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Single time-point kidney dosimetry in ^{177}Lu-PSMA therapy: A comparison between AI-based and manual segmentation approaches

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ABSTRACT

Background: Single time-point (STP) dosimetry has become a practical and efficient approach for personalised radioligand therapy (RLT), with 48-hours post-injection identified as optimal for kidney dose estimation in ^{177}Lu-PSMA therapy for prostate cancer. However, segmentation accuracy remains a critical factor affecting dosimetry reliability. AI-based segmentation has recently been integrated into commercial software to improve efficiency and reduce variability.

Objectives: This study aims to quantify kidney absorbed doses in patients receiving ^{177}Lu-PSMA therapy using STP dosimetry and to compare the accuracy and consistency of AI-based segmentation versus manual segmentation techniques.

Materials and methods: Eight treatment cycles from 5 patients of ^{177}Lu-PSMA were retrospectively analysed. In this work, whole-body SPECT/CT imaging was performed approximately 48 hours post-injection. Then, kidney dosimetry was calculated using voxel-based STP (Hänscheid method) within MIM SurePlan™ MRT software. Kidney volumes of interest (VOIs) were segmented using three approaches: 1) AI-based automatic segmentation, 2) AI-based with manual refinement, and 3) fully manual segmentation. Mean absorbed doses and VOI volumes were compared across methods. Statistical analyses included ANOVA, Dice Similarity Coefficient (DSC), and Jaccard Similarity Coefficient (JSC).

Results: No significant differences in mean kidney absorbed doses were found across segmentation methods (p=0.964), while kidney VOI volumes showed significant variation (p<0.05). AI-based segmentation achieved high concordance with manual delineation (DSC: 0.898±0.019; JSC: 0.816±0.031).

Conclusion: AI-based segmentation provides comparable absorbed dose results to manual segmentation, with reduced time and inter-observer variability.

Introduction

While the Medical Internal Radiation Dose (MIRD) Committee recommends multi-time-point (MTP) imaging to determine time-integrated activity (TIA) and absorbed dose accurately, MTP protocols are often impractical in routine clinical settings due to time and resource constraints.[8] To address this, Hänscheid et al. proposed a simplified single time-point (STP) method that estimates absorbed dose using one single quantitative SPECT/CT image and an assumed effective half-life to address.[9] Recent studies, including those by Brosch-Lenz et al.,[10] have validated

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the accuracy of kidney absorbed dose estimation using STP at approximately 48 hours post-injection, showing minimal deviation compared to MTP-derived references for ^{177}Lu-PSMA in prostate cancer patients, which was in the same way as other related STP dosimetry studies.[11-13]

One of the primary sources of uncertainty in image-based dosimetry is organ segmentation. Accurate delineation of the kidneys directly impacts the volume and activity quantification, and thus the calculated absorbed dose.[14,15] Although widely used, manual segmentation is time-consuming and operator-dependent, leading to inter-observer variability and potential inconsistencies.[16-18] In contrast, artificial intelligence (AI)-based segmentation, particularly using deep learning (DL), offers the potential for rapid, reproducible, and standardized delineation, and has been increasingly integrated into commercial dosimetry platforms such as MIM SurePlan™ MRT (version 7.3.6) and Hermes Voxel-based Dosimetry (version 3.0).[18-20]

Therefore, this study aims to quantify kidney absorbed doses in patients receiving ^{177}Lu-PSMA therapy using STP dosimetry and to compare the accuracy and consistency of AI-based segmentation versus manual segmentation techniques.

Materials and methods

Patient selection

This study was conducted on eight treatment cycles in five ^{177}Lu-PSMA patients treated at the Department of Nuclear Medicine, Faculty of Medicine, Ramathibodi Hospital, Bangkok, Thailand, from January 2024 to December 2024. This retrospective study was approved by the local ethics committee of the Faculty of Medicine Ramathibodi Hospital, Mahidol University. Patients were aged 58-88 years (mean: 67.49±11.56 years). The mean administration activity was 6731.57±1026.49 MBq. Whole-body single time-point SPECT/CT scans were performed approximately 48 hours post-injection (mean: 49.18±2.61 hours post administration) as shown in Table 1. Patient data were tabulated.

Table 1. Patient demographic Information.

Overall (N=8)	Age (years)	Administration activity (MBq)	Acquisition time point (h p.i.)
Mean±SD	67.49±11.56	6731.57±1026.49	49.18±2.61
Median	65.00	6710.15	50.22
Range	58.00-88.00	5607.70-8103.00	43.77-51.95

Image acquisition protocol

A dual-head hybrid SPECT/CT scanner (GE Discovery 870 DR, GE Healthcare, MI, USA) equipped with a Medium Energy General Purpose (MEGP) collimator was used for image acquisition. Each bed position was acquired using 60 frames per head at 5 seconds per frame, resulting in a total acquisition time of approximately 7 minutes.

Quantitative image reconstruction was performed using an Ordered Subset Expectation Maximisation (OSEM) algorithm in Hermes Hybrid Recon 3.0 (Hermes Medical Solutions, Sweden), with 16 iterations, 9 subsets, and a matrix size of 128×128.

