

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
5 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) (mp-MRI) is frequently used to build robust Computer-Aided Detection and Diagnosis (CAD) systems
10 to detect, localize, and grade PCa. In general, CAD systems are based on mp-MRI which potentially combines several of the following modalities (Lemaître et al., 2015): T₂ Weighted (T₂-W)-MRI, Dynamic Contrast-Enhanced (DCE)-MRI, Apparent Diffusion Coefficient (ADC) maps, and Magnetic Resonance Spectroscopy Imaging (MRSI).

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15 In DCE-MRI, a contrast media is injected intravenously and a set of images is acquired over time. Consequently, each voxel in an image corresponds to a dynamic signal 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).

20 The former group of approaches uses pharmacokinetic modelling based on a bicompartiment model, namely Brix (Brix et al., 1991) and Tofts (Tofts et al., 1995) models. The parameters of the Brix model are inferred assuming a linear relationship between the media concentration and the MRI signal intensity. This assumption has shown, however, to lead to inaccurately estimate the pharmacokinetic parameters (Heilmann et al., 2006). In the contrary, Tofts model
25 requires a conversion from MRI signal intensity to concentration, which 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). Indeed, the conversion using the non-linear approach requires to
30 acquire a T_1 map which is not always possible during clinical examination. Additionally, the parameter calculation requires the Arterial Input Function (AIF) which is challenging to measure and can also lead to inaccurate estimation.

The latter group of approaches are rather mathematical than pharmacokinetic modelling (Huisman et al., 2001; Gliozzi et al., 2011). These methods
35 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)
40 the inter-patient variability of the data lead to a variation of the parameters estimated and subsequently to poor classification performance while designing CAD systems, and (ii) only few parameters are used to characterize the dynamic signal implying that some information are discarded.

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

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

The paper is organized as follows: Section 2 outlines our normalization strategy (Section 2.3) as well as specificity regarding the state-of-the-art methods used for comparison (Section 2.4). The dataset, experiments, and results are reported in Section 3 while discussed in Section 4 followed by a concluding section.

2. Materials and methods

2.1. Data

The multi-parametric MRI data are acquired from a cohort of patients with higher-than-normal level of Prostate-Specific Antigen (PSA). The acquisition is performed using a 3T whole body MRI scanner (Siemens Magnetom Trio TIM, Erlangen, Germany) using sequences to obtain T₂-W-MRI, DCE-MRI and Diffusion Weighted (DW)-MRI. Aside of the MRI examination, these patients also have underwent a guided-biopsy. The dataset is composed of a total of 20 patients of which 18 patients have biopsy proven PCa and 2 patients are “healthy” with negative biopsies. Therefore, 13 patients have a PCa in the Peripheral Zone (PZ), 3 patients have PCa in the Central Gland (CG), 2 patients have invasive PCa in both PZ and CG and finally 2 patients are considered as “healthy”. An experienced radiologist has segmented the prostate organ — on T₂-W-MRI and DCE-MRI — as well as the prostate zones (i.e., PZ and CG) and PCa on the T₂-W-MRI.

A 3 mm slice fat-suppressed T₂-W fast spin-echo sequence (Repetition Time (TR)/Echo Time (TE)/Echo Train Length (ETL): 3400 ms/85 ms/13) is used to acquire images in sagittal and oblique coronal planes, the latter planes being orientated perpendicular or parallel to the prostate PZ rectal wall axis. Three-dimensional T₂-W fast spin-echo (TR/TE/ETL: 3600 ms/143 ms/109, slice thickness: 1.25 mm) images are then acquired in an oblique axial plane. The nominal matrix and Field Of View (FOV) of the 3D T₂-W fast spin-echo

75 images are 320×256 and 280×240 mm², respectively, thereby affording sub-millimetric pixel resolution within the imaging plane.

