Radiomic Features Variability with Computed Tomography Convolution Kernels

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Abstract

Radiomics refers to the extraction of hand-crafted features from radiographic images. Combined with machine learning and data analysis algorithms, it can provide a valuable tool to enable a phenotypic tumour profile. Based on the hypothesis that quantitative analysis of medical images may have a similar prognosis power to phenotypes and gene protein signatures, radiomics debates with the lack of standardisation and reproducibility issues. CT convolution kernels modify the frequency contents of projection data before back projection during image reconstruction, affecting the values of, mainly, intensity and texture features. This study evaluated the effect of eight convolution kernels from two General Electric (GE) Computed Tomography (CT) scanners on 19 patients. Feature extraction was restricted to the Clinical Target Volume (CTV), manually defined by experts at Instituto Português de Oncologia do Porto Francisco Gentil (IPO-PORTO). Afterwards, the feature set was grouped per patient following the variance computation kernel-wise. Results show that shape-based features are invariant to changes in the convolution kernel, while Gray Level Size Zone Matrix (GLSZM) and Gray Level Run Length Matrix (GLRLM) seem more exposed to such changes. Additionally, results also suggest that first-order features can withstand slight modifications to the kernel, much like Gray Level Co-occurrence Matrix (GLCM).

1 Introduction

Radiomics is an emerging field involving feature extraction from radiographic images using data-characterization algorithms. Combining radiomics with machine learning and data analysis algorithms may provide valuable insights into texture, shape and spatial relationships between pixels unlocking hidden patterns and quantifying phenotypic characteristics in medical imaging [1].

The typical workflow for radiomics studies begins with collecting medical images, usually Computed Tomography (CT) or Magnetic Ressonance Imaging (MRI). Next, images are processed using specialized software that identifies and extracts quantitative features from an Region Of Interest (ROI) in the image data. Finally, statistical analysis is performed on the extracted features to identify patterns and correlations with clinical outputs [2], such as staging, grading, detection, Biochemical Recurrence (BCR) or aggressiveness. Recently, Mendes et al. [4] evaluated CT-based radiomics to predict Prostate Cancer (PCa) aggressiveness with promising results. Although highly valuable in medical imaging, radiomics lack standardisation and presents reproducibility issues. Additionally, radiomics may not account for several factors affecting imaging results, such as patient movement or variations in the imaging equipment.

CT convolution kernels are mathematical algorithms that enhance image contrast and resolution, allowing better visualisation of internal structures. Kernels modify the frequency contents of projection data before back projection during image reconstruction, thus affecting the values of radiomic features, especially intensity and texture features. The CT acquisition parameters such as kVp, mAs, slice thickness and pixel size also affect image quality, introducing differences in extracted features, although resampling and smoothing reduces these effects [3]. This study evaluated the radiomic features using eight CT convolution kernels from General Electric (GE) (Bone, BonePlus, Chest, Detail, Edge, Lung, Soft and Standard). The purpose is to address the variability of extracted features for further studies.

2 Materials and Methods

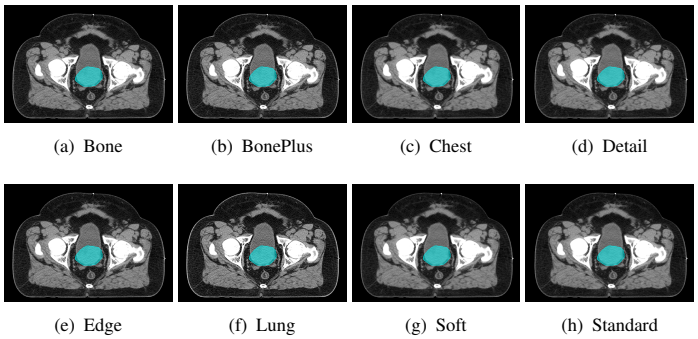
2.1 Image Dataset

The research involved patients who underwent a CT scan at Instituto Português de Oncologia do Porto Francisco Gentil (IPO-PORTO) as part of External Beam Radiotherapy Treatment (EBRT). All images were acquired using a GE Lightspeed or Brightspeed scanner featuring 2.5mm of slice thickness, 120 Kvp, and automatic tube current modulation in retrospect. The dataset contains a total of 30928 images from 19 patients: three from GE LightSpeed and 16 from GE Optima, both 16 slices scanners. The series spanned from October 18th, 2022 to May 29th, 2023, and the age range of the patients included those between 60 and 84 years old. There are eight distinct filters available for series reconstruction using both scanners: Bone, BonePlus, Chest, Detail, Edge, Lung, Soft and the commonly used for PCa, Standard. Reconstruction diameter was set to 500 mm and the pixel spacing to 0.977x0.977. Table 1 summarises the acquisition parameters of both scanners.