To correct for collimator-detector response, a Gaussian model was applied during reconstruction, and the specific parameters for the MEGP collimator of the GE Discovery 870 DR were entered into the software. CT images for attenuation correction were acquired using a low-dose protocol to minimise additional radiation exposure.

Voxel-based single time-point dosimetry

Voxel S-value dosimetry for the kidneys was performed using MIM SurePlan™ MRT dosimetry software (version 7.3.6; GE Healthcare, MI, USA). Single time-point dosimetry, which estimates the time-integrated activity (TIA) based on monoexponential decay fitting using the effective half-life (T_{eff}), was applied as proposed by Hänscheid et al.[10] as shown in Equation 1.

$$TIA \approx \frac{A(t)\cdot 2^{\frac{t}{T_{eff}}}\cdot T_{eff}}{\ln(2)} \qquad (1)$$

If the imaging time point was interval 0.75 to 2.5, STP TIA had less than 10% error compared with the MTP TIA.[10,11] STP TIAs were calculated using the measured activity at approximately 48 hours post-injection for ^{177}Lu-PSMA.

For kidneys STP dosimetry, the volume of interest (VOI) was contoured, limited to the renal cortex on each axial slice as illustrated in Figure 1. This VOI was used to determine both the organ volume (in mL) and the mean absorbed dose (in Gy).

To evaluate the effect of segmentation methods on dosimetric outcomes, three different approaches were applied for kidney delineation:

(a) AI-based automatic segmentation

This method utilized the deep learning algorithm Contour ProtégéAI®, integrated within MIM SurePlan™ MRT software (version 7.3.6). The segmentation process was fully automated and initiated upon image import. The AI algorithm was trained to segment normal organs (including kidneys) based on CT datasets, providing a consistent and time-efficient alternative to manual contouring.

(b) AI-based segmentation with manual modification

In this approach, the automatically generated VOIs from Contour ProtégéAI® were reviewed and manually adjusted by a trained operator to improve anatomical accuracy, particularly in regions where the AI model may have under- or over-segmented the renal cortex. This method represents a hybrid of AI support with human expert refinement.

(c) *Manual segmentation (reference standard)*

Full manual segmentation was performed on CT images by a medical physicist with one year of experience in dosimetry. The segmentation was conducted slice-by-slice, with careful delineation of the renal cortex. This method served as the reference standard for comparison. Importantly, all manual segmentations were performed independently and blinded to the AI-generated results, ensuring unbiased evaluation.

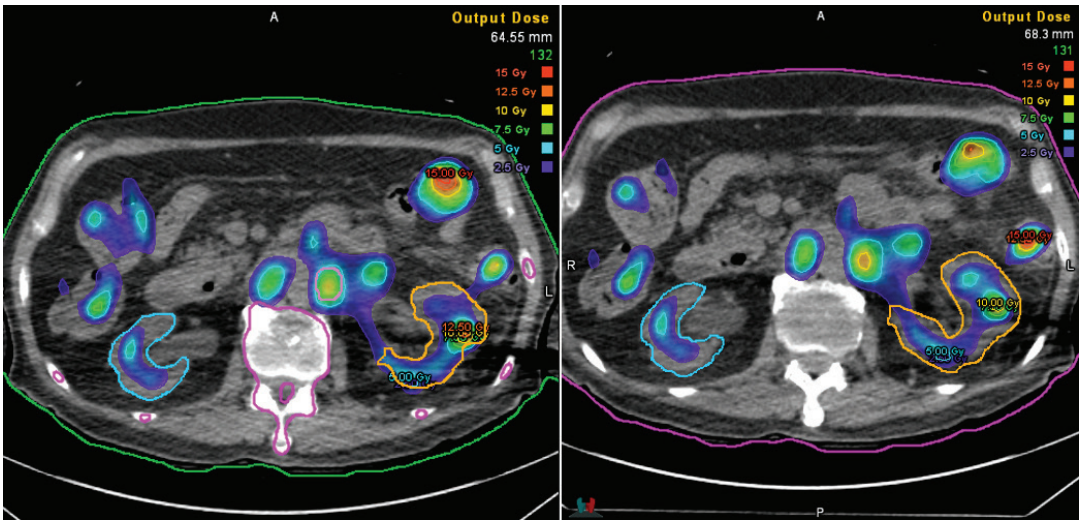

Figure 1. *Kidneys contouring. Left: AI-based segmentation, and right: manual segmentation.*

Each segmentation method was subsequently used to calculate the kidney absorbed dose using the MIM SurePlan MRT dosimetry workflow, which incorporates quantitative SPECT/CT data and voxel-based dose computation. The comparison among segmentation methods aimed to assess the consistency in dosimetric outcomes and segmentation accuracy. Specifically, the mean absorbed dose and contouring volume of the kidneys were compared across the three segmentation techniques using percentage difference. For evaluating segmentation accuracy, Dice Similarity Coefficient (DSC) and Jaccard Similarity Coefficient (JSC) were calculated to quantify the overlap between segmented volumes. These metrics were computed using Python (Version 3.13.2).

