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ARTIFICIAL INTELLIGENCE IN TUMOR TARGETING

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Abstract: Tumors are common, dangerous, and sometimes life-threatening. Artificial intelligence (AI), also referred as machine intelligence, is widely utilized in medical field to accelerate medical advancements. The explosive rise of artificial intelligence (AI) has created significant prospects for improving the accuracy and efficiency of tumor diagnosis and therapy. Malignant tumors are the primary focus of medical study, as well as clinical diagnosis and therapy. Tumors are prevalent, harmful, and can be life-threatening. One of the primary challenges in cancer nanomedicine is the low transport efficiency of nanoparticles (NPs) to tumors. Novel techniques in artificial intelligence (AI) and machine learning provide new tools for addressing this issue.AI has the potential to improve tumor image interpretation in a variety of ways, including more precise tumor volume delineation, more accurate tumor genotyping, and better clinical outcome prediction. AI-assisted brain surgery can cure brain cancers effectively and safely. Artificial intelligence has the power to increase diagnostic accuracy, accelerate therapeutic decision-making, and personalize treatment strategies. AI applications in oncology promise potential improvements in patient outcomes as the technology evolves.

Index Terms - Artificial intelligence, machine learning, Nano particles, Genotyping, personalized treatment

I. INTRODUCTION

Tumours are the abnormal mass of tissues that grows in the form of lumps in uncontrollable manner at anywhere in the body. According to the recent stats i.e. 2022-2023 by WHO there are 300-350 million people are suffering from different types of tumors all over the world, in that 53-55 million people are suffering from cancerous tumors and 250-300 million people are suffering from non-cancerous tumors. so, tumors are one of the major health issues. To cure tumors, we use different treatment methods like Chemotherapy, Radiation therapy, Targeted therapy, Immune therapy. Many novel drug inventions are invented to cure tumors in that one of the major is through sending nanoparticles to the site of tumors but low delivery efficiency of nano particles of the tumor is a critical task. AI is one of the trend set in now-a-days. At the Dartmouth Summer Symposium in 1956, the phrase "artificial intelligence (AI)" was first used to refer to the earlier concepts of "thinking machines." AI is the ability of a machine to learn on its own, finding patterns and connections in large amounts of sample data to make effective decisions in novel situations. AI has the potential to fundamentally alter the medical sector in a number of areas, including

helping physicians diagnose patients to reduce misdiagnosis and missed diagnosis; increasing diagnostic efficiency to alleviate the imbalance between the supply and demand of medical resources; offering early disease risk warning and health consultation services; supporting drug research and development while boosting pharmaceutical productivity; and improving surgical robots and operational accuracy.The application of AI in healthcare is expanding quickly.[1]By 2026, the global healthcare AI market is projected to reach $150 billion. The rising digitization of healthcare data. AI's enhanced capacity to evaluate this data, and the potential advantages of AI in healthcare, including early disease identification, better diagnosis, treatment suggestions, and personalized medicine. The rising digitization of healthcare data, AI's enhanced capacity to evaluate this data, and the potential advantages of AI in healthcare, including early disease identification, better diagnosis, treatment suggestions, and personalized medicineare driving this expansion.AI is becoming more and more crucial to the development of small-molecule drugs.Research has demonstrated that AI-powered image-based diagnostic systems frequently outperform physicians. AI can identify patterns and structures more precisely, which results in more precise diagnoses.AI systems will advance over time based on feedback, expertise, and real-world situations. [2](AI) techniques can uncover practical therapeutic approaches and offer deeper insights into tumor polyclonality. Using ligand-receptor interaction analysis, clonal trajectory reconstruction, network and pathway modeling.[20]AI, such as data privacy protection and the interpretability of algorithms, which require further research and resolution.[17]

