrates sound waves to compose visual symphonies, revealing the hidden contours of the prostate in its meticulous performance, while a biopsy involves collecting tissue samples from the prostate for analysis in a laboratory. These tests help determine the presence and extent of cancer cells in the prostate. Seeking guidance from a healthcare expert becomes paramount for delving into fitting health evaluations and diagnostic approaches for prostate malignancy. In the United States, prostate cancer claims the bronze in cancer-induced mortality in 2017, encapsulating 19 % of emerging cancer instances and contributing to 8 % of fatalities attributed to cancer. Marked by 161,360 fresh diagnoses and 26,730 demises, prostate cancer distinctly reverberates across the landscape of public health. Non-invasive diagnostic approaches, such as MRI, CT, H&E images are commonly used for prostate cancer detection. MRI allows for detailed imaging of the prostate gland, aiding in the diagnosis and staging of the disease. However, to achieve early-stage diagnosis and improve survival rates, a computer-aided detection (CAD) system is crucial. These systems assist in analyzing medical images and identifying potential abnormalities associated with prostate cancer. Researchers have dedicated significant effort to developing various approaches for diagnosing prostate cancer, with a particular utilization of AI's driven approach (ML/DL). These methods leverage biological images of the prostate to train algorithms and enhance diagnostic accuracy. The use of advanced technologies like ML and DL holds promise in increasing the effectiveness and accuracy of prostate cancer diagnosis (Bulten et al., 2022). Fig. 6 of the DiagSet and PANDA database provides visual examples of prostate biopsies, aiding in the understanding and interpretation of the disease (Kozłowski et al., 2021).

4.1.4. Colorectal cancer

In the anatomical region of the lower abdomen, colorectal cancer, ranking as the 3rd most prevalent cancer globally and standing as the second leading cause of cancer-related deaths on a global scale, originates within the rectum or colon—integral components of the intricate digestive system. Despite notable strides in the realms of diagnosis and treatment, survival rates persist at relatively modest levels, thereby

representing a formidable threat to human well-being. The year 2017 witnessed the global reporting of 1.4 million fresh instances of colorectal cancer, leading to approximately 50,260 fatalities. The genesis of colorectal cancer is influenced by factors encompassing suboptimal dietary habits, excessive smoking, and other injurious behaviors, with genetic and environmental variables further amplifying susceptibility. The pivotal significance of early detection, instrumental in augmenting patient outcomes and survival metrics, is underscored by the endoscopic elimination of precancerous lesions, notably polyps, efficaciously mitigating the risk of colorectal cancer emergence. It is judiciously recommended for individuals exhibiting risk factors or harboring a familial history of the ailment to undergo periodic screenings and diagnostic evaluations. Timely discernment and tailored interventions play a decisive role in elevating survival rates for colorectal cancer patients. Medical progressions, inclusive of cutting-edge imaging modalities like colonoscopy, alongside the advent of targeted therapeutic approaches, exhibit promising potential in enhancing patient prognosis. Embracing alterations in lifestyle, characterized by the adoption of a healthful diet, regular engagement in physical exercise, and the cessation of smoking, constitutes a substantive stride towards diminishing the risk landscape associated with colorectal cancer. The study was carried out with the purpose of identifying cases of colorectal cancer by applying ML/DL classifiers applied to histological (H&E) images. The sample histology pictures taken from the Kather-CRC-2016 (KCRC-16) dataset is shown in Fig. 7.

4.1.5. Leukemia (Blood Cancer)

Blood cancer, a spectral invader originating within the marrow's sacred confines, manifests in three haunting forms: leukemia, lymphoma, and myeloma. Leukemia, a spectral uprising, unfurls when the body, possessed, spawns an excess of aberrant white blood cells. Non-Hodgkin lymphoma, a mystical metamorphosis in the lymphatic realm, weaves from lymphocytes, while the enigmatic Hodgkin lymphoma is marked by the appearance of the arcane Reed-Sternberg entity. Multiple myeloma, an arcane enchantment, begins its sorcery within the blood's very essence. Rarer specters of blood and marrow mysteries may also lurk. In this ethereal dance, early divination and intervention wield the power to shape destinies. Chronic leukemia, a subtle whisper in the marrow's secret chambers, unveils two faces: the elusive chronic lymphocytic leukemia (CLL) and the enigmatic chronic myelogenous leukemia (CML) (Nagiub Abdelsalam et al., 2019). CLL, a wisp in the white

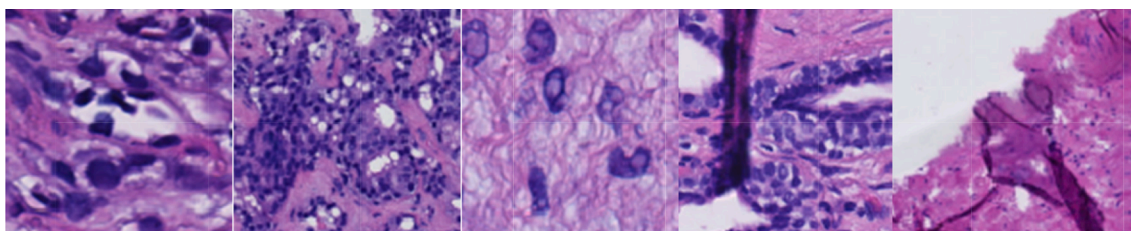


Fig. 6. Randomly selected sample image patches of prostate cancer from DiagSet and PANDA datasets.

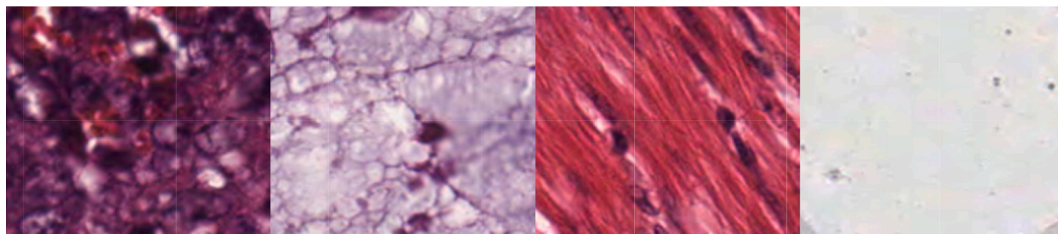


Fig. 7. Sample colorectal histological tissue components (TUMOR, DEBRIS, STROMA, ADIPOSE) from KCRC-16 database.

realm, germinates amidst the marrow's snow. CML, a symphony of shadows, births among the myriad blood kin – red, platelet, and white. In stark contrast, acute leukemia, a tempest of urgency, beckons swift attendants to its arcane masquerade, marked by a tumultuous proliferation of unnatural blood progeny, often luring the unsuspecting children into its vortex. Blood cancer, an ominous specter, orchestrates its macabre ballet, with an anticipated arrival of 178,520 new actors and a fateful departure of 58,100 souls upon the mortal stage in the year 2021 (Depto et al., 2023; Nazari et al., 2020). Leukemia is the most frequent kind of blood cancer, followed by lymphoma and myeloma. These diseases are impacted by age, gender, and heredity, with males and specific family groupings having greater incidence. Early identification and treatment are critical to improving survival rates. Medical therapies have advanced throughout time, considerably improving prognosis for patients affected by these blood malignancies. Fig. 8 shows images of different types of leukemia: Chronic Lymphocytic Leukemia (CLL), Mantle Cell Lymphoma (MCL), Acute Myeloid Leukemia (AML), and Acute Lymphoblastic Leukemia (ALL). These images, taken from the ALL-IDB database, illustrate the distinct characteristics of each leukemia type.

4.2. Datasets

The procurement of data stands as a pivotal undertaking in any AI's driven endeavor, particularly in the area of pattern recognition such as cancer identification, diseases detection, segmentation, etc. Different datasets offer unique opportunities for researchers to develop classifiers and detectors tailored to specific types of cancer. These datasets encapsulate an array of data modalities, such as imaging data (MRI, CT, H&E, Ultrasound, X-Ray), signals data (ECG, EMG, EEG, PPG), text data (Genomic, Electronic Health Records (EHR), Pathology Reports, clinical notes), categorical data, surgical data, etc. Real-time data acquisition is more prevalent in cancer diagnosis, although offline data analysis also plays a significant role.

In this segment, we embark on a panoramic exploration of noteworthy, benchmarked datasets tailored for the identification of various cancer categories, encompassing brain, lung, skin, breast, prostate, colorectal, and leukemia. Each dataset boasts unique attributes and modalities, enriching the tapestry of cancer detection research. Table 2 unfolds a meticulous panorama, presenting an exhaustive synopsis of benchmarked datasets meticulously crafted for the discernment of diverse cancer category. Each database is categorized upon the type of

cancer it focuses on and provides a download link for easy access. The descriptions of the datasets highlight the key features, such as the number of samples or images available, the modality of data (e.g., gene expression data, histological images, CT scans), and the unique characteristics that make them suitable for cancer detection research. Researchers and practitioners can utilize these datasets to develop and evaluate algorithms, explore gene expression patterns, study molecular signatures, and analyze various aspects of cancer detection for specific cancer types.

4.3. Preprocessing

Preprocessing emerges as the artful choreographer, orchestrating the symphony of pattern recognition, image processing, image segmentation, object detection, and all types of classification and prediction tasks. A protagonist in the drama of data, it weaves its significance in the preparation ritual, crafting the dataset into a canvas primed for profound analysis and the extraction of meaning. As the curtains rise post-data collection, the spotlight shifts to the stage where preprocessing takes center stage, unraveling the nuances and intricacies encoded in the pixels of the dataset. The collected dataset can consist of various types of data, such as text, numerical, time series, categorical, signal, image, 2D, or 3D data. Any action performed on the dataset after data collection is considered part of the preprocessing stage. In some cases, feature engineering is also included as part of preprocessing. The term “pre-processing” itself signifies that is orchestrated prior to delving into the data, a prelude before the grand processing, designed to unearth the profound and significant insights encrypted within the dataset's intricate tapestry. The purpose of pre-processing is to clean, filter, rectify, resize, crop, scale, normalize, standardize, enhance, or transform the data. These operations aim to address issues such as noise, blur, missing information, different shapes or sizes, pixel count variations, or orientation differences in the data. The typology of data and the inherent character of the dataset assume a pivotal role in dictating the judicious selection of pre-processing methods to be employed. For example, image data requires different pre-processing techniques compared to text data or time series data. In the realm of pristine and standardized data, the elaborate dance of pre-processing steps may gracefully bow out, revealing an untouched canvas ready for the symphony of analysis. In the intricate tapestry of data, the omission of pre-processing, especially in the presence of cacophony and distortion, can cast a shadow on the prowess of classifiers, impeding their harmonious performance. Preprocessing is

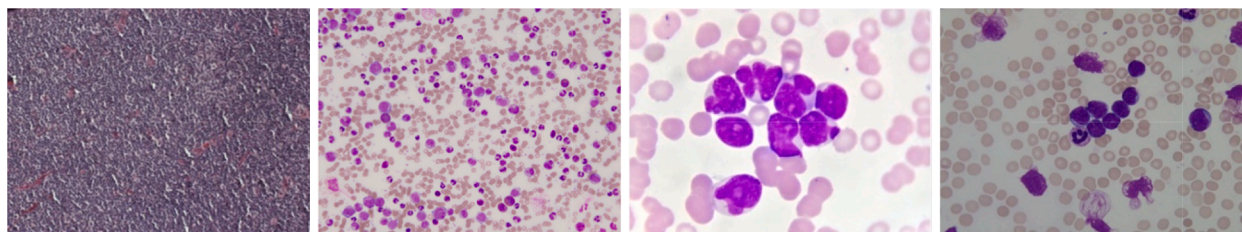


Fig. 8. Sample images of chronic lymphocytic leukemia (CLL), mantle cell lymphoma (MCL), acute myeloid leukemia (AML), and acute lymphoblastic leukemia (ALL) from ALL-IDB Dataset.

Table 2

Comprehensive overview of benchmark datasets for cancer detection across multiple cancer types.

Database Name	Cancer Category	Link	Database Description
ExpressionSet	Leukemia	https://t.ly/9fS45	The dataset consists of 60 samples of bone marrow, encompassing a wide range of conditions from healthy bone marrow to various types of leukemias. The leukemia categories include chronic lymphocytic leukemia, chronic myeloid leukemia, acute lymphoblastic leukemia, and acute myeloid leukemia. This comprehensive collection provides a diverse representation of bone marrow samples.
Gene Expression Omnibus (GEO)		https://t.ly/tnm1N	Common GEO datasets fall into two categories: GEO-GSE9476 is a dataset with 22,283 gene expression assays for acute myeloid leukemia (AML) microarrays, consisting of 36 patients (10 controls and 26 AML cases). It provides insights into gene expression patterns and molecular signatures associated with AML. GEO-GSE28497 is a leukemia classification dataset with gene expression data for 22,285 genes across 281 samples. It offers opportunities to explore gene expression profiles and subtypes of leukemia. Researchers can use it for classification algorithms and understanding the molecular mechanisms of leukemia.
ALL-IDB		https://t.ly/z9yK	The ALL_IDB dataset, focusing on Acute Lymphoblastic Leukemia images, is segregated into two segments: ALL_IDB1 and ALL_IDB2. 1. ALL_IDB1: It consists of 108 images from September 2005's collection, containing over 39,000 blood components. Skilled oncologists have manually identified lymphocytes in these images, making it a valuable resource for studying leukemia. 2. ALL_IDB2: This dataset includes 260 microscopic blood coagulation images. Among them, 130 images are from leukemia patients, and the other 130 are from healthy subjects.
Gland Segmentation in Histology Images Challenge (GlaS)	Colorectal	https://t.ly/-xOCm	The GlaS dataset, dedicated to gland segmentation in colorectal cancer histological images, features 165 images from 16 histological sections stained with hematoxylin and eosin (H&E) of stage T3 or T4 colorectal adenocarcinoma. The dataset encompasses 37 benign and 48 malignant images for training, along with 37 benign and 43 malignant images for testing.
Lung and Colon Histopathological Image Dataset (LC25000)		https://t.ly/GUBgJ	The LC25000 database, a visual symphony of 25,000 vivid images elegantly categorized into 5 distinct classes, unveils the intricate landscapes of colon and lung cancers. Within each class, boasting 5,000 captivating images, unfolds the artistic portrayal of entities such as colon adenocarcinoma, benign colonic tissue, lung adenocarcinoma, lung squamous cell carcinoma, and benign lung tissue. Every image, a visual sonnet, graces the canvas in jpeg format with dimensions of 768 × 768 pixels, adding a poetic touch to the realm of medical datasets.
National Cancer Institute-Prostate, Lung, Colorectal and Ovarian (NCI-PLCO)	Prostate	http://surf.li/qpycr	The Prostate dataset is a comprehensive collection of data from the PLCO study, including information on approximately 77,000 male participants. It covers screening, incidence, and death analysis of prostate cancer, providing valuable insights into the disease. Researchers can analyze various aspects such as screening effectiveness, disease progression, and overall survival using this dataset.
PROSTATE-DIAGNOSIS (PDD)		http://surf.li/qpyci	The PDD database, a visual saga of dynamic contrast-enhanced images, unfolds the intricate narrative of prostate cancer diagnosis. The captivating imagery, acquired pre, during, and post-injection of gadolinium-DTPA, paints a vivid canvas of medical exploration. Each frame, a masterpiece captured by the 1.5 T Philips Achieva scanner with a harmonious blend of surface and endorectal coil, adds to the rich tapestry of diagnostic artistry. This dataset, comprising 32,537 images, becomes a visual anthology drawn from the medical journeys of 92 individuals.
Digital Pathology Dataset for Prostate Cancer Diagnosis (DPDPCD)		https://zenodo.org/record/5971764#.ZG7O6XZBzIV	The DPDPCD stands as a mosaic of digitized whole-slide images (WSIs), each imbued with the distinct hues of hematoxylin and eosin (H&E). The dataset was obtained from 99 prostate cancer patients who underwent treatment at Tan Tock Seng Hospital in Singapore. It includes 40 prostatectomy samples and 59 core needle biopsy samples, resulting in a total of 99 WSIs. Every specimen within is encapsulated within the confines of a singular WSI, serving as a visual compendium for the meticulous scrutiny and analysis of prostate cancer.
DiagSet		https://ai-econsilio.diag.pl	The DiagSet dataset stands as an exhaustive histopathological compendium tailored for the identification of prostate cancer. A staggering 2.6 million tissue patches, meticulously extracted from 430 annotated scans, populate this dataset. The dataset also includes 4675 scans with binary diagnoses and 46 scans with independent diagnoses by a panel of histopathologists. Boasting a diverse array of 430 distinct cases, the DiagSet dataset emerges as an invaluable asset.
Medical segmentation decathlon (MSD) (Antonelli et al., 2022).	Pancreas	http://medicaldecathlon.com/	The MSD dataset includes a specific subset called the Pancreas dataset. Intricately unfolding the nuances within the realms of pancreatic parenchyma and mass, this dataset comprises 420 CT images with portal-venous phase from individuals undergoing pancreatic mass resection, navigating through the intricacies of cysts and tumors. The database was

(continued on next page)

Table 2 (continued)

Database Name	Cancer Category	Link	Database Description
Pancreas-CT dataset (PCT)		http://surl.li/qpycf	preferred for its label imbalance, particularly between the large background, medium-sized pancreas, and small tumor structures The PCT database unveils itself as a meticulously curated anthology of 82 abdominal contrast-enhanced three-dimensional (3D) CT images, illuminating the intricate landscape of the pancreas. These images elegantly unfold approximately 70 s after the ballet of intravenous contrast injection in the portal-venous phase. The dataset includes images from 80 participants (53 males and 27 females), with each participant associated with one study and one series.
The Clinical Proteomic Tumor Analysis Consortium Pancreatic Ductal Adenocarcinoma Collection (CPTAC-PDA)		http://surl.li/qpybz	The CPTAC-PDA database is a comprehensive collection of imaging data and pathology images for studying pancreatic ductal adenocarcinoma. It includes CT, MR, PT, and ultrasound scans, plus pathology (H&E) images. This database comprises of 129 studies involving 107 participants. Among the initially obtained 60 CT scans, 18 were excluded for specific reasons, resulting in 42 CT scans for analysis. The CT modality has a total of 129,910 images, while the pathology modality has 557 images. This dataset provides valuable resources for studying pancreatic cancer using multiple imaging modalities and pathology data.
Esophageal Adenocarcinoma TCGA, PanCancer Atlas (EA-TCGA)	Esophageal	https://datacatalog.mskcc.org/dataset/10413	The EA-TCGA dataset is a collection of summary data visualizations and clinical information from 182 esophageal adenocarcinomas (EA) and their corresponding patients. This dataset, intricately woven into the fabric of the PanCancer Atlas initiative, serves as a rich tapestry within the expansive realm of the TCGA dataset. Unveiling a mosaic of clinical intricacies, it encapsulates mutation counts.
Multi-organ Abdominal CT Reference Standard Segmentations (MACTRS)		https://zenodo.org/record/1169361	The MACTRS dataset intricately encapsulates reference segmented images derived from 90 abdominal CT scans. These meticulous segmentations meticulously outline diverse organs in the abdominal milieu, including the duodenum, pancreas, stomach, liver, esophagus, gallbladder, left kidney, and spleen. This dataset offers precise and standardized reference segmentations, fostering applications in medical image analysis, organ localization, and computer-aided diagnosis.
MICCAI 2015		http://surl.li/qpybl	The MICCAI 2015 dataset unfolds as a captivating tapestry, meticulously curated for the MICCAI 2016 EndoVis Challenge. Comprising 100 evocative lower esophagus endoscopic images drawn from 39 unique narratives, it weaves a story where 22 protagonists bear the mantle of Barrett's esophagus, and 17 characters whisper early inklings of esophageal adenocarcinoma. Within its frames, 50 images stand as witnesses to the intricate dance of cancerous tissue, while an equal number unveil the enigma of Barrett's esophagus. Annotations by seasoned scribes illuminate the canvas, marking the subtle cues of suspicion in the realm of cancerous imagery.

crucial for achieving high accuracy in detection or segmentation tasks and for enhancing the effectiveness of classifiers. It guarantees that the data are in a right form to be fed into the ML models for final analysis. In the realm of raw datasets or real-time data, embarking on the journey of pre-processing stands as an essential prerequisite, paving the way for results steeped in reliability and robustness. There are numerous pre-processing techniques available, including filtering operations, data cleaning, RGB to gray conversion for image data, data transformation, normalization, standardizing, cropping, resizing, scaling, and sampling, among others. Navigating the intricacies of pre-processing, the selection of techniques becomes a bespoke journey tailored to the dataset's unique demands and the aspirations of the analysis. In Table 3, a narrative unfolds, offering a descriptive panorama of pivotal pre-processing techniques in the domain of cancer identification. Beyond mere listing, the table delves into the very essence, unveiling the arcane formulas that breathe life into each pre-processing task.

4.4. Feature engineering

Embarking on the journey through the realm of ML, the significance of feature engineering becomes akin to the masterful strokes of an artist, intricately shaping the canvas that is our dataset, patterns, and classification processes. In the landscape of ML classifiers, including SVM, DT, RF, MLP, BPNN, feature engineering stands as the artisanal touch that refines and enhances the predictive power of these models. Delving into the depths of DL, a different symphony plays out. Here, the process of feature extraction takes on an automatic cadence, as DL models possess

the innate ability to unravel salient features from the given datasets. This automatic revelation of features underscores the complexity and intricacy of DL architectures. It is in this intricate dance that the understanding of features emerges, akin to the enhanced weight of a fairy's enchantment. Feature engineering transforms into a form of alchemy, where vital features are drawn or crafted from the dataset or proposed answer set. These features, resembling the mystical ingredients in a potent potion, serve as inputs for ML models.