Statistical analysis

Following kidneys dosimetry, dosimetric parameters from each segmentation method, including absorbed dose and contouring volume, were reported. Comparisons of kidney absorbed doses and contouring volume across segmentation methods were conducted using One-way analysis of variance (ANOVA) in IBM SPSS Statistics. The $p<0.05$ was considered statistically significant.

Results

Kidney dosimetry and contouring volume

The kidney mean-absorbed dose, estimated using the single time-point (STP) method, along with corresponding contouring volumes, was evaluated using three segmentation approaches: manual, AI-assisted, and AI-assisted with manual adjustment. Details of these measurements, including percentage differences compared to manual segmentation (used as the reference), are presented in Table 2. Additionally, segmentation performance was assessed using Dice Similarity Coefficients (DSC) and Jaccard Similarity Coefficients (JSC), as shown in Table 3.

Table 2. Mean absorbed dose (Gy) and kidney volume (mL), including percentage differences (%), derived from manual segmentation and two alternative methods: AI-based segmentation and AI-based segmentation with manual modification, for each patient.

Study No.	Mean absorbed dose (Gy) (Percentage difference)*			Contouring volume (mL) (Percentage difference)*		
	AI-based with			AI-based with		
	Manual segmentation	Manual modification segmentation	AI-based segmentation	Manual segmentation	Manual modification segmentation	AI-based segmentation
1	1.82	2.00 (9.42)	2.04 (11.40)	446.13	366.85 (-19.50)	332.13 (-29.30)
2	1.84	1.93 (4.77)	1.95 (5.80)	376.59	337.62 (-10.91)	321.49 (-15.79)
3	1.61	1.70 (5.44)	1.72 (6.61)	404.33	363.63 (-10.60)	347.34 (-15.16)
4	2.57	2.71 (5.30)	2.76 (7.13)	290.12	254.82 (-12.96)	247.96 (-15.67)
5	5.17	5.37 (3.80)	5.37 (3.80)	342.36	267.60 (-21.25)	276.60 (-24.51)
6	2.89	3.05 (5.39)	3.11 (7.33)	303.30	271.01 (-11.24)	254.67 (-17.43)
7	2.47	2.49 (0.81)	2.50 (1.21)	354.79	351.57 (-0.91)	346.92 (-2.24)
8	2.09	2.21 (5.58)	2.22 (6.03)	367.13	337.98 (-8.27)	329.44 (-10.82)
Mean±SD	2.39±1.41	2.52±1.17	2.54±1.16	357.46±50.91	315.79±46.47	309.94±39.08

Note: The number in brackets quantifies the relative change as a percentage derived from manual segmentation.

Table 3. Dice similarity coefficient and Jaccard similarity coefficient comparing manual segmentation with two alternative methods—AI-based segmentation and AI-based segmentation with manual modification—for kidney volumes in each patient.

Study No.	Dice similarity coefficient (DSC)		Jaccard similarity coefficient (JSC)	
	AI-based segmentation	AI-based with manual modification segmentation	AI-based segmentation	AI-based with manual modification segmentation
1	0.867	0.881	0.765	0.788
2	0.913	0.928	0.840	0.866
3	0.920	0.933	0.849	0.875
4	0.908	0.915	0.831	0.844
5	0.905	0.926	0.826	0.862
6	0.913	0.930	0.839	0.869
7	0.873	0.890	0.774	0.802
8	0.893	0.903	0.807	0.824
Mean±SD	0.898±0.019	0.9131±0.020	0.816±0.031	0.840±0.033

Comparison of absorbed dose and contouring volume

Figures 2 and 3 show the distribution of kidney absorbed dose across the three segmentation techniques, both overall and for individual cases. The AI-assisted method yielded the highest mean absorbed dose (2.54±1.16 Gy), followed closely by the AI-assisted with manual adjustment (2.52±1.17 Gy), while the manual method resulted in a slightly lower mean value (2.39±1.41 Gy).

A similar trend was observed in kidney contouring volumes (Figure 4). The manual approach produced the largest volume (357.46±50.91 mL), followed by AI with manual adjustment (315.79±46.47 mL), and then AI-only segmentation (309.94±39.08 mL).

DSC and JSC values, which reflect how well the automated contours matched the manually segmented ones, are summarised in Table 3. Overall, segmentation with manual adjustment outperformed AI-only: the average DSC improved from 0.898±0.019 to 0.913±0.020, and the JSC from 0.816±0.031 to 0.840±0.033. These differences are visualised as box plots in Figures 5 and 6.

Statistical comparison

A one-way ANOVA was conducted to examine differences in absorbed dose and kidney volume among the three segmentation methods, as shown in Table 4.

While the absorbed dose did not significantly differ between methods ($p>0.05$), kidney volumes did show statistically significant differences ($p<0.05$), particularly between manual and AI-only segmentation. This suggests that while absorbed dose estimates remained consistent, the accuracy of kidney contouring varied depending on the segmentation approach used.