1. AI for Tumor detection and segmentation

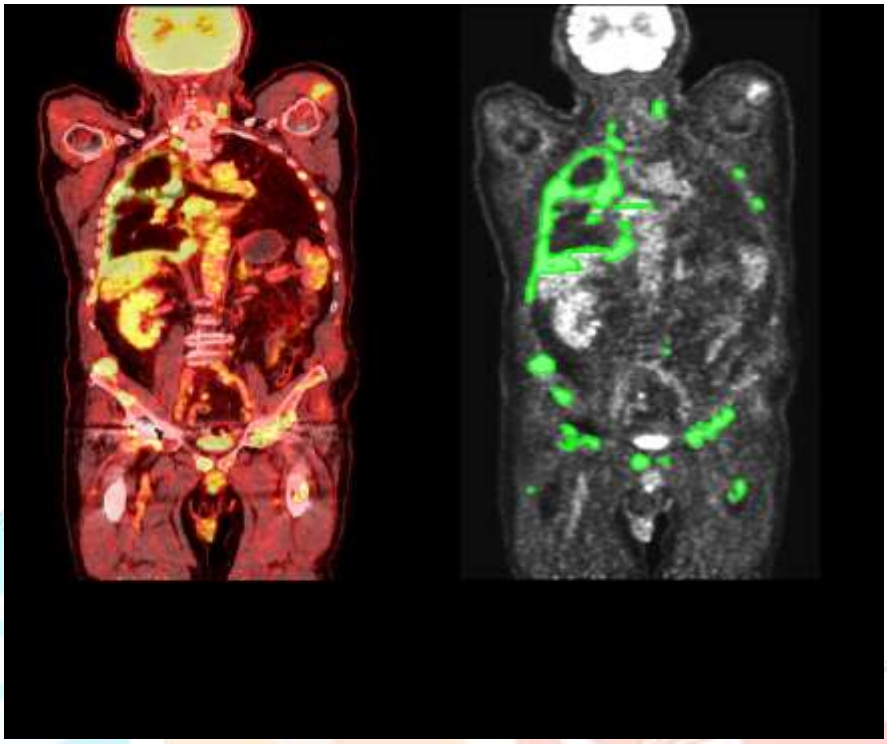
Artificial intelligence, especially deep learning (DL), has shown great promise in the identification of foci, prognosis prediction, microenvironment characterisation, metastasis detection, and other pathological investigations for tumor diagnosis in recent years. Numerous tumor types, including colorectal, gastric, nasopharyngeal, and breast cancers, have been treated with pathological AI.[1]

1.1 Whole slide imaging [WSI]

Whole slide imaging (WSI), as AI solutions help train next-generation pathologists by offering on-demand, standardized, and interactive digital slides that can be shared among numerous users anytime and anywhere. WSI systems featuring automation, high speed, and high resolution have demonstrated a significant impact on medical quality assurance (QA), particularly when supported by AI, which readily provides digital slides to pathologists via laboratory information systems or intranets for various QA tasks, such as remote consultation, measuring inter- and intra-observer differences, competency testing, and slide archiving.They developed two DL algorithms based on WSI to predict the survival rate of patients with hepatocellular carcinoma who underwent surgical excision, with both models outperforming the traditional method based on comprehensive scores of all survival-related baseline variables, and they further validated the models' prognostic value in The Cancer Genome Atlas (TCGA) dataset.[1]

1.2 PET/ICT

Neoadjuvant chemotherapy (NAC) response can be predicted by AI-enhanced PET radiomics.Additionally, AI technologies used in PET radiomics improve the identification and description of distant metastases and lymph nodes, increasing the precision of breast cancer patients' staging.[1]When combined with ML, FDG PET/CT radiomics may help distinguish between diffuse large B-cell lymphoma (DLBCL), HL, and sarcoidosis.[15]



1.3 Detection of eyelid tumor detection system:

This study initially created an ETDS using the Faster-RCNN, an object detection network based on region proposal algorithms31, to automatically discover and clip eyelid malignancies from photographic pictures because one photographic image may display one or more eyelid tumors of various types. In order to properly train the ensuing deep learning-based classification networks, this process can also eliminate the background noise surrounding tumors in photographic images. A tight bounding box was used to identify each eyelid tumor in a picture in order to train the Faster-RCNN model. There is only one eyelid tumor in each cropped image.[3]

