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Revolutionizing Colorectal Cancer Imaging: AI-Driven Insights with RECOMIA for Enhanced PET Metrics and Precision Medicine

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Abstract

Purpose: Colorectal cancer (CRC) poses a significant global health challenge, with accurate staging and restaging being critical for effective treatment planning. Traditional reliance on standardized uptake values (SUV) from ^{18}F-FDG PET/CT imaging is limited by image noise, inter-patient variability, and segmentation inconsistencies. Advanced metrics like Metabolic Tumor Volume (MTV) and Total Lesion Glycolysis (TLG) provide a more comprehensive assessment but are hindered by the need for precise tumor segmentation, a challenge with conventional methods. **Methods:** This retrospective observational study analyzed ^{18}F-FDG PET/CT scans from 15 CRC patients at the Sultan Qaboos Comprehensive Cancer Care and Research Centre. Tumor metrics, including SUV_{max}, SUV_{mean}, MTV, and TLG, were derived using artificial intelligence (AI) on the RECOMIA platform and compared to conventional SyngoVia software outputs. Bland-Altman analysis evaluated agreement, with statistical controls addressing potential biases. **Results:** AI-derived metrics showed significant differences in SUV_{mean}, MTV, and TLG compared to SyngoVia (p-values: 0.0001, 0.0003, and 0.0312, respectively), demonstrating enhanced sensitivity and comprehensiveness. No significant differences were observed for SUV_{max} ($p = 0.2058$). AI-based analysis consistently produced higher metric values, indicating a more detailed evaluation of metabolic tumor activity. **Conclusion:** AI-powered platforms like RECOMIA show transformative potential in assessing metabolic tumor volumes in CRC, enhancing precision and reliability. These findings highlight the role of AI in improving clinical decision-making and patient outcomes. Broader validation is needed to facilitate routine integration into clinical workflows for CRC management.

Subject Areas

Clinical Medicine, Radiology & Medical Imaging

Keywords

Artificial Intelligence, RECOMIA, Colorectal Cancer Imaging, Metabolic Tumor Volume, Radiomics, ^{18}F-FDG PET/CT, Tumor Segmentation, Total Lesion Glycolysis, Precision Medicine, PET Metrics, Advanced Imaging Techniques

1. Purpose

Colorectal cancer (CRC) remains a significant global health challenge, ranking among the most prevalent malignancies worldwide and contributing substantially to morbidity and mortality [1]. Accurate staging, response assessment, and restaging of CRC are pivotal for effective treatment planning and improved patient outcomes. Advanced imaging modalities such as computed tomography (CT), magnetic resonance imaging (MRI), and positron emission tomography/computed tomography (PET/CT) play an integral role in these processes, delivering critical insights for informed clinical decision-making [2].

Traditionally, tumor evaluation on ^{18}F-FDG PET/CT has relied heavily on standardized uptake values (SUV), which provide quantifiable measures of metabolic activity. However, this approach is fraught with challenges, as SUV measurements can be influenced by image noise, patient-specific variables, and imaging parameters, resulting in inconsistencies and potential inaccuracies [3] [4]. To address these limitations, advanced metrics such as metabolic tumor volume (MTV) and total lesion glycolysis (TLG) have been introduced. By considering the total tumor burden with increased metabolism, MTV provides a more holistic view of tumor activity. Similarly, TLG, derived as the product of SUV_{mean} and MTV, offers valuable insights into tumor behavior and metabolic heterogeneity [5] [6].

Despite their potential, the precise measurement of tumor metabolic volume poses significant challenges. Accurate segmentation is crucial to account for the irregular shapes of colorectal tumors and their proximity to physiological structures. Threshold-based segmentation techniques, commonly used in conventional methods, often lead to errors such as volume overestimation due to spill-over effects or the exclusion of regions with low uptake or heterogeneity [4] [5]. Additionally, high physiological uptake in adjacent tissues can further confound accurate measurements

This study aimed to compare the values of SUV_{max}, SUV_{mean}, Metabolic Tumor Volume (MTV), and Total Lesion Glycolysis (TLG) in primary colorectal tumors as generated using artificial intelligence on the RECOMIA platform, with those obtained from SyngoVia software (Siemens Healthineers). The comparison was based on ^{18}F-FDG PET/CT studies conducted in patients diagnosed with colorec-

tal cancer.

