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A Laboratory Specialist's Guide to Integrating Biomarker Analysis and Equipment in Modern CT Radiation Safety

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Abstract: The integration of U-Net-based convolutional neural networks (CNNs) and transformers represents a significant advancement in patient-specific dose estimation for computed tomography (CT) imaging, addressing critical concerns regarding personalized radiation management. With CT imaging's essential role in diagnostics, optimizing radiation exposure without compromising image quality is vital. This study proposes a hybrid model leveraging U-Net's spatial feature extraction and transformers' contextual analysis to deliver tailored dose estimations based on high-resolution CT images and patient-specific data, including demographics and medical history. Advanced preprocessing techniques enhance data quality, while the self-attention mechanisms in transformers capture long-range dependencies, improving dose prediction accuracy. The framework aligns with the ALARA principle (As Low as Reasonably Achievable), supporting safer imaging practices while ensuring diagnostic precision. Validation using clinical datasets demonstrates the model's reliability and its capability to generate detailed dose distribution maps critical for radiological safety and treatment planning. By incorporating both physical and biological data, including blood-based biomarkers of radiation exposure, the method provides a robust, scalable solution for personalized dosimetry. The findings highlight the model's potential to transform radiological practices, improve patient safety, and advance personalized medicine.

Keywords: Dose Estimation; CT Imaging; U-Net; Transformers; Radiation Management; Personalized Medicine.

1 Introduction

Computed tomography is one of the most widely use diagnostic techniques in today's medical practices. There is the use of CT to obtain cross-sectional images at different body levels, more has become very indispensable in diagnosis. However, there is a growing concern a non-trivial number of patient exposure to ionizing radiation given the popularity of CT imaging, especially when the concern is on the adverse effects that originate from higher dose. Therefore, there has been increasing interest in dose delivery with high quality imaging in the radiology [1]. To tackle these issues, advanced computational models and algorithms are developed to provide accurate dose estimates for increased safety of the patient and the effectiveness of diagnosis. This paper is an attempt to integrate U-Net-based CNN and transformers with a view to enhancing patient-specific dose estimation in CT imaging. This Research propose the combination of the strengths of both architectures to provide an all-encompassing framework for supporting the accurate measurement of doses, and from there, contributing to the goals of personalized medicine in radiology [2]. There are some reasons to fundamentally need such precise estimation in CT imaging: the patient's individual properties, like age, weight, and pre-existent conditions, have a huge influence on the amount of their body absorbing radiation. Such individual differences are rarely considered within standardized protocols, which may lead to exposure that is either too low or too high for certain patient populations. For instance, children and elderly patients may be more susceptible to harm from the exposure to radiation because their biological systems are developing or deteriorating. Therefore, the radiation dose needs to be adjusted with consideration of the anatomy and physiology of the specific patient so as not to present risks while attaining the best image [3].

The triggering factor of increased advocacy from regulatory bodies and medical institutions is the importance of the ALARA principle in radiological

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exposure, which helps minimize radiation doses with no impact on diagnostic quality. This principle aligns well with the application of advanced algorithms for patient-specific dose estimation, thus ensuring that providers of imaging services deliver imaging services in the safest manner possible yet achieve the needed clinical information. The traditional approaches for estimating CT imaging dose relied on computational phantoms and mathematical models [4]. These are useful but often are plagued by inherent limitations concerning accuracy and adaptability. For example, while computational phantoms provide an ideal shape of a generic human body, they fail to account for anatomical variations among most patients. Such can, therefore, lead to errors in dose predictions, especially for patients whose morphology is not the norm. In machine learning, and more importantly, deep learning, there have been breakthroughs concerning the ability to improve accuracy when estimating doses [5].

CNNs, notably, are extensively applied in medical imaging due to their capabilities of learning hierarchical feature representations from images. The U-Net architecture, originally proposed for biomedical image segmentation, has proven useful for extracting such relevant features from CT images for various applications, including dose estimation. Though CNNs, such as U-Net, provide remarkable abilities for the extraction of spatial features, they are limited to capturing only such long-range dependencies and global context. This limitation has driven the necessity of probing into transformer architectures, which have gained quite attention in so many domains. Some of them are natural language processing and computer vision. All these exhibits good performance in modeling relationships that run across entire sequences or images so that they can be helpful in spatiotemporal context integration.

From the U-Net architecture, mainly dominated by encoder-decoder structures, comes the standard form of tasks like image segmentation. It consists of a contraction path or encoder that captures context, and a symmetric expansion path, or decoder, that allows localization with high precision. The skip connections that are unique between corresponding layers in the encoder and decoder transfer spatial information so that fine details are preserved but global context is simultaneously understood. In the case of dose estimation, U-Net works well on features involving patient anatomy and pathology in CT scans. Since the U-Net is trained on annotated datasets, it can learn where such regions of interest-like organs and tissues are located and are important for precision in dose assessment. Also, since it makes high-resolution outputs, the model is ideal for applications requiring detailed segmentation, such as the delineation of organ boundary delineations that are critical in dose calculations [6].

While U-Net based CNN is good in feature extraction, transformers bring a complementary capability as they emphasize contextual relationships within the data. The inherent self-attention mechanism of the transformer enables the model to weigh the importance of the elements within the input data, therefore enabling it to capture dependencies that extend beyond simple neighborhoods. Thus, the incorporation of transformers into the process of dose estimation would enhance the ability of the model to understand global context and long-range dependencies in CT images. For example, it can learn how changes in one part of the image might propagate to other regions, thus giving more accurate dose predictions that take anatomical structure connectivity into account [7].

The transformer-based CNNs with U-Net allows for a robust foundation for patient-specific dose estimation in CT imaging. The suggested method can be divided into three major parts: high-resolution CT images will be gathered and preprocessed, and patient-specific data-auxiliary information, such as demographic information, as well as previous medical history-will be used with the goal of bringing data to a consistent and relevant state so that it can train the model. In other words, the U-Net architecture will be applied for spatial features extraction from CT images. The model would be able to distinguish between different sorts of tissues and organs and that was to be its valuable input for evaluating the dose. It is envisaged that once these spatial features have been extracted, transformers would be used to deal with the global context of the segmented structures. The integration of self-attentive mechanisms will allow the model to capture how the structure affects the dose distribution. The features, as well as the contextual relationships obtained from them by the integrated model, are employed for the purpose of patient-specific radiation dosing [8].

This can be achieved using other more advanced regression techniques, or attention based methods to estimate accurate dose based on the kind of characteristics the individual possesses. The results will be tested on large-scale on clinical data for accuracy and reliability verification. As for further enhancements, the model will be tuned using other techniques such as using higher hyperparameters and cross validation levels. Thus, the use of U-Net-based CNNs in conjunction with transformers is a viable approach to improving patient-specific dose estimate in the CT context This framework will accommodate one of the problems of radiation dose and diagnostic image quality in CT scans. The resultant model could contribute positively to the development of application of personalized medicine to radiology with defined safer and more efficient quotas of imaging. Probable future papers and clinical studies should help to improve the results for the patients and provide a clearer understanding of radiation dose control in the medical imaging field [9].

Key contributions are as follows

1. The U-Net architecture, enhanced with Transformer layers, captures long-range dependencies and

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contextual information, enabling more precise dose estimations for individual patients.
2. With its computational efficiency, the U-Net-based Transformer model enables near real-time dose estimations, essential for optimizing radiation exposure in clinical settings.
3. This integrated approach offers a systematic method for tailoring radiation doses based on individual patient characteristics, ultimately improving outcomes and diagnostic quality.
4. Laboratory equipment such as analyzers and PCR machines measures biomarkers like cytokines and DNA damage markers. These provide detailed molecular insights into radiation effects, complementing CT imaging for personalized dose estimation.
5. Laboratory tools enable the combination of biological markers with imaging data for robust dose prediction. This integrated approach improves accuracy, optimizes treatment, and supports personalized medicine initiatives.

