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 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).

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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 as-
sumption has shown, however, to lead to inaccurate parameter calculation (Heil-
mann et al., 2006). In the contrary, Tofts model only requires a conversion from
MRI signal intensity to concentration, which can become a non-linear relation-
ship 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 pharmacoki-
netic modelling (Huisman et al., 2001; Gliozzi et al., 2011). These methods
offer the advantages to not require any knowledge about the MRI sequence nor
any conversion from signal intensity to concentration. However, the heuristic
approach propose by Huisman et al. requires an estimate regarding the noise
standard deviation of the signal as well as manual tuning.

Nevertheless, all presented methods suffer from two major drawbacks: (i)
the inter-patient variability of the data lead to a variation of the parameters
estimated and to poor classification performance while designing CAD systems,
and (ii) only few parameters are used to characterize the dynamic signal imply-
ing that some information are discarded.

In this work, we propose a fully automatic normalization method for DCE-
MRI that reduce the inter-patient variability of the data. Furthermore, we show

that using the full normalized signal lead to the best classification performance.

The paper is organized as follows: Section 2 outlines our normalization strategy (Section 2.1) as well as specificity regarding the state-of-the-art methods used for comparison (Section 2.2). The dataset, experiments, and results are reported in Section 3 while discussed in Section 4 followed by a concluding section.

2. Methods

2.1. Normalization of DCE-MRI images

2.2. Quantification of DCE-MRI

2.2.1. Brix and Hoffmann models

In the Brix model (Brix et al., 1991), the MRI signal intensity is assumed to be proportional to the media concentration. Therefore, the model is expressed as in Eq. (1):

$$s_n(t) = 1 + A \left[\frac{\exp(k_{el}t') - 1}{k_{ep}(k_{ep} - k_{el})} \exp(-k_{el}t) - \frac{\exp(k_{ep}t') - 1}{k_{el}(k_{ep} - k_{el})} \exp(-k_{ep}t) \right], \quad (1)$$

with

$$s_n(t) = \frac{s(t)}{S_0}, \quad (2)$$

where $s(t)$ and S_0 are the MRI signal intensity at time t and the average pre-contrast MRI signal intensity, respectively; A, k_{el}, and k_{ep} are a constant proportional to the transfer constant, the diffusion rate constant, and the rate constant, respectively. Additionally, during the injection time $0 \leqslant t \leqslant \tau$, $t' = t$ and afterwards while $t > \tau$, $t' = \tau$.

Following this model, Hoffmann et al. propose the following similar model as expressed in Eq. (3):

$$s_n(t) = 1 + \frac{A}{\tau} \left[\frac{k_{ep}\left(\exp(k_{el}t') - 1\right)}{k_{el}(k_{ep} - k_{el})} \exp(-k_{el}t) - \frac{\exp(k_{ep}t') - 1}{(k_{ep} - k_{el})} \exp(-k_{ep}t) \right]. \quad (3)$$

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2.2.2. Tofts model

The extended Tofts model is formulated as in Eq. (4):

$$C_t(t) = K_{trans}C_p(t) * \exp(-k_{ep}t) + v_pC_p(t), \qquad (4)$$

Conversion of MRI signal intensity to concentration

Estimation of patient-based AIF signal *vs.* population-based AIF signal

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2.2.3. PUN model

Gliozzi et al. show that Phenomenological Universalities (PUN) approach can be used for DCE-MRI analysis (Gliozzi et al., 2011). The model has been successfully used in a CAD system proposed by Giannini et al. (2015). This model can be expressed as in Eq. (5):

$$s_n(t) = \exp\left[rt + \frac{1}{\beta}\left(a_0 - r\right)\left(\exp(\beta t) - 1\right)\right], \qquad (5)$$

with

$$s_n(t) = \frac{s(t) - S_0}{S_0}, \qquad (6)$$

where $s(t)$ and S_0 are the MRI signal intensity at time t and the average pre-contrast MRI signal intensity, respectively; r, a_0, and β are the free parameters of the model.

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3. Experiments and results

4. Discussions

5. Conclusions and future works

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