In this symbiotic relationship between feature engineering and ML, the models are bestowed with a refined and nuanced understanding. These extracted features act as the compass, guiding the ML models to navigate the labyrinth of classifications. The result is a harmonious convergence of artistry and science, where feature engineering breathes life into the predictions of ML models, enriching the grand tapestry of classification outputs. In the symphony of feature engineering, each stage unveils a unique composition, akin to crafting a masterpiece. feature creation, reminiscent of an artist's canvas, finds its place in text datasets, where the meticulous cleaning and normalization transform the dataset into a refined tableau. As we transition to image datasets, the spotlight shifts to feature extraction, a process akin to mining jewels from the raw ore of Rao image datasets. These extracted features, akin to the gems in a treasure trove, serve as inputs for the intricate dance of ML algorithms. The narrative takes a turn with feature selection, a meticulous curation where the plethora of expected features is distilled, leaving only the most pertinent elements. In a choreographed dance, feature fusion steps in, weaving a tapestry of selected features into a cohesive message that harmonizes with our ML models. Peering into the future,

Table 3
Preprocessing alchemy with formulas and summary.

Preprocessing	Description	Formula
Filtering Technique	Filtering operations are used to enhance image quality by removing noise or smoothing edges. These operations help to improve the clarity and visual appearance of the data. Different filters like Gaussian blur, Median filter, and Bilateral filter can be applied based on the characteristics of the noise and the desired effect.	$Filtered_value = Filter(Input_data, Filter_parameters)$
Data Cleaning	Embarking on the odyssey of data cleaning entails the nuanced task of navigating through missing values and outliers within the dataset. It aims to ensure data integrity and prevent potential biases or errors in the analysis. Various techniques such as removing rows without values, outlier detection, imputation can be employed.	Not applicable
RGB to Gray Conversion	RGB to gray conversion is a technique used to convert color images represented in the RGB format into grayscale images. Grayscale images contain only shades of gray and are commonly used in various computer vision tasks. The transformation is conventionally executed by computing the luminance value for each pixel, employing weighted averages derived from the red, green, and blue channels.	$Gray_value = (0.2989 * Red_value) + (0.5870 * Green_value) + (0.1140 * Blue_value)$
Data Transformation	It is akin to a metamorphosis, reshaping the very essence of data into a new form or scale, unveiling its potential in a novel light. This technique can be used to address issues such as skewness, non-linearity, or heteroscedasticity in the data. Common transformations include logarithmic transformation, power transformation, or applying mathematical functions to change the distribution of the data.	$Transformed_value = Transformation_function(Input_data)$
Normalization	Normalization orchestrates a symphony of data, harmonizing disparate features onto a unified scale or distribution. This meticulous process safeguards against the tyranny of dominance, ensuring equitable contribution from each feature in the analytical composition. Exemplary normalization methods encompass the dance of Min-Max normalization, elegantly bounding values within a defined range, and the rhythmic Z-score normalization, orchestrating values based on the cadence of mean and standard deviation.	$Normalized_value = \frac{(Input_value - Min_value)}{(Max_value - Min_value)}$
Standardizing	Standardizing, also known as z-score standardization, involves scaling of data with zero mean (μ) and unit variance (σ^2). This technique is useful when features have significantly different scales and helps algorithms that rely on distance measures or assume normally distributed data. It ensures that all features contribute equally to the analysis.	$Standardized_value = \frac{(Input_value - Mean_value)}{Standard_deviation}$
Cropping	Cropping is the process of removing unwanted parts of an image or dataset. It helps focus on the relevant region of interest and eliminates irrelevant or distracting elements. Cropping can be done based on specific dimensions or by defining regions to extract.	$Cropped_data = Select_ROI(Input_data, Crop_parameters)$
Resizing	Resizing involves changing the dimensions of an image or dataset. It is useful when dealing with images of different sizes or when a specific size is required for further analysis or compatibility. Resizing can be done by specifying the desired width and height or by scaling based on a ratio.	$Resized_data = Resize(Input_data, Resize_parameters)$
Scaling	Scaling adjusts the scale of features or data values to a desired range. It ensures that all features have a similar magnitude and avoids selected features from governing the analysis based on their original scales. It is commonly used in ML algorithms that rely on distance calculations or gradient-based optimization.	$Scaled_value = \frac{(Input_value - Min_value)}{(Max_value - Min_value)}$
Sampling	Sampling, a meticulous endeavor, entails the judicious selection of a subset of data points from the expansive landscape of the dataset. This can be done randomly or with specific considerations, such as stratified sampling to maintain the proportion of classes or features. Sampling is useful when working with large datasets, reducing computational requirements, or balancing imbalanced datasets.	Formula for sampling depends upon the type of sampling used. The formula for simple random sampling is as follows: Desired sample size(n) = population size(N)*sampling fraction(f)
Binarization	Binarization stands as a transformative technique wielded to metamorphose an image of grayscale into the binary realm, where pixels delineate themselves into distinct binary entities, embracing the simplicity of 0 s and 1 s. It separates objects of interest from the background by assigning black and white values to pixels based on a threshold. This simplifies subsequent tasks like object detection and segmentation. By comparing pixel intensities with the threshold, pixels are assigned white or black values. The threshold determines the separation between foreground and background pixels.	The formula for binarization can be described as follows: $Iff(x, y) > Threshold, setf(x, y) to white(1). Iff(x, y) <= Threshold, setf(x, y) to black(0).$ Where $f(x, y)$ represents the pixel value of grayscale images.

the art of feature fusion takes center stage, as disparate features converge into a symphony of expected futures. Advertising, in this context, becomes a conduit for extracting richer features, akin to alchemists distilling essence from raw elements. Yet, in this grand orchestration, the importance of well-crafted features cannot be overstated. Even the most powerful ML models can falter if faced with overly complex or extraneous features. Hence, the artistry of feature

engineering assumes a pivotal role in orchestrating optimal outcomes. In Table 4, we find the maestros of feature engineering, especially in the domain of cancer classification. Among these virtuosos, Tara stands out, and we shall delve into a brief exploration of their expertise in this intricate domain.

Table 4
Frequently harnessed Key-features in the symphony of ML driven techniques.

Feature	Description
ABCD Rule	ABCD Rule, an acronymic sentinel, meticulously scrutinizes skin lesions through the lens of Asymmetry, Border characteristics, Chromatic variations, and Diameter, elucidating a diagnostic ballet.
Color Moments	Color Moments, the palette virtuoso, intricately dissects the spectrum of hues, capturing the nuanced brushstrokes of color diversity that weave an enchanting visual narrative.
Discrete Cosine Transform (DCT)	DCT, the mathematical virtuoso, unveils the visual symphony's score by translating subtle frequencies into an artistic mathematical notation, resonating in the realm of signal and image processing.
Entropy	Entropy, the metric poet, delves into the pixel poetry of chaos or order, measuring the randomness within a visual sonnet, revealing the intricate dance of complexity as pixels unfold their visual verse.
First Order Features (FOF)	FOF, the statistician's sonneteer, weaves tales of mean, median, and variance, casting light on the distribution saga of pixel intensity, narrating the nuanced landscape of visual data.
Fourier Transform	Fourier Transform, the spectral virtuoso, unravels the image's melody into its frequency notes, creating a harmonious cadence in the realm of signal and image processing.
Gabor Transform (GT)	GT, the texture alchemist, captures tactile nuances in an image, employing its potion in the wizardry of image processing and vision, revealing intricate texture details.
Gradient Map Features (GMF)	Gradient Map Features (GMF), the artist's palette of intensity gradients, depicts transitions and edges, revealing the strokes of visual art in a captivating canvas of visual complexity.
Gray Level Co-Occurrence Matrix (GLCM)	GLCM, a mosaic of pixel relationships, unravels intricate texture patterns, crafting a canvas of spatial ties in the rich kingdom of pixel relationships, offering profound insights into texture patterns.
Gray Level Size Zone Matrix (GLSZM)	GLSZM, a cartographer of size and intensity realms, maps the domains of connected regions, revealing the topography of pixel kingdoms with its size and intensity insights, providing a detailed cartography of pixel landscapes.
Gray-Level Run Length Matrix (GLRLM)	GLRLM, an epic tale of pixel legacies, measures the lengths of harmonious runs, unveiling the poetry of texture in the grand symphony of image analysis, offering detailed insights into the pixel narrative.
Haralick	Haralick, the texture bard, harmonizes metrics from the co-occurrence matrix, crafting lyrical textures in the grand symphony of image analysis, offering profound insights into texture patterns with its sophisticated harmonies.
Hu Invariant Moments	Hu Invariant Moments, the chameleons of mathematical melody, dance with rotation, scale, and translation in the pixel ballad, offering a versatile and invariant representation of image features in the grand concert of image analysis.
Histogram Oriented of Gradient (HOG)	HOG, the maestro of gradients, orchestrates a visual symphony capturing the distributional movements of gradients, widely applauded in the realm of object detection for its ability to provide insights into object shape and structure.
Local Binary Patterns (LBP)	LBP, a tale of local patterns etched in pixel folklore, is the weaver of texture tales frequently summoned in the kingdom of texture classification, offering detailed insights into local image patterns with its intricate storytelling.
Local Entropy	Local Entropy, a local poet's meter, measures the verses of information or disorder, taking a lyrical stroll in the pixels' garden of complexity, providing insights into the local entropy variations within an image, revealing detailed narratives in the complexity of local pixel relationships.
Morphological	Morphological operations, the sculptor's chisel on pixel marble, shape the form and structure of objects,

Table 4 (continued)

Feature	Description
	a symphony of dilation and erosion creating visual sculptures with enhanced features and clarity, providing a detailed artistic touch to the visual canvas.
Radiomic	Radiomic analysis, the healer extracting whispers from medical images, offers a quantitative exploration of tumor chronicles, revealing the tales of inner landscapes with detailed radiomic features, enhancing the diagnostic capabilities in the medical realm.
Shape	Shape analysis, the geometric philosopher pondering area, perimeter, and eccentricity, shapes the visual philosophy of objects in the pixel universe, offering detailed insights into the geometric properties of visual elements in the grand discourse of pixel geometry.
Statistical	The statistician's sonnet, Statistical features sing an ode with measures of mean, median, and standard deviation, a visual aria in the symphony of statistical verses, providing a comprehensive statistical view of visual data.

4.5. Classifiers

4.5.1. Machine learning classifiers

In this segment, we immerse ourselves in the intricacies of ML, directing our focus specifically on the domain of traditional ML classification, and undertake a comprehensive analysis. As conscious entities, we acknowledge that a ML classifier, particularly those rooted in tradition, is meticulously architected for the purpose of categorizing, predicting, or discerning diverse patterns contingent upon specific databases. The efficacy of such classifiers is contingent upon a database that undergoes scrupulous processing to ensure its integrity and relevance. The training regimen entails the initiation and optimization of weights, along with the deployment of anticipated features as input parameters. This process involves fine-tuning the model's parameters to enhance its predictive capabilities. Subsequently, the dataset undergoes a meticulous partitioning into training and test sets, with the former serving as the crucible for the model's learning process. The classifier embarks on a self-training odyssey utilizing the training set. Through iterative processes, it refines its internal parameters, adapting to the intricacies of the data. Once trained, the classifier scrutinizes its mettle against the test set, delineating the provided inputs into one or more pre-defined categories. This validation process ensures that the model can generalize well to new, unseen data, a crucial aspect of its reliability.

An array of ML classifiers is at our disposal, each with its unique strengths and applications. For tasks related to cancer identification, traditional stalwarts such as the Back Propagation Neural Network (BPNN), Random Forest classifier, Artificial Neural Network (ANN), SVM, Decision Tree, k-Nearest Neighbors Classifier (k-NN), Logistic Regression, Linear Discriminant Analysis (LDA), Probabilistic Neural Network (PNN), and more are commonly applied. Each of these classifiers has distinct characteristics and excels under certain conditions, making them valuable tools in the realm of cancer detection. [Table 5](#) delves into a detailed scrutiny of these indispensable classifiers, providing nuanced insights into their attributes, with a particular emphasis on traditional ML classifiers, accompanied by comprehensive delineations.

[Fig. 9](#) succinctly captures the architecture of the support vector machine, a pivotal ML classifier. This algorithm excels in categorizing data into multiple classes by optimizing hyperplanes for maximal separation in the feature space. The diagram visually outlines key components, including input data, feature extraction, kernel function, support vectors, decision boundaries, and final classification output, providing a quick insight into the multi-class SVM's operational framework.

Table 5
Frequently employed ML classifiers for cancer prediction with descriptions and analysis.

ML Classifiers	Description	Analysis
Support Vector Machine (SVM)	A discriminant that segregates data points employing hyperplanes while optimizing the margin between distinct classes. This method proves efficacious particularly in handling data sets characterized by a high dimensionality.	SVM is a powerful classifier that excels at handling high-dimensional data, particularly when features outnumber samples. SVM, which uses a nonlinear kernel, captures complex relationships in data. Optimal performance necessitates meticulous tuning of the kernel and regularization parameters. RF handles both numerical data and categories, making it useful for a variety of tasks. Unlike individual decision trees, it excels at handling large, complex datasets and has a built-in defense against overfitting. This ensemble approach minimizes the impact of a single data point.
Random Forest (RF)	RF is a machine learning technique that uses multiple decision trees to forecast outcomes. Each RF tree is trained on a random subset of data and features. For classification tasks, RF employs a voting mechanism to determine the final prediction, whereas for regression tasks, predictions are averaged across trees.	AdaBoost and Gradient Boosting are examples of ensemble classifiers, which combine weak learners to improve classification accuracy. They are effective at capturing complex patterns while minimizing bias. However, they may be sensitive to noisy or mislabeled data, and model selection and training time should be taken into account.
Ensemble Classifier (EC)	It combines the predictions of multiple models to reach a final decision. It leverages the strengths of multiple classifiers, combining their outputs to improve accuracy and robustness. This approach improves overall performance by combining the diverse insights of various models, reducing errors and increasing adaptability.	ANNs are highly effective learning machines. Unlike simpler models, they can detect complex patterns in data, especially when there are multiple hidden layers. This makes them ideal for tasks such as image recognition and natural language processing. To avoid overfitting, ANNs must be trained with a large amount of data and carefully tuned architecture, activation functions, and techniques.
Artificial Neural Network (ANN)	ANNs mimic the complex organization of biological neural networks by interconnecting artificial neurons to form a network. Inspired by the natural design of brains, ANN excels at identifying intricate patterns and relationships in data. This classifier is as versatile as its biological counterpart, with a remarkable ability to understand and process complex information.	DT can handle both numbers and categories and can detect complex relationships in data. This makes them simple to understand, like following a story. However, on very complex datasets, DTs can become overly specific to training data (overfitting). It is a straightforward yet powerful classifier. Unlike most models, it does not require extensive training. Instead, it predicts using the closest data points (k neighbors). This makes KNN useful for detecting local patterns and nonlinear relationships in data. However, its performance is
Decision Tree (DT)	DT navigates decisions in a structured tree-like model, making decisions using a series of if-else statements. Each branch of the DT represents a choice based on specific criteria, resulting in a clear and interpretable decision or prediction.	
K-Nearest Neighbors (KNN)	KNN is a classifier that accepts new instances by consulting their k nearest neighbors in the feature space. Its strength is in identifying local patterns and effectively managing complex, non-linear decision boundaries. KNN works on the assumption that similar instances are likely to have	

Table 5 (continued)

ML Classifiers	Description	Analysis
	the same class label, making it especially useful for tasks involving clustering or proximity-based relationships.	dependent on selecting the correct number of neighbors (k) and a suitable distance metric. Additionally, scaling features may be required for optimal results.
Naive Bayes (NB)	Naive Bayes is a classifier that predicts outcomes using Bayes' theorem and the assumption that features are independent. This method is renowned for its simplicity, speed, and efficacy, particularly on small datasets. NB compute probabilities and predict outcomes by assuming that features are conditionally independent given the class label.	Naive Bayes is fast and effective, especially for small datasets. These classifiers are well-known for their speed and ability to work with limited training data. While they assume feature independence (which is not always the case), they frequently outperform expectations, particularly in tasks such as text classification and sentiment analysis.
Logistic Regression (LR)	LR is excellent at predicting probabilities for two categories. Unlike linear regression, it employs a sigmoid function to convert numerical data into a probability between 0 and 1. This makes LR ideal for tasks like spam filtering and categorizing emails as important or not important.	LR estimates the likelihood that a given class of data points—such as spam or not—will exist. When there is a straight line that represents the relationship between features and class, LR performs well. It can handle both numbers and categories. For tasks where it's crucial to comprehend the reasoning behind predictions, this makes LR a useful tool.
Gradient Boosting (GB)	With gradient boosting, weak learners are paired with strong classifiers. It creates a sequence of models one after the other, fixing each one's mistakes. Because of this, GB is effective with imbalanced data, or datasets with disparate class sizes. GB is a useful tool despite not being the simplest model due to its capacity to learn complex patterns.	Class imbalances and complex data are ideal environments for gradient boosting. It creates a series of models, each one fixing the flaws in the one before it. Collaborative efforts reveal latent patterns and enhance its efficacy in tasks such as fraud identification. Like XGBoost and LightGBM, it is strong, but careful tuning is required to prevent overfitting.
Back Propagation Neural Network (BPNN)	Artificial neural network training is conducted by BPNN, which calculates the gradient of the loss function with respect to the network's weights and performs a symphony of weight changes. By fine-tuning its parameters through this iterative process, BPNN maximizes the network's capacity to learn and generate precise predictions based on the given data.	Capable of processing both categorical and numerical data, BPNNs are highly effective learners. Complex tasks such as language translation and image recognition are areas in which they excel. To prevent overfitting, however, BPNNs need a large amount of training data and careful setup.
Linear Discriminant Analysis (LDA)	LDA is a classifier that uses linear combinations of features to project data onto a lower-dimensional space with the goal of maximizing separation between classes. It works well, especially when dealing with balanced datasets, by optimizing data representation in a way that improves classification accuracy based on distinct class features.	Both data complexity reduction and data point classification are addressed by LDA. The most effective feature combinations to distinguish between various classes are found. Weighted datasets with well-defined class distributions are ideal for LDA. It does not, however, always hold true because it depends on the assumption of normality in the data and equal variances within classes.

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Table 5 (continued)

ML Classifiers	Description	Analysis
Probabilistic Neural Network (PNN)	PNNs are a type of feedforward neural network that classify data using a kernel density estimation technique. It performs exceptionally well in pattern recognition tasks, particularly when dealing with smaller datasets, by accurately estimating the underlying distribution of data points and generating probabilistic predictions from there.	Pattern recognition in small to medium datasets is an area where PNNs excel. They are helpful for tasks like spam filtering because they estimate probabilities for various classes. Nevertheless, when training with big datasets, PNNs may be memory-intensive and sluggish.

4.5.1.1. Deep learning classifiers. Deep learning, a transformative paradigm, obviates the need for manual feature selection in cancer detection. Particularly effective with large biomedical images, deep neural networks learn intricate patterns directly from raw data, enhancing diagnostic accuracy by capturing nuanced features at pixel-level. This heralds a paradigm shift in medical imaging, promising new frontiers in understanding and treating diseases. These models, such as Convolutional Neural Networks (CNN), Fully Convolutional Networks (FCN), Recurrent Neural Networks (RNN), You Only Look Once (YOLO), Deep Convolutional Neural Networks (DCNN), Generalized Adversarial Networks (GAN), and Long Short-Term Memory Networks (LSTM), stand at the forefront of various classification and segmentation works. In the realm of cancer identification, a plethora of CNNs takes center stage, including renowned architectures like AlexNet, ResNet, UNet, VGG, EAI, EfficientNet, and ShuffleNet. These formidable models excel at precisely discerning cancerous cells or tissues within medical images, paving the way for early diagnosis and intervention. Furthermore, researchers frequently leverage tailored iterations of CNNs, such as OCNN, ACCNN, CNN + AlexNet, and SE-CNN, to enhance performance in the intricate domains of cancer detection.

DL classifiers excel in object recognition and segmentation, leading to their increased adoption in recent decades. They have consistently been shown to be effective in processing complex biomedical images and extracting meaningful features automatically. By leveraging DL techniques, accurate identification of tumor characteristics, localization of

abnormalities, and prediction of cancer subtypes can be achieved. Overall, DL models like CNN, LSTM, DCNN, GAN, NLP, and their variations have significantly contributed to cancer detection and segmentation. These groundbreaking models have transformed the landscape, ushering in an era of automated feature extraction and precise identification of cancerous tissues within imaging datasets. This paradigm shift enables early detection and augments the efficacy of subsequent treatments. Table 6 encapsulates a broad outline of diverse DL classifiers employed in the domain of cancer detection. Each model is elucidated, delineating its unique characteristics and applications in scrutinizing medical images.

The CNN stands out as the predominant and extensively employed DL model for diverse cancer detection tasks. Beyond cancer detection, CNN models take center stage in decision-making tasks utilizing a DL approach. Various types, including modified versions, of CNN models like Le-Net5, AlexNet, VGG-16, VGG-19, ResNet, and numerous others are at the forefront. For clarity, Fig. 10 illustrates the layered structure of the VGG-16 CNN model.