1.4 Image diagnosis of bone tumors

In musculoskeletal oncology, radiographic distinction between infection and cancer is infamously challenging. Wang et al. trained an ensemble of convolutional and Transformer models on 1,992 radiographs and paired clinical features in a multicenter study. Excellent external-set performance (accuracy = 0.895) clearly outperformed junior readers while matching senior radiologists. The same team demonstrated how maps of saliency represent localized periosteal reaction patterns and cortical damage, offering explainability that is essential for tumor boards to accept. These multimodal networks are currently being retrained on dual-energy CT and low-field MRI, opening the door to completely automated AJCC or Enneking staging dashboards.[4]

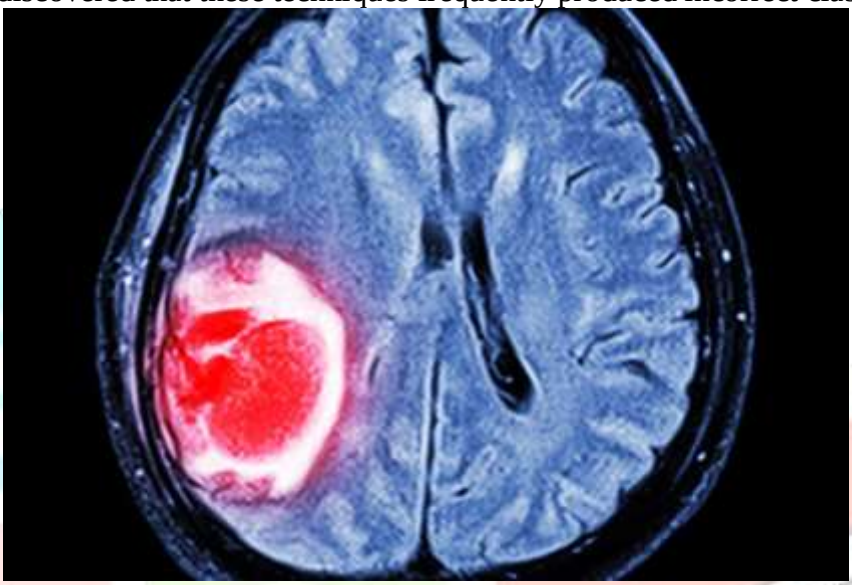
1.5 Diagnosing Mediastinal Malignant Tumors

Prior to the invention of the first CT scanner in 1970, chest radiography was primarily used to diagnose mediastinal cancers, with a 30% qualitative diagnostic rate. For patients with thymic epithelial tumors, Chowdhary et al. created an AI-based prognostic model that had an AUC of 0.90 and an overall accuracy of 84.2% and 87.0% in the training and validation cohorts, respectively. There is a lot of room for improvement in advanced imaging technologies like contrast-enhanced ultrasound and multi-physical coupled imaging, which are constantly being investigated and updated. These techniques would be further refined by combining them with sophisticated machine learning. The various clinical behaviours of mediastinal tumors, such as their primary and metastatic nature, complicated mediastinal structural placements, and occult onset, have long made diagnostic imaging of these tumors difficult.These new AI-

powered tools are able to collect tissue features and precisely detect minor traits like lymph node metastases and microvascular invasion. A precise diagnosis makes it simple to create a customized treatment plan.[5]

1.6 Brain Tumor Imaging

In the upcoming years, the market for brain tumor diagnostics is anticipated to expand quickly. The market is projected to grow from its 2021 valuation of $844.63 million to $2476.14 million by 2028. brain regions that can offer vital information for diagnosis and therapy. Lung cancer, breast cancer, brain tumors, and other cancers have been successfully diagnosed by AI-based imaging algorithms such as the CXR-vision model, LIDC IDRI model, LUNA16 model, and CT-based volumetric analysis. The location of a brain tumor is predicted using a deep wavelet autoencoder (DWAE) model that analyses multimodal data, including PET scans, perfusion MRI pictures, and MRI images.Deep learning-based brain tumor segmentation is a widely used technique due to its automation and state-of-the-art outcomes. For instance, the latent-dynamic condition random field (LDCRF) and deep capsule network (CapsNet) can be used to automatically segment brain tumors. On the other hand, a research of deep learning-based techniques for tiny tumor detection discovered that these techniques frequently produced incorrect classifications.[2]