Table 1: GE LightSpeed and GE Optima aquisition parameters.

Thickness (mm)	Kvp	mAs	Diameter (mm)	Pixel spacing
2.5	120	Auto	500	0.977x0.977

Experts at the institution delineated the Clinical Target Volume (CTV) that contains the gross demonstrable extent and location of the tumour, which may also include metastatic regional nodes and distant metastasis if they are indistinguishable from the primary tumour plus a margin that reflects the probability of subclinical disease occurrence. The study was conducted according to the guidelines of the Declaration of Helsinki. The study was approved by the IPO-PORTO Porto Healthcare Ethics Committee (protocol code CES.274/020 and date of approval October 1st 2020). Figure 1 shows an example CT image reconstructed with GE convolution kernels and in blue the manually drawn CTV.



(a) Bone (b) BonePlus (c) Chest (d) Detail

(e) Edge (f) Lung (g) Soft (h) Standard

Figure 1: CT images reconstructed with GE convolution kernels.

2.2 Feature Extraction

Radiomics extracts two types of features: semantic and agnostic. Semantic features describe lesions with prognostic values, such as size, shape or necrosis. Agnostic features provide first-order, second-order or higher-order statistics. First-order statistics focus on individual voxels reducing the volume to a single value. Second-order descriptors are texture features grouping voxels with similar statistics and are very useful to measure tumour heterogeneity. Higher-order statistics search for pattern repetitions

in the volume. Table 2 shows some of the features that can be extracted with PyRadiomics [5].

Table 2: Extracted features.

Feature Class	# Features
First Order Statistics	19
Shape based (3D)	16
Shape based (2D)	10
Grey Level Co-occurrence Matrix (GLCM)	24
Grey Level Run Length Matrix (GLRLM)	16
Grey Level Size Zone Matrix (GLSZM)	16
Neighbouring Gray Tone Difference Matrix (NGTDM)	5
Gray Level Dependence Matrix (GLDM)	14
Total	**120**

Features comply with the Image Biomarker Standardisation Initiative (IBSI), an independent international collaboration that aims at standardizing the extraction of image biomarkers for high-throughput quantitative analysis (radiomics).

All features from Table 2 were extracted from the original image, restricted to the CTV, using an isotropic resampling ([1, 1, 1]), a B-spline interpolation, a bin width of 25 and a voxel size of 2 for 3D feature extraction. The full analysis was performed on an Intel(R) Core(TM) i7-6500U CPU@2.50GHz 2.60 GHzz, with 16 Gb of RAM and an Nvidia GeForce 930M (2Gb DDR3).

3 Results and Discussion

This work studied the variability of some radiomic features with different convolution kernels used in the CT image reconstruction algorithm. Features were standardized with z-score, subtracting the mean and dividing by the standard deviation. Next, features were grouped by patient, and the variance was computed along the convolution kernels.

The obtained results suggest that shape-based features are invariant to the used convolution kernel as expected since the CTV was the same for all reconstructions. These features are descriptors of the size and shape of the CTV independent of the grey-level intensity distribution. The applied convolution kernels work at the frequency level leaving the shape and size of the structures unchanged. The other features present some variation. First-order features describe the distribution of voxel intensities within the image region [5]. Gray Level Co-occurrence Matrix (GLCM), Gray Level Size Zone Matrix (GLSZM) and Gray Level Run Length Matrix (GLRLM) are highly dependent on grey-level values in the image dataset. The Neighbouring Gray Tone Difference Matrix (NGTDM) quantifies the difference to the average grey-level neighbourhood values, and the Gray Level Dependence Matrix (GLDM) quantifies grey-level dependencies. Figure 3 shows the ten features that presented a higher variance.