4.5.1.2. ML vs DL classification. The classification approach employing AI techniques is broadly divided into two main categories: the ML driven approach and the DL driven approach, with several subcategories such as supervised, semi-supervised, unsupervised, and reinforcement learning existing within them. In the realm of cancer classification and segmentation, these two primary AI-based approaches, ML and DL, are predominantly employed. Fig. 11 illustrates the fundamental distinctions between them, primarily focusing on dataset utilization and feature extraction (Khan et al., 2021; Lin & Wong, 2018). The key differences include the deep and rigorous training steps and the requirement for larger datasets in DL, whereas ML-driven approaches can also perform well with smaller datasets, followed by shared preprocessing steps. In ML-driven approaches, feature extraction necessitates additional techniques such as wavelet, Fourier, statistical, morphological, shape, texture, color, etc. In contrast, DL approaches are inherently capable of automatically extracting the required features.

Another significant difference lies in the training steps, where DL models require extensive and deep training on very large datasets. If the dataset is insufficient in size, techniques like data augmentation, data oversampling, and synthetic data generation are applied to bolster the dataset. ML approaches employ neural network-based classifiers, such as

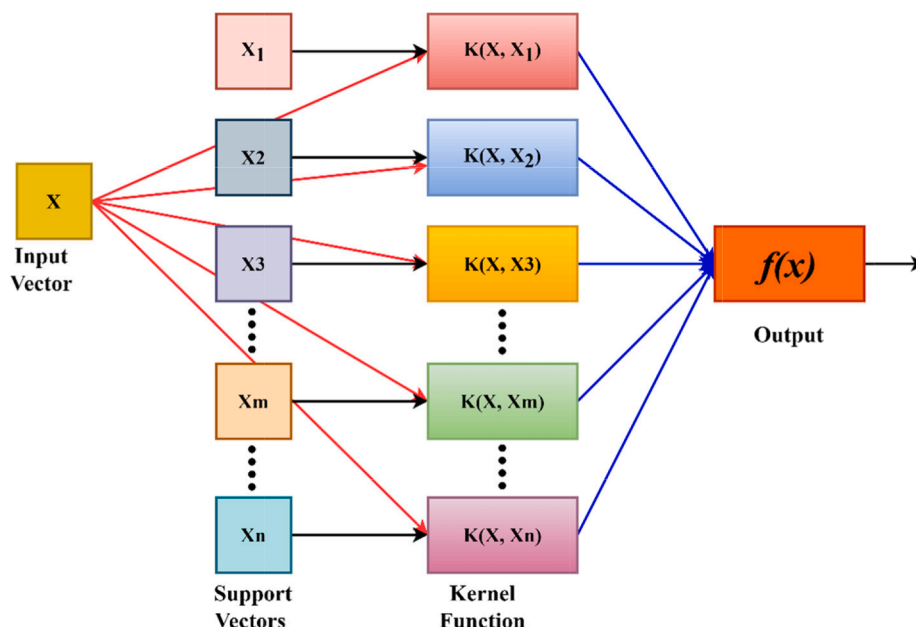


Fig. 9. Schematic diagram of support vector machine (Yoon et al., 2011).

Table 6
An exploration of deep learning classifiers employed in cancer classification.

Deep Learning Models	Description	Analysis
Convolutional Neural Networks (CNN)	CNNs (Convolutional Neural Networks) specialize in deep learning and can perform complex image analysis tasks such as object recognition and image segmentation. VGG, ResNet, and GoogLeNet are well-known CNNs, each with its own set of capabilities for handling large amounts of visual data accurately and efficiently.	CNNs have revolutionized cancer detection by achieving remarkable accuracy in analyzing medical images, including mammograms, CT scans, and histopathological images. Their power to inevitably discover complex categorized features enables the identification of tumor characteristics, localization of abnormalities, and prediction of cancer subtype, contributing to early identification and improved clinical outcomes.
Long Short-Term Memory Networks (LSTM)	LSTM is an advanced subset of recurrent neural networks (RNNs) that is particularly well-suited for sequential data analysis, such as time series or natural language. They coordinate and interpret the complex patterns in the data they process.	In cancer detection, LSTMs are applied to analyze sequential input data, including clinical time-series data, time-series gene expression data, and longitudinal patient records. By capturing temporal dependencies and contextual information, LSTMs enable accurate prediction of disease progression, identification of prognostic factors, and personalized treatment recommendations.
Deep Convolutional Neural Networks (DCNN)	In the extraction of intricate features from image data, the specialized variant of CNNs, known as DCNNs, not only excels but demonstrates expertise with their deeper architecture. This depth enables them to extract more intricate, complex, and abstract features from images, showcasing their proficiency in image analysis.	DCNNs have demonstrated superior performance in cancer detection tasks by leveraging their deeper architecture to capture fine-grained details and subtle patterns. They excel at feature extraction, enabling precise localization of tumors, identification of microscopic structures, and differentiation between benign and malignant tissues. The improvement in diagnostic accuracy and reduction of false positives is achieved through the utilization of DCNNs.
Generalized Adversarial Networks (GAN)	GANs are a type of deep learning network capable of synthetically producing realistic data. They contain two neural networks in their structures: the generator and the discriminator. The generator creates synthetic data that resembles real data, while the discriminator determines the generated data's authenticity.	The challenge of limited annotated data in cancer research can be addressed by training the generator network to produce synthetic medical images using GANs. It can augment the available dataset, enabling more robust and diverse training of cancer detection models. GAN-generated data can enhance model generalization, improve performance on rare or unbalanced classes, and facilitate research on novel imaging modalities.
You Only Look Once (YOLO)	YOLO is a great real-time object detection tool that strikes a good balance between accuracy and speed. YOLO uses a single network to process the	YOLO has shown promising results in cancer detection by rapidly identifying and localizing tumors in medical images. Its real-time processing capabilities make

Deep Learning Models	Description	Analysis
	entire image in a single pass, in contrast to traditional methods that require multiple passes over an image.	it suitable for applications where timely and accurate detection is crucial, such as during surgical procedures or screening tests. YOLO's speed and accuracy contribute to improved diagnostic efficiency and patient outcomes.
Region-based Convolutional Neural Networks (RCNN)	RCNNs are a type of object detection model. They operate in two stages: first, they identify potential regions in an image that may contain objects (region proposals). The regions are then classified, and the object's location is refined.	In cancer detection, RCNNs have been utilized to identify and localize tumors in medical images, differentiating them from surrounding tissues. By combining region proposal techniques and CNNs, RCNNs improve the precision of tumor identification and assist in treatment planning. Their ability to handle complex image structures and varying tumor sizes enhances their utility in cancer detection.
EfficientNetB	EfficientNets are CNN architectures designed to achieve high accuracy with fewer parameters. They outperform other models by scaling network width, depth, and resolution simultaneously. This enables EfficientNets to be more efficient (using less memory and compute power) while still maintaining high accuracy.	Promising results in cancer detection have been demonstrated by EfficientNet models, striking a harmonious balance between model size and accuracy. Their efficient architecture allows for faster inference times while maintaining high performance. EfficientNet models can effectively analyze medical images, including those with large resolutions, enabling accurate tumor detection and classification. They contribute to improved efficiency and scalability in cancer detection systems.

feed-forward networks, backpropagation, SVM, decision trees, random forests, naive Bayes, artificial neural networks, evolutionary computing, gradient descent, etc., during the classification stage. Conversely, DL classifiers utilize architectures like CNNs (AlexNet, ResNet, MobileNet, EfficientNet), GANs, YOLO, LSTMs, Transformers, FCNs, etc. Additionally, DL approaches often necessitate GPU processing, especially with large image datasets, whereas ML approaches can function efficiently on robust CPU processors without requiring GPU support. Researchers and scholars select their approach based on factors like dataset size, data types, hardware support, and specific application requirements. Over the last 5–10 years, DL models have gained prominence due to the availability of large datasets and their versatility across various applications, leading to exponential growth. This review article separately analyzes cancer classification tasks under ML-driven and DL-driven approaches, providing insights into their distinctive characteristics and applications.

4.6. Performance assessment metrics (PAM)

Algorithms in the field of artificial intelligence (AI), particularly ML and DL, deal with the difficult task of classification. We use several key metrics to assess their performance: precision, Specificity, AUC-ROC (Area Under the Receiver Operating Characteristic Curve), recall, F1-score, PNR, FNR, MCC, and accuracy (Tharwat, 2018). These metrics

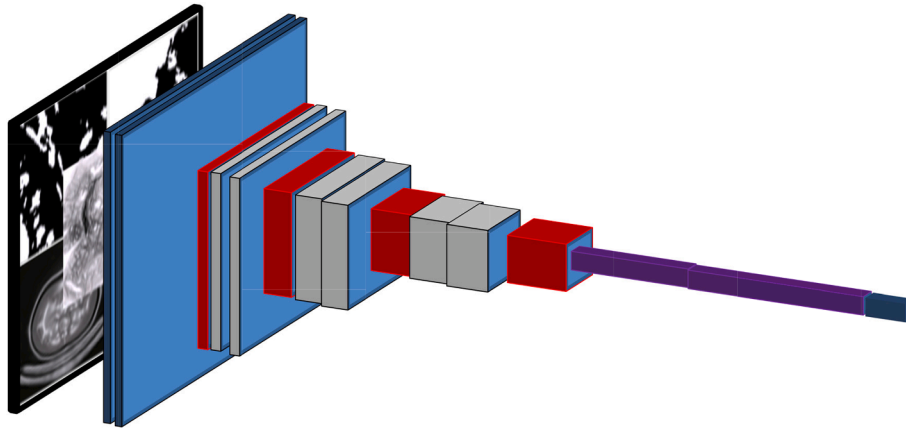


Fig. 10. Layer-wise Structure of VGG-16 Convolutional Neural Network Model.

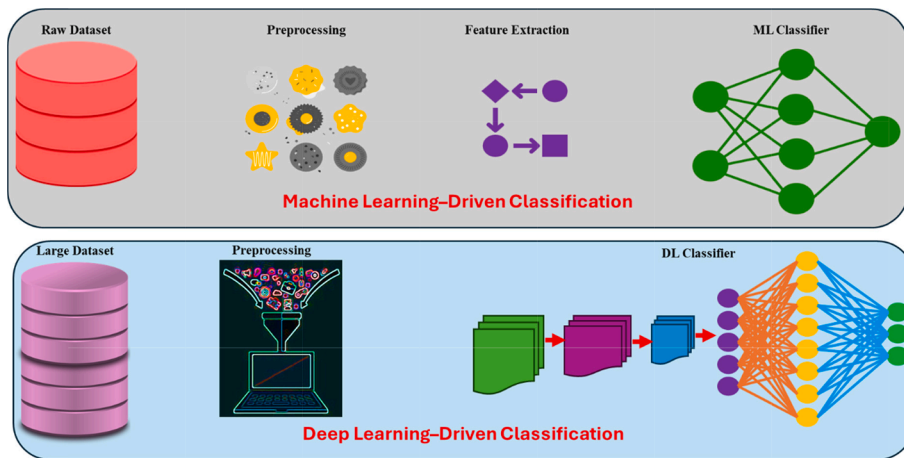


Fig. 11. ML vs DL driven approach in cancer classification.

serve as objective judges, assessing the models' ability to distinguish between different categories. Researchers employ a wide range of metrics, each providing a distinct perspective on the model's strengths and weaknesses. Choosing the right metrics is an important step that must be tailored to the specific classification task and application requirements. These metrics are critical in areas such as cancer detection, guiding classifier evaluation across binary and multi-class problems. The confusion matrix offers a visual representation that makes clear the relationship between actual outcomes and the classifier's predictions, especially in binary classification where outcomes can be either positive or negative. Fig. 12 shows the binary class confusion matrix visually, with each of its four main components—TP, TN, FP, and FN—distinguished by different colors. This visual aid improves understanding and clarity by distinguishing each category with a distinct color.

Performance Assessment Metrics (PAMs) become our compass when assessing machine learning models in classification tasks. Together, these metrics allow for the analysis of a model's performance in differentiating between various categories, such as the classification of medical images or the detection of spam emails. The confusion matrix serves as the basis for classifier evaluation. This matrix, which shows the breakdown of the model's predictions in relation to the actual data, functions as a scorecard. The confusion matrix consists of four fundamental parts: True Positive (TP), False Positive (FP), True Negative (TN), and False Negative (FN). TP is the precision with which the positive class is identified, allowing for the successful localization of instances within the positive category. On the other hand, TN denotes the accurate identification of the negative class, skillfully recognizing examples

		Actual	
		1	0
Predicted	1	TP	FP
	0	FN	TN

Fig. 12. Binary classification confusion matrix.

within the negative category. But the complexities come with FP, which stands for the incorrect identification of the positive class—cases of the negative class that are mistakenly identified as positive. Conversely, FN represents the false negative class identification, whereby positive class instances are mistakenly identified as negative (Tharwat, 2018). Key PAMs for classification tasks include the following:

Accuracy: This metric assesses how accurate the model's predictions are generally. It is computed using the formula in equation (1), much

like a general indicator.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (1)$$

Precision: It is a metric that assesses how well a classifier predicts the positive outcomes. It measures the ratio of true positive predictions—that is, correctly identified positive cases—among the classifier's total positive predictions. The following equation (2) provides the precision formula:

$$Precision = \frac{TP}{TP + FP} \quad (2)$$

Recall: This metric evaluates how well a classifier finds every positive instance in a dataset. It is also referred to as sensitivity or true positive rate, or TPR. It calculates the percentage of real positive cases that the model correctly identified. The following equation (3) provides the recall formula:

$$Recall = \frac{TP}{TP + FN} \quad (3)$$

Specificity: True Negative Rate, or Specificity, is another crucial parameter for assessing classification models (TNR). This measure focuses on how well the model can detect occurrences of negativity. Put more simply, it indicates the percentage of real negative situations that the model accurately identified as negative. The specificity is computed using equation (4).

$$Specificity = \frac{TN}{TN + FP} \quad (4)$$

F1-Score: A fair evaluation of a classifier's performance is offered by the F1-score, a metric that integrates recall and precision into a single score. It shows the model's effectiveness in maximizing true positive identification and reducing false positives. Equation (5) represents the formula for the F1-score.

$$F1 - Score = \frac{2 \cdot (Precision \cdot Recall)}{Precision + Recall} \quad (5)$$

FPR: The percentage of negative cases that the model mistakenly classified as positive is known as the False Positive Rate, or FPR. If there are serious outcomes from misclassifying something as positive, a high FPR may be an issue. Equation (6) is used to calculate it.

$$FPR = \frac{FP}{FP + TN} \quad (6)$$

FNR: The percentage of positive cases that the model misclassified as negative is known as the False Negative Rate, or FNR. If missing true positives is a big worry, a high FNR may be an issue. Equation (7) is utilized to express the confusion matrix and calculate it.

$$FNR = \frac{FN}{FN + TP} \quad (7)$$

MCC: With imbalanced classes (where one class predominates over the other), the Matthews Correlation Coefficient (MCC) offers a balanced performance measure that is especially helpful. MCC is defined by equation (8) and goes from -1 (indicating complete disagreement between predictions and actual outcomes) to $+1$ (indicating perfect predictions):

$$MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP + FP) \times (TP + FN) \times (TN + FP) \times (TN + FN)}} \quad (8)$$

AUC-ROC: The model's performance is displayed graphically across various classification thresholds using the AUC-ROC (Area Under the Receiver Operating Characteristic Curve) metric. Better performance is

indicated by an AUC-ROC score that is higher (closer to 1).

5. ML/DL approach for cancer detection

In this section, we have presented a block diagram illustrating techniques for cancer identification through the application of both ML and DL approach. The diagram unfolds a combined approach, functioning as a classification system for cancer detection. This comprehensive explanation captures the intricacies of both ML and DL within a unified visual representation. Fig. 13 utilizes distinct colors to highlight main processes common and unique to both ML and DL classifiers. Blocks outlined by the red line delineate shared processes, encompassing data processing and testing and prediction stages between ML and DL. The green line specifically represents DL-based techniques in cancer classification, while the blue line symbolizes ML-driven techniques. The common stages between both approaches include data processing, covering data collection, preprocessing, data augmentation, and data distribution. Additionally, in the testing and prediction stage, both approaches involve model testing on the test dataset and data classification. In the ML based approach, feature engineering plays a crucial role, including sub-parts such as extraction of features, selection of features, and reduction of features. These are essential and mandatory components of the ML-based approach, where the model is trained on feature-engineered data input. The performance of the classifiers relies on the suitability and optimization of these features. Contrastingly, in the DL based approach, the feature engineering process is not required, as DL classifiers have the capability to automatically extract features based on the input dataset. For a more profound understanding, the subsequent subsections, 4.1 and 4.2, elaborate on the ML Approach for Cancer Detection and Machine DL Approach for Cancer Detection, respectively.

5.1. ML approach for cancer detection

Here, we present prediction methods using an ML-driven approach for five types of cancers: Esophageal, Prostate, Pancreatic, Colorectal, and Leukemia. The selection of these five cancer categories is considering their elevated fatality rates and the limited coverage in existing research reviews. The generalized ML-driven classification techniques rely on benchmarked medical cancer datasets, serving as the foundation for ML-based detection methods. However, raw datasets may not be directly suitable for processing, leading to several preprocessing steps. These include color transformation, RGB to gray conversion, denoising, pixel enhancement, normalization, and standardization, preparing the dataset for subsequent analysis stages. The pre-processed dataset undergoes feature engineering, where various types of features are extracted using appropriate techniques. This step aims to capture meaningful information and details from the preprocessed data for the classification task. To effectively train and evaluate ML models, the preprocessed data is distributed into training, testing, and validation datasets. This ensures a comprehensive evaluation of the model's training and verification on these datasets. The ML model predicts cancer types in binary-class or multi-class classification, and its accuracy is assessed using various evaluation metrics. Subsequent subsections provide a detailed review of each cancer type based on various parameters, focusing on utilizing ML approaches for cancer detection and highlighting specific methods and findings for each type of cancer.

5.1.1. ML for pancreatic cancer detection

Table 7 encapsulates a compendium of avant-garde ML methodologies, showcasing the pinnacle of methods in the landscape of the detection of pancreatic cancer. The table includes 16 studies published between 2018 and 2023, evaluating different literature, features, Optimal method, utilized databases or number images or number of data, and the highest accuracy metrics of each study. The studies employ diverse ML algorithms such as SVM, RF, EL-SVM, XGBoost, and Naïve Bayes, among others. The features utilized in the studies range from

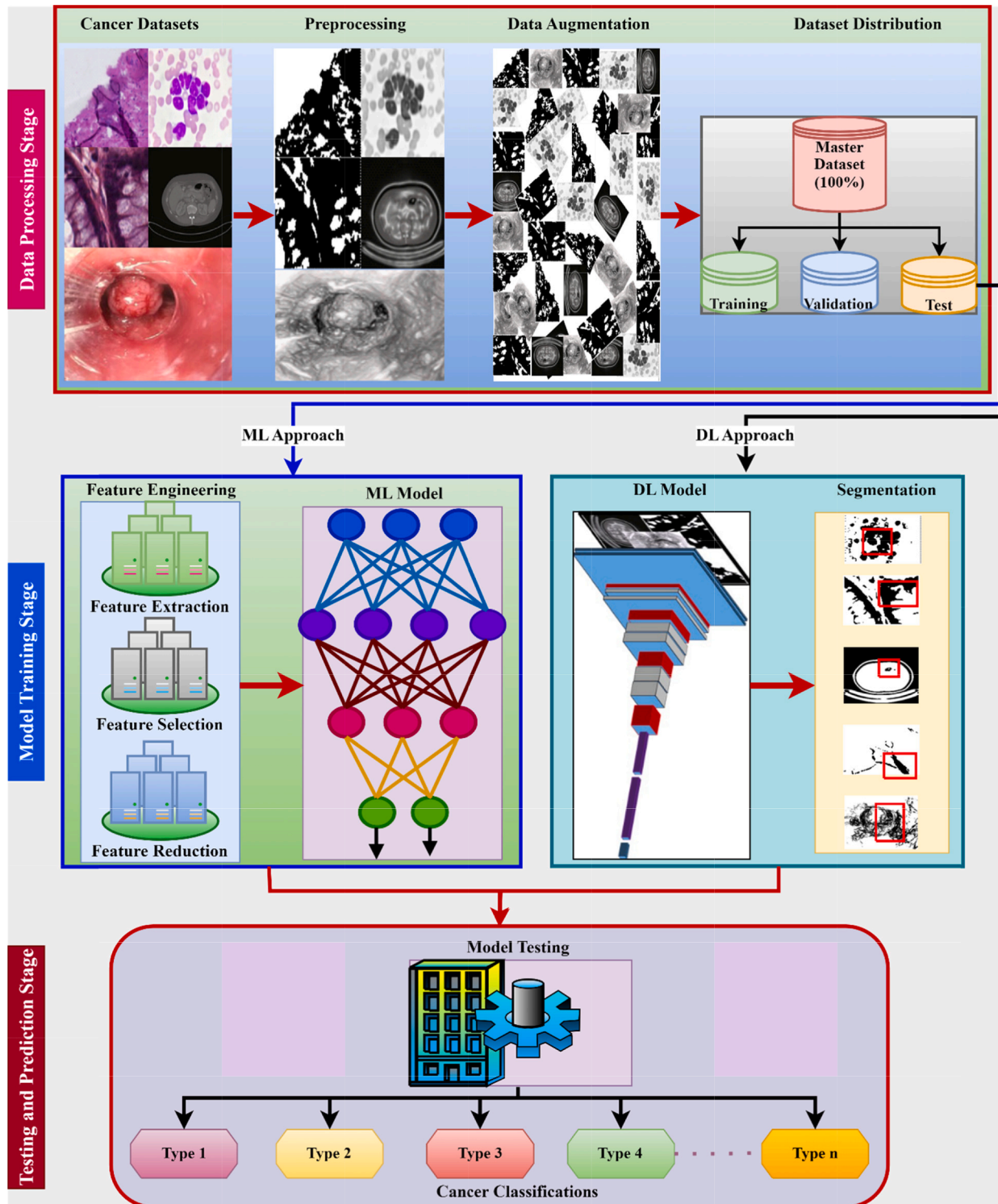


Fig. 13. Block diagram of AI-driven (ML/DL) approach for cancer prediction.