2.AI in Brain Tumors

A brain tumor is a mass of tissue that is formed by an accumulation of abnormal brain cells. Most brain tumors are primary tumors that originate in the brain, and they are mainly benign without aggression to surrounding tissues.[19]Deep learning models and medical imaging are crucial for the early detection and diagnosis of brain tumors, enabling prompt treatment and enhancing patient outcomes.[14]Automatic diagnosis benefits from the useof AI in medical imaging, which depends on image interpretation. Diagnostic radiology is becoming a more objective discipline with the use of AI. [16]

2.1 Radiomics in brain tumor diagnosis

Radiomics gives vital information on tumour responses to therapy by introducing artificial intelligence (AI) into the glioblastoma multiforme (GBM) tumor assessment utilizing image data. Radiomics uses sophisticated image analysis technologies, including as diffusion and perfusion imaging, to deliver precise diagnoses and treatments for GBM. Radiomics based on deep learning requires larger datasets to produce better results due to the high correlation between extracted features and input data. However, the dataset's limited availability restricts radiomic use in a variety of research fields. On the contrary, transfer learning is a technique that eliminates this constraint. Transfer learning uses pre-trained neural networks to train interrelated things. For example, a neural network trained on imaging data to segment gliomas can be applied to the segmentation of brain metastases. In one study, researchers established a pattern of 11 radiographic markers that predicts both survival and classification in patients with newly diagnosed glioblastoma. The radiomic signature showed better performance than established radiological and clinical risk models. Radiomics is expanding rapidly. Radiomics will play an essential role in precision diagnostics in oncology in the future as clinical data grows and machine learning approaches progress. To increase radiomic acceptance, emphasis on reproducibility and interpretability is important. According to a study, radiomics can increase the accuracy of cancer diagnosis up to 20%. [2]

Most of the studies published in this field on the use of ML for the evaluation of radiomic features in p-CNS focused mainly on tumor characterization, especially those of the PF.[18]

2.2 Radiogenomics

Radiogenomics ('imaging genomics') is a fastly emerging area that investigates the association between a disease's genomic characteristics and imaging biomarkers. The heterogeneity of brain cancers limits radiogenomics' clinical use. This constraint can be addressed by completing entire tumour analysis using radiogenomics. In response to current chemotherapy/immunotherapy and radiation therapy, radiomics and radiogenomics offer promise in terms of accurate diagnosis, prognosis prediction, and tumor response evaluation.[2]Radiogenomics is the application of existing MR imaging features to the molecular properties of brain tumors in order to more accurately diagnose and characterize diseases. Precision medicine, individualized treatment planning, and imaging biomarkers at various patient phases are all made possible by the promising fields of radiogenomics and radiomics in cancer research and treatment.[6]

3.AI in Cancerous Tumors

Cancerous tumors recent developments in nanotechnology have made it possible to create drug formulations based on nanoparticles (NPs) that have better qualities than conventional small molecule chemotherapy, such as high drug loading, precise targeting and delivery, and the capacity to control the release of the anticancer medication in a sustained or controlled manner, but Nano particles were shown to have a poor tumor delivery efficiency. Physiologically based pharmacokinetic (PBPK) models were created to mimic the biodistribution of various NPs in order to address the earlier problem. In recent years the development of advanced data analysis algorithms, various machine learning (ML), and artificial intelligence (AI) techniques has made it possible to forecast the toxicity of chemicals or nanoparticles as well as their absorption, distribution, metabolism, and excretion (ADME) characteristics.The relation between the physicochemical characteristics and the tumor delivery effectiveness of NP is determined by the more advanced ML and DNN computational techniques.[7]

3.1 Model development

In this study, nine modeling algorithms were used. These algorithms fall into four classes: neural networks, support vector machines (SVMs), ensemble models, and traditional models. The two traditional models that were employed as the basic machine learning methods were simple linear regression (LR) and k-nearest neighbors (KNN). Three decision tree methods were employed as ensemble models: Random Forest (RF), Bagged model (Bag), and Gradient boosting model (Gbm). Three variations of the linear basis kernel-based SVM models were used for SVMs: regular SVM (R-SVM), least-squared (LS-SVM), and L2 Regularized (L2-SVM) models. R software (version 4.02) was used to create these methods using machine learning tools including kernlab (version 0.9–25),[39] randomForest,(version 4.6–12) and xgboost model creation (version 0.4–4).Each machine learning model's hyperparameters were optimized using the random search technique built into the R package caret.