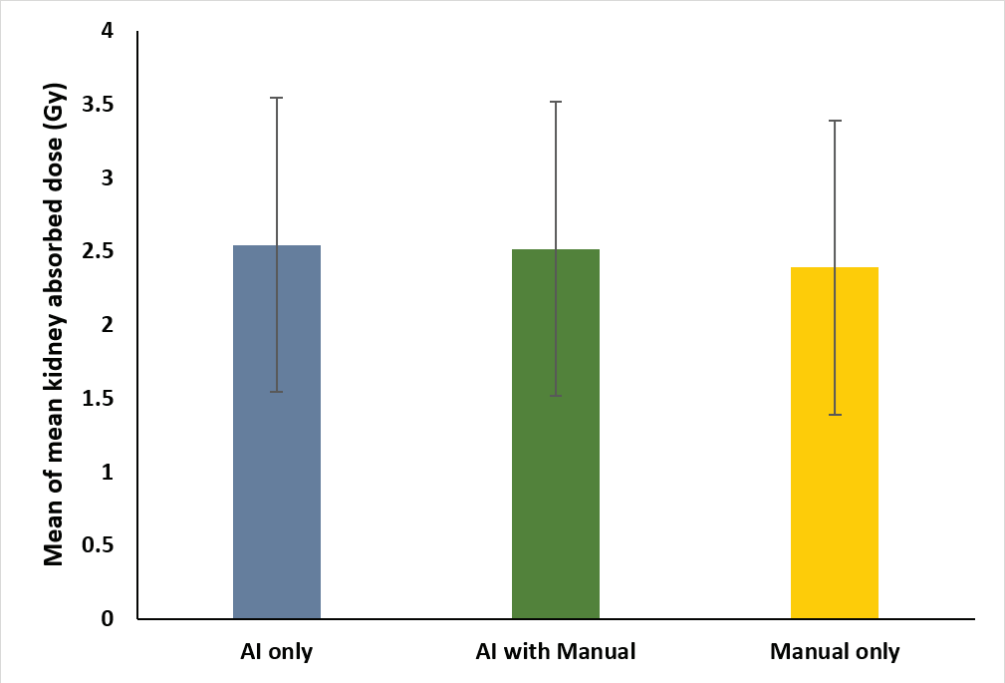

Figure 2. *Comparison of the mean kidney absorbed dose (±SD) obtained using three different segmentation methods: AI-based segmentation, AI-based segmentation with manual modification, and manual segmentation.*

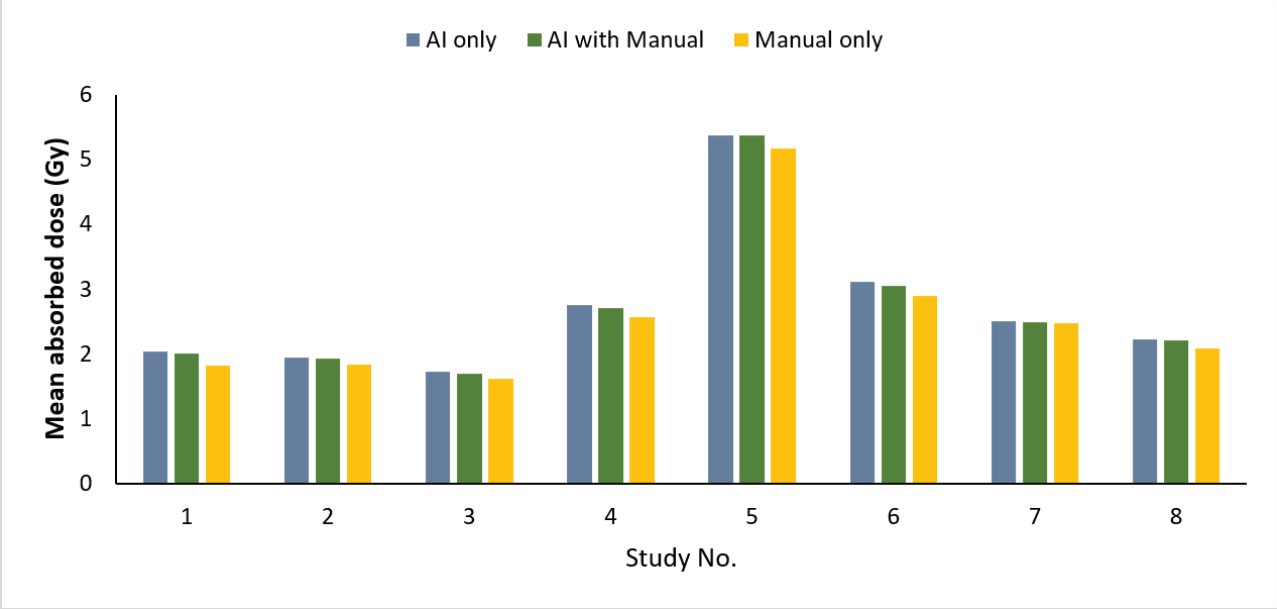

Figure 3. *Comparison of the mean kidney absorbed dose obtained using three segmentation methods: AI-based segmentation, AI-based segmentation with manual modification, and manual segmentation across individual studies.*