MSLF, GIST, and radiomics to shape-based features and histogram-based features. The datasets/images used in the studies vary in size, ranging from 55 to 1,477 samples. The performance metrics, measured in percentage accuracy, achieved by the studies for the pancreatic cancer classification differs from 81.19 % to 99.20 %.

Based on the information shown in Table 7, a state-of-the-art evaluation for ML-driven pancreatic cancer identification is provided below.

A. Highest Accuracy (Radiomics with RF):

- The technique achieving the highest accuracy is based on Radiomics with RF, as mentioned in the study by (Chu, Park, Kawamoto, Fouladi, et al., 2019).
- Radiomics is used as the feature set, which engages extracting quantitative features from the utilized dataset.
- The reported accuracy for this technique is 99.20 %, indicating excellent performance in accurately detecting pancreatic cancer.
- The high accuracy suggests that Radiomics combined with RF is effective in accurately classifying pancreatic cancer cases.

Table 7

State-of-the-Art comparative review of ML-based techniques for pancreatic cancer classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Li et al., 2018)	MSLF	HFB-SVM-RF	80 Cases	96.47
(Hussein et al., 2019)	GIST, Deep features	SVM	171 Images	84.22
(Qiu et al., 2019)	Histogram, Run Length, Co-Occurrence	SVM	56 Images	86.00
(Yang et al., 2019)	Radiomics	RF + LASSO	78 Images	85.00
(Chu, Park, Kawamoto, Fouladi, et al., 2019)	Radiomics	RF	380 cases	99.20
(Li et al., 2020)	WT, GLDS, Shape, GLGCM, GLRLM, GLCM	EL-SVM	168 Images	91.63
(Chang et al., 2020)	Radiomics, ICC	SVM + LASSO	401 Patients	90.10
(Qiu et al., 2021)	MSTA	SVM	312 Cases	81.19
(Liu et al., 2021)	Radiomics, MIP	SVM	112 Patients	89.91
(Ruano et al., 2022)	SURF	SVM-RBF	55 Cases	92.10
(Cheng et al., 2022)	1037 radiomics features	SVM	60 Images	86.70
(Mukherjee et al., 2022)	GLDM, GLSZM, GLRLM, GLCM, PCA algorithm	SVM	420 Images	92.20
(Ansari et al., 2022)	Radiomics	PSO SVM	420 Images	95.00
(Ebrahimian et al., 2022)	Radiomics	RF	103 Cases	89.00
(Qureshi et al., 2022)	Radiomic	Naïve Bayes	108 Images	86.00
(Chang et al., 2023)	Radiomics	XGBoost, LR	1,477 Images	87.50

B. Lowest Accuracy (MSTA with SVM):

- The technique with the lowest accuracy is based on MSTa with SVM, as mentioned in the work by (Qiu et al., 2021).
- The specific ML algorithm used for feature extraction is MSTa.
- The reported accuracy for this technique is 81.19 %, which is relatively lower compared to other techniques in the table.
- The lower accuracy suggests that the use of MSTa with SVM may face challenges in accurately classifying pancreatic cancer cases.

C. Comparative Differences:

- **Accuracy Range:** The range of accuracies observed among the ML-based techniques for pancreatic cancer detection is substantial, with a difference of 18.01 % between the highest accuracy (99.20 %) and the lowest accuracy (81.19 %). This indicates a notable variation in the performance of different ML techniques in detecting pancreatic cancer. The wide range suggests that certain techniques have been able to achieve higher levels of accuracy, while others have demonstrated comparatively lower accuracy. It highlights the need for further exploration and refinement of ML-driven methods to improve the overall outcome and consistency in pancreatic cancer detection.
- **Algorithm Variation:** Different ML algorithms such as RF, SVM, EL-SVM, SVM + LASSO, PSO-SVM, Naïve Bayes, XGBoost, and LR are utilized in the techniques, showcasing the exploration of various algorithms for pancreatic cancer detection.
- **Feature Variation:** The techniques utilize various types of features such as MSLF, GIST, Deep features, Histogram, Run Length, Co-Occurrence, Radiomics, Shape, GLCM, GLRLM, GLGCM, GLDS, WT, ICC, MIP, SURF, GLCM, GLRLM, GLSZM, GLDM, and PCA. The variation in feature types highlights the importance of capturing

different aspects of pancreatic cancer characteristics for accurate classification.

- **Dataset Variation:** The datasets and images utilized in the studies examining ML-based techniques for pancreatic cancer detection exhibit notable variations in size, ranging from 55 to 1,477 samples. These datasets differ in terms of their origin, specific characteristics (such as cases, images, or patients), and potentially other factors. The diversity in dataset characteristics can substantially affect the performance of the ML classifiers because of the variations in quality of dataset, diversity, and representation. The dimension and composition of the database used for the classification also have an essential role in training accurate and robust models. Therefore, researchers must carefully consider these variations and their potential effects on model performance when developing and evaluating ML-based techniques for pancreatic cancer detection.
- **Advancements over time:** The presence of more recent techniques achieving superior accuracy in the area of ML-driven pancreatic cancer prediction indicates a trend of ongoing advancements and improvements over time. This suggests that researchers and practitioners are persistently investigating new methods, algorithms, and methods to boost the performance and efficiency of ML-based techniques in detecting pancreatic cancer. The advancements over time may be attributed to various factors, such as improved understanding of the disease, availability of larger and more diverse datasets, refinement of ML algorithms, and advancements in computing resources.

5.1.2. ML for esophageal cancer detection

Table 8 presents a contrasted examination of ML approaches for the identification of esophageal cancer. It includes various literature references, the features utilized, the best technique employed, the dataset or number of data utilized, and the corresponding highest metrics value. The table below presents a broad outline of 17 different ML-based approaches for esophageal cancer diagnosis, spanning the years 2018 through 2023. Various features such as radiomics, wavelet transform, diagnostic features, and blood indicators are utilized. Models include ANN, RF, LR, SVM, XGBoost, and LGBM. Datasets/images range from 8 patients to 10,588 patients/images. The performance metrics, achieved by the studies for the classification of esophageal cancer vary from 77.10 % to 99.70 %.

Considering the data encapsulated within Table 8, an exhaustive analysis has been undertaken to elucidate the cutting-edge landscape in esophageal cancer identification through the utilization of ML algorithms, and the ensuing outcomes are delineated herewith.

A. Highest Accuracy (ResNet with ELM, ASODTL-ECC):

- The technique achieving the highest accuracy is based on ResNet architecture with ELM (Extreme Learning Machine) and ASODTL-ECC model, as mentioned in the study by (Alharbe et al., 2022).
- The specific DL algorithm used for feature extraction is ResNet.
- The reported accuracy for this technique is 99.70 %, indicating excellent performance in accurately detecting esophageal cancer.
- The high accuracy suggests that the combination of ResNet with ELM and ASODTL-ECC is effective in accurately classifying esophageal cancer cases.

B. Lowest Accuracy (DL, HRF with SVM):

- The technique with the lowest accuracy is based on the use of DL and HRF with SVM, as mentioned in the research by (Hu et al., 2021)
- The specific ML algorithm used for feature extraction is not mentioned.
- The reported accuracy for this technique is 77.10 %, which is relatively lower compared to other techniques in the table.
- The lower accuracy suggests that the use of DL and HRF with SVM may face challenges in accurately classifying esophageal cancer cases.

C. Comparative Differences:

Table 8

State-of-the-Art comparative review of ML-based techniques for Esophageal cancer classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Hou et al., 2018)	Radiomics	ANN	68 Images	84.30
(Xiong et al., 2018)	Radiomics	RF	30 Images	93.30
(Ou et al., 2019)	Radiomics	LR	591 Images	86.00
(Yusantay et al., 2019)	WT, Tamura Algorithm	SVM	400 cases	98.67
(Hu et al., 2020)	Radiomics	SVM	231 Images	84.30
(Rosenfeld et al., 2020)	Diagnostic Features	LR	1299 Patients, 398 Patients	84.51
(Sun et al., 2020)	SOM	SVM	180 Patients	95.56
(Li et al., 2021)	QRF	EC	334 Patients	81.60
(Hu et al., 2021)	DL, HRF,	SVM	231 Images	77.10
(Gong et al., 2021)	Categorical, Numerical	XGBoost	10,588 Patients	87.50
(Nazarian et al., 2022)	DRS	XGB, LGBM	34 patients	96.20
(Wang et al., 2022a)	MRMR	IAOA-SVM	298 patients	95.60
(Huang et al., 2022)	PCA,	LDA + XGB + SVM	8 patients	90.30
(Wang et al., 2022b)	FS-GA	BES-LSSVM	360 patients	97.01
(Alharbe et al., 2022)	Deep feature	ASODTL-ECC	750 Images	99.70
(Wang et al., 2023)	Blood Indicators	CS-SVM	398 Samples	98.43
(Shi et al., 2023)	LASSO, Radiomics	LR	28 Patients	92.70

- **Accuracy Range:** The range of accuracy values observed among the ML-based techniques for esophageal cancer detection is substantial, with a difference of 22.6 % between the maximum accuracy of 99.70 % and the minimum accuracy of 77.10 %. This considerable variation in performance highlights the diverse outcomes achieved by different ML models in accurately detecting esophageal cancer.
- **Algorithm Variation:** Different ML algorithms such as ANN, RF, LR, SVM, XGBoost, XGB, LGBM, IAOA-SVM, LDA + XGB + SVM, BES-LSSVM, CS-SVM, ELM, ASODTL-ECC, TCLDAASCA, JDPCA, MRMR, DRS, HRF, QRF, and Radiomic-LR & LASSO are utilized in the techniques, showcasing the exploration of various algorithms for esophageal cancer detection.
- **Feature Variation:** The techniques utilize various types of features such as Radiomics, WT, Tamura Algorithm, Diagnostic Features, SOM, Categorical, Numerical, DRS, PCA, FS-GA, Blood Indicators, Shape, FOF, Texture, and WT. The variation in feature types highlights the importance of capturing different aspects of esophageal cancer characteristics for accurate classification.
- **Dataset Variation:** Datasets used in esophageal cancer detection techniques vary in size, origin, and characteristics. They range from small datasets with 8 patients/images to large datasets with up to 10,588 patients/images. Dataset variations impact model performance due to differences in data quality, diversity, and representation. Larger and more diverse datasets generally lead to better accuracy, while smaller or less diverse datasets may limit

performance. Considering dataset characteristics is crucial for reliable and accurate esophageal cancer detection.

- **Advancements over time:** Advancements in ML-based techniques for esophageal cancer detection have been observed over time, with studies conducted between 2018 and 2023. Notably, some of the techniques achieving high accuracy are more recent, indicating ongoing improvements and advancements in the field. This suggests that researchers are continuously exploring and developing new ML approaches to increase the accurateness and effectiveness of esophageal cancer classification work.

5.1.3. ML for prostate cancer detection

A contrast of the latest advancements in ML-driven classification methodologies for the identification of prostate cancer is presented in Table 9. The table lists 18 different studies, various literature references, the features utilized, the best technique employed, the dataset or number of data utilized, and the corresponding highest metrics value. The studies utilize a range of techniques, including KNN, SVM, LR, RF, and

Table 9

State-of-the-Art Comparative review of ML-based techniques for prostate cancer classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Reda et al., 2018)	Level Set, GGMRF	KNN	DWI Images	94.40
(Barlow et al., 2019)	Segmentation	ADABOOST	NCI-PLCO	91.00
(Li et al., 2018)	mpMRI-IF	SVM	152 Images	97.60
(Liu et al., 2019)	Size, Statistics, HOS GLRM, GLSZM, FOF, GLCM, Shape	LR	mpMRI	90.00
(Yoo et al., 2019)	Deep Features	Random Forest	DWI images	87.00
(Chen et al., 2019)	Form Factors, Haralick features, GHF, FOF	LR	381 MRI	99.10
(Akamine et al., 2020)	Statistical features	Hierarchical Clustering	40 MRI	97.80
(Huang et al., 2020)	GMRf, LBP, Texture	SVM	Ultrasound/ 342 Images	70.93
(Ellmann et al., 2020)	Random Forest	CADx-EGB	mpMRI/195 Images	82.10
(Salama & Aly, 2021)	ResNet50	SVM	1765 Patients	98.79
(Rustam & Angie, 2021)	6 features	Random Forest	185 Observations	97.30
(Wang et al., 2022)	SCAD	Random Forest	PHDA Dataset	96.80
(Ramkumar et al., 2022)	HCCA	Decision Tree	PAS Data	97.30
(Koc et al., 2022)	Deep Features	KNN	352 Images	98.00
(Akinuwesi et al., 2023)	PCA	SVM	10,000 Images	90.00
(Yu et al., 2023)	BorutaShap	SVM	AFM Images	82.50
(Anand et al., 2023)	GLCM	KNN	80 MRI	90.00
(Qi et al., 2023)	WT, FOF, NGDM, GLSZM, GLRM, GLCM, GLDM, Shape	Random Forest	519 cases	83.00

DT, and features such as GLCM, texture, and statistics. The datasets used for the studies range from DWI images to ultrasound and MRI scans, with the number of images used ranging from 10,000 to 185 observations. The metrics for prostate cancer classification varies from 70.93 % to 99.10 %, with the highest accuracy achieved using LR on 381 MRI scans.

The data in Table 9 has been utilized to conduct a thorough comparative evaluation of the contemporary state-of-the-art in the identification of prostate cancer through the application of ML algorithms, and the results are elucidated below.

A. Highest Accuracy (FOF, GHF, Haralick, form factor with LR):

- The technique achieving the highest accuracy is based on FOF, GHF, Haralick, and form factor with LR, as given in the paper by (Chen et al., 2019).
- The specific features used in this technique include FOF, GHF, Haralick, and form factor.
- The reported accuracy for this technique is 99.10 %, indicating excellent performance in accurately detecting prostate cancer.
- The high accuracy suggests that the combination of these features with LR is effective in accurately classifying prostate cancer cases.

B. Lowest Accuracy (Texture, LBP, GMRF with SVM):

- The technique with the lowest accuracy is based on Texture, LBP, GMRF (Gaussian Markov Random Field), and SVM, as cited in the work by (Huang et al., 2020).
- The specific features used in this technique include Texture, LBP, and GMRF.
- The reported accuracy for this technique is 70.93 %, which is the lowest among all performances in the table.
- This lower metrics suggests that the use of these features with SVM may face challenges in accurately classifying prostate cancer cases.

C. Comparative Differences:

- **Accuracy Range:** The ML-driven methods for the identification of prostate cancer exhibit a significant variation in performance, as indicated by the accuracy range of 28.17 %. The highest accuracy achieved among the techniques is 99.10 %, while the lowest accuracy is 70.93 %. This wide range of accuracies highlights the diversity in the effectiveness of different ML approaches for prostate cancer detection. It suggests that some techniques are highly accurate in correctly identifying prostate cancer cases, while others may face challenges in accurately classifying the disease.
- **Algorithm Variation:** Different ML algorithms such as KNN, SVM, RF, DT, ADABOost, Hierarchical Clustering, and BorutaShap are utilized in the techniques, showcasing the exploration of various algorithms for prostate cancer detection.
- **Feature Variation:** The techniques utilize various types of features such as Level Set, GGMRF, mpMRI derived imaging features, Segmentation, FOF, GHF, Haralick, form factor, Statistics, Shape, Size, GLCM, GLRM, GLSZM, HOS, Texture, LBP, GMRF, SCAD, HCCA, GLDM, NGDM, and GLCM. The variation in feature types highlights the importance of capturing different aspects of prostate cancer characteristics for accurate classification.
- **Dataset Variation:** Dataset variation is evident in the techniques employed for pancreatic cancer detection, with differences observed in terms of size, origin, and specific characteristics of the datasets. The dataset sizes vary from the highest 10,000 images to the lowest 185 observations. Such variations in dataset characteristics can significantly influence the performance of the models due to differences in data quality, diversity, and representation.
- **Advancements over time:** Over the period from 2018 to 2023, a total of 18 studies have been conducted on prostate cancer identification using an ML-driven approach. It is noteworthy that some of the more recent techniques have demonstrated high accuracy, indicating continuous advancements and improvements in ML-driven methodologies for the classification of prostate cancer. The evolving nature of these techniques suggests an ongoing effort to

boost the accurateness and effectiveness of prostate cancer prediction work.

5.1.4. ML for colorectal cancer detection

A presentation of various methodologies based on ML algorithms for the identification of colorectal cancer is delineated in Table 10. The table lists 18 studies, various literature references, the features utilized, the best technique employed, the dataset or number of data utilized, and the corresponding highest metrics value. The studies utilize a range of techniques, including Naïve Bayes, SVM, RF, and XGBoost, and features such as genes characteristic, statistical, and color characteristics. The datasets used for the studies range from Kaggle to TCGA and include a variety of images such as Affymetrix, MALDI MSI, and SEKN. The metrics values for the prediction of colorectal cancer differs from 65.83 % to 100 %, with the highest accuracy achieved using a hybrid model on LC25000/2800 images.

Table 10

State-of-the-Art comparative review of ML-based techniques for colorectal cancer classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Salmi & Rustam, 2019)	6 attributes	Naïve Bayes	209 cases	95.24
(Yang et al., 2019)	CHFSPW, CSQ	SVM	Local/180 Images	96.01
(Zhao et al., 2019)	LR, ROC Curve	SVM-RBF	ENA	91.20
(Shafi et al., 2020)	MDA, MDG	RF	Affymetrix, Hum6000	95.16
(Park et al., 2020)	Random Features	AdaBoost	PLCO	80.00
(Mohalder & Talukder, 2021)	CNN	XGBoost	10,000Images	99.00
(Battista et al., 2021)	Gini Importance, PCA	SVM + XGB + MLP	345 Patients	98.03
(Nazari et al., 2021)	PCA	SVM	GEO	91.89
(Mittal et al., 2021)	BmzP	NN	MALDI MSI	98.00
(Qarmiche et al., 2022)	EHLI, Age	SVC	MMSD	65.83
(Alqudah & Alqudah, 2022)	Haralick, 3D GLCM, HSV Color Space	QDA	KCRC-16/5000 Images	97.32
(Hage Chehade et al., 2022)	Statistical, GLCM, Hu invariant moments	XGBoost	LC25000	95.60
(Talukder et al., 2022)	Deep Features	Hybrid Model	LC25000/2800 Images	100.00
(Su et al., 2022)	Genes Characteristic	RF	TCGA	99.81
(Arowolo et al., 2023)	785 attributes	RF	Kaggle/5000 Instances	96.00
(Lo et al., 2023)	Clinical	SE-KNN	1729 Images	94 0.00
(Khazae Fadafen & Rezaee, 2023)	Dilated ResNet	DeepSVM	KCRC-16, CRC-5000, NCT-CRC-HE-100 K	99.76
(Tripathi et al., 2023)	color characteristics	Categorical Boosting	NCT-CRCHE-7 K	90.67

Based on the data presented in Table 10, an extensive comparative analysis of the latest developments in Colorectal Cancer identification using ML algorithms has been conducted, and the results are outlined below.

A. Highest Accuracy (Deep Features with Hybrid Model):

- The technique achieving the highest accuracy is based on deep features with a hybrid model, as stated in the work by (Talukder et al., 2022).
- The specific features used in this technique are deep features extracted from images.
- The reported accuracy for this technique is 100 %, indicating excellent performance in accurately detecting colorectal cancer.
- The high accuracy suggests that the grouping of deep features and the hybrid classifiers is efficient in accurately classifying colorectal cancer cases.

B. Lowest Accuracy (EHLL, Age with SVC):

- The technique with the lowest accuracy is based on EHLL, Age, and SVC (Soft Voting Classifier), as cited in the research by (Qarmiche et al., 2022).
- The specific features used in this technique include EHLL and Age.
- The reported accuracy for this technique is 65.83 %, which is the lowest among all in the table.
- The lower metrics suggest that the use of these features with SVCC may face challenges in accurately classifying colorectal cancer cases.