To forecast the delivery efficiency of cancer nanomedicines, a deep learning neural network was built for artificial neural networks. The R package "h2o" (Version 3.32.0.5), a R interface for a multilayerfeedforward neural network model,was used to carry out DL. The DL model's architecture featured five dense layers (three hidden levels). To carry out non-linear transformations,the ReLu was employed as an activation function.The learning rate and the regulation function with L1 [Lasso Regression] and L2 [Ridge Regression] were optimized using the training dataset. The DL model in this work was assembled using the Adam and root mean square error (RMSE) as optimizers and loss functions. The early stopping ruleand dropout functionwere employed to enhance the model's generalisation error and mitigate overfitting. Additionally, the Gedeon approach was used to calculate the variable importance for the DL model.[8]

3.2 Model Performance Evaluation

In the evaluation process, the initial dataset was divided at random into a test set (20% of the data) for external validation of the model and a training set (80% of the data) for internal validation using 5-fold cross-validation. The training set was subsequently divided into five equal-sized subgroups for the 5-fold cross-validation study. Four of the five subsets were utilised to construct the model, and one subset was retrained as validation data to assess the final model. After that, this cross-validation procedure was repeated five times, ensuring that every subset had been used for validation. [8]

3.3 Nano-Tumour Database

The majority of datasets came from research that used passive targeting (68%). The data covered a wide range of cancer kinds, including breast (30%), liver (17%), colon (8%), cervix (7%), and lung (6%) among others (32%). The mouse tumor models included Allograft Heterotopic (AH, 38%), Allograft Orthotopic (AO, 12%), Xenograft Heterotopic (XH, 38%), and X bbfdenograft Orthotopic (XO, 12%). In terms of physicochemical features, organic NPs accounted for the majority (71%). Polymeric (40%), gold (17%),

liposomes (9%), hydrogels (6%), silica (6%), iron oxide (2%), dendrimers (2%), and others (18%) were among the key materials used. [8]

3.5 Development and Validation of NP Tumour Delivery Efficiency Models

Among the selected ML model algorithms, the RF model performed better in predicting each endpoint, with higher R2 and lower RMSE or MAE values than other ML algorithms. The KNN model was the weakest modeling approach, with R2 values for all endpoints less than 0.1. The R2 and RMSE values for RF varied from 0.11 to 0.29 and 3.17 to 7.15 for each endpoint in the test set, respectively, whereas the values in the training set ranged from 0.15 to 0.19 and 2.06 to 3.72.Although the L2-SVM model outperformed the others in the DE168 test set, the findings may not be valid due to large variations in R2 and RMSE values between the training and test sets. When forecasting the performance of the DL model, the results beat all ML approaches, with the greatest R2 values and significantly lower RMSE and MAE values across all endpoints than those from other algorithms. These findings indicate that the DL model outperformed all other ML and DL models in predicting endpoints across the training and test sets.[8]

3.6 Results

Our published Nano-Tumor Database provided all information on the physicochemical characteristics of NPs, tumor model, and cancer type. 5 36 models were created by combining nine modeling algorithms with four different response variable types (delivery efficiency at various time points following IV injection, such as DE24 and DE168). In particular, the factors associated with the description of tumor research and the physicochemical characteristics of NPs were employed as input features to forecast the tumor delivery efficiencies of various NPs. The models were created using several modeling algorithms following data preparation. The 5-fold cross-validation approach was used to evaluate the final models, and each model's quality was assessed using training and test data sets independently using a number of metrics, such as R2, RMSE, and MAE.[8]Pathologists who used AI model aid diagnosed patients faster (0.03±0.01) seconds than those who used conventional techniques [13]