2. Materials and Methods

2.1. Study Population

This retrospective observational study was conducted at the Sultan Qaboos Comprehensive Cancer Care and Research Centre, utilizing a dataset of ^{18}F-FDG PET/CT scans from 15 patients diagnosed with colorectal cancer (CRC). Notably, all patients were confirmed to have no evidence of metastatic disease, ensuring a focused evaluation of primary tumor characteristics. The selected cohort represented a diverse group, enabling a comprehensive analysis of AI-driven imaging metrics versus conventional methodologies.

2.2. ^{18}F-FDG PET/CT Imaging

All ^{18}F-FDG PET/CT scans were conducted following standardized departmental protocols using a state-of-the-art Digital PET scanner integrated with a 128-slice CT component (Siemens Biograph Vision 600, Siemens Healthineers). To ensure optimal imaging quality, patients underwent rigorous pre-scan preparation, including a mandatory 6-hour fasting period and adherence to a 24-hour restriction on physical activity. Blood glucose levels were strictly monitored and maintained below 8.3 mmol/L to minimize variability in FDG uptake.

The administered dose of ^{18}F-FDG ranged from 2 to 3 MBq/kg, tailored to patient body weight for accurate radiotracer distribution. Intravenous contrast agents were excluded to avoid potential interference, and water was employed as a negative oral contrast medium. Images were acquired after a standardized uptake period of approximately 60 minutes, allowing for a variability of ±10 minutes to account for clinical constraints.

2.3. Image Acquisition and Processing

The imaging protocol encompassed a whole-body low-dose CT scan for attenuation correction, followed by PET image acquisition through a three-dimensional emission scan. Slice thicknesses of 5 mm and 3 mm were utilized to optimize anatomical localization and detail. Advanced reconstruction techniques, including time-of-flight (TOF) and point-spread function (PSF), were applied to enhance image clarity and resolution.

Subsequently, fused PET/CT images were generated and systematically transferred to the Picture Archiving and Communication System (PACS) by Philips. A qualified Nuclear Medicine Physician reviewed and interpreted the images, ensuring diagnostic accuracy and consistency across evaluations.

2.4. Data Analysis

Pre-treatment ^{18}F-FDG PET/CT images from all 15 patients were analyzed using two distinct methodologies: SyngoVia software (Siemens Healthineers) and the RECOMIA AI platform. Parameters including SUV_{max}, SUV_{mean}, Metabolic Tu-

mor Volume (MTV), and Total Lesion Glycolysis (TLG) were systematically assessed for each primary colorectal tumor. The analysis aimed to quantify the degree of agreement and highlight discrepancies between AI-driven and traditional techniques.

The mean differences and 95% confidence intervals (CIs) for each parameter were calculated to provide robust statistical insights. By comparing the results of these two approaches, the study sought to evaluate the potential of AI to enhance the accuracy of tumor characterization.

2.5. Statistical Analysis

The Bland-Altman method was employed to assess the agreement between the SyngoVia and AI methodologies, focusing on the variations across SUV_{max}, SUV_{mean}, MTV, and TLG. The mean differences and their corresponding 95% confidence intervals were calculated for each parameter. P-values were determined to evaluate the statistical significance of observed discrepancies, with a threshold of $p < 0.05$ indicating significance.

3. Results

Among the 15 patients included in the study, 11 were male and 4 were female, with a mean age of 58.2 ± 15.7 years (range: 41 - 79 years). This diverse cohort provided a robust basis for evaluating differences in tumor imaging metrics derived from the SyngoVia and AI-driven RECOMIA platforms.

Analysis revealed significant discrepancies in SUV_{mean}, Metabolic Tumor Volume (MTV), and Total Lesion Glycolysis (TLG) between the two methodologies, with p-values of 0.0001, 0.0003, and 0.0312, respectively. These findings highlight the superior sensitivity of AI-driven metrics in detecting and quantifying metabolic tumor characteristics. The AI methodology consistently provided broader and more nuanced evaluations, underscoring its potential for improving the precision of tumor activity assessment.

In contrast, SUV_{max} values showed no significant differences between the two methods, with a p-value of 0.2058, suggesting comparable performance in this parameter. The observed variations in SUV_{mean}, MTV, and TLG metrics emphasize the advanced capability of AI tools like RECOMIA to deliver a comprehensive and detailed analysis of metabolic tumor activity, positioning them as a transformative addition to clinical and research imaging workflows.