C. Comparative Differences:

- **Accuracy Range:** The accuracy range among ML-based techniques for colorectal cancer detection is significant, with a difference of 34.17 % between the highest (100 %) and lowest (65.83 %) accuracies. This indicates a notable variation in performance among different techniques for accurately classifying colorectal cancer cases.
- **Algorithm Variation:** Different ML algorithms such as RF, Neural Network, Naïve Bayes, SVM, XGBoost, SVC, QDA (Quadratic Discriminant Analysis), DeepSVM, and Categorical Boosting are utilized in the techniques, showcasing the exploration of various algorithms for colorectal cancer detection.
- **Feature Variation:** The techniques utilize various types of features such as attributes, CHFSPW, CSQ, LR (Logistic Regression), ROC Curve, MDA, MDG, Gini Importance, PCA (Principal Component Analysis), BmzP, Haralick, 3D GLCM, HSV Color Space, Statistical, GLCM, Hu invariant moments, Genes Characteristic, FEViT, Clinical, color characteristics, etc. The variation in feature types highlights the importance of capturing different aspects of colorectal cancer characteristics for accurate classification.
- **Dataset Variation:** The datasets used in different techniques vary in terms of size, origin, and specific characteristics (e.g., cases, images, patients, instances). The variation in dataset characteristics can impact the classifiers outcome because of the differences in data quality, diversity, and representation.
- **Advancements over time:** The inclusion of studies from 2019 to 2023 in the table indicates the presence of ongoing research and advancements in ML-based techniques for colorectal cancer detection. Furthermore, the observation that some of the techniques achieving high accuracy are more recent suggests continuous improvements and progress in ML-based techniques for the detection of colorectal cancer.

5.1.5. ML for leukemia detection

In the eloquent confines of Table 11, a ballet of comparison unfolds, spotlighting avant-garde ML methods ingeniously harnessed for the intricate task of leukemia classification. The tabulation encapsulates 18 studies, complete with their corresponding references, feature extraction methodologies, optimal techniques, utilized databases or the quantity of data, and the pinnacle of accuracy metric percentages achieved. The studies range from 2018 to 2023 and utilize a range of

Table 11

State-of-the-Art comparative review of ML-based techniques for Leukemia classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Mirmohammadi et al., 2018)	Shape, Statistical	SVM	312 Images	97.00
(Vogado et al., 2018)	Deep Features	SVM	ALL-IDB 1, ALL-IDB 2	99.20
(Abdeldaim et al., 2018)	Shape, Color, Texture	KNN	ALL-IDB1, ALL-IDB2	96.01
(Jothi et al., 2019)	Statistical, Texture, Color, WT, Morphological	EC	ALL-IDB/ 300 Images	99.00
(Mishra et al., 2019)	DOST, Morphological, Textural, Color	ADBRF	ALL-IDB1/ 799 Cells	99.66
(Shahin et al., 2019)	Shape, Texture, Complex	SVM	WBC/2551 Images	96.10
(Sharma & Kumar, 2019)	SVD, PCA	ABC-BPNN	MLdata Repository	98.70
(Claro et al., 2020)	Deep Features	AlexNet	2,415 Images	97.18
(Dasariraju et al., 2020)	Shape, Size, Color	RF	18,365 Images	93.45
(Bodzas et al., 2020)	Morphological, Statistical	ANN	241 Images	97.52
(Sahlol et al., 2020)	VGGNet-19	SVM	ALL-IDB2	96.11
(Jusman et al., 2021)	Hu invariant moments	SVM	800 Image	95.00
(Mirmohammadi et al., 2021)	Geometric, Statistical	RF	312 Images	98.00
(Elhassan et al., 2022)	CNN-Based	RF	AML-C-LMU	97.57
(Liu & Hu, 2022)	Morphological, Radiomics, Clinical	RF	TCIA	99.80
(Das et al., 2022)	MobileNetV2	SVM	ALLIDB1, ALLIDB2, ASH	99.39
(Emam Atteia, 2023)	GoogleNet, Inception-v3 (CNNs)	SVM	ALL-IDB	100.00
(Anil et al., 2023)	Cell-based features	MLP	ALL-IDB1, ALL-IDB	98.40

techniques, including SVM, KNN, RF, and MLP, and features such as deep features, Statistical features, color, Geometric, shape, Morphological features, and texture. The datasets used for the studies range from ALL-IDB to TCIA and include a variety of images such as AML-C-LMU, ML data Repository, and WBC. The highest metrics values for the identification blood cancer differs from 93.45 % to 100 %, with the highest accuracy achieved using GoogleNet and Inception-v3 on ALL-IDB.

The information presented in Table 11 has been used to conduct a state-of-the-art review for ML-driven algorithms for the prediction leukemia, and the key findings are presented below.

A. Highest Accuracy (GoogleNet and Inception-v3 with SVM):

- The technique achieving the highest accuracy is based on the combination of GoogleNet and Inception-v3 (CNNs) with SVM, as mentioned in the study by (Emam Atteia, 2023).
- The specific features used in this technique are not explicitly mentioned.
- The reported accuracy for this technique is 100.00 %, indicating excellent performance in accurately detecting leukemia.
- The high accuracy suggests that the combination of GoogleNet and Inception-v3 CNNs with SVM is effective in accurately classifying leukemia cases.

B. *Lowest Accuracy (Shape, Size, and Color Features with RF):*

- The technique with the lowest accuracy is based on the use of shape, size, and color features with the RF classifier, as refer to the paper by (Dasariraju et al., 2020).
- The specific ML algorithm used for feature extraction is not explicitly mentioned.
- The reported accuracy for this technique is 93.45 %, which is the lowest among all.
- The lower accuracy suggests that the combination of shape, size, and color features with RF may face challenges in accurately classifying leukemia cases.

C. *Comparative Differences:*

- **Accuracy Range:** The small difference of 6.55 % between the highest accuracy (100.00 %) and the lowest accuracy (93.45 %) in ML-based techniques for leukemia detection suggests a relatively consistent performance across different methods. This indicates that the variation in accuracies may be attributed to factors such as the specific dataset used, or the techniques employed by researchers. It highlights the importance of dataset quality and the choice of appropriate techniques in achieving higher accuracies in leukemia detection using ML-based approaches.
- **Algorithm Variation:** Different ML algorithms such as SVM, KNN, EC, ADBRF, ABC-BPNN, RF, ANN, MLP, and their combinations are utilized in the techniques, indicating the exploration of various algorithms for leukemia detection.
- **Feature Variation:** The techniques utilize various types of features such as shape, statistical, deep features, morphological, wavelet, color, texture, DOST, Hu invariant moments, geometric, radiomics, and clinical features. The variation in feature types indicates the importance of capturing different aspects of leukemia characteristics for accurate classification.
- **Dataset Variation:** The datasets used in different techniques vary in terms of size, origin, and specific leukemia subtypes (e.g., ALL-IDB1, ALL-IDB2, AML-C-LMU). The variation in dataset characteristics can impact the classifier performance due to differences in diversity, data quality, and representation.
- **Advancements over time:** Over the years, from 2019 to 2023, there has been a notable progression in ML-based techniques for leukemia detection, as evident from the studies included in the table. The inclusion of more recent techniques achieving high accuracy implies that there are continuous advancements and improvements in this field. Researchers are actively exploring novel approaches and refining existing techniques to augment the performance and efficacy of leukemia detection using ML-based methods. This ongoing research indicates a dedicated effort to stay at the forefront of leukemia detection by leveraging the potential of ML algorithms.

5.2. *DL approach for cancer detection*

The schematic representation in Fig. 13 succinctly outlines the utilization of DL and ML approaches for categorizing various cancer types. This comprehensive overview encompasses the classification of five distinct cancer categories employing DL algorithms. Initiating the process, the first stage involves obtaining a benchmarked and authenticated dataset tailored for the specific cancer type under investigation. This dataset may suffer from various forms of noise or may lack the appropriate format for direct utilization in the classification process. Consequently, in the subsequent stage, diverse preprocessing methods are generally employed to filter and organize the raw dataset into a useful and appropriate format. The choice of preprocessing methods varies depending on the nature of the data acquired for the classification task. Despite the fact that feature engineering is not imperative in DL-driven algorithms, as these models automatically extract deep features, many researchers still employ various feature engineering techniques to enhance classification performance. In a DL-based approach, a substantial amount and size of data are essential, as DL classifiers require

extensive training to discern intricate patterns. Therefore, if the dataset is not sufficiently large, augmentation techniques are applied to increase the dataset by augmenting images and data. The augmented data, which may be substantial for training the classifiers, is then provided to the models. However, before that, it is imperative to apply data distribution, where the dataset is divided into training, test, and validation sets. The proportion of training and validation data is notably high, ranging from 60 % to 95 % of the total data, while the remaining 40 % to 10 % is reserved for testing the model performance, ensuring that this portion remains unexposed during the training process. Following the training phase, the DL model, now equipped for cancer type prediction or classification, is applied to new, unseen data to estimate or classify the presence of cancer. The prediction may take a binary form (e.g., cancer/non-cancer) or be multi-class, depending on the specific application and dataset utilized. In certain instances, post-processing methods such as segmentation are employed as a subsequent step. Segmentation entails accurately delineating or isolating cancerous regions from surrounding tissues or structures. This segmentation process facilitates further analysis or specific localization of the detected cancer types.

5.2.1. *DL for pancreatic cancer detection*

Table 12 delineates a comprehensive comparative analysis of cutting-edge techniques within the realm of DL for the prediction of pancreatic cancer. The table lists 21 studies, with various parameters such as the literatures with author names and years, extraction of features, optimal methods of classification, utilized database or number of data, and highest metrics percentage (Accuracy). The studies range from 2019 to 2023 and utilize a range of techniques, including CNN, ResNet, CapsNet, and Attention U-Net, and features such as CT images, EUS images, nCLE, and biomarkers. The datasets used for the studies range from TCIA to BioGPS and include a variety of images such as CT, EUS, and video frames. The studies performance for the classification of pancreatic cancers using DL methods varies from 66.80 % to 100 %, with the highest accuracy achieved using CNN and MobileNet on CT images.

The significant findings and observations derived from a DL-driven methods for detecting Pancreatic Cancer, as inferred from the information outlined in Table 12, are elucidated below.

A. *Highest Accuracy (CNN with YCNN and MobileNet):*

- The technique achieving the highest accuracy is based on a CNN with YCNN and MobileNet architectures, as mentioned in the work by (Dinesh et al., 2023).
- The feature extraction is not performed, used automatically extracted feature by DL model.
- The reported accuracy for this technique is 100.00 % and 99.50 % for two different models, indicating excellent performance in accurately detecting pancreatic cancer.
- This high accuracy suggests that the CNN-based approach with the specific models used in this study is effective in accurately classifying pancreatic cancer cases.

B. *Lowest Accuracy (ViT with CNN):*

- The technique with the minimal accuracy is based on an amalgamation of ViT (Vision Transformer) and CNN, as stated in the work by (Fleurentin et al., 2023).
- The feature extraction is not performed, used automatically extracted feature by DL model.
- The reported accuracy for this technique is 66.80 %, which is the lowest.
- The lower accuracy suggests that the ViT and CNN-based approach with the specific dataset used in this study may face challenges in accurately classifying pancreatic cancer cases.

C. *Comparative Differences:*

- **Accuracy Range:** The significant difference of 33.20 % between the highest accuracy (100.00 %) and the lowest accuracy (66.80 %) highlights a substantial change in the outcomes of DL-based techniques for pancreatic cancer classification. This indicates that

Table 12

State-of-the-Art comparative review of DL-based techniques for pancreatic cancer classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Chu, Park, Kawamoto, Wang, et al., 2019)	×	DCNN	575 CT Images	87.80
(Kuwahara et al., 2019)	CEUS	ResNet50	3,970 EUS Images	94.00
(Zhang et al., 2020)	GLCM, LBP, LFE, GMM	CNN	TCIA	99.90
(Zhang et al., 2020)	×	ResNet	19,487 Images	82.40
(Si et al., 2021)	×	FEE-DL	250,981 Images	82.70
(Udristoiu et al., 2021)	×	CNN-LSTM	2,688 Images	98.30
(Nguon et al., 2021)	×	ResNet50	211 Images	82.75
(Marya et al., 2021)	×	ResNet50V2	1,174,461 EUS Images	75.60
(Machicado et al., 2021)	nCLE	VGG-16	15,027 Video Frames	85.70
(Vilas-Boas et al., 2022)	×	CNN	505 Images	98.50
(Althobaiti et al., 2022)	CapsNet	ODL-PTNTC	BioGPS	98.40
(Kronberg et al., 2022)	×	ResNet18-CNN	17,842 Image	94.00
(Bonmati et al., 2022)	×	CNN	143 Pairs of Image & Voice	76.00
(Oh et al., 2022)	×	Attention U-Net	57 Images364 images	98.30
(Fleurentin et al., 2023)	ViT	CNN	786 EUS	66.80
(Tang et al., 2023)	×	UNet++	4342 EUS Images	93.80
(Kuwahara et al., 2023)	×	EfficientNetV2-L	22,000 Images	87.90
(Dinesh et al., 2023)	CNN	YCNN, MobileNet	7,245 CT Images	100.0099.50
(Lee et al., 2023)	CLAHE	VGG19	22,424 Frames	98.00
(Karar et al., 2023)	Biomarkers	CNN + LSTM	590 Samples	97.00
(Thanya et al., 2023)	Histogram	DCNN,DBN	534 Patients	99.60

different DL models and approaches can yield significantly different outcomes in terms of accuracy. Such variations may arise due to various factors, including differences in network architectures, training strategies, hyperparameters, and the size and quality of the datasets applied for training and evaluation. It is vital to consider these execution disparities when selecting and evaluating DL models for pancreatic cancer detection, as it emphasizes the need to identify and employ the most effective techniques to achieve accurate and reliable results.

- **Algorithm Variation:** The table highlights the utilization of different DL algorithms for pancreatic cancer detection, showcasing the exploration and adoption of various DL models in this domain. Some of the mentioned DL algorithms include CNN, ResNet, CapsNet, Attention U-Net, UNet++, EfficientNetV2-L, VGG19, among others. These DL models offer different architectures, design principles, and capabilities, allowing researchers to investigate their effectiveness in classifying pancreatic cancer. By leveraging a diverse range of DL algorithms, researchers aim to increase the efficacy and performance of pancreatic cancer prediction systems and explore the potential of these models in addressing the challenges of this disease.

- **Feature Variation:** The table provides information on the features used in the studies for pancreatic cancer detection. These features encompass a wide range of characteristics related to pancreatic cancer, including texture, shape, and cell structures. Some of the mentioned features include GLCM, LBP, LFE, GMM, nCLE, Biomarkers, Histogram, among others. By leveraging these diverse features, researchers aim to capture different aspects of pancreatic cancer, enabling more comprehensive and accurate detection using ML-based techniques.
- **Dataset Variation:** The datasets used for pancreatic cancer detection vary in terms of their sources, including TCIA and BioGPS, and imaging modalities such as CT, EUS, and video frames. The dataset sizes range from as high as 1,174,461 images to as few as 57 images. These variations in dataset characteristics can impact the model's performance, considering differences in data quality, diversity, and representation.
- **Advancements over time:** The table includes studies conducted between 2019 and 2023, indicating recent research efforts in the area of pancreatic cancer classification with DL-driven techniques. The studies utilize various DL models such as CNN and MobileNet, showcasing the diversity of approaches in the field. The obtained metrics values range from 66.80 % to 100 %, highlighting the variability in performance among the different techniques. The maximum metrics value attained using CNN and MobileNet on CT images suggests the efficacy of DL models in pancreatic cancer recognition. These findings demonstrate the continuous advancements and improvements in DL-based techniques for the recognition of pancreatic cancer over the years.

5.2.2. DL for esophageal cancer detection

Table 13 delineates a comprehensive comparative analysis of cutting-edge techniques within the realm of DL for the prediction of esophageal cancer. The table lists 21 studies, with various parameters such as the literatures with author names and years, extraction of features, optimal methods of classification, utilized database or number of data, and highest metrics percentage (Accuracy). The studies range from 2019 to 2023 and utilize a range of techniques, including CNN, DCNN, ResNet-UNet, and DL-FCN, and features such as ME + NBI, CAD-NBI+, and BiT-M. The datasets used for the studies range from 379 to 29,794 images and include a variety of imaging modalities such as endoscopy and CT. The metrics attained for the classification of esophageal cancer differs from 80.60 % to 98.10 %, with the highest accuracy achieved using DCNN on 13,083 images.

The key findings and observations of esophageal cancer detection using a DL-driven methodology, based on the data presented in Table 13, are provided below.

A. Highest Accuracy (DCNN with 98.10 % Accuracy):

- The technique achieving the highest accuracy is with utilizing DCNN classifier, as declared in the work by (Liu et al., 2022).
- Feature Engineering methods are not utilized separately, utilized DL Automatic features extracted by the DL model.
- The reported accuracy for this technique is 98.10 %, indicating excellent performance in accurately detecting esophageal cancer.
- The high accuracy suggests that the use of DCNN is effective in accurately classifying esophageal cancer cases.

B. Lowest Accuracy (BiT-M with 80.60 % Accuracy):

- The technique with the lowest accuracy is based on BiT-M (Big Transfer Model), as mentioned in the research performed by (Tani et al., 2023).
- Feature Engineering methods are not utilized separately, utilized DL Automatic features extracted by the DL model.
- The reported accuracy for this technique is 80.60 % is the lowest classification accuracy among entire studies.
- The lower accuracy suggests that the use of BiT-M may face challenges in accurately classifying esophageal cancer cases.

Table 13

State-of-the-Art comparative review of DL-based techniques for esophageal cancer classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Horie et al., 2019)	×	CNN	9,546 Images	98.00
(Tomita et al., 2019)	×		379 Images	85.00
(Cai et al., 2019)	×	DNN	2,615 Images	91.40
(Nakagawa et al., 2019)	×	DCNN	15,252 Images	91.00
(Everson et al., 2019)	ME + NBI	CNN	7,046 Images	93.30
(Zhao et al., 2019)	×	DL-FCN	1,350 Images	93.00
(Hashimoto et al., 2020)	×	CNN	1,835 images	95.40
(de Groof et al., 2020)	×	ResNet-UNet	1,704 Images	89.00
(de Souza et al., 2020)	CNN	DCGAN, CNN	176 Images	90.00
(Ohmori et al., 2020)	×	CNN	23,289 Images	81.00
(Liu et al., 2020)	×	CNN	1,272 Images	85.83
(Tokai et al., 2020)	×	CNN	2,042 Images	95.50
(Shimamoto et al., 2020)	×	CNN	23,977 Images	89.00
(Fukuda et al., 2020)	×	DCNN	23,746 images	88.00
(Li et al., 2021)	×	CAD-NBI+CAD-WLI	5,367 Images	94.90
(Kumar & Mubarak, 2022)	CNN	ResNet50	1,800 Images	94.46
(Yuan et al., 2022)	×	DCNN	7,094 Images	91.30
(Tajiri et al., 2022)	×	BiT-M	29,794 Images	80.90
(Liu et al., 2022)	×	DCNN	13,083 Images	98.10
(Tani et al., 2023)	×	BiT-M	237 Lesions	80.60
(Yuan et al., 2023)	×	CNN	10,047 Images	92.40

C. Comparative Differences:

- **Accuracy Range:** The significant difference of 17.5 % between the highest accuracy (98.10 %) and the lowest accuracy (80.60 %) highlights the variation in performance observed among the DL-driven methodologies for esophageal cancer identification. This variation suggests that different DL models and approaches can yield diverse outcomes in the form of accuracy when used to the task of esophageal cancer detection. The variation may stem from differences in the design of DL architectures, training methodologies, feature extraction techniques, or the specific datasets used. It underscores the importance of carefully selecting and optimizing DL models to achieve higher accuracy and reliability in esophageal cancer detection.
- **Algorithm Variation:** Different DL algorithms such as CNN, DNN, DCNN, ResNet-UNet, DCGAN, BiT-M, etc., are utilized in the techniques, showcasing the exploration of various DL models for esophageal cancer detection.
- **Feature Variation:** The table incorporates diverse feature engineering techniques, and noteworthy is the observation that some researchers have not employed any specific feature engineering methodology. However, it highlights features like ME + NBI, CAD-NBI+, CAD-WLI, etc. These features are designed to encapsulate

various aspects of esophageal cancer, including morphology, color, and texture.

- **Dataset Variation:** The datasets used in the studies for esophageal cancer detection exhibit a wide range in terms of the number of images, spanning from 379 to 29,794. These datasets encompass diverse imaging modalities, including endoscopy and CT scans. Such variation in dataset characteristics can significantly influence the competence of the models employed for esophageal cancer detection. Furthermore, variations in data quality, such as variations in imaging resolution, noise levels, or data preprocessing techniques, can also affect the Model capability in classification work. Therefore, it is crucial to consider dataset characteristics and ensure their representativeness and quality when developing and evaluating ML models for esophageal cancer detection.
- **Advancements over time:** The inclusion of studies from 2019 to 2023 in the table suggests that there is ongoing research and continuous advancements in DL-driven methodologies for esophageal cancer classification. This indicates that researchers are actively exploring and developing new approaches to upgrade the accuracy and effectiveness of esophageal cancer identification using DL methods. The continuous research and advancements in DL-driven approach for classification of esophageal cancer indicate a commitment to addressing the challenges and improving the overall efficiency of early recognition and diagnosis. This ongoing progress is essential for potentially improving patient outcomes, guiding treatment decisions, and reducing the burden of esophageal cancer on individuals and healthcare systems.

5.2.3. DL for prostate cancer detection

Table 14 presents a comparative review of the state-of-the-art in DL-driven approach for prostate cancer categorization. The table lists 20 studies conducted between 2019 and 2023, providing details such as authors, publication years, literature sources, features used, best techniques employed, dataset or image sources, and the corresponding best accuracy achieved. Various DL models including CNN, ResNet, 3D U-Net, and VGG16 were utilized, leveraging diverse features such as CEUS data, mpMRI images, and slide tiling. The datasets encompassed a wide range, with image counts spanning from 70 to 47,579, and modalities including CEUS, mpMRI, and DWI. The reported accuracies ranged from 76.00 % to 99.38 %, with the highest accuracy achieved through the application of CNN on 5000 MRI images. Collectively, these studies reveal the possibility of DL-driven algorithms in enhancing prostate cancer classification and diagnosis.

