difference in BMI, weight loss, tumor stage, or ECOG score between muscularity groups. The LM group had a lower skeletal muscle area ($p < 0.001$), lower visceral adipose tissue area ($p = 0.01$), and there is no difference in skeletal muscle radiodensity ($p = 0.85$), subcutaneous adipose tissue area ($p = 0.76$), and intramuscular adipose tissue area ($p = 0.46$) when compared to normal muscularity group. A lower handgrip strength was also observed in the LM group ($p < 0.01$). Regarding insulin sensitivity, the LM group had a higher M-value adjusted for Free Fat Mass (FFM) ($p = 0.01$) and M-value adjusted for Total Body Weight (TBW) ($p = 0.0347$). Additionally, a significant negative correlation was found between muscularity and M-value-FFM (rho = -0.5047, $p = 0.004$) and M-value-TBW (rho = -0.4742, $p = 0.0076$). There was no difference in M-value between cachexia and non-cachexia patients. No statistical difference was observed in inflammatory markers (C-reactive protein, Glasgow prognostic score (mGPS), and neutrophil-to-lymphocyte ratio (NLR)) according to muscularity groups. **Conclusion:** There is no insulin resistance associated with LM or cachexia. It is possible that the main determinant of insulin sensitivity is the amount of visceral adipose tissue and systemic inflammation. The LM group exhibits a lower area of visceral adipose tissue, with no discernible difference in inflammatory markers. This study highlights the importance of expanding investigations into the determinants of metabolic changes and body composition in cancer cachexia.

Keywords: Cachexia, Insulin resistance, Metabolism, Muscularity, Rectal neoplasia.

https://doi.org/10.1016/j.htct.2024.04.057

DEEP LEARNING FOR CT IMAGES SEGMENTATION

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Introduction/Justification: Computed tomography (CT) scans are integral to cancer patient diagnosis, revealing changes in body composition linked to survival progression. The conventional approach to body composition analysis using CT scans is labor-intensive and expensive, demanding skilled professionals and licensed software for manual segmentation of Regions of Interest (ROIs). To address these challenges, we introduce a Deep Learning algorithm designed for automated CT image segmentation, presenting an efficient alternative that overcomes the limitations of the current methodology. Beyond the advantages of speed, automation enhances result uniformity and enables uncertainty estimation. In this presentation, we will show preliminary results from our algorithm, highlighting its potential contributions to survival analysis in cancer patients. **Objectives:** The primary goal of this study was to develop an automated segmentation algorithm for CT scans using Deep Learning models. **Materials and Methods:** In developing segmentation algorithms, a dataset of 453 CT slices at the L3 lumbar vertebral level from gastric cancer patients was utilized, with an 80% training and 20% testing partition. Employing the UNET+ResNet18 deep learning architecture, supervised training utilized manually generated segmentation masks as references. Four dedicated UNET+ResNet18 algorithms were trained for distinct ROIs: Skeletal Muscle (SM), Intramuscular Adipose Tissue (IMAT), Visceral Adipose Tissue (VAT), and Subcutaneous Adipose Tissue (SAT). Segmentation performance on the test set was evaluated using the Dice Coefficient, underestimation and overestimation percentages, Bland-Altman analyses, and qualitative visual inspection of segmented images. **Results:** The UNet+ResNet18 models demonstrated superior segmentation performance for SM, VAT, and SAT, achieving mean Dice scores exceeding 0.95. In comparison to manual segmentation, the Deep Learning algorithm exhibited minor average underestimations and overestimations, both below 5% for these tissues. However, IMAT segmentation exhibited relatively lower performance, with a mean Dice score of approximately 0.86 and underestimation and overestimation percentages around 15% and 13%, respectively. The Bland-Altman analysis revealed mean bias and limits of agreement for mean radiodensities of SM, VAT, SAT, and IMAT as follows: 0.14 [-0.82, 1.10] HU, -0.53 [-2.03, 0.98] HU, -0.18 [-1.70, 1.33] HU, and 0.48 [-3.86, 4.82] HU, respectively. **Conclusion:** The Deep Learning approach provides a standard and fast solution for CT image segmentation, demonstrating good results for SM, VAT and SAT. For these tissues, derived radiomics features could provide valuable insights into the analysis of cancer patient outcomes. Further studies are necessary for enhancing IMAT segmentation, given its challenging small area. Additionally, future investigations should focus on uncertainty estimation in CT images, exploring its impact on segmentation procedures and radiomic feature extraction.

Keywords: Automated body composition analysis, Computed tomography, Deep learning.

https://doi.org/10.1016/j.htct.2024.04.058

AUTOMATED SYNTHESIS AND IN VITRO STUDIES OF [68GA]GA-FAPI-46 IN HOSPITAL RADIOPHARMACY

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