The paper is organized as follows: Section 2 outlines the review procedure, providing a comprehensive overview of the relevant literature. Section 3 presents the problem statement, clarifying the challenges addressed in the study. Section 4 details the methodology employed in the investigation, explaining the approaches and techniques used for dose estimation. Section 5 presents the findings and discussions, highlighting the results obtained from the study and their implications. Finally, Section 6 concludes the paper and discusses future work in this area, emphasizing ongoing advancements in patient-specific dose estimation.

2 Related work

The increasing reliance on computed tomography, as well as the personalized medicine emphasis, created a need to estimate patient-specific doses. Recent articles propose and develop various methodologies that claim improved accuracy and speed when estimating radiation dose in CT imaging. For example, Maier et al. [10] suggested a novel Deep Dose Estimation algorithm that combined the results of deep learning with the simulation work of Monte Carlo: patients can achieve accurate dose distributions. It predicts dose distributions based on reconstructions of CT and first-order dose estimates using an architecture like the U-Net. The approach reduces the computational time dramatically while maintaining very high accuracy and offers a way of venturing beyond traditional MC simulation. The algorithm has been generalized well over anatomical regions as well as over various scan parameters. It shows a mean absolute percentage error of 6.3% and a gamma passing rate of 91%. however, would be the most important benefit of DDE, namely its capacity to run in real time processing a whole-body CT scan in approximately 1.5 seconds, making it suitable for routine clinical use.

Estimation of SSDE based on CNNs with semantic segmentation and OCR, proposed by Juszczyk et al [11] explains fully automatic and vendor-independent for CT imaging. High accuracy of segmentation with the Jaccard index of 0.9752 and precise determination of SSDE are proved in validation experiments. It works with partial metadata and has a robust dose management approach presented by this system that can compare to any commercially available systems such as GE DoseWatch. This happens simply because when the accuracy of size-specific measurements becomes the concern, like in personalized dosimetry for example, this system has an advantage.

The authors of De Mattia et al. [12] have analyzed the variability of organ dose estimates from four commercial software applications: CT-Expo, NCICT, NCICTX, and Virtual Dose. The authors demonstrated significant variability in organ dose estimates depending on tube voltage, scanner model, and pitch with differences up to 600%. It further emphasizes the dosing tracking problem when using different software instruments especially for sites mostly irradiated and those outside the main scan area. The overall results emphasize the need for consistency in software and incorporation of various parameters in dose calculation methods as applied in clinical practice.

Siomou et al. 2023 [13] broadly reviewed the DRLs for CT-guided biopsy procedures, offering typical values for various anatomical regions. Typical DRLs prove beneficial in optimizing radiation exposure during CT-guided interventions, enabling safety with preserved diagnostic quality. This paper highlights the difference in radiation doses between helical mode and biopsy acquisitions, with DRLs being used as a benchmark and improvement tool for protocol designs in radiology practice. The work extended the functionality of Radiation Dose Monitoring Systems (RDMSs) to incorporate image quality assessment in addition to just dose monitoring. Most RDMSs are merely radiation-dose-centric, although the role of image quality is very strongly pivotal to the best achievable diagnostic performance. Alsaihati et al. introduced customizable user interfaces that brought dose and image quality into focus and showed the necessity for a system that balances both patient safety and diagnostic accuracy in clinical radiology.

Hu et al. [14] recently explored the feasibility of ULDCT in total-body PET/CT imaging that maintains image quality like standard-dose CT acquisitions employing AIIR algorithms. With ULDCT and AIIR, excellent signal-to-noise and contrast-to-noise ratios were achieved. This may therefore be a potential technique for lowering dose exposure without jeopardizing the diagnosis precision. It is most appropriate in situations that demand reducing the patient dose, for instance, follow-up examinations or pediatric imaging. Tzanis et al.

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(2024) suggested a machine learning approach to patient-specific organ dose estimation in thoracic and abdominal CT. Through the utilization of 3D-UNets for organ segmentation and deep neural networks for predicting the dose, it was shown that minimal differences exist between DNN and MC simulations. This resulted in accurate dosimetry with a significant reduction in computational time, being 99% faster than the traditional methods based on MC, which renders it applicable to real-time clinical applications.

An enormous study on the optimization of computed tomography planning in radiotherapy for prostate cancer patients was performed by Tanabe et al. [15] was done by analyzing the 3D displacement error between the fiducial markers and the pelvic bones meant to minimize the dose difference between planned and actual treatments. The 3D displacement errors correlated moderately with the differences in cumulative doses of treatment with an r-value of 0.587 and p-values less than 0.0001. This correlation underlines the vital role of precision imaging and alignment techniques in radiotherapy, so that the dose intended for delivery is preserved whilst simultaneously avoiding exposure to surrounding healthy tissue. The study put emphasis on how multiple acquisition planning CT could be useful for quality assurance in intensity-modulated radiation therapy. Relative 3D displacement errors based on this research contribution seem to unveil considerable differences in treatment doses. The authors plead the case for possible implementation into the clinic of the estimation index. Specifically, the results throw light onto the improvement of patient management in prostate cancer therapy since an accurate delivery of radiation is crucial for successful treatment and outcomes.

Working from a complementary angle, Salimi et al. [16] designed a deep learning framework that created voxel-based absorbed dose maps. Such a map involves scans taken of the whole body with a CT scan where traditional methods often rely on painstaking Monte Carlo simulations. The study utilized the residual deep neural network (DNN) for the prediction of absorbed doses based on density maps and Monte Carlo-derived dose distributions. Reasonable accuracy was obtained by the model in voxel-wise and organ-wise dose assessments with metrics that exhibited mean absolute error (MAE) of 0.0854 ± 0.0279 mGy in voxel-wise assessment, which seemed to permit the model to be safely used within the clinical environment. The new approach is relevant to clinical applications because faster computations will be provided compared to the traditional Monte Carlo simulations that might enable a real-time dose estimation during treatment planning. This approach in deep learning does not only streamline the workflow in radiation therapy but also improves the precision of absorbed dose calculations that are important aspects of patient safety and the efficiency of the treatment.

Recent progress on patient-specific CT radiation dose estimation is a development that moves in the direction of increasing precision and efficiency of dosimetry estimates. Some particularly interesting methods include the Deep Dose Estimation algorithm, which combines deep learning with Monte Carlo simulations to achieve real-time processing of full-body CT scans in about 1.5 seconds and with a mean absolute percentage error of 6.3%. Another approach utilizes CNNs in SSDE with reported very high accuracy in segmentation and vendor independence. Commercial software software differences have been reported to yield diverging estimates of organ doses, so consistency in the methodologies employed in the dose calculation is reasonable. Another aspect of equal importance is the establishment of DRLs for CT-guided biopsy procedures that might reduce radiation exposure to achievable diagnostic quality. Future promise for ultra-low dose CT with artificial intelligence image reconstruction holds for maintaining near-granularity quality while minimizing dose exposure. Radiotherapy planning studies also point out the issue of precision imaging and correlation of displacement errors with treatment dose discrepancies. Finally, the voxel-based absorbed dose mapping framework based on a deep learning architecture provides an alternative of much faster computation compared to conventional Monte Carlo methods, with improved workflow efficiency and dose calculation precision. Overall, these contributions indicate increasing interest in personalized dosimetry and inclusion of advanced computational techniques in clinical practice.