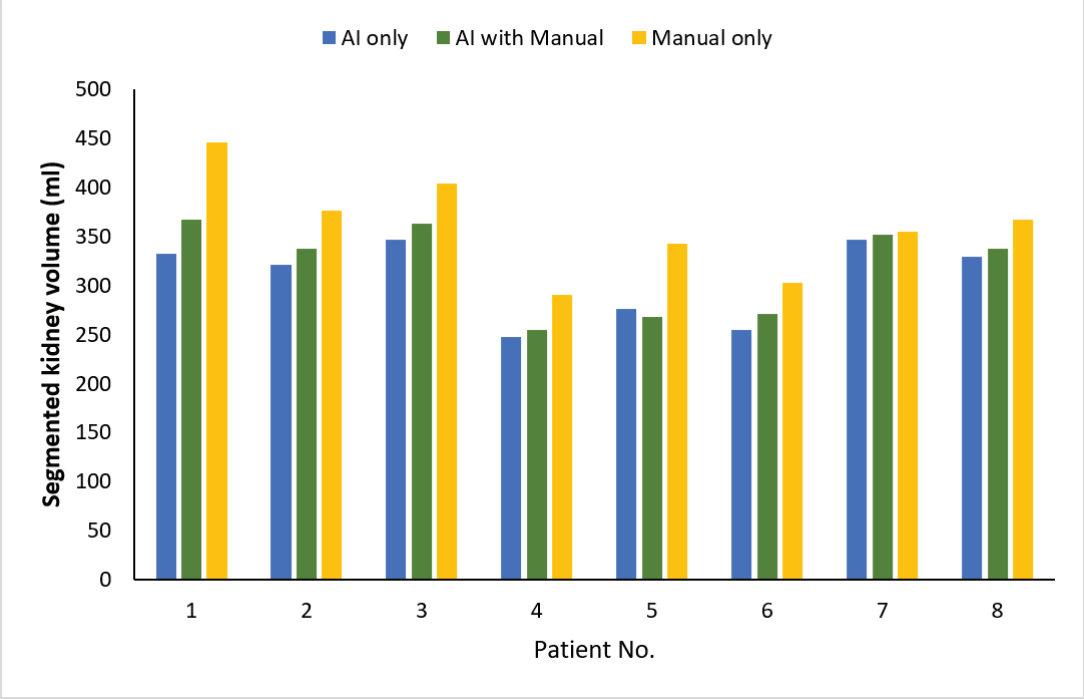

Figure 4. *Comparison of the mean kidney contouring volume (±SD) obtained using three segmentation methods: AI-based segmentation, AI-based segmentation with manual modification, and manual segmentation.*

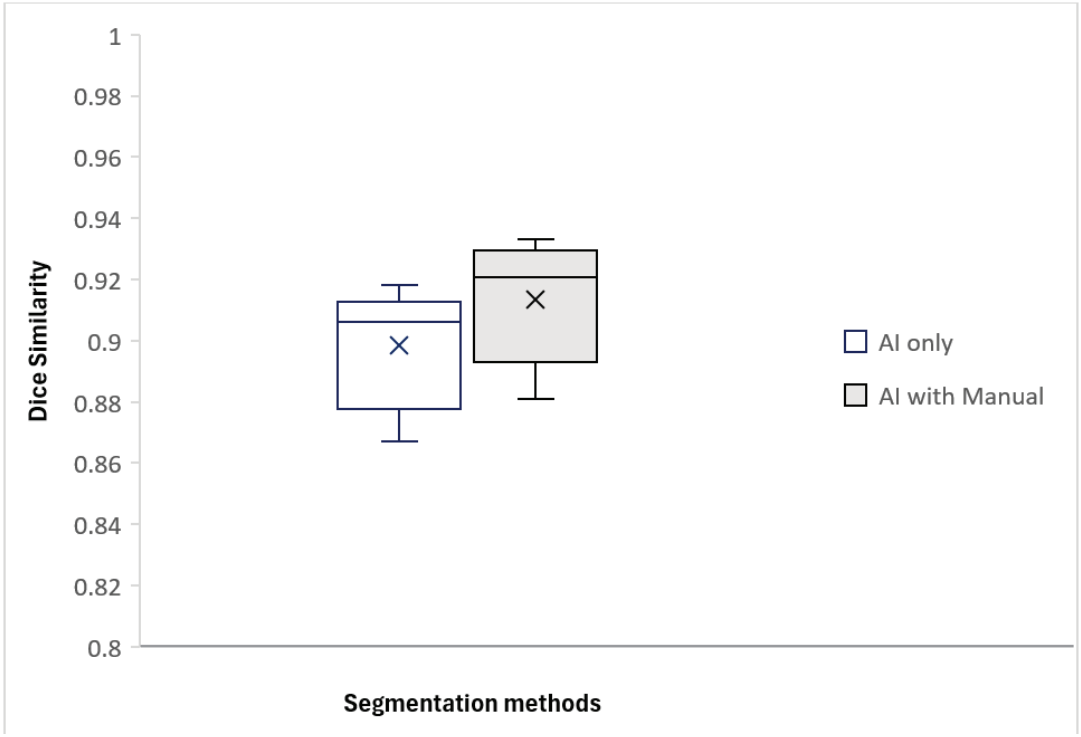

Figure 5. *Box plot of dice similarity coefficient (DSC) for kidney contouring volumes obtained from AI-based segmentation and AI-based segmentation with manual modification.*