DCE-MRI are performed using a fat suppressed 3D T1 VIBE sequence (TR/TE/Flip angle: 3.25 ms/1.12 ms/10°; Matrix: 256×192 ; FOV: 280×210 (with 75% rectangular FOV); slab of 16 partitions of 3.5 mm thickness; tempo-
80 ral resolution: 6 s/slab over approximately 5 min). A power injector (Medrad, Indianola, USA) is used to provide a bolus injection of Gd-DTPA (Dotarem, Guerbet, Roissy, France) at a dose of 0.2 ml Gd-DTPA/kg of body weight.

These DCE-MRI sequences are resampled using the spatial information of the T₂-W-MRI and missing data are interpolated using linear interpolation.
85 The volumes of the DCE-MRI dynamic are rigidly registered, to remove any patient motion during the acquisition. Furthermore, a non-rigid registration is performed between the T₂-W-MRI and DCE-MRI in order to propagate the prostate zones and PCa ground-truths. The resampling is implemented in C++ using the Insight Segmentation and Registration Toolkit (Ibanez et al., 2005).

90 2.2. Implementation

The implementation of the registration (C++), normalization (Python), and classification pipeline (Python) are publicly available on GitHub¹. The data used for this work are also publicly available².

2.3. Normalization of DCE-MRI images

95 In this work, we propose a method to normalize DCE-MRI prostate data, although it can be applied to any DCE-MRI sequences. The aim of the method is to reduce the intra-patient variations, occurring during the acquisition process. In T₂-W-MRI, these variations imply that the intensity Probability Density Function (PDF) of the prostate region is shifted as well as wider or narrower,
100 from a patient to another. Therefore, these variations can be corrected using a

¹<https://github.com/I2Cvb/lemaitre-2016-nov/tree/master>

²<http://kaggle.com>

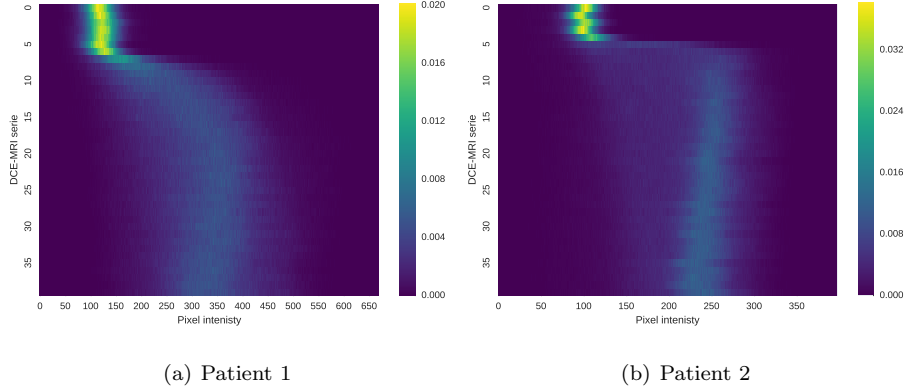


Figure 1: Illustration of the variations of the intensity PDF over time of two patients in a DCE-MRI.

z -score approach, assuming that the data follow a specific distribution (Lemaitre et al., 2016).

In DCE-MRI, the inter-patient variations are more complex due to the over time acquisition. These variations can be highlighted by observing the evolution of the intensity PDF of the DCE-MRI over time, as shown in the heatmap in Fig. 1. Therefore, these variations are: (i) an offset of the peak value before pre-contrast, (ii) a time offset depending of the contrast injection, and (iii) a global scale factor related to the enhancement. Therefore, our normalization method should attenuate all these variations and be performed globally across the different time sequence rather than for each independent sequence.

2.3.1. Graph-based offset correction for each DCE-MRI sequence

Before to standardize each sequence, the first step of the normalization is to cancel the intensity specific at each patient, occurring due to the media injection. In DCE-MRI, the intensity PDF do not always follow either a Rician or a Gaussian distribution over time. Therefore, the mean of these distributions cannot be used as a potential estimate for this offset. Additionally, this offset should be characterized by a smooth transition between series over time. Thus, this problem is solved using the graph-theory: considering the intensity PDF