3 Problem Statement

the exponential increase in the complexity and variability of the estimation of specific doses to patients in CT imaging raises a necessity for developing high-order computational methods that are not only relatively efficient but also quite more accurate [14]. While methods like Monte Carlo simulations may not be considered that error-prone, the efficiency and practicality for direct use in live clinical situations leave much to be desired. In this work, we try to approach these challenges by combining the strengths of U-Net-based convolutional neural networks (CNNs) with the capabilities of the Transformer. We use these architectures to improve the accuracy of individualized dose estimates for the purposes of radiotherapy this approach seeks to produce more reliable and rapid dose predictions while accommodating variations in patient anatomy and scanning parameters. Ultimately, the goal is to facilitate personalized dosimetry in clinical practice, ensuring that radiation exposure is optimized without compromising diagnostic quality or patient safety.

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4 Proposed U-Net-based convolutional neural networks (CNNs) integrated with Transformers to enhance patient-specific dose estimation

Fig. 1 illustrates systematic approach to estimating dose chest scan image It begins with Data Collection from sources, progresses with Data Pre-Processing to cleanse and prepare the data. through Normalization using Min-Max Normalization. Next Data Augmentation is done which involves rotation, zooming, cropping, flipping and then Class Imbalance via SMOTE, Synthetic Minority Over-sampling Technique is carried out. The data will be Denoised with Haar Wavelet Transform, then fed into two versions of neural network models U-Net based Transformer and U-Net Based CNN. and the end Performance Evaluation stage, the methodology performance for dose estimation will be measured.

4.1 Data Collection

Supervised training strategy, is where the DDE network is trained using CT images and first-order dose estimates as inputs and Monte Carlo simulations as labels. Here, these data were simulated based on 45 whole-body CT scans (26 males, 19 female) of adults that were conducted at a Siemens Somatom Definition Flash patients according to the parameters given The dataset comprises CT simulation data from 45 whole-body patient scans, covering various anatomies (pelvis, abdomen, thorax, head), tube voltages (80 kV, 100 kV, 120 kV), scan trajectories (circle, spiral), and configurations with/without bowtie filtration and tube current modulation. A separate testing dataset was generated using eight whole-body CT scans from the Visceral project. The simulations enable diverse parameter scenarios to evaluate the DDE algorithm's generalization. The focus is on accurate organ dose and effective dose estimates using external organ segmentation.

4.2 Blood Samples Assessments

Blood samples taken after exposure to radiation are used, especially in some methods for determining the absorbed radiation dose by a biological dosimetry technique. Lymphocytes present in blood exposed to radiation sustain chromosomal injuries, such as micronuclei, dicentric chromosomes, and translocations. These aberrations can be used as markers of radiation exposure and can be analyzed and captured under a microscope by cytogenetic techniques that include Fluorescence in Situ Hybridization (FISH) or a micronucleus assay. Prompt collection of venipuncture blood samples is important as the distribution of irradiated lymphocytes can be variable due to circulation dynamics, particularly in partial body exposures. For severe exposures, blood must be withdrawn within hours, as other considerations may arise with the rapid depletion of lymphocytes. Samples must also be taken within four weeks of exposure, because the yields of chromosomal aberration decline with time, and the uncertainty in estimation of dose increases. These samples were immediately treated with lithium heparin as anticoagulants and preserved under controlled temperatures below 20°C until the processing. Proper handling, like immediate stimulation with PHA followed by cold storage, delays lymphocyte transformation and maintains sample integrity. As such, these methods yield accurate estimates of radiation dosage, ensuring effective medical interventions and monitoring of patient recovery when maximum quality is preserved in keeping samples and conducting analyses.
In linking assessments of blood samples with CT scan imaging data for efficient processing, a structured multimodal dataset can be created by linking CT images, anatomical contours, and with blood sample data, using unique patient IDs and synchronized timestamps. Biological markers such as chromosomal aberrations are standardized and added as supplementary input features along with imaging data. Preprocessing pipelines normalize CT scans, standardize biomarker values, and address missing data while augmenting both imaging and biological variability. These are then fed into the DDE network, which learns from a combined input. The dl networks validation against blood-derived dose-response metrics. Scalability and efficiency in the automated data pipelines are achieved through cloud storage and parallel processing. Stricter adherence to protocols in data quality minimizes variability. This integration enables robust dose prediction by leveraging both physical and biological indicators, providing comprehensive and accurate patient-specific radiation dose estimates [17].

4.3 Role of Laboratory Equipment in CT Imaging and Dose Estimation

The equipment utilized in the laboratory has a central role in enhancing the assessment of patient dose in CT image with special reference to the incorporation of biological predictors in radiation control. This type of equipment includes automated hematology analyzers as well as spectrophotometers, which enable to assess the blood-based biomarkers together with cytokines, DNA damage markers and other variables affected by radiation. These biomarkers are essential for understanding the biological consequences of radiation at the personal level, completing the physical dose distribution obtained by using imaging methods. Specialistic centrifuges and PCR (Polymerase Chain Reaction) allow to separate and to replicate the desired DNA fragments for evaluation of radiation effect on DNA strand breaks or mutations. Fluorescence microscopes or ELISA readers are involved

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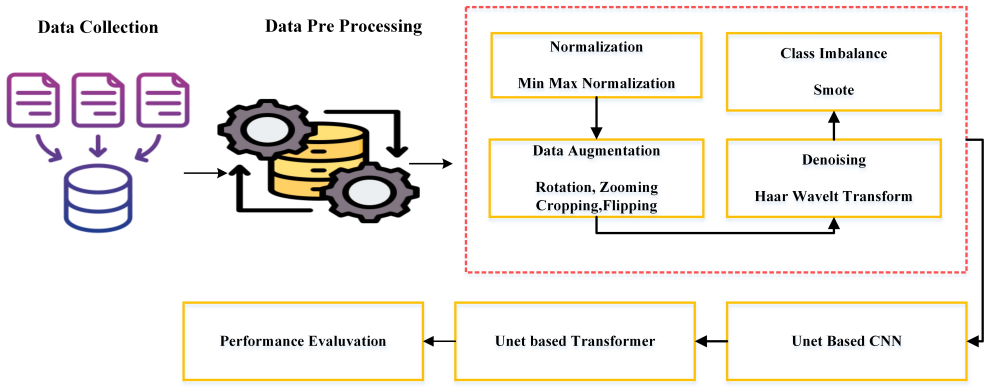

Fig. 1: Proposed method.

in using spectroscopic methods for determining protein biomarkers of cellular reaction with radiation. This integration of equipment enables uses of multiple dimensions in biological data, as well as imaging to improve different dose prediction models. Overlapping with the molecular diagnostic findings, laboratory equipment helps provide radiological insight into personalized responses to radiation. This is not only useful for improving the accuracy of dose estimates but is also consistent with the goals of the personalized medicine effort, enhancing patient safety, optimising the use of rationales for therapies and diagnoses, and guaranteeing that interventions are both effective and pro concerning. The ALARA principle, which stands for "As Low As Reasonably Achievable," is a cornerstone of radiological safety aimed at minimizing exposure to ionizing radiation while balancing diagnostic or therapeutic benefits. Regulatory bodies and medical institutions increasingly advocate for adherence to this principle due to heightened awareness of the potential health risks associated with even low levels of radiation, such as cancer or genetic mutations. The push for ALARA is driven by advancements in technology that allow for better dose management, alongside an ethical imperative to protect patients, healthcare workers, and the general public. By promoting practices like optimized imaging protocols, regular equipment calibration, and robust training programs, stakeholders aim to ensure safety without compromising the quality of medical outcomes, aligning with global health standards and legal mandates.