The techniques for detecting prostate cancer using DL have been analyzed, and the comparison study and its conclusions, which are based on Table 14, are presented below.

A. Highest Accuracy (CNN with 99.38 % Accuracy):

- The technique achieving the highest accuracy utilizing CNN classifier as stated in the research y by (Ali & Mohammed, 2022).
- No additional features were utilized other than automatically extracted by DL-Model.
- The reported accuracy for this technique is 99.38 %, indicating excellent performance in accurately detecting prostate cancer.
- The high accuracy suggests that the use of CNN is effective in accurately classifying prostate cancer cases.

B. Lowest Accuracy (CNN with 76 % Accuracy):

- The technique with the lowest accuracy is based on a CNN with a dataset consisting of 377 patients, as mentioned in the study by (Arif et al., 2020).
- The specific features used in this technique are not explicitly mentioned.
- The reported accuracy for this technique is 76.00 %, which is lowest across all the studies reviewed.

Table 14

State-of-the-Art comparative review of DL-based techniques for prostate cancer classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Feng et al., 2019)	3D-CNN	CNN	47,579 CEUS Data	90.00
(Xu et al., 2019)	×	ResNet	346 Images	93.00
(Lucas et al., 2019)	×	CNN	96 Images	92.00
(Arif et al., 2020)	×	CNN	377 Patients	76.00
(Tolkach et al., 2020)	×	NASNetLarge	TCGA/ 218 Images	98.00
(Kott et al., 2021)	×	ResNet	14,803 image	91.50
(Melo et al., 2021)	×	CNN	1,525 Images	94.10
(Hosseinzadeh et al., 2021)	×	3D U-Net	2,734 mpMRI Images	85.00
(Elmarakeby et al., 2021)	×	DNN (P-NET)	1,013 Prostate cancers	83.00
(Hassan et al., 2022)	VGG16	EAI	1151 Participants	97.00
(Tsuneki et al., 2022)	Slide Tiling, Otsu's	EfcientNetB1	TCGA	99.00
(Ali & Mohammed, 2022)	×	CNN	5000MRI Images	99.38
(Salman et al., 2022)	×	Yolo	500 Images	97.00
(Alshareef et al., 2022)	CIWO-FS	DNN	MGED	97.19
(Ye et al., 2022)	CNN	PSP-Net + VGG16	70 Images	88.00
(Abdelmaksoud et al., 2023)	Spatial, Shape Prior, Intensity	CNN	DWI dataset	94.00
(Hamm et al., 2023)	×	EAI	Prostate dataset	80.00
(Xiang et al., 2023)	RestNet50	GCN-MIL	6,174 Slides	78.50
(Wang et al., 2023)	×	SE-CNN	81 MRI	91.20
(Zhao et al., 2023)	×	DL-CS	1861 Patients	81.40

- The lower accuracy suggests that the CNN-based approach with the specific dataset and features used in this study may face challenges in accurately classifying prostate cancer cases.

C. Comparative Differences:

- **Accuracy Range:** The significant variation in performance among DL-based techniques for prostate cancer detection, as indicated by the 23.38 % difference between the highest accuracy (99.38 %) and the lowest accuracy (76 %), suggests that different techniques yield varying levels of accuracy in identifying prostate cancer. This difference could be assigned to numerous components, involving variations in the algorithms, models, and datasets used in each technique. It highlights the importance of selecting and implementing appropriate DL-based techniques to achieve higher accuracy in prostate cancer detection. Further research and refinement of these techniques can guide improved problem-solving capabilities and patient outcomes.
- **Algorithm Variation:** The techniques for prostate cancer detection involve the utilization of different DL algorithms such as CNN, ResNet, VGG16, EfficientNetB1, DNN, PSP-Net, GCN-MIL, SE-CNN, and more. This diverse set of DL models demonstrates the exploration and experimentation with various architectures and approaches in the field of prostate cancer detection. Researchers aim to pull the depths of these different DL classifiers to upgrade performance,

robustness, and efficiency in detecting prostate cancer, ultimately enhancing diagnostic capabilities and patient outcomes.

- **Feature Variation:** The table mentions the utilization of features such as CEUS data (Contrast-Enhanced Ultrasound), MRI (Magnetic Resonance Imaging) images, intensity, shape prior, spatial information, and more. These features are employed to capture various characteristics of prostate cancer, including texture, shape, signal intensity, and spatial patterns. By incorporating these features into the analysis, researchers aim to augment the overall performance and effectiveness of the task of prostate cancer classification. The combination of different features allows for a comprehensive evaluation of the prostate gland, enabling the identification and characterization of cancerous regions.
- **Dataset Variation:** The datasets utilized in the different techniques for prostate cancer detection exhibit variations in terms of size, origin, and specific characteristics. These characteristics include the utilization of CEUS data, images, TCGA data, mpMRI images, prostate datasets, DWI datasets, slides, and MRI scans. The varied nature of these datasets can exert a considerable influence on the efficacy of the models. The kaleidoscopic variations in data quality, diversity, and representation wield a profound influence on the model's prowess to navigate the intricate landscape of prostate cancer detection. Hence, it becomes paramount to intricately consider the idiosyncrasies embedded within the dataset when crafting and appraising ML-based techniques for unveiling the enigma of prostate cancer.
- **Advancements over time:** The inclusion of studies conducted between 2019 and 2023 in the table suggests a continuous focus on research and advancements in DL-driven approach for the identification of prostate cancer. This temporal framework underscores continuous endeavors aimed at enhancing the precision and efficacy of prostate cancer detection, achieved through the application of DL models. The presence of recent studies further suggests that researchers are actively exploring and developing new approaches to enhance the detection and diagnosis of performance of the DL based approach for prostate cancer.

5.2.4. DL for colorectal cancer detection

Table 15 presents a comparative review of the state-of-the-art in DL-driven approach for colorectal cancer categorization. The table lists 22 studies, providing details such as authors, publication years, literature sources, features used, best techniques employed, dataset or image sources, and the corresponding best accuracy achieved.

Innumerable DL classifiers including, VGG16, LSTM, CNN, ShufNet, VGG19, MSINet, ResNet-50, SSDL, CRCNet, ResNet, Qritive Colon AI, DCNN, Lightweight CNN, ResNet-18, Hybrid U-Net, ConvNeXt, YOLOv3-MSF, and CJT-DEO-EDNN were utilized. The features employed varied, including clinicopathologic features, robust PCA, CRCNet, CLAHE, PCA, and deep features. The datasets or images used ranged from 165 images to 464,105 images, with various sources such as patients, tumors, images, WSI (Whole Slide Images), and polyp frames. The reported best accuracies ranged from 69.00 % to 99.98 %, indicating the high possibility of DL-based approach in colorectal cancer classification.

A comparative review evaluation of the state-of-the-art in detecting colorectal cancer using DL approach has been carried out, and the results of that analysis are described. The analysis is grounded in the data presented in Table 15, which is available below.

A. Highest Accuracy (VGG16 CNN with 99.98 % Accuracy):

- The technique achieving the highest accuracy is based on VGG16 CNN, as reported by the authors in (Dabass et al., 2023).
- No specific feature has been extracted in this work.
- The reported accuracy for this technique is 99.98 %, indicating excellent performance in accurately detecting colorectal cancer.

Table 15

State-of-the-Art comparative review of DL-based techniques for colorectal cancer classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Bychkov et al., 2018)	VGG16	LSTM	420 Patients	69.00
(Wang et al., 2019)	×	CNN	58,152 Patients	92.00
(Echle et al., 2020)	Clinicopathologic Features	ShufNet	8,836 Tumors	96.00
(Sharma et al., 2020)	Robust PCA	VGG19	4,976 Images	95.75
(Zhou et al., 2020)	×	CRCNet	464,105 images	88.20
(Yamashita et al., 2021)	×	MSINet	343 Patients	93.00
(Sarwinda et al., 2021)	CLAHE	ResNet-50	165 Images	88.00
(Yu et al., 2021)	×	SSDL	13,111 WSI	93.00
(Damkhang et al., 2021)	VGG16	CNN	5000 Images	99.00
(Ben Hamida et al., 2021)	×	ResNet	(NCT-CRC-HE-100 K+CRC-5000)	99.98
(Wang, 2022)	DL	ResNet	NCT-CRC-HE-100 K	99.80
(Ho et al., 2022)	ResNet-101	Qritive Colon AI	GLAS	91.00
(Hasan et al., 2022)	PCA	DCNN	LC25000	99.80
(Sakr et al., 2022)	×	Lightweight CNN	LC25000/10,000 Images	99.50
(Kim et al., 2023)	×	ResNet-18	889 WSI	98.50
(Dabass et al., 2023)	×	HU-Net	HosC, LC-25000, GLAS,CRAG	99.98
(Bokhorst et al., 2023)	×	CNN	1054 Images	94.87*
(Palak et al., 2023)	×	VGG 16	7,286 Polyp frames	78.30
(Kumar et al., 2023)	×	CRCN-Net	1,11,555 Images	98.30
(Yengce-Tasdemir et al., 2023)	×	ConvNeXt	10,000 Images	95.00
(Murugesan et al., 2023)	×	YOLOv3-MSF	1000 Images	96.04
(Srivastava et al., 2023)	Deep Features	CJT-DEO-EDNN	LC25000	99.95

*Calculated from the Confusion matrix from the paper (Bokhorst et al., 2023).

- The high accuracy suggests that the use of VGG16 CNN is effective in accurately classifying colorectal cancer cases.

B. Lowest Accuracy (VGG 16 with 69.00 % Accuracy):

- The technique with the lowest accuracy is based on VGG 16, as mentioned by the authors in (Bychkov et al., 2018).
- There are no features extracted by the authors in this work.
- The reported accuracy for this technique is 69.00 %, which is relatively lower compared to other techniques in the table.

- The lower accuracy suggests that this particular VGG 16-based technique may face challenges in accurately classifying colorectal cancer cases.

C. Comparative Differences:

- **Accuracy Range:** The significant difference of 30.98 % between the highest accuracy (99.98 %) and the lowest accuracy (69.00 %) highlights a substantial difference in the performance of DL—driven approach for the detection of colorectal cancer. This wide range underscores the diversity of accuracies achieved by different techniques, suggesting that certain DL models or approaches outperform others in accurately detecting colorectal cancer. The difference in performance can be credited to factors such as variations in the datasets used, the specific DL algorithms employed, the preprocessing techniques applied, and the overall design and implementation of the models. It underscores the imperative for persistent research and fine-tuning of DL-based techniques to augment the accuracy and dependability of colorectal cancer detection.
- **Algorithm Variation:** The table showcases the utilization of many DL algorithms for the classification colorectal cancer, including VGG16, LSTM, CNN, ShufNet, Robust PCA, VGG19, CRCNet, MSI-Net, ResNet-50, SSDL, ResNet, ResNet-101, DCNN, Lightweight CNN, ResNet-18, Hybrid U-Net, CNN, VGG 16, CRCN-Net, ConvNeXt, YOLOv3-MSF, and CJT-DEO-EDNN. The use of different algorithms reflects the exploration of multiple DL models for colorectal cancer detection.
- **Feature Variation:** The table mentions different features used in the techniques, such as clinicopathologic, morphological, statistical, PCA, and deep features. These features capture various characteristics of colorectal cancer, including clinicopathologic factors, cell morphology, statistical patterns, and learned representations. The variation in features highlights the diversity of approaches in feature extraction for colorectal cancer detection.
- **Dataset Variation:** The datasets utilized in the different techniques for colorectal cancer detection exhibit significant variation in terms of size, ranging from 165 images to 464,105 images. These datasets consist of diverse sources such as patients, tumors, images, WSI (Whole Slide Images), and polyp frames. They encompass various specific datasets with unique names and characteristics. Factors such as data quality, diversity, and representation within the datasets can influence the efficacy and reliability of the classifiers. Therefore, the selection of database have a decisive role in evaluating the effectiveness of DL techniques for accurately detecting colorectal cancer. Researchers need to carefully consider the dataset characteristics and ensure they are representative and of high quality to obtain reliable and robust results.
- **Advancements over time:** The table presented includes studies conducted over various years, indicating the presence of ongoing research and advancements in DL-based techniques for the prediction of colorectal cancer. The inclusion of studies from different years suggests that the field is continuously evolving, and researchers are actively working on improving and refining DL models for more accurate detection of colorectal cancer. This ongoing research signifies the commitment to enhancing the performance and effectiveness of DL-based methods in the area of the diagnosis of colorectal cancer. It demonstrates the efforts of researchers to stay up-to-date with the latest developments in DL and apply It illuminates the call for an ongoing symphony of research endeavors, orchestrating the refinement of DL-based techniques, in order to elevate the artistry in the diagnosis of colorectal cancer.

5.2.5. DL for leukemia detection

Table 16 presents a comparative review of the state-of-the-art DL based methodologies for leukemia prediction. The table includes 20 studies conducted between 2018 and 2023, providing information on the authors and year of publication, features extraction methods, optimal methods for classification, dataset or number of data used, and

Table 16

State-of-the-Art comparative review of DL-based techniques for Leukemia classification.

References	Feature Extraction	Optimal method	Database (No. of data)	Highest Accuracy (%)
(Rehman et al., 2018)	CNN	CNN	ACLD /330 Images	97.78
(Ahmed et al., 2019)	Morphological	CNN	ALL-IDB, ASH	88.25
(Jha & Dutta, 2019)	Statistical, LDP	SCA-CNN	ALL-IDB2	98.70
(Nazari et al., 2020)	×	DL	AML, GE	96.67
(C. Zhang et al., 2020)	CNN-HOG	CNN + HOG + SVM	BCCD/ 5000 Images	96.00
(Loey et al., 2020)	×	AlexNet	2,820 Images	100.00
(Bibi et al., 2020)	×	DenseNet-121	ALL-IDB, ASH	99.91
(Genovese et al., 2021)	Var-PCA Net	DCNN	ALL-IDB2	96.84
(Jiang et al., 2021)	×	VIT-CNN	ISBI 2019	99.03
(Das & Meher, 2021)	×	Mobile netV2, Resnet18	ALLIDB1, ALLIDB2	99.39
(Rezayi et al., 2021)	CNN Features	VGG-16	12,528 Images	97.41
(Bukhari et al., 2022)		SE-CNN	ALL-IDB	98.30
(Abir et al., 2022)	Transfer Learning	InceptionV3	ISBI 2019	98.38
(Abhishek et al., 2023)	VGG16	VGG16	1250 Images	84.00
(Talaat & Gamel, 2023)	Alexnet	OCNN	C-NMC 2019	99.99
(Depto et al., 2023)	GAN	DenseNet121	C-NMC, ALLIDB-2	81.67
(Abd El-Ghany et al., 2023)	×	EfficientNet-B3	15,114 Images	98.31
(Manescu et al., 2023)	×	MILLI	ALLIDB1, ALLIDB2	99.00
(Nasir et al., 2023)	×	Transfer Learning	10, 000 Instances	97.30
(Sheet et al., 2023)	×	Mobilenet V2	ISBI 2019	96.58

the corresponding highest metrics (accuracy). Many DL algorithms including, CNN, SCA-CNN, DL, CNN + HOG + SVM, AlexNet, DenseNet-121, DCNN, VIT-CNN, MobileNetV2, ResNet18, VGG-16, InceptionV3, SVM + VGG16, OCNN, DenseNet121, EfficientNet-B3, and MILLI were utilized. The features employed varied, including morphological, statistical, LDP, deep features, and transfer learning. The datasets or images used ranged from 330 images to 15,114 images, with various sources such as ACLD, ALL-IDB, ASH, Gene Expression, AML-Related, BCCD, ISBI 2019, C-NMC, and ALLIDB-2. The reported best accuracies ranged from 81.67 % to 100.00 %, indicating the promising performance of DL utilized techniques in the detection of leukemia.

A thorough comparative analysis was undertaken to assess the recent developments in leukemia detection using DL- based methods. The findings of this analysis are summarized below, based on the data presented in Table 16.

A. Highest Accuracy (AlexNet):

- The technique achieving the highest accuracy is based on AlexNet, as reported in the work of (Loey et al., 2020).
- No features have been extracted in this work by the authors.
- The reported accuracy for this technique is 100.00 %, indicating excellent performance in accurately detecting leukemia.
- The high accuracy suggests that the use of AlexNet is effective in accurately classifying leukemia cases.

B. Lowest Accuracy (GAN with DenseNet121):

- The technique with the lowest accuracy is based on GAN (Generative Adversarial Network), as stated by the authors in (Depto et al., 2023).
- Features were not extracted by the authors in this work.
- The reported accuracy for this technique is 81.67 %, which is relatively lower compared to other techniques in the table.
- The lower accuracy suggests that this particular GAN-based technique may face challenges in accurately classifying leukemia cases.

C. Comparative Differences:

- **Accuracy Range:** The difference of 18.33 % between the highest accuracy (100.00 %) and the lowest accuracy (81.67 %) indicates a notable variation in performance among the DL-based techniques for leukemia detection. This range highlights the diversity of accuracies achieved by different techniques, suggesting that the effectiveness of DL models in leukemia detection can vary significantly depending on the specific approach and methodology employed. It emphasizes the significance of choosing proper DL techniques and optimizing them to accomplish higher accuracies in leukemia detection tasks. The range also signifies the potential for further advancements and improvements in DL-based techniques for more accurate and reliable leukemia detection.
- **Algorithm Variation:** The table showcases the utilization of various DL algorithms for leukemia detection, including CNN, SCA-CNN, DL, CNN + HOG, AlexNet, DenseNet-121, Trained Var-PCA Net, VIT-CNN, MobileNetV2, ResNet18, VGG-16, SE-CNN, Transfer Learning (InceptionV3, EfficientNet-B3), GAN, MILLIE, OCNN, and more. The use of different algorithms reflects the exploration of multiple DL models for leukemia detection.
- **Feature Variation:** The table mentions different features used in the techniques, such as morphological features, statistical features, LDP (Local Directional Pattern), DL features, CNN features, transfer learning, and more. These features capture various characteristics of leukemia, including cell morphology, statistical patterns, and learned representations. The variation in features highlights the diversity of approaches in feature extraction for leukemia detection.
- **Dataset Variation:** The datasets used in the techniques vary in terms of size, origin, and specific characteristics. Examples include ACLD, ALL-IDB, ALL-IDB2, GE, AML-Related, BCCD, C-NMC, C-NMC 2019, ISBI 2019, and 10,000 Instances. The variation in dataset characteristics can impact the model's performance due to differences in data quality, diversity, and representation. The preference of dataset provides a key role in evaluating the effectiveness of DL techniques for leukemia detection.
- **Advancements over time:** The table includes studies from 2018 to 2023, indicating ongoing research and advancements in DL-based techniques for leukemia detection. The inclusion of recent studies suggests that the field is evolving, with researchers continuously improving and refining DL models for accurate leukemia detection.

6. Discussion

In this segment, we embark on a journey through the vast landscape of cancer detection, navigating the intricacies of traditional ML models. A symphony of literature sources unfolds before us, meticulously curated for various cancer types, casting a spotlight on the distinctive dance between ML and DL models. Our voyage commences with the unveiling of the sheer volume of literature sources scrutinized for each

cancer type, meticulously categorized into the realms of ML and DL techniques. This unveiling provides a glimpse into the depth of research, a testament to the focused attention bestowed upon the domain of ML and DL. As we delve deeper, a comparative ballet takes center stage, gracefully choreographed to showcase the pinnacle performers among ML and DL classifiers for every category of cancer. This dance offers a profound harmony of the evolutionary strides and performance zeniths attained by diverse techniques in the expansive domain of cancer classification. The juxtaposition of ML and DL models unveils visions into their unique findings and limitations, painting a vivid portrait of their suitability for distinct cancer types. It's a narrative that beckons us to discern the nuances, to appreciate the intricacies of each approach. Our odyssey reaches its zenith with a contemplative discourse on the delta between the zenith and nadir of performance, expertly navigating the divergence among models employing ML and DL techniques for every cancer category. This chasm in performance serves as a beacon, underscoring the remarkable diversity within models and fervently signaling the need for continued exploration and enhancement in the realm of cancer detection. This narrative, a tapestry woven from literature analysis, performance evaluations, and nuanced comparisons, lays the groundwork for the future. It is a clarion call echoing through the corridors of research, propelling us towards a future where the accuracy and efficacy of cancer detection techniques, wielded by the artistry of ML and DL models, reach new summits.

6.1. Literature utilization ML/DL

In the intricate tapestry of Fig. 14, a masterful portrayal unfolds, offering a nuanced and comprehensive analysis of the literary landscape spanning various cancer realms. With a keen focus on the realms of ML and DL, the data orchestrates a dance of revelation, laying bare the distribution of scrutinized literature sources across diverse cancer types. As our gaze falls upon the canvas of pancreatic cancer, a narrative of 16 meticulously reviewed literature sources for ML techniques materializes. A nod to the deft deployment of ML algorithms, these findings carve a testament to the exploration and utilization of ML methodologies in the domain of pancreatic cancer classification and diagnosis. Yet, the plot thickens as 21 literature sources converge around DL techniques, a resounding declaration of the profound emphasis placed on the application of DL models and frameworks in the realm of pancreatic cancer research. Together, the amalgamated total of 37 literature sources forms a magnum opus, a testament to the exhaustive exploration of ML and DL approaches in unraveling the intricate challenges entwined with pancreatic cancer detection and classification. Shifting the spotlight to the realm of esophageal cancer, the analysis unfolds a narrative of 17

literature sources scrutinized for ML techniques. A striking tableau that speaks volumes, signifying a considerable congregation of studies dedicated to the exploration of ML-based approaches for the detection of esophageal cancer.