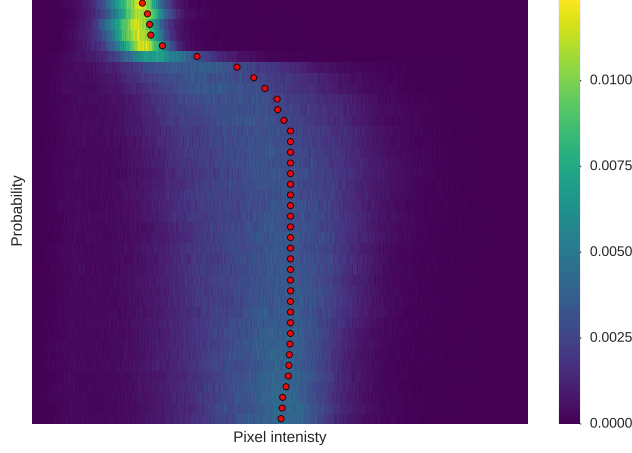


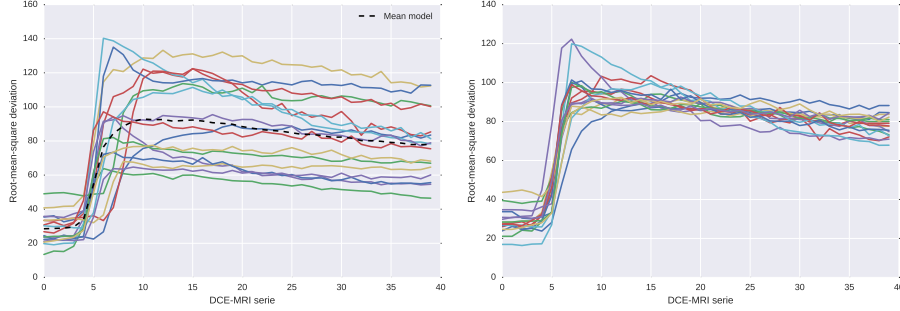
Figure 2: Illustration of the estimator found using the shortest-path through the graph.

over time as shown in Fig. 1, the offset is the boundary splitting the heatmap in
 120 two partitions such that it is as close as possible to the peak of the intensity PDF
 (see Fig. 2 for an illustration). Given the heatmap, a directed weighted graph
 $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ is built by taking each bar of the heatmap as a node and connecting
 each pair of bars by an edge. The edge weight w_{ij} between two nodes i and
 j corresponding to two pixels at position (x_i, y_i) and (x_j, y_j) , respectively, is
 125 defined as in Eq. (1):

$$w_{ij} = \begin{cases} \alpha \exp(1 - \frac{H(i)}{\max(H)}) & \text{if } x_j = x_i + 1 \text{ and } y_j = y_i, \\ (1 - \alpha) \exp(1 - \frac{H(i)}{\max(H)}) & \text{if } x_j = x_i \text{ and } y_j = y_i + 1, \\ 0 & \text{otherwise,} \end{cases} \quad (1)$$

where H is the heatmap, α is a smoothing parameter controlling the partition-
 ing.

Therefore, the offset is estimated by finding the shortest-path to cross the
 graph using Dijkstra's algorithm. The entry and exiting nodes are set to be
 130 the bin with the maximum probability for the first DCE-MRI serie and the bin
 corresponding to the median value for the last DCE-MRI serie, respectively. To
 ensure a robust estimation of the offset, the process of finding the shortest-path



(a) RMSD computed for each patient of our dataset. (b) RMSD after alignment using the curve parametric model.

Figure 3: Illustration of the correction of the time offset and the data dispersion.

is iteratively repeated by shifting the data and updating the heatmap as well as the graph \mathcal{G} . The procedure is stopped once that the offset found do not
 135 change. In general, this process is not repeated more than 3 iterations. An example of the offset found using this approach is presented in Fig. 2. Finally, for each DCE-MRI serie, the intensities are shifted by this offset.