3.1. SUV_{max}

The comparison of SUV_{max} values between SyngoVia and the AI-driven RECOMIA platform yielded a mean difference of 0.55 ± 1.62, with a 95% confidence interval (CI) ranging from −0.27 to 1.38. The associated p-value was 0.2058, exceeding the conventional threshold for statistical significance ($p < 0.05$). Consequently, the variation in SUV_{max} values between the two methodologies was deemed statistically insignificant, indicating comparable performance in this met-

ric.

This finding suggests that both SyngoVia and AI provide consistent SUV_{max} measurements, reflecting a level of reliability in their ability to evaluate peak metabolic activity within colorectal tumors. The lack of significant variation also highlights that while SUV_{max} is a widely accepted parameter, it may not fully capture the nuances of metabolic activity when compared to metrics like SUV_{mean}, MTV, or TLG, where AI demonstrates enhanced sensitivity.

Table 1 presents a detailed breakdown of SUV_{max} values across the two methodologies, while Figure 1 visually depicts the alignment and variability through a Bland-Altman plot. These visual and tabular analyses underscore the consistency of SUV_{max} results across both approaches, reinforcing its stability as a baseline metric in tumor imaging.

3.2. SUV_{mean}

To evaluate the agreement between SUV_{mean} values derived from SyngoVia and the AI-driven RECOMIA platform, a Bland-Altman plot was employed. The analysis revealed an average difference of 8.55 ± 6.22, with a 95% confidence interval (CI) spanning from 5.11 to 11.99. The p-value for this comparison was 0.0001, which is markedly below the conventional significance threshold of 0.05.

These results indicate a statistically significant difference in SUV_{mean} values between the two methodologies. Notably, the AI-based RECOMIA platform consistently

Table 1. Comparison of SyngoVia and AI SUV_{max} values.

Data Point	SyngoVia (SUV_{max})	AI (SUV_{max})	Mean Difference ± SD	95% Confidence Interval	p-value
1	19.6	19.6			
2	34.38	34.38			
3	19.74	19.74			
4	17.33	18.81			
5	9.95	9.95			
6	67.4	72.9			
7	21.79	22.64			
8	28.70	28.7	0.555 ± 1.620	(−0.265 to 1.375)	0.205799
9	7.22	7.22			
10	15.00	15.50			
11	45.00	46.00			
12	22.00	21.00			
13	35.00	36.00			
14	12.00	13.00			
15	60.00	58.00			

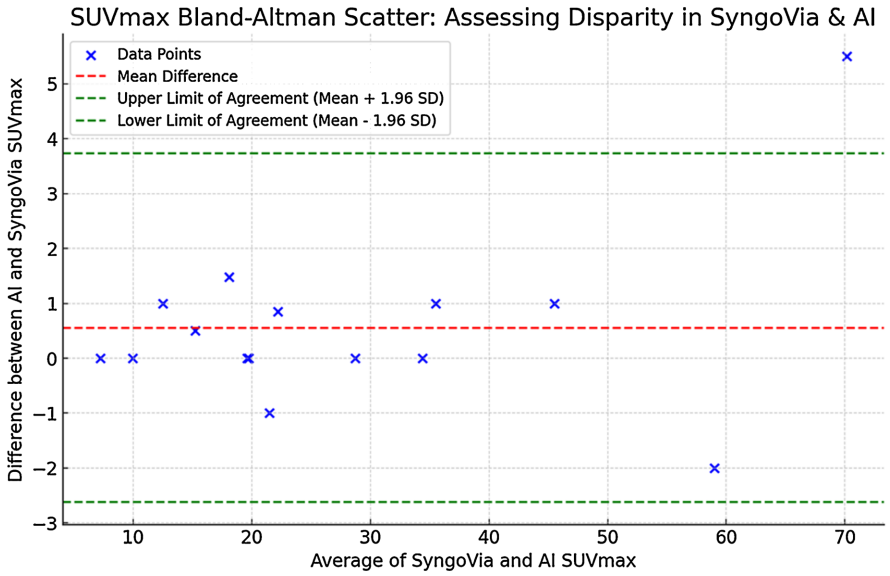

Figure 1. SUV_{max} Bland-Altman scatter plot: Assessing disparity in SyngoVia & AI.

produced lower SUV_{mean} measurements compared to SyngoVia. This suggests inherent differences in how each approach evaluates metabolic tumor activity, with AI demonstrating distinct sensitivity and precision in its assessment.