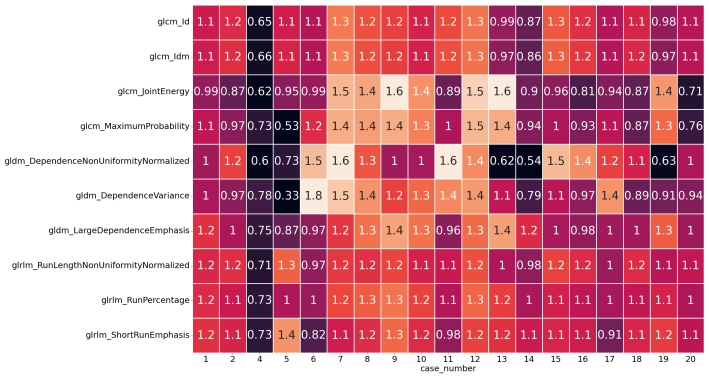


Figure 2: Variance Matrix: 10 features with higher variance across convolution kernels.

Case number 3 was excluded from this analysis since it was reconstructed with a diameter of 650mm. For patients 6 and 17, the GLDM DependenceVariance feature, which measures the variance in dependence size in the image, had the highest variance value. For patients 9, 10, 12,13 and 19, the GLCM JointEnergy feature presented the highest variance value. The JointEnergy measures homogeneous patterns in the image. A high value may indicate a higher heterogeneity change with the convolution kernel. Patients 7, 11, 15 and 16 had a high variance for the GLDM DependenceNonUniformityNormalized feature indicating more heterogeneity among dependencies in the image. Patients 1, 2 and 4 had very similar variances along convolution kernels. Patient 5 presented a high variance value for the GLRLM ShortRunEmphasis feature indicating a higher variance on the fine textural textures.

The mean-variance of GLSZM and GLRLM features is notably high in each patient, particularly in patients 5, 8, 9, and 13. However, note that the variance is highly dependent on the patient. With the exception of patient 6, who shows high mean-variance values, and patient 4, who shows low mean-variance values, all patients exhibit similar mean-variance values for their first-order features, much like the GLCM. The mean-variance for all feature groups was the lowest for Patient 4, while GLDM features were found to be significant for every patient. Additionally, NGTDM had the lowest mean variance for all patients. Figure 3 shows the mean variance by feature group per patient.

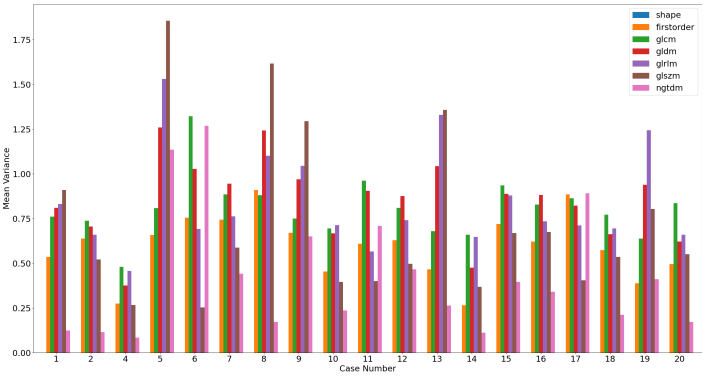


Figure 3: Mean variance by feature group.

4 Conclusions

Radiomic studies present several reproducibility issues, such as a dependence on the acquisition parameters, patient movements and other factors affecting image quality. This research shows that radiomic features depend at some level on the convolution kernel used for CT image reconstruction. For further radiomic studies involving CT images, these findings may suggest using a convolution kernel other than the Standard. Although more investigation is needed to determine which kernel may be most effective in radiomic studies, in building a classifier or finding a radiomic signature, this work highlights a potential issue. Shape-based features are invariant to changes in the convolution kernel used for image reconstruction if the same volume is used for feature extraction. On the other end, GLSZM and GLRLM are the ones that present the highest variance among all patients. First-order features seem to withstand slight modifications to the kernel, much like GLCM.

References

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