2.3.2. Time offset and data dispersion correction

The next variations to correct are the time offset and the data dispersion. By
 140 computing the Root-Mean-Square Deviation (RMSD) of the intensities for each DCE-MRI serie, one can observed these two variations as shown in Fig. 3(a). Therefore, to correct these variations, we propose to register each patient RMSD to a mean model which corresponds to the mean of all patients RMSD. The parametric model to perform the registration is formulated as in Eq. (2):

$$T(\alpha, \tau, f(t)) = \alpha f(t - \tau), \quad (2)$$

145 where α and τ are the two parameters handling the time offset and global scale, respectively, $f(\cdot)$ is the RMSD function.

Therefore the registration problem is equivalent to:

$$\arg \min_{\alpha, \tau} = \sum_{t=0}^N [T(\alpha, \tau, f(t)) - \mu(t)]^2, \quad (3)$$

where $\mu(\cdot)$ is the mean model, N is the number of DCE-MRI serie.

Illustration of the correction applied to each RMSD patient is shown in
 150 Fig. 3(b). Once all these parameters have been inferred, the data can be shifted
 as well as scaled.

2.4. Quantification of DCE-MRI

2.4.1. Brix and Hoffmann models

In the Brix model (Brix et al., 1991), the MRI signal intensity is assumed to
 155 be proportional to the media concentration. Therefore, the model is expressed
 as in Eq. (4):

$$s_n(t) = 1 + A \left[\frac{\exp(k_{el}t') - 1}{k_{ep}(k_{ep} - k_{el})} \exp(-k_{el}t) - \frac{\exp(k_{ep}t') - 1}{k_{el}(k_{ep} - k_{el})} \exp(-k_{ep}t) \right], \quad (4)$$

with

$$s_n(t) = \frac{s(t)}{S_0}, \quad (5)$$

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 pro-
 160 portional to the transfer constant, the diffusion rate constant, and the rate
 constant, respectively. Additionally, during the injection time $0 \leq t \leq \tau$, $t' = t$
 and afterwards while $t > \tau$, $t' = \tau$.

Following this model, Hoffmann et al. propose the following similar model
 as expressed in Eq. (6):

$$s_n(t) = 1 + \frac{A}{\tau} \left[\frac{k_{ep}(\exp(k_{el}t') - 1)}{k_{el}(k_{ep} - k_{el})} \exp(-k_{el}t) - \frac{\exp(k_{ep}t') - 1}{(k_{ep} - k_{el})} \exp(-k_{ep}t) \right]. \quad (6)$$

165 The parameters are estimated by fitting the model using non-linear least-
 squares optimization solved with Levenberg-Marcquardt.

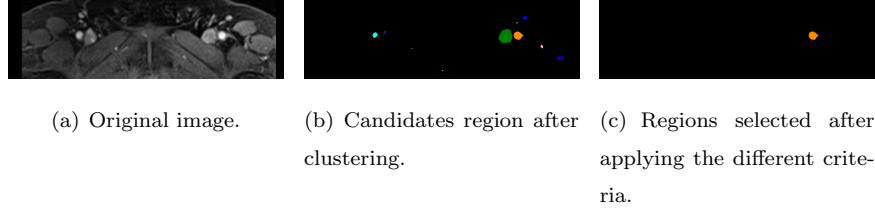


Figure 4: Illustration of the segmentation of the area used to determine the AIF.

2.4.2. Tofts model

The extended Tofts model is formulated as in Eq. (7):

$$C_t(t) = K_{trans}C_p(t) * \exp(-k_{ep}t) + v_pC_p(t), \quad (7)$$

where $*$ is the convolution operator; $C_t(t)$ and $C_p(t)$ is the concentration of
 170 contrast agent in the tissue and in the plasma, respectively; K_{trans} , k_{ep} , and v_p
 are the volume transfer constant, the diffusion rate constant, and the plasma
 volume fraction, respectively.

Therefore, Tofts model requires to: (i) detect candidate voxels from the
 femoral or iliac arteries and estimate a patient-based AIF signal, (ii) convert
 175 the MRI signal intensity (i.e., AIF and dynamic signal) to a concentration, and
 (iii) in the case of a population-based AIF, estimate an AIF signal.