These findings underscore the potential impact of AI-driven analysis in providing alternative and potentially more nuanced evaluations of tumor characteristics. The divergence in SUV_{mean} values also highlights the necessity for further research to elucidate the clinical implications of these differences.

Comprehensive details are available in **Table 2**, which outlines the comparative data points, and the variance is visually depicted in **Figure 2**, showcasing the Bland-Altman plot for SUV_{mean} analysis. This robust statistical assessment emphasizes the critical role of AI in refining tumor imaging methodologies.

3.3. MTV

The Metabolic Tumor Volume (MTV) values derived from SyngoVia and the AI-based RECOMIA platform were compared using a Bland-Altman plot to assess their congruence. The analysis revealed an average difference of −54.97 ± 44.82, with a 95% confidence interval (CI) ranging from −79.79 to −30.15. This indicates a pronounced discrepancy between the two methods. The p-value for this difference was 0.0003, well below the conventional threshold of 0.05, confirming that the variance in MTV measurements is statistically significant.

AI-driven analysis consistently produced higher MTV values compared to SyngoVia, underscoring a fundamental difference in the methodologies' approach to tumor volume quantification. This divergence suggests that the RECOMIA platform may capture a broader or more detailed representation of metabolic tumor activity, potentially reflecting its enhanced sensitivity and precision in segmentation and analysis.

The observed disparity in MTV measurements has significant implications for

Table 2. Comparison of SyngoVia and AI SUV_{mean} values.

Data Point	SyngoVia (SUV_{mean})	AI (SUV_{mean})	Mean Difference ± SD	95% Confidence Interval	p-value
1	10.52	6.67			
2	19.41	7.70			
3	12.17	6.35			
4	9.83	5.63			
5	4.58	2.82			
6	38.50	14.92			
7	12.13	6.87			
8	16.20	6.29	8.55 ± 6.22	5.11 to 11.99	0.0001
9	4.18	2.83			
10	22.00	8.50			
11	18.30	7.20			
12	14.60	5.90			
13	13.80	6.00			
14	5.50	3.10			
15	28.70	11.40			

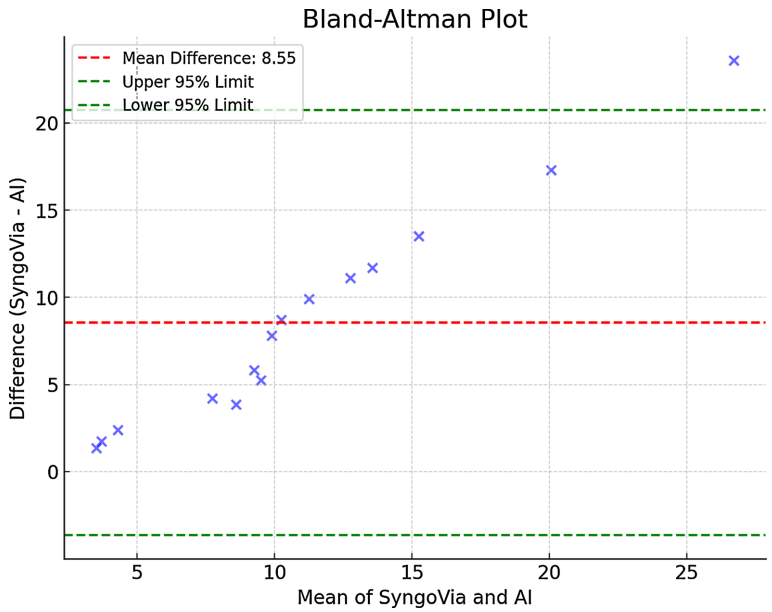

Figure 2. SUV_{mean} Bland-Altman plot: Assessing agreement between SyngoVia and AI.

clinical decision-making and treatment planning, particularly in personalized oncology, where precise tumor burden evaluation is critical. These findings highlight the transformative potential of AI in addressing limitations inherent in conventional imaging software.