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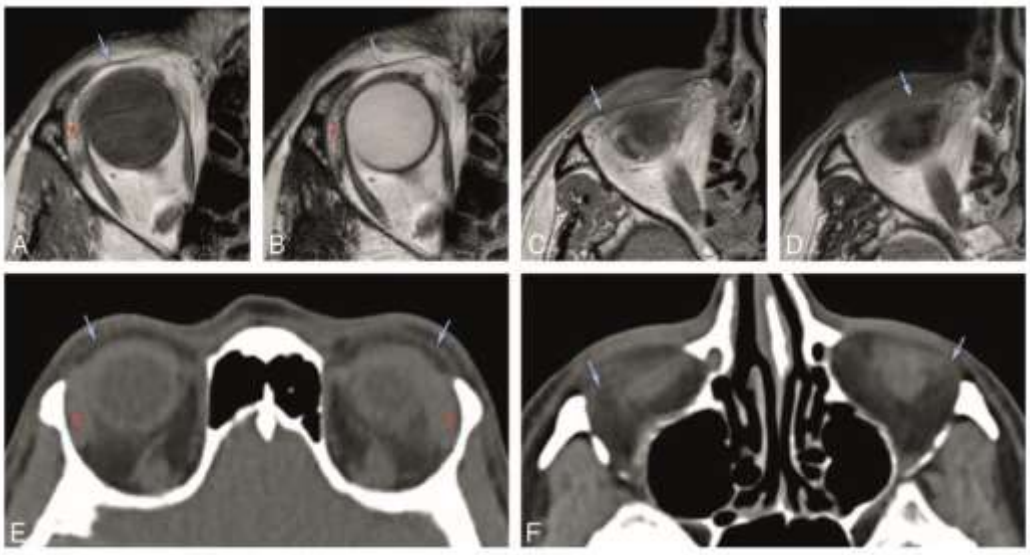
4.AI in Eyelid tumors

Tumors of the eyelids are the most frequent neoplasm seen indaily ophthalmology practice. Since eyelids include a lot of tissue,types, various benign and malignant tumors can develop.[3]



4.1 AI Models

Models to differentiate between benign and malignant eyelid cancers were trained using four traditional deep learning algorithms: DenseNet121, ResNet50, Inception-v3, and VGG16. The expert categorized a total of 36 photos (12 images of malignant tumors and 24 images of benign tumors) into the borderline case group (eyelid tumors of unknown malignant origin). In this group, the best algorithm, DenseNet121, distinguished between benign and malignant eyelid tumors with an accuracy of 77.8%, a sensitivity of 83.3%, and a specificity of 75.0%.[3]

4.2 Development of a deep learning classification system

To categorize eyelid cancers, researchers developed a deep learning system. Cropped photos taken from the NEH dataset served as its foundation. 70% of that dataset was used for training, 15% for validation, and 15% for testing. There was no overlap between any of the sets.
In the process, they examined four well-known CNN designs. DenseNet121, ResNet50, Inception-v3, and VGG16 were among them. With its dense layer connections, which significantly enhance feature flow throughout the network, DenseNet121 stands out. ResNet50 relies on skip connections to make training those deeper networks less of a hassle. Inception-v3 introduces inception modules that significantly reduce the computing loads.VGG16, which is based on stacks of 3 x 3 filters, keeps things simple even when it gets deep. From the beginning, transfer learning was used. Weights pretrained on ImageNet were used to start each model. Every image, whether 224 by 224 or 299 by 299, was adjusted to meet the precise input sizes required. All of them were adjusted to fall between 0 and 1. Additionally, augmentation assisted with flips, rotations, and brightness adjustments. Ultimately, the training set expanded from 883 photos to 5,298. The entire training was conducted on four Nvidia 2080Ti GPUs using PyTorch.The entire training was conducted on four Nvidia 2080Ti GPUs using PyTorch. The total batch size was set at 128. Adam was the optimizer, and it ran continuously for 80 times with a learning rate of 0.001. Accuracy checks for training and validation, together with loss values, concluded each period. The model that had the highest validation accuracy was saved. The internal set was used to test the selected model initially. For a more complete picture, it then switched to an independent external test set. All of this was done to ensure that everyone performed well. The t-SNE visualization provided a satisfying conclusion. In a two-dimensional feature space, it described how the model separated different types of tumors.[3]