Segmentation of artery voxels and patient-based AIF estimation

The AIF signal from DCE-MRI can be manually estimated by selecting the
 most-enhanced voxels from the femoral or iliac arteries (Meng et al., 2010).
 180 Few methods have been proposed to address the automated extraction of
 AIF signal. Chen et al. filter successively the possible candidates (Chen
 et al., 2008): (i) dynamic signals with small peak are rejecting by thresh-
 olding, (ii) voxels with a small wash-in are rejected by thresholding, (iii)
 a blob detector is used and large enough regions are kept, and (iv) circu-
 185 lar and cylindricity are used to reject the last false positive. Zhu et al.
 propose an iterative method selecting voxels which best fit a gamma vari-
 ate function (Zhu et al., 2011). However, it requires to compute first and

second derivatives as well as maximum curvature points. Shanbhag et al. propose a 4-steps algorithm (Shanbhag et al., 2012; Fennessy et al., 2015):
 190 (i) remove slices with artefacts and find the best slices based on intrinsic
 anatomic landmarks and enhancement characteristics, (ii) find the voxel
 candidates using the maximum enhanced voxels and a multi-label maxi-
 mum entropy based thresholding algorithm, (iii) excluding region next to
 the endorectal coil, and (iv) selecting the best 5 candidates which meet
 195 enhancement characteristics and that are correlated.

All the above methods are rather complex and thus we propose a method
 which is based on the following simple assumptions: (i) all possible AIF
 signal candidates should have a similar shape, (ii) an high enhancement,
 and (iii) the arteries should be almost round and within a size range.
 200 Therefore, each slice is clustered into regions using K-means clustering
 with $k = 6$. The cluster with the highest enhancement—i.e. corresponding
 to the 90th percentile of the maximum of each dynamic signal—contain the
 arteries and is selected. Finally, regions with an eccentricity smaller than
 0.5 and an area in the range of $[100, 400]$ voxels are kept. Additionally,
 205 to remove voxels contaminated by partial volume effect, only the 10%
 most enhanced voxels of the possible candidates are kept as proposed
 by (Schabel and Parker, 2008) and the average signal is computed. A
 summary of the different segmentation steps is presented in Fig. 4.

Conversion of MRI signal intensity to concentration To estimate the free
 parameters of the Tofts model (see Eq. (7)), the concentration $C_t(t)$ and
 $C_p(t)$ need to be computed from the MRI signal intensity and the AIF sig-
 nal, respectively. This conversion is based on the equation of the FLASH
 sequence—see Appendix A for details—and is formulated as in Eq. (8):

$$c(t) = \frac{1}{TR \cdot r_1} \ln \left(\frac{1 - \cos \alpha \cdot S^* \frac{s(t)}{S_0}}{1 - S^* \frac{s(t)}{S_0}} \right) - \frac{R_{10}}{r_1}, \quad (8)$$

with,

$$S^* = \frac{1 - \exp(-TR \cdot R_{10})}{1 - \cos \alpha \cdot \exp(-TR \cdot R_{10})}, \quad (9)$$

where $s(t)$ is the MRI signal, S_0 is the MRI signal prior to the injection of the contrast media, α is the flip angle, TR is the Repetition Time (TR), R_{10} is the pre-contrast tissue relaxation time also equal to $\frac{1}{T_{10}}$, r_1 is the relaxivity coefficient of the contrast agent.

T_{10} can be estimated from the acquisition of a T_1 map. However, this modality was not part of the clinical trial in this research and the value of T_{10} was fixed to 1600 ms for both blood and prostate as stated in the literature (Fennessy et al., 2015; De Bazelaire et al., 2004; Carr and Carroll, 2011).

Estimation of population-based AIF While estimating the pharmacokinetic parameters from Tofts model, the AIF concentration $C_p(t)$ can be computed either from the patient or a population. We presented in the two previous sections the algorithms which allows to estimate the patient-based AIF concentration. To compare with the previous approach, we also computed a population-based AIF which will be also later used to compare the performance of both approaches. In that regard, the population-based AIF was estimated as in (Meng et al., 2010) by fitting the average patient-based AIFs to the model of Parker et al. (2006) which is formulated as in Eq. (10):

$$C_p(t) = \sum_{n=1}^2 \frac{A_n}{\sigma_n \sqrt{2\pi}} \exp\left(\frac{-(t - T_n)^2}{2\sigma_n^2}\right) + \frac{\alpha \exp(-\beta t)}{1 + \exp(-s(t - \tau))}, \quad (10)$$

where A_n , T_n , and σ_n are the scaling constants, centers, and widths of the n^{th} Gaussian, α and β are the amplitude and decay constant of the exponential; and s and τ are the width and center of the sigmoid function, respectively.