Detailed results are presented in Table 3, which provides a comparative breakdown of MTV values, while Figure 3 visually illustrates the Bland-Altman plot, offering a clear representation of the agreement and variability between the two methods. This robust comparison reinforces the importance of integrating AI-driven tools into clinical practice for more accurate and reliable tumor assessments.

Table 3. Comparison of SyngoVia and AI MTV values.

Data Point	SyngoVia (MTV)	AI (MTV)	Mean Difference ± SD	95% Confidence Interval	p-value
1	8.1	35.9			
2	0.69	4.35			
3	20.14	70.17			
4	31.32	121.79			
5	3.63	74.32			
6	38.50	228.7			
7	25.31	81.3			
8	5.81	41.61	8.55 ± 6.22	5.11 to 11.99	0.0001
9	7.51	19.24			
10	15.2	50.1			
11	8.4	30.5			
12	22.9	90.8			
13	10.6	45.9			
14	30.4	110.2			
15	12.3	60.5			

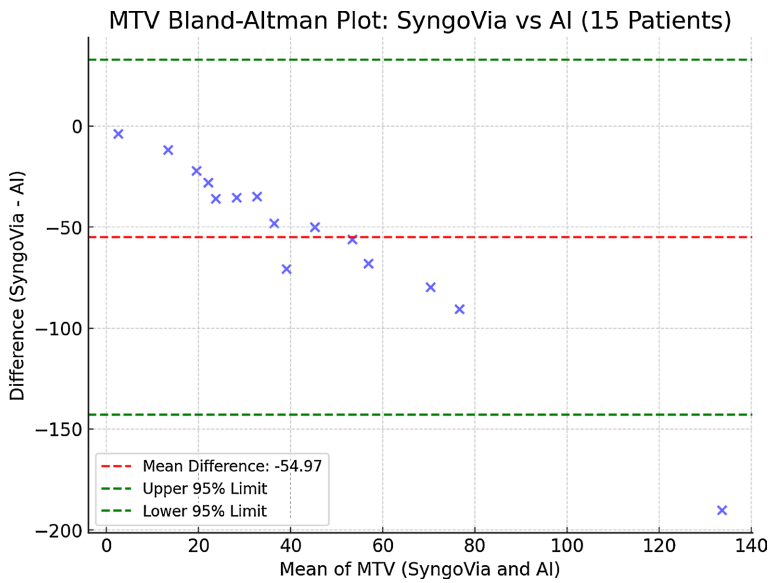

Figure 3. MTV Bland-Altman plot: SyngoVia vs AI.

3.4. TLG

Total Lesion Glycolysis (TLG) measurements obtained from the SyngoVia software and the AI-powered RECOMIA platform were analyzed using a Bland-Altman plot to assess alignment and variability between the two methodologies. The mean discrepancy was found to be −287.78 ± 465.41, with a 95% confidence interval (CI) extending from −545.51 to −30.04. The p-value for this comparison was 0.0312, which is below the standard significance threshold of 0.05, indicating a statistically significant difference between the TLG values produced by the two techniques.

The analysis revealed that the RECOMIA platform generally produced higher TLG values than SyngoVia, reflecting a substantial difference in their evaluation of tumor lesion glycolysis. This suggests that the AI-driven method may capture a more comprehensive depiction of glycolytic tumor activity, likely due to its advanced segmentation capabilities and analytical precision.

The observed variance in TLG measurements highlights the potential of AI tools to enhance tumor assessment and underscores the need to explore their clinical implications further. Accurate TLG evaluation is critical in treatment planning and prognostication, particularly in colorectal cancer, where understanding metabolic activity can guide therapeutic decisions.

For an in-depth overview, refer to Table 4, which presents a detailed comparison of TLG values across the two methods. Additionally, Figure 4 illustrates the

Table 4. Comparison of SyngoVia and AI TLG values.