In a captivating parallel, our gaze extends to 21 literature sources, each meticulously examined for the nuances of DL methods in the realm of esophageal cancer. A crescendo of interest unfolds, echoing the growing allure and deployment of DL models in the intricate tapestry of esophageal cancer research. The amalgamated total of 38 literature sources stands as a testament to the profound exploration of both ML and DL methods, tirelessly seeking to elevate the precision and adeptness of esophageal cancer diagnosis. Transitioning to the realm of prostate cancer, our analysis unfurls a narrative spun from 18 scrutinized literature sources dedicated to ML techniques. This revelation paints a canvas adorned with the fruits of extensive research, delving into the realm of ML-based methodologies for the detection and characterization of prostate cancer. Mirroring this narrative, 20 literature sources emerge from the shadows, showcasing the blossoming embrace of DL models and algorithms in the domain of prostate cancer research. The confluence of 38 literature sources stands as a beacon, underscoring the indispensable role of both ML and DL approaches in the pursuit of advancing the detection and classification of prostate cancer. A similar symphony resonates in the context of colorectal cancer, where 18 literature sources lay bare the rich landscape of ML techniques. This tableau unfolds as a testament to the application of ML algorithms and strategies, etching the contours of colorectal cancer detection and diagnosis. The rhythm intensifies as 22 literature sources come into focus, capturing the crescendo of DL models ascending to meet the challenges entwined with colorectal cancer. The harmonious total of 40 literature sources reverberates, symbolizing an exhaustive exploration of both ML and DL techniques, working harmoniously to enhance the accuracy and efficiency of colorectal cancer detection and classification.

In the realm of leukemia, 18 literature sources weave a narrative of ML techniques, underscoring the use of ML algorithms and approaches in the intricate fabric of leukemia research. A harmonious counterpart emerges with 20 literature sources, mirroring the rise of DL models and frameworks in the pursuit of leukemia detection and classification. The cumulative total of 38 literature sources resonates as a comprehensive saga, emblematic of the intricate investigation into both ML and DL techniques in the captivating landscape of leukemia research. In summation, the analysis encapsulated in the presented figure serves as a gateway to understanding the ebb and flow of ML and DL techniques across diverse cancer realms. It not only unveils the ascendancy of DL models in recent times but also pays homage to the enduring significance of ML approaches. The collective resonance of 191 literature

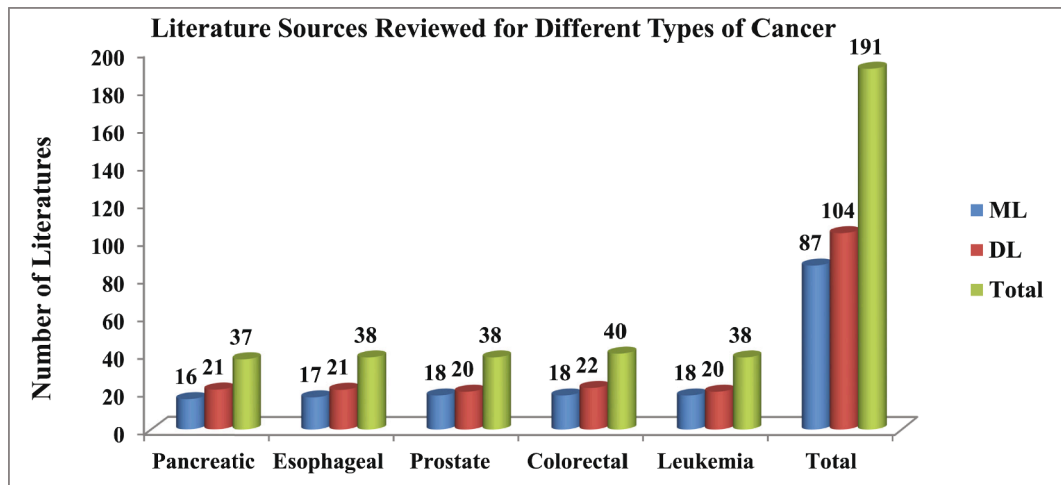


Fig. 14. Number of literature sources utilized for review in different types of cancer detection techniques.

sources echoes the vast expanse of research endeavors, bearing witness to the ceaseless efforts to refine and elevate the accuracy and effectiveness of cancer detection techniques.

6.2. Best performing models

Fig. 15 unfolds as a gallery showcasing the virtuosity of the best-performing ML models across various cancer types, each adorned with their respective accuracies – a testament to their prowess in the realm of the classification of cancers. In the field of pancreatic cancer classification, the Random Forest (RF) classifier emerges as the virtuoso, achieving an unparalleled accuracy of 99.2 %. This symphony of precision signifies the RF model's exceptional ability to discern pancreatic cancer cases with an extraordinary level of accuracy, setting a formidable benchmark in the field. For esophageal cancer, the stage belongs to the hybrid ensemble of the ELM and ASODTL-ECC, reaching a crescendo with an impressive accuracy of 99.7 %. This harmonious collaboration underscores the model's efficacy in pinpointing esophageal cancer cases with remarkable accuracy, a performance that resonates with a sense of excellence. In the realm of prostate cancer, the Logistic Regression (LR) model takes center stage, achieving a notable accuracy of 99.1 %. The LR model's eloquence lies in its ability to discern and classify prostate cancer cases with remarkable precision, weaving a narrative of proficiency in cancer detection. In the enigmatic landscape of colorectal cancer detection, a hybrid model shrouded in mystery attains a perfect accuracy of 100 %, standing as an exemplar of exceptional performance. This veiled virtuosity showcases the model's unprecedented ability to accurately identify colorectal cancer cases, leaving an indelible mark in the annals of cancer detection. The denouement arrives in the domain of leukemia detection, where the Support SVM model graces the stage, achieving a flawless accuracy of 100 %. This zenith of precision accentuates the SVM model's capability to categorically classify leukemia cases with unparalleled accuracy, a triumph in the realm of cancer detection. Collectively, these best-performing ML models emerge as luminaries, casting their brilliance across the diverse landscapes of cancer detection. They stand not only as benchmarks for comparison but also as beacons illuminating the path toward a deeper understanding of the effectiveness of ML algorithms in the intricate dance of cancer detection.

Fig. 16 unfolds as a captivating panorama, unveiling the epitome of DLbrilliance across diverse cancer types, each adorned with their corresponding accuracies—a testament to the extraordinary efficacy of DL classifiers in the detection of various cancers. In the realm of pancreatic cancer detection, the YCNN and MobileNet model take center stage, achieving an immaculate accuracy of 100 %. This symphony of perfection attests to the classifiers unmatched competence to discern and classify pancreatic cancer cases with unparalleled accuracy, etching a milestone in the field. For esophageal cancer, the DCNN graces the canvas, achieving an accuracy of 98.1 %. This ballet of precision underscores the DCNN model's capacity to accurately identify esophageal

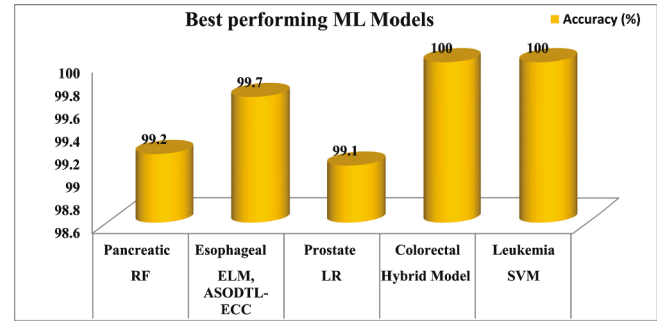


Fig. 15. Comparative analysis of best performing machine learning models in cancer detection.

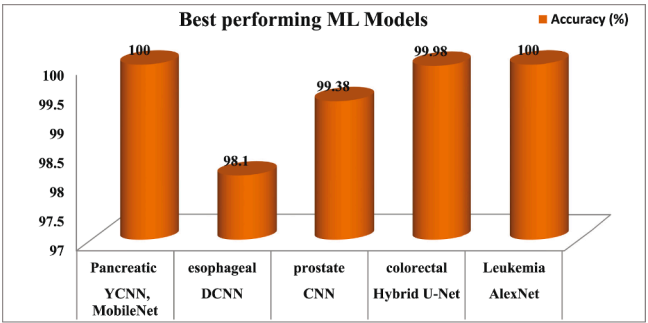


Fig. 16. Comparative analysis of best performing machine learning models in cancer detection.

cancer cases with a meticulous touch, a performance that resonates with a sense of profound excellence. In the realm of prostate cancer detection, the CNN model emerges as a luminary, achieving an accuracy of 99.38 %. This eloquent demonstration showcases the model's prowess in accurately classifying prostate cancer cases, unraveling a narrative of sophistication in cancer detection. In the enigmatic landscape of colorectal cancer detection, the Hybrid U-Net model unveils its brilliance, achieving an unparalleled accuracy of 99.98 %. This masterpiece of performance highlights the exceptional capabilities of this model in accurately identifying colorectal cancer cases, leaving an indelible mark in the symphony of cancer detection. The grand finale arrives in the domain of leukemia detection, where the AlexNet model takes the spotlight, achieving a perfect accuracy of 100 %. This zenith of precision accentuates the AlexNet model's ability to categorically classify leukemia cases with unwavering accuracy, a triumph in the realm of cancer detection. Collectively, these best-performing DL models stand as luminaries, illuminating the frontier of cancer detection with their brilliance. They not only represent the pinnacle of current achievements but also foreshadow the continuous evolution and effectiveness of DL algorithms in the intricate tapestry of identifying diverse types of cancer.

Fig. 17 unfolds as a harmonious canvas, offering a comparative ballet between the zeniths of ML and DL classifiers across diverse cancer types, their respective accuracies weaving a narrative of their efficacy in the nuanced domain of classification of cancers. In the realm of the detection of pancreatic cancer, the ML approach, adorned with the Random Forest model, achieves a noteworthy accuracy of 99.2 %. Contrasting this, the DL approach, orchestrated by the YCNN model, attains perfection with a flawless accuracy of 100 %. This duet of approaches demonstrates their highly effective nature, with the DL approach slightly edging past its ML counterpart in the realm of pancreatic cancer detection. For esophageal cancer, the ML approach, guided by the ELM model, achieves a resounding accuracy of 99.7 %. In a complementary dance, the DL approach, featuring the DCNN model, achieves an accuracy of 98.1 %. This pas de deux underscores the effectiveness of both ML and DL approaches in esophageal cancer detection, with the ML approach claiming a slight advantage in accuracy. For the classification of prostate cancer, the ML approach, steered by the Logistic Regression (LR) model, attains an accuracy of 99.1 %. Counterpointing this, the DL approach, curated with the CNN model, achieves a marginally higher accuracy of 99.38 %. This symphony suggests the efficacy of both methods in prostate cancer detection, with the DL approach exhibiting a nuanced advantage in accuracy.

In the intricate tapestry of colorectal cancer detection, the ML approach, harmonized with the Hybrid Model, achieves a perfect accuracy of 100 %. Its counterpart, the DL approach, donned with the Hybrid U-Net model, achieves an exceptional accuracy of 99.98 %. This duet resonates with exceptional performance, showcasing the highly effective nature of both ML and DL approaches in accurately classifying colorectal cancer cases. The grand finale unfolds in the realm of leukemia detection, where both the ML approach, led by the SVM model, and

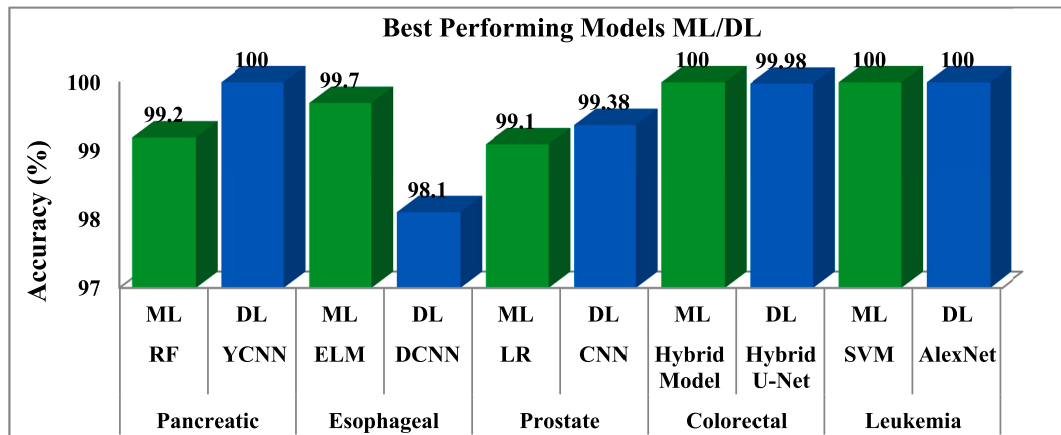


Fig. 17. Comparison of best performing ML and DL models for cancer classifications.

the DL approach, choreographed by the AlexNet model, achieve a perfect accuracy of 100 %. This crescendo exemplifies the equal effectiveness of both ML and DL approaches in detecting leukemia cases with unwavering precision. In summary, this comparative analysis is a symphony that underscores the harmonious effectiveness of both ML and DL approaches in the intricate dance of cancer detection. While nuances in accuracy may exist between the two approaches for specific cancer types, both have demonstrated their remarkable capability to accurately detect and classify various forms of cancer. The choice between ML and DL approaches may be guided by considerations such as data availability, computational resources, and the specific requirements of the application.

6.3. Worst ML/DL techniques

Fig. 18 paints a candid portrait, shedding light on the challenges faced by the worst-performing ML models across diverse cancer types, each accompanied by their respective accuracies—an acknowledgment of the nuances in their efficacy in the intricate area of cancer classifications. In the arena of pancreatic cancer detection, the SVM model takes the stage, achieving an accuracy of 81.19 %. This revelation, while indicative of some clinical value, stands in contrast to the zenith achieved by the best-performing models, signifying a relatively lower performance. Similarly, for esophageal cancer detection, the SVM model grapples with an accuracy of 77.1 %, portraying a scenario where accuracy falls below the peaks attained by the best-performing models. This echoes the challenges faced by the SVM model in capturing the intricacies of esophageal cancer. In the domain of prostate cancer detection, the SVM model contends with an accuracy of 70.93 %, trailing behind the prowess demonstrated by the best-performing models. This modest accuracy underscores the hurdles faced by the SVM model in the

intricate landscape of prostate cancer detection. The stage shifts to colorectal cancer detection, where the SVC model struggles with an accuracy of 65.83 %. This portrayal of lower accuracy emphasizes the challenges encountered by the SVC model in accurately classifying colorectal cancer cases compared to its more proficient counterparts. Finally, leukemia detection sees the Random Forest model facing the challenges with an accuracy of 93.45 %. While this accuracy may still hold clinical value, it acknowledges the lower performance compared to the zenith achieved by the best-performing models in leukemia detection. It's pivotal to note that the performance of these worst-performing ML models may possess clinical utility to some extent, but their lower accuracy underlines the imperative for continuous improvements and refinements. Further strides in ML models, feature selection techniques, and data preprocessing are essential to bolster their performance in detecting these specific types of cancers.

Fig. 19 emerges as a beacon, casting a spotlight on the luminaries among ML models across diverse cancer types, each adorned with their corresponding accuracies—a celebration of their high accuracy and effectiveness in the intricate dance of cancer classification. In the realm of pancreatic cancer detection, the RF model ascends to greatness, achieving a remarkable accuracy of 99.2 %. This stellar performance underscores the RF model's proficiency in accurately detecting pancreatic cancer, setting a formidable standard. For esophageal cancer detection, the ELM model with ASODTL-ECC takes center stage, achieving an impressive accuracy of 99.7 %. This symphony of precision showcases the ELM model's exceptional effectiveness in detecting esophageal cancer with a nuanced touch. In the domain of prostate cancer detection, the LR model asserts its dominance with an accuracy of 99.1 %. This eloquent demonstration highlights the LR model's robust performance in accurately detecting prostate cancer, weaving a narrative of excellence. Colorectal cancer detection witnesses the triumph of a Hybrid Model, achieving a perfect accuracy of 100 %. This masterpiece

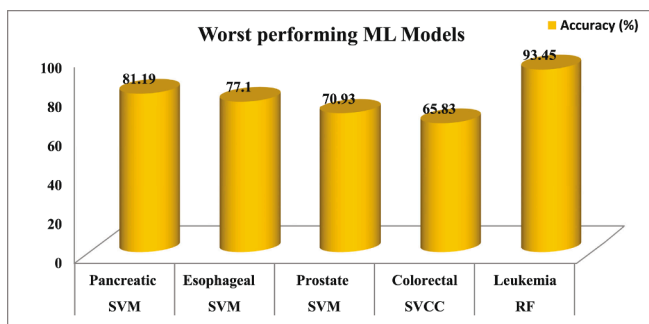


Fig. 18. Comparative analysis of worst performing machine learning models in cancer detection.

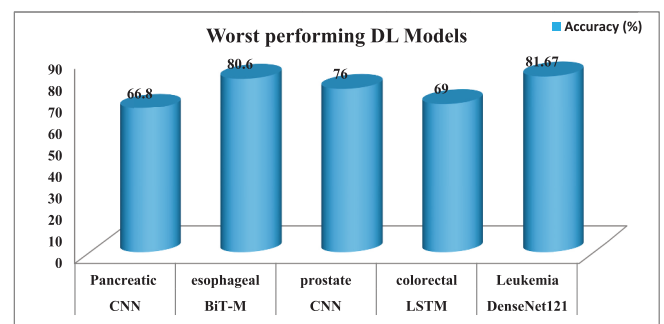


Fig. 19. Comparative analysis of worst performing deep learning models in cancer detection.

of accuracy exemplifies the Hybrid Model's exceptional ability to accurately detect colorectal cancer, leaving an indelible mark in the symphony of cancer detection. In the grand finale, leukemia detection sees the SVM model achieving a perfect accuracy of 100 %. This zenith of precision accentuates the SVM model's unparalleled capability to categorically classify leukemia cases with unwavering accuracy, a triumph in the realm of cancer detection. Collectively, these best-performing ML models stand as beacons of excellence, illuminating the path toward high accuracy and effectiveness in the intricate landscape of cancer detection. While acknowledging their achievements, it is paramount to consider various factors, including the dataset used, feature selection, and model optimization techniques, to ensure the robustness and generalizability of these models in real-world scenarios.

Fig. 20 unveils the intricate landscape of challenges faced by the worst-performing models for the classifications of various cancers, encompassing both classical ML and DL approaches. Each model is accompanied by its corresponding accuracy, providing insights into the complexities and limitations encountered in accurately classifying different categories of cancers. In the arena of pancreatic cancer detection, the SVM classifier, harnessed by the ML approach, grapples with an accuracy of 81.19 %. Contrasting this, the CNN model, steering the DL approach, faces a more formidable challenge with a lower accuracy of 66.8 %. This divergence in performance underscores the nuanced challenges between ML and DL in the context of pancreatic cancer detection. Esophageal cancer detection introduces the SVM model under the ML approach, achieving an accuracy of 77.1 %. In contrast, the BiT-M under the DL approach contends with a slightly lower accuracy of 80.6 %. This subtle interplay accentuates the intricacies and nuances present in the detection of esophageal cancer using distinct ML and DL approaches. Prostate cancer detection witnesses the SVM model, guided by the ML approach, achieving an accuracy of 70.93 %. In the DL realm, the CNN model steps into the spotlight, showcasing a marginal improvement with a slightly higher accuracy of 76 %. This delicate dance highlights the challenges faced by both ML and DL approaches in accurately discerning prostate cancer cases. The domain of colorectal cancer detection unfolds with the SVC model, navigating its challenges under the ML approach with an accuracy of 65.83 %. In the DL arena, the LSTM model grapples with a slightly higher accuracy of 69 %. Additionally, the RF model, treading the ML path, achieves a relatively higher accuracy of 93.45 %, while the DenseNet121 model, dwelling in the DL landscape, contends with an accuracy of 81.67 %. These variations underscore the multifaceted challenges in accurately classifying colorectal cancer cases, revealing nuances between ML and DL approaches. In essence, these worst-performing models serve as compass points, guiding us through the labyrinth of challenges and limitations in cancer detection. To overcome these hurdles, further investigation and

refinement are imperative. Factors such as feature selection, data quality, model optimization, and domain-specific considerations should be carefully considered to propel these models toward enhanced performance in the intricate realm of cancer detection applications.