The parameters are estimated by fitting the model using non-linear least-squares optimization solved with Levenberg-Marquardt.

2.4.3. 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. (11):

$$s_n(t) = \exp \left[rt + \frac{1}{\beta} (a_0 - r) (\exp(\beta t) - 1) \right], \quad (11)$$

with

$$s_n(t) = \frac{s(t) - S_0}{S_0}, \quad (12)$$

230 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.

The parameters are estimated by fitting the model using non-linear least-squares optimization solved with Levenberg-Marcquardt.

235 2.4.4. Semi-quantitative analysis

The semi-quantitative analysis of the DCE-MRI is equivalent to extract curve characteristics directly from the signal without a strict theoretical pharmacokinetic meaning. In this work, we use the model presented by Huisman et al. (2001) which formulate the MRI signal as in Eq. (13):

$$s(t) = \begin{cases} S_0 & 0 \leq t \leq t_0 \\ S_M - (S_M - S_0) \exp\left(\frac{-(t-t_0)}{\tau}\right) & t_0 < t \leq t_0 + 2\tau \\ S_M - (S_M - S_0) \exp\left(\frac{-(t-t_0)}{\tau}\right) + w(t - t_0 + 2\tau) & t > t_0 + 2\tau \end{cases} \quad (13)$$

240 where $s(t)$ is the MRI signal intensity, S_0 is the pre-contrast signal intensity, t_0 is the time corresponding to the start of enhancement, S_M and τ is the maximum of the signal and the exponential time constant, and w is the slope of the linear part.

Huisman et al. argue that curve fitting via least-squares minimization using
245 Nelder-Mead algorithm leads to inaccurate estimation of the free parameters:

mainly the issue come from an incorrect estimation of the start of enhancement t_0 leading to incorrect estimation of the other parameters. Therefore, they propose to: (i) estimate robustly t_0 , (ii) estimate S_0 by averaging the samples between 0 and t_0 (ii) estimate w depending if the slope is significant or not, (iii) estimate S_M which should be the point at the intersection of the most probable slope line and the plateau.

Instead of these successive estimations, we propose a unified optimization in which t_0 is fixed since that this is a key parameter. Therefore, t_0 is robustly estimated from the AIF signal since that this is the most enhanced signal in which the start of enhancement is easily identifiable. The AIF signal is computed as in Section 2.4.2. t_0 is estimated by finding the maximum in the beginning of the first derivative of the MRI signal. Then, the function in Eq.(13) is fitted using non-linear least squares with Trust Region Reflective algorithm. Furthermore, the parameters τ and S_M are bounded during the optimization to ensure robust estimations.

From Eq.(13), the following features are extracted: (i) the wash-in corresponding to the slope between t_0 and $t_0 + 2\tau$, (ii) the wash-out corresponding to the parameter w , (iii) the area under the curve between t_0 and the end of the signal, (iv) the exponential time constant τ , and (v) the relative enhancement $S_M - S_0$.

3. Experiments and results

3.1. Classification of individual parameter for each model

The first experiment consists in comparing the classification performance using each individual parameter for the different models, to assess the potential benefit of the normalization method. Therefore, each feature is individually classified using a Gaussian Naive Bayes (NB) classifier in a Leave-One-Patient-Out Cross-Validation (LOPO CV) fashion. NB is used due to its simplicity and it enables to check the fitted parameters for interpretation. The results are summarized in Table 1. It can be noted that in the majority of the cases,