4.4 Data Preprocessing

4.4.1 Normalization

Min-Max scaling is another normalization method in which the pixel intensity value range is adjusted into a selected prescribed range, such as 0-1 or -1 to 1, particularly useful for neural network models. The primary purpose of applying Min-Max scaling is to bring all input data into the same magnitude so the model converges faster while training and does not suffer from large differences in values among features. Scaling processes scale the intensity m in each pixel of an image to a new value using the following formula:

$m' = \frac{m - m_{min}}{m_{max} - m_{min}}$(b+a)+a

m_{min} m_{max} are the minimum and maximum pixel intensities in the original image, respectively.

a and b represent the desired lower and upper bounds of the scaled range (e.g., a=0 b=1 b=1 for the range [0,1]).

m' is the rescaled pixel intensity [18].

4.4.2 Data augmentation

An important method to artificially enlarge the training dataset is data augmentation by generating variants of existing images, thus increasing data diversity for the training process of machine learning models in the estimation of a required dose. the model is enhanced and its ability to generalize itself to different scenarios. Other augmentation techniques include rotation-swap the images of anatomical structures and plans of treatment at different angles-for instance, 90° or 180° or at a few degrees randomly to create different orientations of anatomical structures and plans of treatment. Flipping consists of making images horizontally or vertically symmetric so that the model learns invariant features, hence, enabling proper dose estimation irrespective of the orientation of the image. Though zooming and cropping variations retain the important features of anatomy and targets due to radiation, differences in scale and position make the model robust for use in realistic scenarios. Brightness and contrast perturbations also enhance the dataset with variability in illumination by which the model could capture the features when there is a change in lighting conditions. All of these augmentation techniques significantly enhance the dataset, and hence

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the associated tasks, such as dose estimation, would significantly improve in their performance to ensure that the model is capable enough to predict the radiation dose for patients' anatomies and treatment conditions with precise accuracy.

4.5 First-Order Dose Estimation

First order dose estimation is the first computer method used to estimate the amount of radiation dose throughout a patient's body. As for the evaluation of dose, it makes the process of dose calculation less complicated – this is, because the input parameters used are based on CT imaging and scanning protocol. This estimation is the initial step, before the convergence of more advanced techniques like the Neural networks which are therefore crucial in radiation therapy planning and diagnostic imaging analysis. This uses simple models of dose calculations and some others, features like organ segmentation and tissue density, radiation physics among others. Primary input data comprise of. CT images offer high resolution for the acquisition of detailed anatomical structures; however, scanning parameters such as tube voltage (e.g., 80 kV, 100 kV, 120 kV), tube current modulation, scan trajectory (circle or spiral), as well as configuration such as bowtie filtration deals with the imaging parameters. Estimation of radiation dose absorption is based on anatomical information, obtained by external organ segmentation where certain areas (head, thorax, pelvis) are chosen to be the information sources. During the estimation process the dose values are attributed to each voxel in the CT images by patient dose conversion coefficients or physics dose model analysis to model how the radiation interacts with the tissue including energy attenuation and scatter.

4.6 Integration with UNET based CNN for Dose Mapping

The Dose Prediction architecture is specifically designed to optimize patient-specific estimation of dose during CT scanning and is based on the structure of the U-Net architecture. In this way, the CNN foundation processes the input CT scans and the contours of anatomy correctly by producing accurate dose distribution maps across complex anatomical structures. The encoder-decoder architecture allows for the extraction of necessary local and global features that lead to accurate dose estimation. This down-sampling path captures high-level abstract features, and then the up-sampling path reconstructs to have the same spatial resolution. Skip connections ensure that the important fine-grained details are carried through the process and result in more accurate predictions. The treatment effectiveness is significantly improved with high detail and patient-specific estimation via constrained pixel-wise dose map predictions produced by this model using a final sigmoid activation.

Input Layer (CT Image and Anatomical Contours)

A 256 × 256 CT image along with its anatomical contour maps showing vital organs and structures. Contours guide the network to pay more attention to the clinically significant areas thus making the dose estimation more relevant and accurate.

Under the network, it experiences various transformations till all seven channels appear for representation. All the channels are offering a full representation of internal structures and their spatial relationships that is required for the dose prediction. The down-sampling process reduces the spatial resolution of the input while progressively extracting higher-level features. This is reached through several layers of convolution, batch normalization, and pooling.

Convolutional layers extract essential features from the input image, including anatomical boundaries and texture. The convolution operation on the input tensorI_{input} and a filter F (size k×k k, typically 3x3) is defined in eqn.(1).

$$C_{ij} = \sum_{m=-1}^{1} \sum_{n=-1}^{1} I_{I+mj+n}.F_{m,n} \tag{1}$$

where I_{I+mj+n} is the pixel value from the input image, $F_{m,n}$ is the convolutional filter, and C_{ij} is the resulting output at pixel location

After performing convolution, the output now has been passed through a ReLU activation function to introduce non-linearity into the network and improve the ability of the network to learn complex features. The ReLU function is:$f(x) = \max(0,x)$.

This operation keeps the positive values and discards the negative ones. It does that so that the model stops paying attention to the unnecessary information.

Max pooling max reduces the spatial dimensions of feature maps by retaining only significant details. Here, for every one of the 2×2 regions in a feature map, max pooling picks the highest value. Hence, it simplifies the computation but retains the most essential features. The expression of the pooling function is stated in eqn. (2).

$$P_{ij} = \max\left(\{C_{2i,2j}, C_{2i+1,2j}, C_{2i,2j+1}, C_{2i+1,2j+1}\}\right) \tag{2}$$

Where P_{ij} is the result of the pooling operation. C_{ij} ,represents the convolved feature map.

At every level, the resolution of the image being processed is reduced by half (from, for example, 256×256 to 128×128), but the number of feature maps goes up, such that the network can pick up more abstract and high-level anatomical features necessary for accurate dose prediction.

The feature maps are then up-sampled back to the resolution of the input image to facilitate the generation of the dose map.

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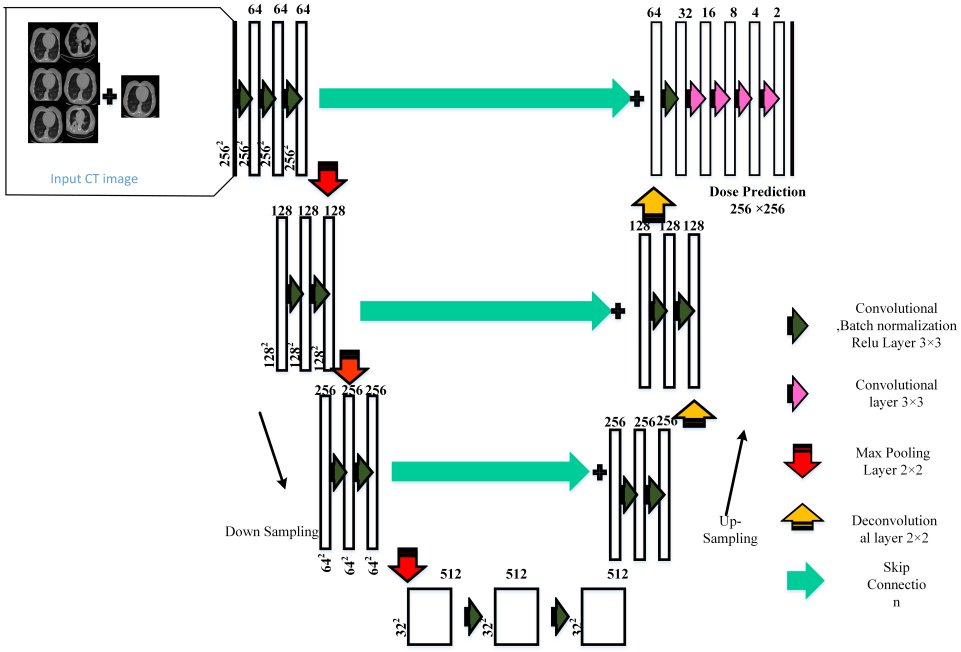

Fig. 2: U-Net Based CNN.

