
Harmonization of 18F-FDG PET images for multicenter radiomic studies

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Résumé

Introduction:

Radiomics is a promising method which has undergone rapid development over the last few years. However, it has been shown that different acquisition/reconstruction parameters could introduce biases in PET-based textural feature calculation [1,2]. The aim of this study was (i) to evaluate the impact of voxel size, spatial resolution (SR) and signal-to-noise ratio (SNR) on feature values, (ii) to propose a harmonization method of 18F-FDG PET images based on phantom acquisitions to reduce the impact of SR and SNR on radiomic indices.

Methods:

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115 cervical cancer patients were included retrospectively. Two groups were defined according to the PET scanner used for baseline image acquisition (G1: Siemens Biograph I; G2: GE Discovery-690). Eleven radiomic features were extracted from a spherical non-pathological hepatic volume of interest (VOI). The impact of voxel size was investigated by resampling all images into three different matrix sizes: 5.3 mm \times 5.3 mm \times 3.4 mm (G1 grid size), 2.7 mm \times 2.7 mm \times 3.4 mm (G2 grid size), 2.0 mm \times 2.0 mm \times 2.0 mm.

In addition, two FDG-filled phantoms (homogeneous: HP, triple-line: TLP) were acquired on a GE Discovery-690 PET/CT with seven acquisition and reconstruction protocols, by changing the iteration number and post-filtering FWHM and with or without PSF modeling. SR was evaluated for all sets using TLP and all images were convolved by a 3D-Gaussian function (referred to harmonization filter HF hereafter) with a specific standard deviation so that all filtered images had the same SR as when using the clinical protocol. SNR was evaluated using the homogeneous phantom before and after HF. Radiomic features were also calculated in 22 spherical VOI (19.5 mL) before and after HF on the homogeneous phantom. Bland-Altman plots were used to characterize the dispersion of values between original and HF images. P-values from permutation tests were calculated between the two sets.

Results:

At least 4 features (SUVmax, SUVpeak, Homogeneity, SRE) were highly dependent on the PET scanner in the three sets of patient images ($p < 0.05$, Wilcoxon test). Spatial resampling was not sufficient to eliminate this dependence.

Original images of the phantoms showed large differences in both SR (3.3–7.9mm) and SNR (9.2–25.7). A large variability of radiomic feature values was observed between different reconstruction protocols, especially for those with point-spread function correction. After filtering all images to the clinical SR (7.9mm), feature values were less scattered according to Bland-Altman analysis (figure 1). The difference in feature values between 2 mm and 6.4 mm FWHM post-filtering was highly significant on original images (permutation test, $p < 0.001$) but not significant after HF for SUVmax, Entropy, SRE and HGZE ($p > 0.05$).

The whole analysis will be reproduced on a Philips Gemini PET device (work in progress).

Conclusions:

A high variability of feature values was observed on clinical data due to the gap in technology between the two imaging devices. Gaussian filtering showed promising results on phantom data, by reducing the differences in textural feature values between protocols. When applied on highly different PET devices, this method might eliminate some biological signal. A combination of Gaussian filtering and voxel resampling will be investigated on patient data to assess the clinical use of such method on more recent devices.

References:

- Bailly *et al.*, PloS One. 2016
- Yan *et al.*, J Nucl Med. 2015

Mots-Clés: radiomics, texture, PET