4.3 Result

An eyelid tumor identification system (ETDS) was established and evaluated using a total of 1,417 photos with 1,533 eyelid tumors delimited by tight bounding boxes after 150 photographic images lacking histopathological diagnosis were eliminated. The deep learning classification method was developed and evaluated using 1,533 cropped pictures produced by the ETDS (1,161 images of benign tumors and 372 images of malignant tumors).[3]

5. AI in Bone Tumor

5.1 AI-empowered radiotherapy workflow for primary bone tumors

Artificial intelligence (AI) is gradually permeating every technical stage of contemporary radiotherapy, resulting in a data-driven "learning loop" that reduces planning cycles, standardizes quality, and customizes decision-making. AI provides a way to take advantage of multicenter experience without sharing raw data for the relatively uncommon but physiologically varied primary bone tumors, where surgical margins can be narrow, organ-at-risk (OAR) limitations difficult, and prospective trials limited. Here, we map the state of the art throughout the whole irradiation chain, emphasizing methods that have advanced past proof-of-concept and are currently passing multicenter or prospective review.[4]

5.2 Automatic tumour and OAR contouring

Osteogenic sarcoma target delineation might be labor-intensive due to skip lesions and post-biopsy artifacts. According to Yin et al., a nnU-Net-based pipeline trained on pelvic and extremity MRI achieved a mean Dice similarity coefficient (DSC) of 0.77 ± 0.05 for gross tumor volume (GTV) segmentation, outperforming an atlas-only workflow by 11 percentage points and reducing manual editing time by half (23). The work used open-sourced weights and cross-scanner data, which expedited external validation despite the small test population (n = 52). The current focus is on hybrid CNN–atlas cascades that improve DSC at the tumor–marrow interface, where relapse frequently occurs, by initially propagating bony masks as geometric priors before fine edge refinement.[4]

5.3 AI-optimised FLASH radiotherapy

Ultra-high rate of dosage (≥40 Gy s^{-1}) The millisecond time dimension introduced by FLASH is beyond the scope of manual quality assurance. Since 2021, FLASH-AI articles have increased fivefold, with normal-tissue sparing and beam-monitoring becoming popular subjects, according to bibliometric mapping. In order to maintain dose-rate variation within ±3%—a need for the sub-second closed-loop therapy envisioned for pre-clinical bone-metastasis FLASH trials—prototype amorphous-silicon detectors now track individual 2-μs micro-pulses, and deep-learning observers flag beam-current drift in real time. Adaptive replanning

within the same breath-hold is made possible by algorithms such as iDoTA, which anticipate the entire 3D photon or proton dose in 50–100 ms.[4]

6. Tumor Micro Environment

6.1 Analysis of the use of CNNs and deep learning

The accuracy of diagnosis is one of the most significant issues in oncopathology. The prognosis and the best course of therapy for a patient are determined by an accurate diagnosis (PTT). This causes considerable difficulty among pathologists and results in a lack of consensus on interpretations of these parameters. One of these factors is a detailed assessment of the tumor microenvironment (TME) and the presence of tumor buds.

On the basis of histology pictures, CNNs and deep learning are reasonably accessible techniques for identifying and forecasting the progress of CRC in patients. 10, 13 CNNs can tackle tissue classification problems more effectively than both conventional machine learning techniques and specialist equipment for histological tissue classification because of their ability to adapt to the spatial structure of the data. The quality of AI model predictions is comparable to the quality of manual assessment or even higher: implementation of a semi-automated method surpassed manual assessment approximately 2.5 times in tumor clusters detection, and when implementing deep learning algorithms, the estimated potential was even higher.[9]