6.4. ML vs DL analysis

Embark on a detailed exploration of the intricate tapestry woven by the comparative analysis between ML and DL methods for every cancer category in Fig. 21. The canvas unfolds, revealing the nuances and differences in performance throughout various classifiers. In the realm of pancreatic cancer, the ML approach paints a picture of contrasts. A stellar best accuracy of 99.2 % signifies the prowess of traditional ML models in detecting pancreatic cancer with precision. However, the shadows are cast with the worst accuracy of 81.19 %, revealing the struggles faced by some ML models in this intricate dance. The 18.01 % difference between the zenith and nadir echoes the significant variation in performance among ML models. On the DL stage, a triumphant best accuracy of 100 % showcases the dominance of DL models in pancreatic cancer detection. Yet, the darker hues emerge with the worst accuracy of 66.8 %, illustrating challenges faced by some DL models. The broader 33.2 % gap between the pinnacle and abyss emphasizes the notable variation in DL model performance, still surpassing their ML counterparts. Esophageal cancer's canvas is painted with contrasting strokes. The ML approach presents a majestic, best accuracy of 99.7 %, signaling strong performance. However, the darker undertones of the worst accuracy at 77.1 % hint at the struggles faced by certain ML models. The 22.6 % difference between the zenith and nadir unfolds a significant performance variation in ML models. On the DL canvas, a slightly diminished best accuracy of 98.1 % is still a testament to DL's prowess. Yet, the shadows deepen with a worst accuracy of 80.6 %, revealing hurdles faced by some DL models. The 17.5 % difference between the pinnacle and abyss suggests a moderate variation in DL model performance for esophageal cancer detection. Prostate cancer takes center stage with a theatrical interplay between ML and DL. The ML approach boasts a stellar best accuracy of 99.1 %, showcasing its capabilities. However, the shadows loom with a worst accuracy of 70.93 %, underlining the challenges encountered by certain ML models. The grand 28.17 % difference between the zenith and nadir unfolds a significant performance variation in ML models. In the DL realm, a higher best accuracy of 99.38 % steals the spotlight, surpassing the best ML model. Yet, the shadows persist with a worst accuracy of 76 %, unveiling the hurdles faced by some DL models. The 23.38 % difference between the pinnacle and abyss signifies a notable variation in DL model performance for prostate cancer detection. Colorectal cancer's narrative unfolds with a dramatic contrast. The ML approach paints a picture of

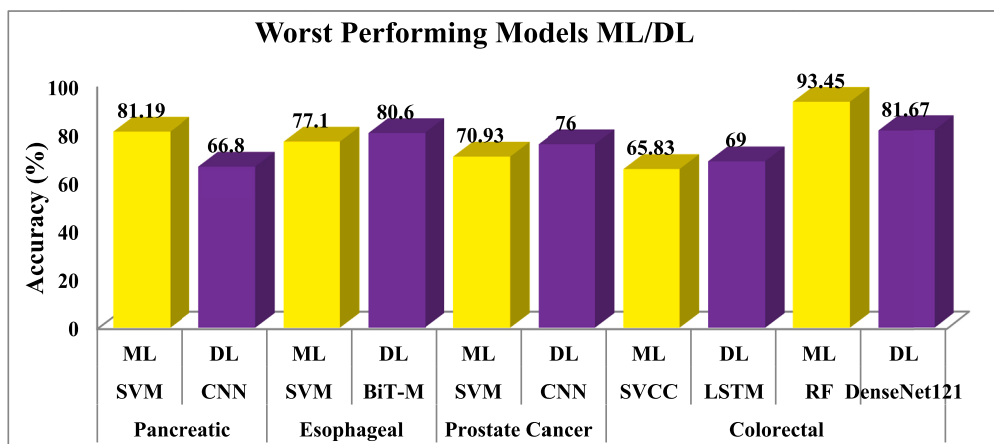


Fig. 20. Comparison of worst performing ml and dl models for cancer classification.

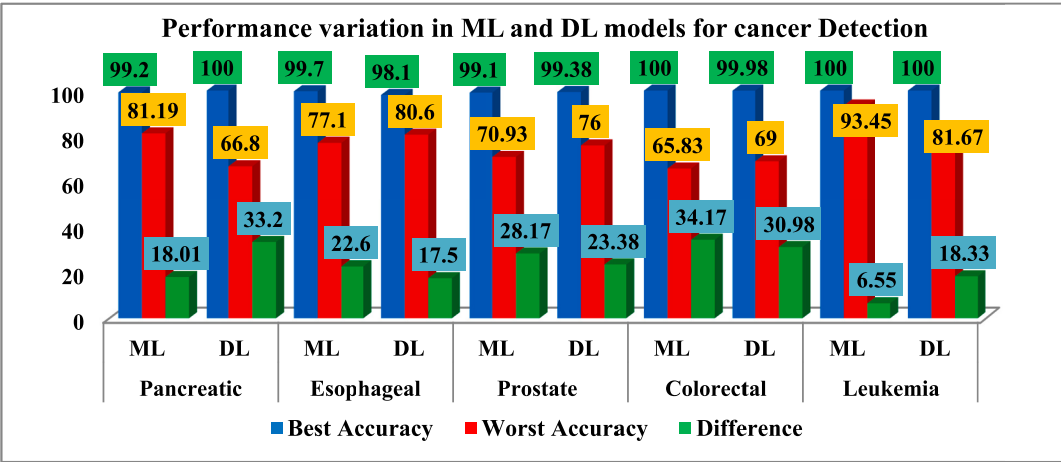


Fig. 21. Comparative evaluation of best and worst classifiers for each cancer category.

excellence with a perfect best accuracy of 100 %, a testament to traditional ML model capabilities. However, shadows creep in with the worst accuracy of 65.83 %, indicating challenges faced by certain ML models. The substantial 34.17 % difference between the zenith and nadir reveals a significant variation in ML model performance. On the DL stage, a superior best accuracy of 99.98 % steals the limelight. Yet, shadows persist with a worst accuracy of 69 %, unveiling the hurdles faced by some DL models. The 30.98 % difference between the pinnacle and abyss underscores a notable variation in DL model performance for colorectal cancer detection. In the realm of leukemia detection, both ML and DL approaches share a harmonious crescendo with a perfect best accuracy of 100 %. However, the ML approach grapples with a higher worst accuracy of 93.45 %, hinting at challenges faced by certain ML models. The modest 6.55 % difference between the zenith and nadir suggests a relatively small variation in performance among ML models. The DL approach mirrors the harmony with a similar best accuracy of 100 %, yet the shadows deepen with a lower worst accuracy of 81.67 %. The 18.33 % difference between the pinnacle and abyss unveils a notable variation in DL model performance for leukemia detection. In summary, this detailed analysis unfolds a narrative where DL models generally outshine ML models in pancreatic, esophageal, and colorectal cancer detection, attaining higher accuracies in the best-performing classifiers. However, both ML and DL models showcase robust performance in leukemia detection. The variations in performance among the best and poor performing classifiers underscore the importance of meticulous model selection and optimization for achieving reliable and accurate cancer detection across diverse cancer types. The canvas of cancer detection is complex and nuanced, revealing visions into the intricate interplay of ML approaches.

In the enchanting tableau of Table 17, a narrative unfolds, woven with threads of literature sources, model performances, and the captivating dance between ML and DL approaches. Like a celestial map guiding us through the cosmos of cancer detection research, it beckons

us to explore its secrets.

The disparities in performance accuracies among the models are intricately linked to a multitude of influential factors within the classification paradigm. Foremost among these factors is the magnitude of the dataset employed for both training and testing, wielding a profound impact on the model's performance. While larger datasets can potentially enhance generalization, they concurrently present computational challenges. Furthermore, the choice of methodologies for feature extraction assumes paramount significance. The adoption of specific techniques such as wavelet, Fourier, statistical, morphological, shape, texture, or color extraction critically influences the model's acuity in discerning pertinent patterns. The cardinality of features integrated into the classification process constitutes another pivotal facet. The judicious selection of an optimal feature set emerges as a key determinant in refining model accuracy. The classifier itself, whether grounded in neural network architectures characteristic of DL or conventional algorithms like SVMs, decision trees, or random forests intrinsic to ML, introduces an additional stratum of variability. Fine-tuning the parameters inherent to these classifiers further compounds the intricate orchestration of model performance. The presence of imbalanced data sets, particularly prevalent in the domain of cancer classification, wherein certain cancer types may exhibit lower prevalence, begets potential disparities in performance. Consequently, rectifying this imbalance becomes an imperative consideration. Lastly, a caveat is cast upon the reliance solely on accuracy as a singular metric for evaluation. Metrics encompassing recall, sensitivity, and the F1 score become indispensable in offering nuanced insights into the model's capacity to discern instances of interest, especially in medical applications wherein misclassifications hold consequential ramifications. Thus, the holistic contemplation of these multifaceted factors proves indispensable for a nuanced and comprehensive evaluation of cancer detection models.

Table 17
Overall Comparative analysis of ML and DL classifiers for cancer prediction: performance, model comparison, and literature review.

Types of Cancer	Approach	Best Accuracy (%)	Best Model	Worst Accuracy (%)	Worst Model	Difference (%)	No. of Literatures	Total Literatures
Pancreatic	ML	99.2	RF	81.19	SVM	18.01	16	37
	DL	100	YCNN, MobileNet	66.8	CNN	33.2	21	
Esophageal	ML	99.7	ELM, ASODTL-ECC	77.1	SVM	22.6	17	38
	DL	98.1	DCNN	80.6	BiT-M	17.5	21	
Prostate	ML	99.1	LR	70.93	SVM	28.17	18	38
	DL	99.38	CNN	76	CNN	23.38	20	
Colorectal	ML	100	Hybrid Model	65.83	SVC	34.17	18	40
	DL	99.98	Hybrid U-Net	69	LSTM	30.98	22	
Leukemia	ML	100	SVM	93.45	RF	6.55	18	38
	DL	100	AlexNet	81.67	DenseNet121	18.33	20	

6.5. Key findings and challenge

6.5.1. Overall Findings

Performance Variability:

- The discernible dissimilarity in accuracy between the most proficient and least effective classifiers varies markedly across each cancer type.
- For example, in the detection of pancreatic cancer, the proficient ML model RF attained 99.2 % of accuracy, while the worst ML model (SVM) got only 81.19 % accuracy, causing a deviation of 18.01 %.
- Similarly, in the classification of esophageal cancer, the difference in accuracy between the best ML model (ELM, ASODTL-ECC) and the worst ML model (SVM) was 22.6 %.

Superiority of Models:

- DL models consistently outperformed ML models in terms of accuracy across most cancer types.
- In pancreatic cancer detection, the DL model (YCNN, MobileNet) produced 100 % accuracy of classification, superior to the best ML model.
- Similarly, in the classification of prostate cancer, the DL model (CNN) produced 99.38 % accuracy, while the best ML model (LR) achieved an accuracy of 99.1 %.

Dataset Size and Diversity:

- The article used doesnot provide specific information about the dataset characteristics, such as size and diversity.
- Nevertheless, it is crucial to acknowledge that disparities in data quality, diversity, and representation have the potential to influence the efficacy of both ML and DL classifiers.
- Larger and more diverse datasets can contribute to better model operation and simplification.

Specificity to Cancer Types:

- Different models and approaches were used for different cancer types, indicating the need for specific models tailored to the characteristics of each cancer type.
- For example, the Hybrid Model showed superior performance in colorectal cancer detection, achieving 100 % accuracy in the ML approach.
- The choice of models and approaches may be influenced by the specific challenges and features correlated with each category of cancer.

Advancements over Time:

- The inclusion of studies from different years in this study suggests ongoing research and advancements in ML and DL-driven approach for the identification of cancers.
- This indicates that researchers are continuously improving and refining models to achieve more accurate detection and diagnosis.

Adequate Literature:

- The investigation reveals that a substantial quantity of articles underwent review for each specific cancer category and approach.
- The cumulative count of the articles scrutinized in this paper stands at 191, demonstrating a comprehensive review conducted to gather relevant information on ML and DL models for cancer detection.

6.5.2. Challenges

- **Scarcity of number of articles:** Although the study reviewed a considerable number of literature sources (ranging from 37 to 40), the total number of articles for each category of cancer is completely less. This limited pool of literature sources may pose challenges in terms of obtaining a comprehensive understanding of the field and potentially restrict the diversity of approaches and models considered.
- **Variability in model performance:** This article demonstrates a significant difference between the highest and lowest metrics values for each cancer type, with differences ranging from 18.01 % to 34.17 %. This indicates a notable variability in model performance. Understanding the reasons behind such variations and addressing the factors that contribute to lower accuracy models can be a challenge in this field.
- **Lack of standardized evaluation metrics:** This study presents accuracy percentages as the primary evaluation metric for model performance. While accuracy is an essential metric, it may not provide a complete picture of a model's capabilities, especially when overfitting might be a concern. The absence of standardized evaluation metrics, such as precision, recall, F1-score, or area under the curve (AUC), makes it challenging to comprehensively verify and evaluate the classifiers, particularly regarding their generalizability to real-world settings. The absence of standardized evaluation metrics, such as precision, recall, F1-score, or area under the curve (AUC), makes it challenging to comprehensively verify and evaluate the classifiers.
- **Dataset characteristics and representativeness:** This paper does not provide detailed information about the datasets used for training and evaluation. The lack of information regarding the size, diversity, quality, and representativeness of the datasets can hinder the assessment of the models' robustness and generalization capabilities. Without understanding the dataset characteristics, it becomes challenging to draw definitive conclusions about the models' performance.
- **Potential bias in literature selection:** The study's findings are based on the literature sources reviewed. The selection of literature sources might introduce bias based on the inclusion criteria and search methodology. The potential omission of relevant studies or the inclusion of studies biased towards certain approaches or models could impact the overall findings and conclusions.
- **Limited representation of cancer types:** The study focuses on five specific cancer types (Pancreatic, Esophageal, Prostate, Colorectal, and Leukemia). While these cancers are significant and have a high impact on public health, the study may not encompass the full spectrum of cancer types. The limited representation of cancer types restricts the generalizability of the findings to other cancer types.
- **Lack of information on model interpretability:** This paper primarily focuses on model accuracy and does not provide insights into model interpretability or the ability to explain the underlying decisions. The lack of information on model interpretability limits our understanding of how and why the models make certain predictions, which can be vital for gaining faith and approval in clinical settings.

Addressing these challenges will require further research and exploration to overcome the limitations and improve the reliability, generalizability, and interpretability of ML and DL models for cancer detection.

6.6. Proposed methodology

After a meticulous review of around 190 research articles and 16 review articles, we have devised a comprehensive methodology for the classification of diverse cancer types utilizing the most proficient classifiers from both ML and DL. Illustrated in Fig. 22, our methodology is a

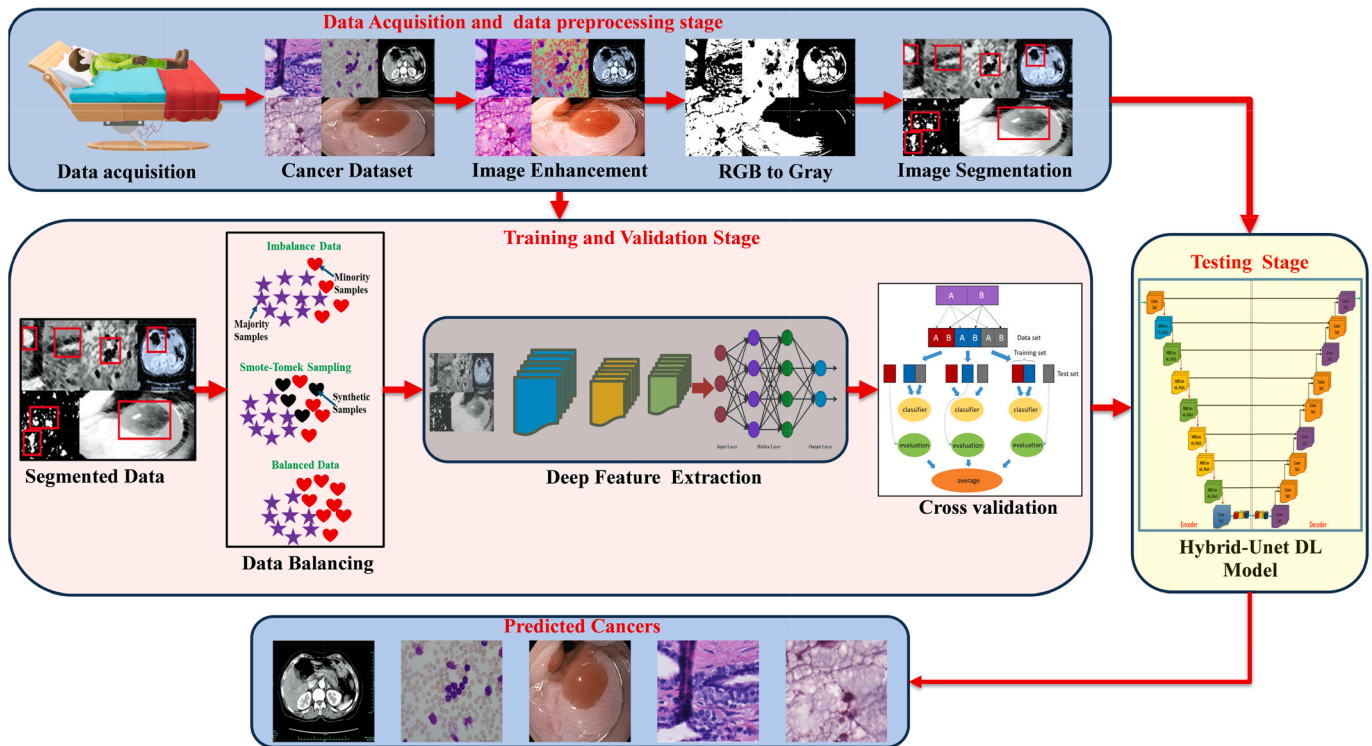


Fig. 22. Proposed methodology for classification of various cancer categories based on the review outcome.

culmination of insights gleaned from existing literature and our inventive approaches, segmented into three integral stages: data acquisition and preprocessing, training and validation, and testing and prediction. In the initial stage of data acquisition and preprocessing, cancer data is sourced from reputable entities such as hospitals or research centers. Subsequently, we propose three preprocessing techniques: image enhancement to refine image quality, RGB to gray conversion for improved generalization, and data segmentation, especially crucial for image datasets to isolate specific cancer regions. Moving on to the training and validation stage, segmented images from the preprocessing phase serve as input data. To address potential data imbalances, we introduce the SMOTE-Tomek approach, a hybrid of oversampling and undersampling techniques. Additionally, deep feature extraction techniques are employed to capture pertinent features for subsequent stages. The final testing and prediction stage involve a U-Net-based hybrid DL model, designed for simultaneous segmentation and classification tasks. To optimize training, we incorporate k-fold cross-validation, ensuring effective model training and validation. The trained model is then rigorously tested on an independent dataset to predict and classify various cancer types. This proposed methodology aims to guide scholars and researchers in choosing an optimal approach for the classification of different cancer categories using ML/DL methods. By integrating innovative preprocessing steps, data balancing strategies, and feature extraction techniques, along with a specialized hybrid DL model, our goal is to enhance the accuracy and effectiveness of cancer classification systems.

7. Conclusion

This review article provided a broad review and state-of-the-art analysis for the classification of various categories of cancers utilizing AI-driven methods (ML and DL). By examining recently published literature from 2018 to 2023, the study focuses on five types of cancers with high mortality rates: pancreatic, esophageal, prostate, colorectal, and leukemia. The analysis encompasses 191 literature sources, with 87 papers utilizing traditional ML models and 104 papers employing DL

techniques for cancer detection. Various parameters, including different literatures, features, Optimal method, utilized databases or number images or number of data, and the highest accuracy metrics of each study, are thoroughly examined to proffer insightful perspectives into the research topography. Benchmarked and open access databases for the five categories of cancer are described and provided source link for assisting access to these resources. The study also presents the most commonly utilized features for cancer detection, providing brief descriptions of each feature. Furthermore, a concise analysis of commonly used preprocessing techniques, along with a generalized formula, enhances understanding of the preprocessing stage. Based on the review conducted, we have noted that both types of models attained maximum accuracies of 100 %, while the lowest accuracy observed was 66.8 % utilizing DL models. The difference of accuracy between highest and lowest using ML model was 34.17 % and using DL Model it was 33.2 %. This huge difference in the classification accuracy shows that there is scope of improvement of more than 30 % in both types of approaches for cancer detection techniques. The substantial difference in accuracy, with a gap of 34.17 % for ML and 33.2 % for DL, underscores the significance of selecting the appropriate approach, classifier, dataset, and preprocessing techniques to enhance detection outcomes. These findings underscore the significance of fine-tuning multiple factors in cancer detection models to attain elevated accuracy and mitigate the likelihood of misdiagnosis. In its entirety, this review article functions as an invaluable resource for researchers, medical practitioners, and stakeholders in the field of cancer detection. It feeds a thorough understanding of the existing state-of-the-art techniques, their strengths, and areas for improvement. The understandings gotten from these findings can potentially lead to advancements in cancer diagnosis, ultimately benefiting patients by enabling early detection, personalized treatment, and improved overall survival rates.

In future research, we plan to integrate explainable AI into cancer detection, enhancing transparency. Clinical practice data will be incorporated for improved overall performance and acceptance. This augmentation will be complemented by the inclusion of pertinent clinical practice data, seeking to enhance the overall robustness and

acceptability of the review performance. The incorporation of explainable AI not only adds a layer of transparency to the decision-making processes of the models but also aligns with the imperative for interpretable outcomes in critical domains such as medical diagnosis.

CRedit authorship contribution statement

Hari Mohan Rai: Conceptualization, Methodology, Writing – original draft, Writing – review & editing, Visualization. **Joon Yoo:** Methodology, Writing – review & editing, Supervision. **Abdul Razaque:** Writing – review & editing, Visualization, Validation.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Hari Mohan Rai reports administrative support and writing assistance were provided by Gachon University.

Data availability

No data was used for the research described in the article.

Acknowledgement

This work was supported by the National Research Foundation of Korea (NRF) Grant funded by the Korea government (MSIT) (NRF-2021R1F1A1063640).

Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

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