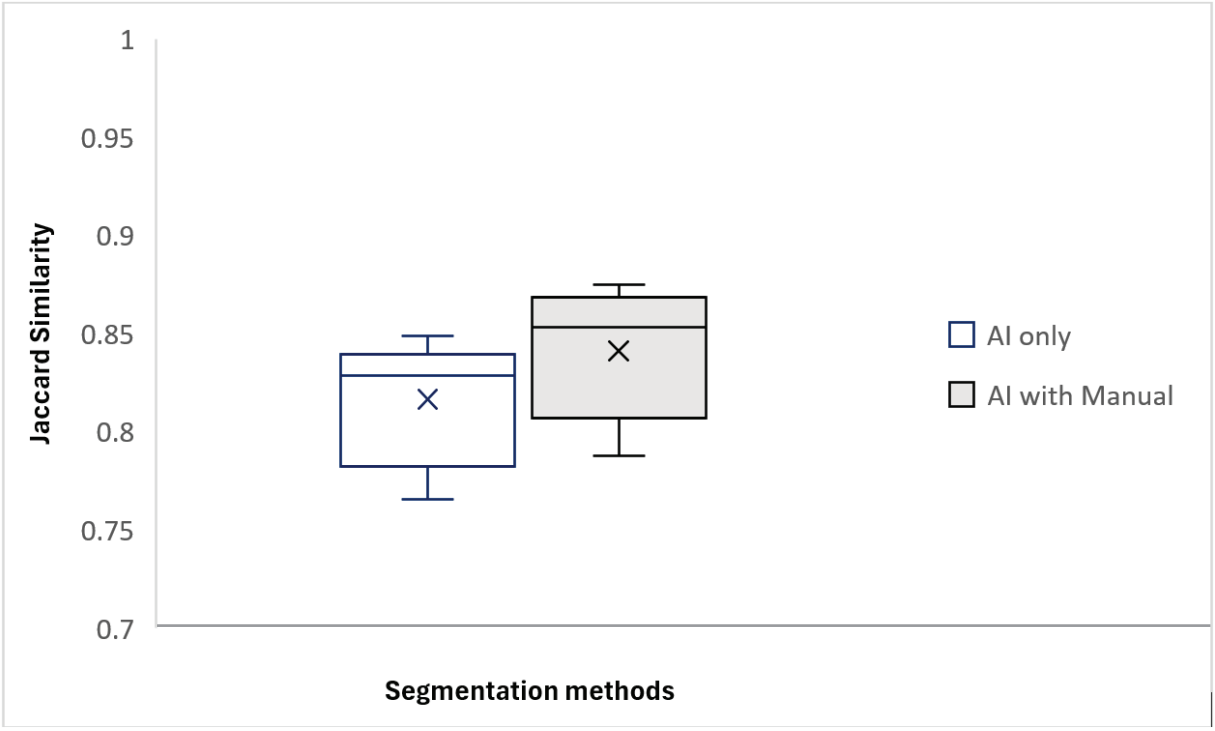

Figure 6. *Box plot of Jaccard Similarity Coefficient (JSC) for kidney contouring volumes obtained from AI-based segmentation and AI-based segmentation with manual modification.*

Statistical comparison

A one-way ANOVA was conducted to examine differences in absorbed dose and kidney volume among the three segmentation methods, as shown in Table 4. While the absorbed dose did not significantly differ between methods ($p>0.05$), kidney volumes did show statistically significant differences ($p<0.05$), particularly between manual and AI-only segmentation. This suggests that while absorbed dose estimates remained consistent, the accuracy of kidney contouring varied depending on the segmentation approach used.

Table 4. The p values from one-way ANOVA comparing kidney mean absorbed dose and contouring volume obtained using manual segmentation, AI-based segmentation, and AI-based segmentation with manual modification.

	Manual vs AI-based	Manual vs AI with manual modification	AI-based vs AI with manual modification	All segmentation methods
Mean absorbed dose	0.813	0.821	0.992	0.964
Contouring volume	$p<0.05$	0.074	0.477	$p<0.05$

Discussion

In this study, three different kidney segmentation approaches for single time-point (STP) dosimetry in patients treated with ^{177}Lu-PSMA was investigated: manual segmentation by a medical physicist, fully automated segmentation, and automated segmentation with manual refinement.

When comparing these methods, the mean absorbed dose to the kidneys did not show a statistically significant difference ($p>0.05$). The percentage difference in absorbed dose between AI-based segmentation and manual segmentation was approximately 6% (range: 0%-11%), while the difference between AI-only and AI with manual modification was about 5% (range: 0%-9%).