6.2 Development of an AI-Powered TME Analyzer

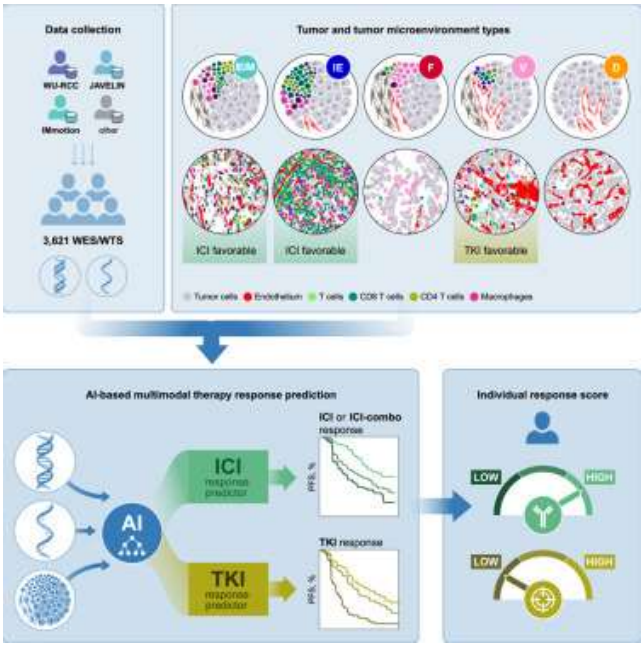
Plans to employ a model of the Mask R-CNN type were also proposed by Kather et aland Lu et al., the Faster R-CNN network demonstrated efficacy by displaying assessment results comparable to manual evaluation by senior pathologists in a significantly shorter amount of time.Two DL-based AI models based on the DeepLabV31 architecture, such as SCOPE HER2, are also included in Lunit SCOPE IO (Lunit), an AI-powered TME analyzer. In addition The Data Supplement (Methods) contains information on the AI-powered HER2 analyzer. While the tissue segmentation model divides regions into CA, cancer stroma (CS), and BG in hematoxylin and eosin (H&E) WSIs, the cell identification model identifies TC, lymphocyte (LC), macrophage (MP), fibroblast (FB), and endothelial cell (EC). Cell density in each location for each cell type was computedby integrating the data from the tissue detection model and the cell detection model. Similar measurements were made for OT (LC-CA, LC-CS, MP-CA, MP-CS, FB-CA, FB-CS, EC-CA, and EC-CS). The density of TCs in the CA and CS was characterized as the TC-CA and TC-CS, respectively (counts/mm2).[10]

6.3 Spatial analysis and imaging: Precision at the micron scale

Clarifying tumor-immune interactions requires spatially resolved study of the TME. Tumor-infiltrating lymphocytes (TILs) and their spatial distribution across tumor types have been quantified using CNNs, finding patterns associated with immunological subgroups and treatment responses. Another study found 43 TIL spatial characteristics in breast cancer that were highly correlated with immune pathways and treatment outcomes by using machine learning to evaluate whole-slide histopathology pictures. AI and imaging mass cytometry have made it possible to track immune cell interactions in high resolution. Recent developments have shown that regional patterns of T-cell depletion are predictive of treatment resistance in colorectal cancer.In order to view the interactions between stromal and immune cells at the micron scale, AI-driven 3D spatial reconstructions of the TME are being constructed. This opens up new possibilities for immune exclusion zone targeting. Deep learning combined with multiplex imaging data provides real-time insights into intratumoral heterogeneity, improving the accuracy of diagnosis and treatment.[11]

6.4 HALO AI Nuclear Phenotyper Algorithm

The format was a tiled TIFF file in SVS format, which was subsequently compressed to JPEG. There was no usage of Z-stacking. The HALO software was loaded with the photos, and the AI nuclear phenotyper algorithm was trained for 556,930 iterations using a total of 34,427 nuclei from 52 different samples. The accuracy of the final nuclear phenotyper algorithm was verified by pathologists at the Markey Cancer Center. For each murine lung section, the tumor areaswithapproximately50mmsurroundingareawere hand-annotated for analysis. For the KRAS/Lkb1-null tumors, adenocarcinoma and squamous cell carcinoma regions were manually sub-annotated by an experienced researcher.[12]



7. CONCLUSION

AI is the major evolution in the medical industry. AI becomes the most far-advanced to treat various types of tumors, like mentioned in the review article, it treats brain tumors, cancer tumors, bone tumors, eyelid tumors, and various other tumors, like breast tumors , lung tumors colorectal tumors .Various model deep learning models are evolved to diagnose treat , prevent and cure cancers. By 2030 technology in AI evolves to great extent in treating Tumors.

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