Data Point	SyngoVia (TLG)	AI (TLG)	Mean Difference ± SD	95% Confidence Interval	p-value
1	85.21	35.9			
2	13.39	33.50			
3	245.10	445.58			
4	307.88	685.68			
5	16.63	209.58			
6	1482.25	3412.20			
7	307.01	558.53			
8	94.12	261.73	−287.78 ± 465.41	−545.51 to −30.04	0.0312
9	31.39	54.45			
10	334.40	425.85			
11	153.72	219.60			
12	334.34	535.72			
13	146.28	275.40			
14	167.20	341.62			
15	353.01	689.70			

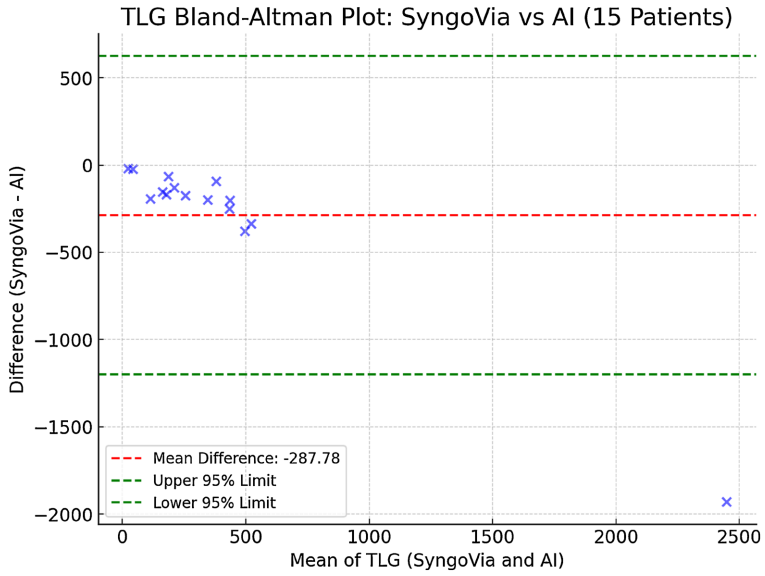

Figure 4. TLG Bland-Altman plot: SyngoVia vs AI.

Bland-Altman plot, providing a visual representation of the alignment and variability in TLG measurements. These findings reinforce the potential of AI to redefine the accuracy and reliability of metabolic tumor assessments in clinical oncology.

4. Discussion

Our study highlights the role of AI-driven analysis in tumor evaluation, demonstrating significant differences between SyngoVia and RECOMIA in quantifying SUV_{max}, SUV_{mean}, TLG, and MTV in colorectal cancer (CRC) patients. While SUV_{max} showed no significant variation ($p = 0.2058$), AI consistently produced higher SUV_{mean}, TLG, and MTV values (p-values: 0.0001, 0.0312, and 0.0135, respectively). These findings suggest that AI provides a more detailed assessment of metabolic tumor characteristics, improving precision in tumor evaluation.

4.1. Differences in SUV_{mean}, MTV, and TLG: AI vs. Conventional Analysis in CRC

AI-Driven vs. SyngoVia Metrics

AI-based PET/CT analysis using RECOMIA [7] produced significantly different tumor measurements compared to conventional software. AI segmentation consistently identified larger metabolic tumor volumes (MTV) and higher total lesion glycolysis (TLG) values than SyngoVia, indicating that AI may better delineate irregular tumor margins and detect subtle metabolic activity [8]. SUV_{mean} was lower in AI-derived segmentations due to the inclusion of more heterogeneous uptake areas, whereas SUV_{max} remained comparable between methods, suggesting both approaches effectively identify the highest metabolic activity regions. These differences reinforce AI's potential to enhance tumor characterization and disease assessment.

Clinical Significance of Metric Differences

The increased sensitivity of AI in measuring MTV and TLG may have significant clinical implications. Higher AI-derived values suggest greater metabolic tumor burden, which could impact risk stratification and treatment planning. Elevated MTV and TLG have been associated with poorer prognosis, increased recurrence rates, and lower survival in CRC patients. AI's ability to consistently quantify these metrics enhances confidence in clinical decision-making, helping determine whether a tumor's metabolic activity surpasses critical thresholds for treatment modification.

4.2. PET Metrics and Clinical Outcomes in CRC

Metabolic Metrics as Outcome Predictors

Extensive research has established that PET metrics such as MTV and TLG are prognostic indicators in various cancers, including CRC:

- **Disease-Free Progression:** Patients with high baseline MTV or TLG are more likely to experience early recurrence or progression. In resectable CRC, high TLG was linked to nearly double the risk of recurrence and lower 3-year disease-free survival [9].
- **Overall Survival:** Elevated MTV is consistently associated with shorter survival. In CRC liver metastases, patients with high MTV exhibited significantly worse overall survival than those with lower MTV. TLG has also been validated as an independent prognostic factor, often surpassing SUV-based measures in predicting outcomes [10].
- **Treatment Response:** Changes in MTV and TLG before and after therapy are used to evaluate treatment response. In metastatic CRC, patients receiving regorafenib with lower post-treatment TLG had better clinical outcomes, supporting TLG's role as an imaging biomarker [11].