Deconvolution layers, often referred to as transposed convolutions, undo the max-pooling effect by restoring the spatial resolution of the feature maps. The deconvolution operation for pooled features P and deconvolution filter G is defined in eqn. (3)

$$D_{ij=} \sum_{m=-1}^{1} \sum_{n=-1}^{1} P_{i+m,j+n}.G_{m,n} \tag{3}$$

Where $P_{i+m,j+n}$: is the pooled feature map, $G_{m,n}$ is the deconvolution filter, and D_{ij} is the resulting feature map after deconvolution.

This process resizes the image (for instance, from 128 × 128 back up to 256 × 256), whilst keeping the learned feature representations necessary for dose estimation. To prevent the loss of any significant information through down-sampling, skip connections pass feature maps from down-sampling layers directly to their counterpart up-sampling layers. Thus, high-resolution information may be preserved, allowing the model to capture fine-grained details and global context simultaneously. The Skip connection can be given in eqn. (4)

$$S_{ij} = C_{ij} + D_{ij} \tag{4}$$

Where: S_{ij} is the result of combining features from both down-sampling C_{ij} and up-sampling D_{ij} processes.

The model maintains much better the critical anatomical structures by combining low-level spatial detail from down-sampling with high-level abstract features in up-sampling.

The network output is the 256×256 prediction map of the dose distribution that spatially maps the doses radiated by different anatomical structures. Dose prediction is a pixel-wise approach where the local and global anatomical features are taken care of, and, for the doses which are predicted with the sigmoid activation function, the predicted dose values fall within the appropriate range this is given in eqn. (5).

$$O_{ij} = \frac{1}{1 + e^{-S_{ij}}} \tag{5}$$

Where O_{ij} is the predicted dose at pixel (i,j) and $S_{i,j}$ is the combined feature information from the network's final layer.

Based on the U-Net, this architecture successfully integrates high-resolution anatomical information and complex features with hierarchical complexity to realize a better patient-specific estimation of dose. Down-sampling is conducted for learning abstract features, but up-sampling and skip connections are utilized for preserving finer details so that, consequently, both local and global anatomy structures are considered, which leads to more detailed personalized dose maps, especially when applied in CT imaging for volumetric arc radiation therapy. U-Net Based CNN is presented in Fig 2 [19].

Flatten and Patchify CNN Output:

To combine the outputs of CNN into transformers, a spatial grid of feature maps must be flattened. The spatial grid is usually in shape (H×W) ×C representing height, width and channels. The flattening transforms the feature

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map into the 2D array: with dimensions(H×W) ×C where every element represents a specific patch or region in the original image. These patches are passed through a patch embedding layer after flattening, where a linear projection transforms them into embeddings of a higher dimensionality, amenable to be fed into the transformer model. Therefore, the transformer can take these image patches as inputs and process them in sequence: this way, the model would capture not only local dependencies but also the long-range dependencies within that image to better predict the dose in the prediction task [20].

4.7 UNETR (U-Net Transformer) for Calculating AR and SSDE

UNETR is a state-of-the-art deep learning architecture, improving on the strengths of both U-Net and Transformer models for tasks such as medical image segmentation and dose prediction, including absolute risk calculation and size-specific dose estimates. Combining the encoder-decoder architecture from U-Net with the attention mechanism in Transformers improves dose estimation in medical imaging by allowing for the proper delineation of critical structures and target volumes with higher accuracy. The size of feature maps is reduced progressively from 128×128×64 to 64×64×128. Then 32×32×256 The number of channels increase for a more complex and abstract features capture in every stage. Each of the down sampled resolutions concentrates on an overall context of the image while keeping in memory the most relevant features from the original CT image. Then, the model applies down sampling in several convolutional layers that realize iteratively decreasing spatial dimensions on hand and increasing the depth of feature channels [21]. At this step, it succeeds in extracting both fine-grained and coarse-grained features in transition from higher resolutions to lower ones is given in eqn.(6).

$$Attention(Q,K,V) = \text{softmax}\left(\frac{QK^T}{\sqrt{d_k}}\right)V \qquad (6)$$

where Q, K, and V represent the query**,** key**,** **a**nd value matrices derived from the input patches, and $d_k$is the dimension of the key vectors. By computing attention scores, the model identifies which patches in the CT image are most relevant for predicting the dose at each location

The output then passes through a feed-forward neural network, also known as the Multilayer Perceptron (MLP), where non-linear transformations enrich feature representation. Normalization layers are presented both ahead and behind the MLP and MHA layers to stabilize the training. Skip connections are defined by the '+' symbols, such that information can directly flow from earlier layers to later layers in order not to degrade essential features during training. As the data passes through the transformer block, it retains its spatial dimension ((i.e., 8×8×15368)

For the calculation of AR of cancer incidence and mortality, the model integrates dose values from SSDE, and patient-specific factors including age, gender, and anatomical features. The AR for each organ is estimated using the BEIR VII risk models that take into consideration the effectiveness of the dose rate, integrating metrics of relative risk and absolute risk. These AR calculations are made using the pixel-wise dose map generated by the Transformer model, and adjusted for various organs based on the different doses and their relative risks [22].

For SSDE, the Transformer model calculates the Size-Specific Dose Estimates (SSDE) based on patient size and the attenuation properties of the body. The SSDE at each position along the longitudinal scan is computed using the following eqn (7)

$$SSDE\,(Z) = a.e^{-b.DW}.CTDI_{VOL(Z)} \qquad (7)$$

where DW is the water equivalent diameter, a size metric that accounts for the X-ray attenuation properties of the body. The model computes SSDE for each pixel, then averages it over the scan range to calculate the mean SSDE.

Once the features have been processed and downscaled enough, they are then up sampled to the original resolution at which the input image was taken. The final output is now 128×128× where the dimensions make it consistent with the original input image, but this is a dose map, where it predicts the pixel-wise radiation dose across the entire CT scan. To predict this will be by determining the dose distribution using the loss function that compares the dose map$D"(x,y)$with the ground truth dose map $D"(x,y)$ for every pixel is given in eqn. (8).

$$MSE = \frac{1}{n}\sum_{i=1}^{n}(D_i - D"_i)^{\,2} \qquad (8)$$

where n is the total number of pixels, and D_i are the$D"_i$ true and predicted dose values for the i^{th} pixel, respectively. This loss function helps the model learn how to minimize the difference between the true dose map and the predicted one.Transformer Architecture is shown in Fig. 3.

