Automatic prostate cancer detection through DCE-MRI images: all you need is a good normalization

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Abstract

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1. Introduction

Prostate Cancer (PCa) is the second most frequently diagnosed men cancer, accounting for 899,000 cases leading to 258,100 deaths (Ferlay et al., 2010). As highlighted by the PI-RADS Steering Committee, the two main challenges to be addressed are (Weinreb et al., 2016): (i) the improvement of detecting clinically significant PCa and (ii) an increase of the confidence in benign or dormant cases, avoiding unnecessary invasive medical exams. In this regard, multiparametric Magnetic Resonance Imaging (MRI) (mpMRI) is frequently used to build robust Computer-Aided Detection and Diangosis (CAD) systems to detect, localize, and grade PCa. In general, CAD systems are based on mpMRI which combines

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several of the following modalities (Lemaître et al., 2015): T_2 Weighted (T_2-W)-MRI, Dynamic Contrast-Enhanced (DCE)-MRI, Apparent Diffusion Coefficient (ADC) maps, and Magnetic Resonance Spectroscopy Imaging (MRSI).

In DCE-MRI, a contrast media is injected intravenously and a set of images is acquired over time. Consequently, each voxel in the image is a dynamic signal which is related to the vascular properties of the tissue. In fact, these properties are automatically extracted using quantitative or semi-quantitative approaches (Lemaître et al., 2015).

The former group of approaches uses pharmacokinetic modelling based on a bicompartment model, namely Brix (Brix et al., 1991) and Tofts (Tofts et al., 1995) models. The parameters of the Brix model are found assuming a linear relationship between the media concentration and MRI signal intensity. This assumption has shown, however, to lead to inaccurate parameter calculation (Heilmann et al., 2006). In the contrary, Tofts model only requires a conversion from MRI signal intensity to concentration, which can become a non-linear relationship using specific equation of MRI sequences (e.g., FLASH sequence). Tofts modelling suffers, however, from an higher complexity (Gliozzi et al., 2011). The conversion using the non-linear approach requires to acquire a T_1 map which is not always possible during clinical examination. Furthermore, the parameter calculation require the Arterial Input Function (AIF) which is challenging to measure and can also lead to inaccurate estimation of the parameters.

The latter group of approaches are rather mathematical than pharmacokinetic modelling.

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