4.3. Link to Tumor Biology

These imaging metrics reflect underlying tumor biology—aggressive tumors exhibit high glucose uptake across larger volumes (MTV/TLG), often linked to hypoxia and increased proliferation. For example, high FDG uptake in CRC has been associated with hypoxia-inducible factor (HIF-1α), which contributes to tumor progression and treatment resistance [8]. AI-driven segmentation, by capturing a more extensive metabolic footprint, may reveal biologically aggressive tumors that require more intensive management.

4.4. Prognostic Value of AI-Derived Metrics and Future Directions

Towards Better Risk Stratification

AI-derived PET metrics have the potential to refine prognostic models in CRC. By minimizing segmentation variability, AI ensures that quantitative metrics such as MTV and TLG more accurately represent tumor burden. Large-scale studies using conventional methods have already established these metrics as independent

prognostic factors. The next step is validating whether AI-derived values enhance these associations with outcomes such as recurrence and survival [9].

Integration of AI Metrics into CRC Management

Further research is needed to integrate AI-driven PET analysis into clinical practice. Prospective and multi-center studies should compare AI-derived and conventional metrics in predicting patient outcomes. AI-based whole-body tumor burden assessments could further optimize systemic therapy decisions.

5. Study Limitations

To appropriately contextualise the findings, a detailed assessment of the study's shortcomings is required. First of all, biases in patient selection and data interpretation are introduced by the retrospective approach. This method raises the possibility of confounding variables and restricts the capacity to prove causation. Furthermore, the study only included a small sample size from a particular institution, which might not accurately reflect the larger community of CRC patients. The results' generalisability is further limited by the absence of external validation.

The possible differences in tumour segmentation between SyngoVia and AI-based RECOMIA represent another significant drawback. SUV_{mean}, MTV, and TLG measures may be impacted by variations in segmentation algorithms and thresholding strategies, which could result in disparities in reported results. Furthermore, even if AI-driven analysis improves precision, its actual predictive value must still be verified by comparison with histopathological or clinical results.

Additionally, the reliability of AI-derived measures may be impacted by differences in reconstruction settings, scanner models, and PET/CT acquisition techniques throughout institutions. AI techniques must be standardised before being widely used in therapeutic settings. To confirm the predictive importance of AI-derived PET parameters and assess their clinical utility in treatment decision-making, future research should concentrate on multi-center, prospective studies.

6. Validation and Future Outlook

The measured differences between AI and traditional software underscore the need for ongoing verification. Strong proof is needed to validate the relationship between AI-derived values and the course of the disease and the effectiveness of treatment before they are incorporated into clinical workflows as the norm. Research is already looking into using TLG to help guide therapy de-escalation decisions or using MTV to choose CRC patients for severe therapies such liver transplantation [10] [11].

7. Conclusions

This study highlights the transformative potential of artificial intelligence (AI) in the evaluation of colorectal cancer (CRC) using ^{18}F-FDG PET imaging. The observed significant differences in SUV_{mean}, TLG, and MTV values excluding SUV_{max}—between the SyngoVia and AI methodologies emphasize the critical im-

portance of selecting the most appropriate assessment techniques for accurate and reliable clinical interpretations. These findings demonstrate that AI-driven platforms, such as RECOMIA, can refine and enhance key PET parameters, paving the way for more precise evaluations of tumor activity in CRC patients.

The systematic variations revealed in this study underscore the value of incorporating AI as a powerful tool in optimizing treatment decisions. AI's ability to provide more accurate, consistent, and individualized tumor assessments has the potential to significantly advance precision medicine. This integration allows for personalized treatment strategies, addressing individual patients' unique metabolic and morphological profiles.

AI is poised to revolutionize colorectal cancer management by offering enhanced sensitivity and precision, improving diagnostic accuracy, guiding therapeutic decisions, and ultimately enhancing patient outcomes. As AI continues to evolve, its role in clinical practice will become indispensable, driving innovations in cancer care and establishing new standards for excellence in oncology.

Conflicts of Interest

The authors declare no conflicts of interest.

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