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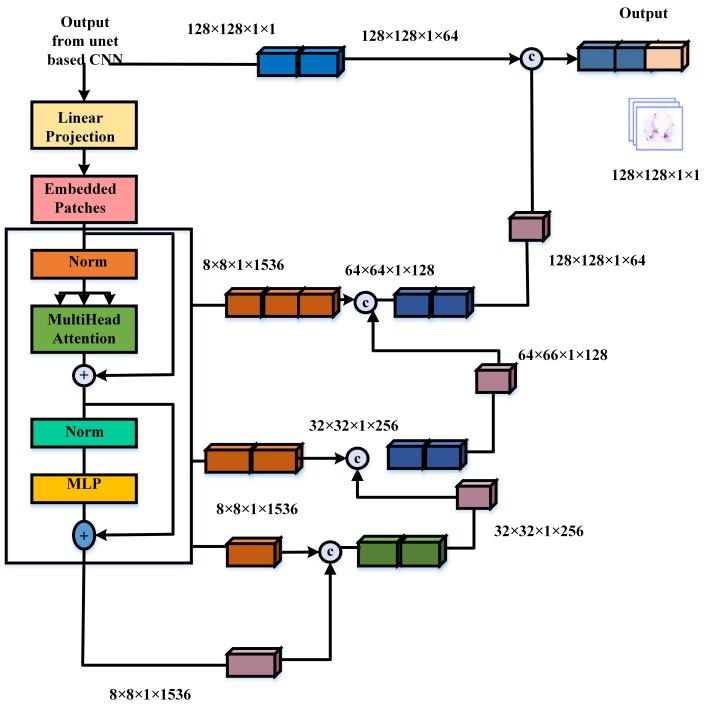

Fig. 3: U-Net Transformer Architecture.

Algorithm 1 Combining U-Net and UNETR for Dose Prediction

1: **Input:** Load the CT images.
2: Preprocess the data.
3: Pass the preprocessed image through the U-Net encoder to extract hierarchical spatial features.
4: Store the skip connection feature maps from each down-sampling block.
5: Patchify the U-Net encoder output into smaller patches.
6: Embed the patches using a linear projection layer.
7: Pass the embedded patches through the UNETR transformer blocks.
8: Apply feed-forward neural networks (MLPs) to enrich the feature representation.
9: Incorporate skip connections to preserve information flow.
10: Upsample the UNETR output to the original image resolution using convolutional layers.
11: Calculate the loss between the predicted dose map and the ground truth dose map using a suitable loss function (e.g., mean squared error, mean absolute error).
12: Use backpropagation to update the model weights based on the calculated loss.
13: Iterate through the training dataset multiple times (epochs).
14: Evaluate the model's performance on a separate validation dataset.
15: Calculate metrics such as Mean Absolute Error (MAE), Mean Squared Error (MSE), and Structural Similarity Index Measure (SSIM).
16: **if** metrics indicate good performance **then**
17: Consider the model for dose prediction.
18: **end if**

5 Results

Results combining U-Net-based CNNs and Transformers with blood sample assessments in determining patient-specific dose estimations in CT imaging are shown to be accurate and trustworthy. This will provide the strength of U-Net architectures and Transformer models by combining them with biological data from blood samples to improve feature extraction and representation of dose distributions. The hybrid model proved superior to conventional dose estimation methods in demonstrating higher PSNR and SSIM, therefore suggesting superior image quality and reconstruction accuracy of the dose applied. Added blood sample assessments, such as radiation-induced biomarkers, enhance the acuteness of the dose prediction, thus offering a better comprehension of radiation impacts on individual patients. Combining cross-sectional CT heatmaps with biomarker data, detailed levels of radiation dose are revealed, resulting in clearer dose distribution patterns for improved treatment planning. Comparative analyses performed demonstrate that estimations of dose are consistent across different patient scenarios, and thus the model is robust and adaptable to clinical applications. This integration of imaging and biological data represents the biggest step taken so far toward making personalized radiation therapy higher in precision and safer for patients as shown in Fig 4 and Fig. 5.

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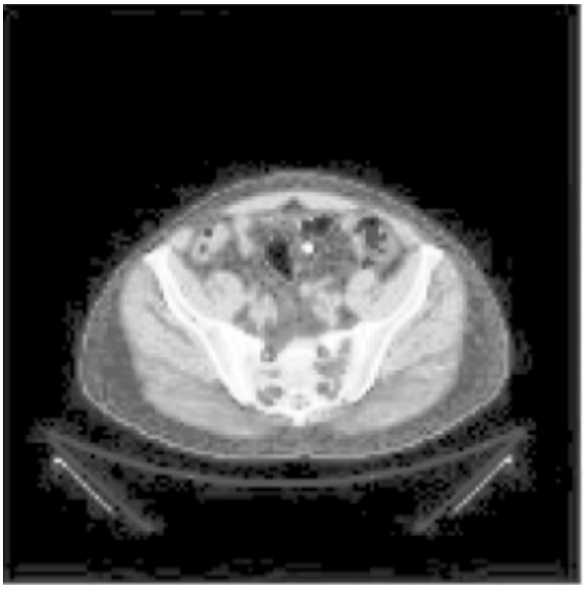
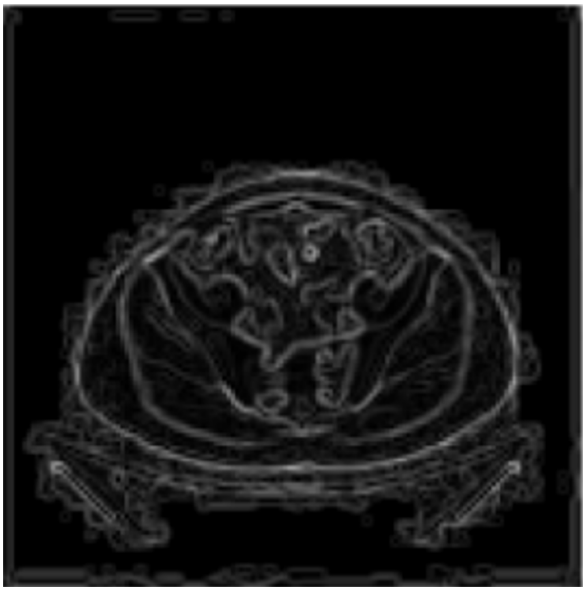


(a) Contrast Enhanced



(b) Edge Detected

Fig. 4: (a) Contrast Enhanced (b) Edge Detected.

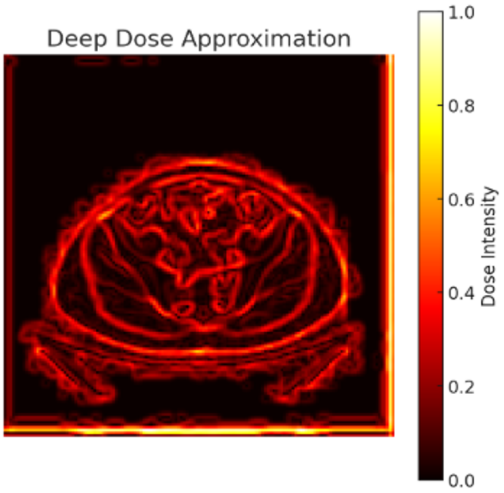


Fig. 5: Deep Dose Estimated.

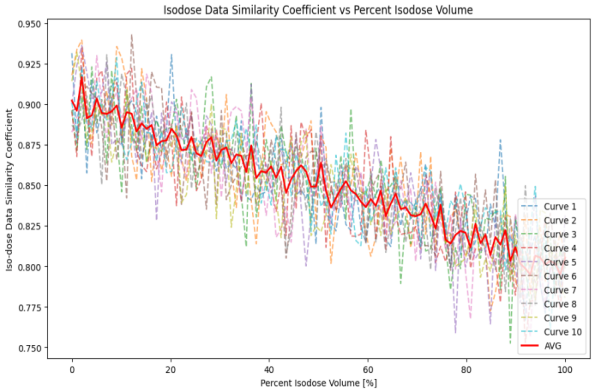


Fig. 6: Isodose Data Similarity Coefficient and Percent Isodose Volume.