These findings align with previous work by Dewaraja et al. who evaluated deep-learning-based kidney segmentation against manual contours in a multiple time-point (MTP) SPECT/CT study following ^{177}Lu-PRRT.[21] They reported mean absorbed dose differences of 3% for CNN-only segmentation and 2% (range: 0%-4%) with manual segmentation. The slightly higher variability observed in our study may be attributed to the use of STP dosimetry based on time-integrated activity (TIA) estimation from a STP approach, while the previous study used MTP. Nonetheless, our results

demonstrated that STP dosimetry performed around 48 hours post-injection can achieve a mean error of less than 10%, consistent with the recommendation by Hänscheid et al.,[9] and supported by Resch et al.,[22] as a practical alternative to MTP approach.

In terms of segmentation accuracy, our study reported average DSC values of 0.898 for AI-only segmentation and 0.913 for AI with manual modification when compared with manual segmentation. These results are comparable to those reported by Dewaraja et al. who found a DSC of 0.91 for deep-learning-only segmentation and 0.93 when manual refinement was included.[21]

Despite the similar absorbed dose estimates, a statistically significant difference was found in the kidney contouring volumes, particularly between manual and AI-only methods. Manual contours tended to include larger volumes, likely due to added margins to account for spill-out activity, limited spatial resolution (partial volume effects), and CT-related artefacts. These factors may lead to underestimation of the absorbed dose when smaller volumes are contoured, potentially impacting dose-response evaluations. This observation is supported by Nazari et al. who reported interobserver variability in manual segmentation due to inconsistent inclusion of spill-out activity beyond CT-defined anatomical boundaries in kidney and liver VOIs during deep-learning dosimetry evaluation. [23]

Limitations

This study has several limitations. First, the patient cohort was relatively small, which may limit the generalisability of the findings. Second, single time-point (STP) dosimetry was not validated against multi-time-point (MTP) dosimetry, as MTP was not routinely performed at our institution as a baseline for voxel-based dosimetry. Lastly, manual segmentation was conducted by a single observer, which may introduce observer bias and limit assessment of interobserver variability.

Conclusion

This study demonstrated that single time-point (STP) dosimetry is a promising approach for voxel-based dosimetry in ^{177}Lu-PSMA therapy and can be feasibly implemented in routine clinical practice. While different segmentation methods resulted in variations, particularly in the segmented kidney volume, the absorbed dose estimates remained comparable across methods. AI-based segmentation produced results consistent with manual segmentation, while offering significant advantages in terms of time efficiency, reliability, accuracy, and consistency, making it a robust alternative for clinical dosimetry workflows.

Ethical approval

This study was approved by the Human Ethics Committee of the Faculty of Medicine Ramathibodi Hospital, Mahidol University (COA No. MURA2025/422).

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Conflict of interest

There is no conflict of interest.

CRediT authorship contribution statement

Thitaya Chaiwongsa: conducted the experiments, analyzed the data, and drafted the manuscript; **Putthiporn Charoenphun:** co-supervised the study; **Wichana Chamroonrat:** supervised the clinical part and verified the VOIs in the study; **Krisanat Chuamsaamarkkee:** drafted the manuscript, prepared the figures and tables, and served as the corresponding author.

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References

[1] Meyer C, Szidonya L, Winters C, Mench A, Mallak N, Mittra E. Quantitative imaging for 177Lu-PSMA treatment response monitoring and dosimetry. Front Nucl Med. 2023; 3: 1291253. doi: 10.3389/fnume.2023.1291253.

[2] Violet J, Jackson P, Ferdinandus J, Sandhu S, Akhurst T, Iravani A, et al. Dosimetry of 177Lu-PSMA-617 in metastatic castration-resistant prostate cancer: Correlations between pretherapeutic imaging and whole-body tumor dosimetry with treatment outcomes. J Nucl Med. 2019; 60(4): 517-23. doi:10.2967/jnumed.118.219352.

[3] Juzeniene A, Stenberg VY, Bruland ØS, Larsen RH. Preclinical and clinical status of PSMA-targeted alpha therapy for metastatic castration-resistant prostate cancer. Cancers (Basel). 2021; 13(4): 779. doi:10.3390/cancers13040779.

[4] Alsadi R, Djekidel M, Bouhali O, Doherty JO. Towards routine clinical use of dosimetry in [177Lu] Lu-PSMA prostate cancer radionuclide therapy: Current efforts and future perspectives. Front Phys. 2022; 10: 1-13 doi:10.3389/fphy.2022.940677.

[5] Ramonaheng K, Qebetu M, Ndlovu H, Swanepoel C, Smith L, Mdanda S, et al. Activity quantification and dosimetry in radiopharmaceutical therapy with reference to 177Lutetium. Front Nucl Med. 2024; 4: 1355912. doi:10.3389/fnume.2024.1355912.

[6] Brosch-Lenz J, Uribe C, Gosewisch A, Kaiser L, Todica A, Ilhan H, et al. Influence of dosimetry method on bone lesion absorbed dose estimates

in PSMA therapy: application to mCRPC patients receiving Lu-177-PSMA-I&T. EJNMMI Phys. 2021; 8(1): 26. doi:10.1186/s40658-021-00369-4.

[7] Gustafsson J, Sundlöv A, Sjögreen Gleisner K. SPECT image segmentation for estimation of tumour volume and activity concentration in 177Lu-DOTATATE radionuclide therapy. EJNMMI Res. 2017; 7(1): 18. doi: 10.1186/s13550-017-0262-7.