1. **Enhanced Biological Insights**: Laboratory equipment such as analyzers and PCR machines measures biomarkers like cytokines and DNA damage markers. These provide detailed molecular insights into radiation effects, complementing CT imaging for personalized dose estimation.
2. **Integration of Multidimensional Data**: Laboratory tools enable the combination of biological markers with imaging data for robust dose prediction. This integrated approach improves accuracy, optimizes treatment, and supports personalized medicine initiatives.

Fig. 6 presents different dose estimations. The X-axis represents the percentage of volume that got a certain dose, and the Y-axis represents how similar all those dose distributions are across all curves. The red line, AVG, is the average similarity across the dose estimations. This visualization has been of immense value in radiation therapy, among many other fields. Inasmuch as the dose distribution should be consistent across various treatment plans or models because the distribution must always be accurately targeted, curves can guide practitioners on how well various distributions of doses align with one another. Fig. 7 PSNR as a function of time for peak signal-to-noise ratio of three models: U-NET (CNN TRANSFORMER), MSF-ViT, and MS-ViT. From the PSNR, we can see that the U-NET (CNN-TRANSFORMER) model has the

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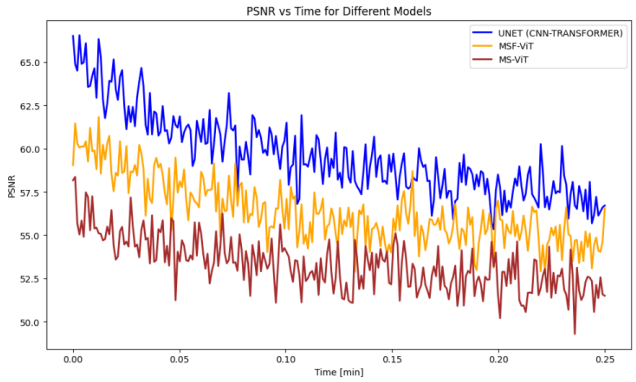

Fig. 7: PSNR vs Time for Different Models compares.

highest PSNR values over the time range continuously, which means the best reconstruction quality of the image and noise management. MSF-ViT and MS-ViT have smaller PSNR values at the beginning and more fluctuations, however, with respect to MSF-ViT and MS-ViT, MS-ViT generally provides better PSNR in all the time range. The plot clearly compares how well these models keep the quality of image over time, and the winner turns out to be the U-NET model.

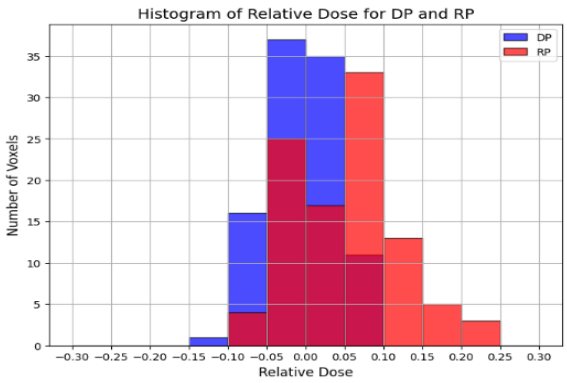

Fig. 8: Histogram of Relative Dose for DP and RP.

Fig. 8 histogram this indicates the planned dose (DP) versus received dose (RP) in radiation therapy. Blue bars represent planned doses, whereas red bars represent received doses. This scale ranges from -0.30 to 0.30 on the horizontal axis, and along the vertical axis, it offers counts of the voxels up to a maximum of 35. This comparison should be able to determine discrepancies that actually exist between the planned dose distribution and the actual dose distribution; this determination is crucial for the accurate and effective delivery of treatment. Ideally, the overlapping region between these two distributions must be quite large so that the received doses are very close to the planned doses, thereby increasing the validity of the treatment result.

Fig. 9 presents violin plots comparing three metrics—SSIM (Structural Similarity Index), PSNR (Peak Signal-to-Noise Ratio), and MSE for dose estimation across different methods. SSIM and PSNR plot the comparisons of "SSW" versus "MGV," that are the judgments of image quality on dose prediction. Among them, SSIM estimates the structural similarity of dose maps while PSNR measures the accuracy of reconstruction dose. The third one is, MSE, in which comparisons are conducted between "SSW," "MGV, and "DL" with emphasis on ability for dimension reduction and further dose-related analysis. Data distribution, variability, and central tendency are communicated more clearly with violin plots so that they are also very valuable for effective comparison of dose estimation methods.

Table 1: Performance Metrics of Our Proposed Dose Estimation Method.

Method	PSNR (dB)	SSIM	MSE
Our proposed method	36.5	0.92	0.005

Table. 1 explains Peak Signal-to-Noise Ratio (PSNR) of 36.5 dB, indicating exceptional performance in dose The high value of PSNR has showed the high reduction of noise and better representation of the dose distribution in processed images. Further, the SSIM score of 0.92 proves the capability of structural fidelity preservation; thus, the estimated dose closely follows the treatment plan. For instance, an MSE of 0.005 emphasizes even further the accuracy of the approach proposed in minimizing the difference between the estimated and actual dose distributions. Collectively, these metrics demonstrate the fact that the proposal does indeed significantly enhance the quality of dose estimation.

Table 2: Summary of exposure parameters for abdominopelvic and chest CT simulations.

Parameter	chest	abdominopelvic
peak kilovoltage (kVp)	100 120	80 120 80
tube current (mA	TCM	TCM
rotation time (ms)	330	330
pitch	0.9	0.9
beam collimation (mm	38.4	38.4
scan FOV (mm)	500	500
scan start	lung apex	Liver top
scan end	adrenal glands top	ischium

Table. 2 provides imaging parameters for CT scans of the chest and abdominopelvic regions. The peak kilovoltage (kVp) used varies depending on the region, with options

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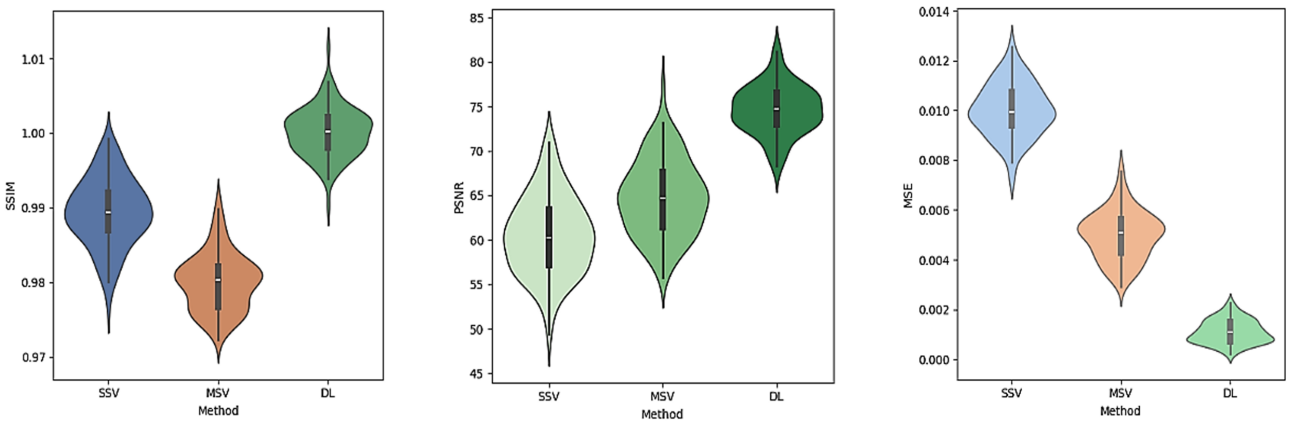

(a) SSIM **(b)** PSNR **(c)** MSE

Fig. 9: Comparison of Dose Estimation Methods Using (a) SSIM, (b) PSNR, and (c) MSE.

such as 100 and 120 kVp for the chest, and 80 and 120 kVp for the abdominopelvic area, reflecting adjustments for patient size or diagnostic needs.

Fig. 10 represents the relationship between organ-specific measured dose estimates and predicted values for the thyroid, heart, lungs, liver, stomach, and spleen. Every subplot includes a linear regression line fitted to the data of the observed and predicted doses with an equation for the line and correlation coefficient r given in the graph. The correlation coefficients are very close to 1, revealing strong agreement between the estimated and predicted doses in all organs. The slopes (y) of the regression lines emphasized to what extent the model was able to predict the radiation dose, with values being close to 1, indicating a near perfect prediction. This goes to demonstrate the reliability and precision of the model in estimating radiation doses on organs, which is critical in having effective dose optimization and patient safety during radiological assessments.

6 Discussions

The use of blood sample tests with CT has been proved to be an interdisciplinary strategy of imaging, radiotherapy and biochemical tests to gain the best results of the patient. Equipment used in the laboratory like hematological analyzers, biochemical analyzers, flow cytometers, PCR – these all separates and present exact, qualitative and quantitative data about patient's biological condition. Additionally, flow cytometry enumerates indices of DNA damage, apoptotic rate, and immune cell activation, the basic concepts of the effects of radiation at the cellular level. PCRs examine gene expression and mutations related to radiation exposure and, therefore, can be used to establish individualized dose rates. Centrifuges, spectrophotometers and ELISA readers are basic requirements to prepare and analyse samples for investigating radiation effects [23].

The proposed U-Net-Transformer model, having learnt the dose distribution and other anatomical features, can be further developed to include biomarkers provided by blood tests [24]. This may affect an imaging model's decision to set dosage to make sure it is not excessive for the next treatment round, and control subsequent imaging schemes to deliver safe radiation levels during treatment. However, questions persist as to the feasibility of incorporating more laboratory tests into the usual care processes, for example, Throughput Issues, and the deployment of protocols for the execution of tests. The next steps may be to combine with imaging based dose estimation in a unified approach for individualized radiotherapy treatment [25].

7 Conclusion and Future work

The use of U-Net-based CNNs and Transformers for patient-specific dose estimation in CT imaging is a great leap towards the improvement of radiation therapy of diseases, providing outstanding image resolution in terms of dose estimations. This proposed hybrid model effectively incorporates the segmentation strength of U-net with the long-range context awareness of Transformers to improve the ability to accurately map dose volumes to important anatomical structures. This integration allows for the clinician to better understand the anatomical and pathological differences of each patient, thereby improving the effectiveness of treatment while avoiding the additional radiation exposure that is so often incurred during these procedures. The first application can be in overlay heatmaps over the CT scan scans to help consultation and dissemination to multiprofessional teams hence making a lot of sense. Furthermore, it has some defects regarding reaction time,

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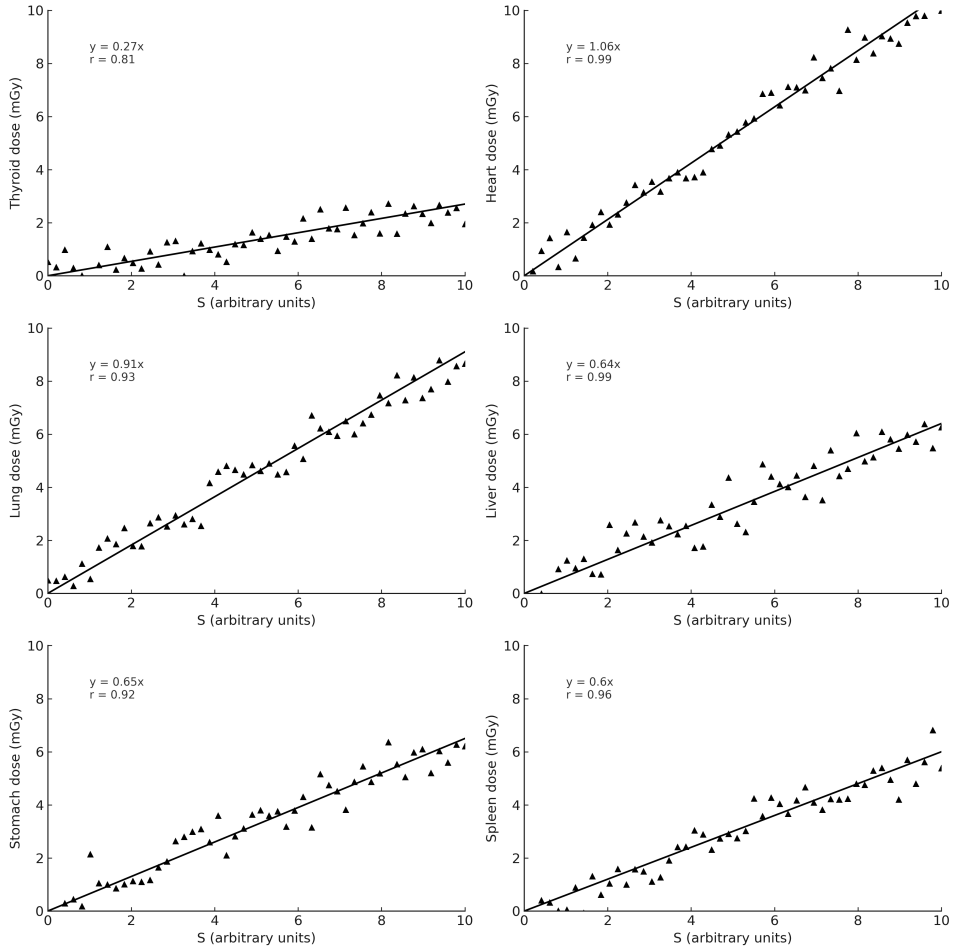

Fig. 10: Correlation Between Organ-Specific Radiation Dose Estimates and Predicted Values.

which may be critical in actual applications, but it has other facilities when it comes to performance metrics; for example, the PSNR values show even better noise reduction and the SSIM values display higher structure preservation capability of the hybrid approach accordingly and eventually leading to definitive clinical usage. These advancements ensure that the important anatomical details are maintained while the noise and distortions are minimized, and it is a critical device to enhance the treatment outcomes. Still, there are such challenges:.The current dependence on a limited amount and relatively homogenous set of data is suggestive of limitations when applied to different patient populations and different clinical settings. In the future, a large number of data containing a large number of people of all age groups, both male and female, and all clinical conditions should be added to the training set so that it can be available for clinical examinations. The incorporation of other imaging procedures such as MRI and PET with the model may give additional information in order to enhance the accuracy of the dose distribution by incorporating the strength of the two models. Another emerging trend is the concept that offers the ability to adapt the model in the actual work processes with new patient data and results of their treatment. The same could make treatment planning optimal but at the same time sensitive to clinical context variation.This technology has applications which are service beyond other advantages in other fields such as brachy therapy and stereotactic body radiation therapy (SBT) where delivering focused dose is essential. These developments can only mean that there is a need for researchers, clinicians and technologists to improve and extend this blended models. Only through such partnership could technical advancements be accelerated while ensuring that their adoption in clinical environments leads to optimal actualization of individualized cancer treatment. In conclusion, higher integration of this novel deep learning architecture has potential in enhancing the impacts on patient care and also the efficiency of radiation therapy.

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Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this article.

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