[8] Siegel JA, Thomas SR, Stubbs JB, Stabin MG, Hays MT, Koral KF, et al. MIRD pamphlet no. 16: Techniques for quantitative radiopharmaceutical biodistribution data acquisition and analysis for use in human radiation dose estimates. J Nucl Med. 1999;40(2): 37S-61S.

[9] Hänscheid H, Lapa C, Buck AK, Lassmann M, Werner RA. Dose mapping after endoradiotherapy with 177Lu-DOTATATE/DTATOC by a single measurement after 4 days. J Nucl Med. 2018; 59(1): 75-81. doi:10.2967/jnumed.117.193706.

[10] Brosch-Lenz J, Delker A, Völter F, Unterrainer LM, Kaiser L, Bartenstein P, et al. Toward single-time-point image-based dosimetry of 177Lu-PSMA-617 therapy. J Nucl Med. 2023; 64(5): 767-74. doi:10.2967/jnumed.122.264594.

[11] Kurth J, Heuschkel M, Tonn A, Schildt A, Hakenberg OW, Krause BJ, et al. Streamlined schemes for dosimetry of 177Lu-labeled PSMA targeting radioligands in therapy of prostate cancer. Cancers (Basel). 2021; 13(15): 3884. doi:10.3390/cancers13153884.

[12] Jackson PA, Hofman MS, Hicks RJ, Scalzo M, Violet J. Radiation dosimetry in 177Lu-PSMA-617 therapy using a single treatment SPECT/CT scan: A novel methodology to generate time- and tissue-specific dose factors. J Nucl Med. 2020; 61(7): 1030-6. doi:10.2967/jnumed.119.233411.

[13] Peters SMB, Mink MCT, Privé BM, de Bakker M, de Lange F, Muselaers CHJ, et al. Optimization of the radiation dosimetry protocol in Lutetium-177-PSMA therapy: toward clinical implementation. EJNMMI Res. 2023; 13(1): 6. doi:10.1186/s13550-023-00952-z.

[14] Gawel J, Rogulski Z. The challenge of single-photon emission computed tomography image segmentation in the internal dosimetry of 177Lu molecular therapies. J Imaging. 2024; 10(1): 27-40. doi: 10.3390/jimaging10010027.

[15] Makris NE, van Velden FH, Huisman MC,Menke CW, Lammertsma AA, Boellaard R. Validation of simplified dosimetry approaches in 89 Zr-PET/CT: The use of manual versus semi-automatic delineation methods to estimate organ absorbed doses. Medical Physics. 2014; 41(10): 102503. Doi: 10.1118/1.4895973.

[16] Vomacka L, Gosewisch A, Delker A, Fendler W, Bartenstein P, Boening G. Automatic image segmentation for 3D dosimetry in Lu-177 DKFZ-PSMA-617 therapy of castrate-resistant metastatic prostate cancer using a robust cluster algorithm on 4D SPECT data. J Nucl Med. 2016; 57(suppl2): 497.

[17] Hesamian MH, Jia W, He X, Kennedy P. Deep learning techniques for medical image segmentation: achievements and challenges. J Digit Imaging. 2019; 32(4): 582-96. doi: 10.1007/s10278-019-00227-x.

[18] Danieli R, Milano A, Gallo S, Veronese I, Lascialfari A, Indovina L, et al. Personalized dosimetry in targeted radiation therapy: A look to methods, tools and critical aspects. J Pers Med. 2022; 12(2): 205. doi: 10.3390/jpm12020205.

[19] Wendler T, Kreissl MC, Schemmer B, Rogasch JMM, De Benetti F. Artificial Intelligence-powered automatic volume calculation in medical images-available tools, performance and challenges for nuclear medicine. Nuklearmedizin. 2023; 62(6): 343-53. doi: 10.1055/a-2200-2145.

[20] MIM software Inc. MIM SurePlan™ MRT for Molecular Radiotherapy Dosimetry User Guide.

[21] Dewaraja YK, Mirando DM, Peterson AB, Niedbala J, Millet JD, Mikell JK, et al. A pipeline for automated voxel dosimetry: Application in patients with multi-SPECT/CT imaging after 177Lu-peptide receptor radionuclide therapy. J Nucl Med. 2022; 63(11): 1665-72. doi: 10.2967/jnumed.121.263738.

[22] Resch S, Ziegler SI, Sheikh G, Unterrainer LM, Zacherl MJ, Bartenstein P, et al. Impact of the reference multiple-time-point dosimetry protocol on the validity of single-time-point dosimetry for [177Lu]Lu-PSMA-I&T therapy. J Nucl Med. 2024; 65(8): 1272-8. doi: 10.2967/jnumed.123.266871.

[23] Nazari M, Jiménez-Franco LD, Schroeder M, Kluge A, Bronzel M, Kimiaei S. Automated and robust organ segmentation for 3D-based internal dose calculation. EJNMMI Res. 2021; 11(1): 53. doi: 10.1186/s13550-021-00796-5.