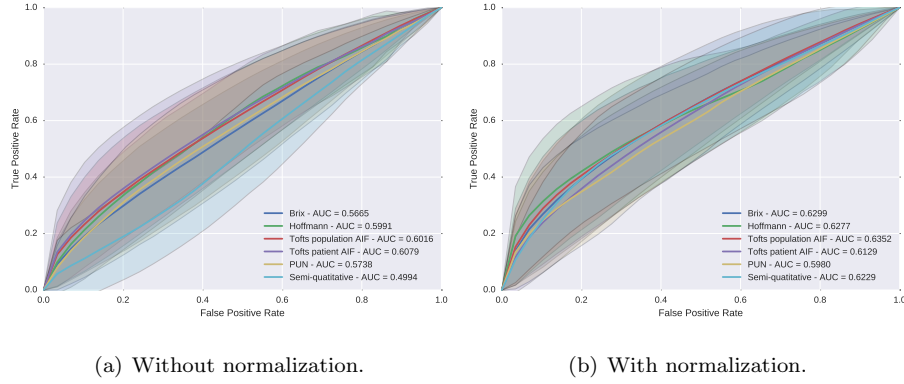


Figure 5: ROC analysis using a RF classifier with and without normalization DCE-MRI data for different pharmacokinetic models.

275 normalizing the data improve the classification performance in terms of Area Under the Curve (AUC). Only the PUN model does not follow this tendency which might due to the fact that the function do not fit the data as good as the other model - WE WILL NEED SOME RMSE FOR EACH FITTING IF WE SAY SO..

280 It could be interesting to check the value of the mean and std of the NB. We could compute a ratio which refer to the class separability.

3.2. Classification by combining the parameters for each model

Usually, the parameters are combined to form a multi-dimensional prior to classify the data. Therefore, for each model, all parameters are combined and classified using a Random Forest (RF) classifier in a LOPO CV fashion. The use of RF is motivated since that it leads to the best performance in the state-of-the-art methods (Litjens et al., 2014). The results are summarized by making Receiver Operating Characteristic (ROC) analysis and computing the AUC, as reported in Fig. 5. It can be noted that in all the cases the normalization of the data improve the classification performance.

Table 1: AUC for each individual pharmacokinetic parameter using a NB classifier.

Features	Un-normalized data	Normalized data
Brix model		
A	0.62	0.67
k_{el}	0.52	0.61
k_{ep}	0.52	0.58
Hoffmann model		
A	0.50	0.56
k_{el}	0.53	0.64
k_{ep}	0.50	0.66
Tofts model with population AIF		
K_{trans}	0.62	0.65
v_e	0.50	0.52
v_p	0.63	0.53
Tofts model with patient AIF		
K_{trans}	0.66	0.65
v_e	0.50	0.52
v_p	0.37	0.65
PUN model		
a_0	0.53	0.51
r	0.59	0.55
β	0.56	0.44
Semi-quantitative analysis		
wash-in	0.64	0.51
wash-out	0.50	0.66
IAUC	0.61	0.64
τ	0.57	0.61
$S_M - S_0$	0.63	0.64

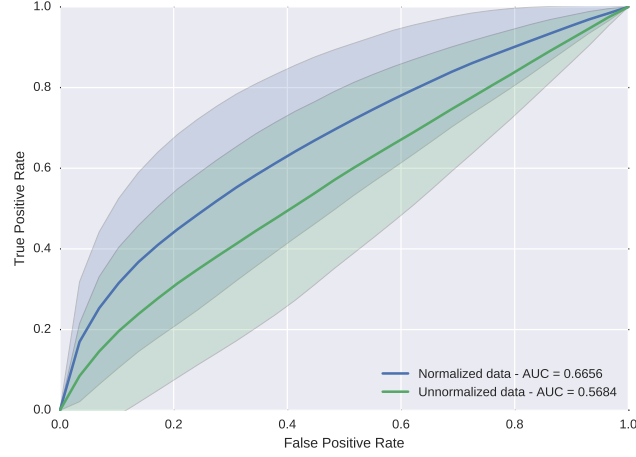


Figure 6: ROC analysis using the entire DCE-MRI signal with and without normalization in conjunction with a RF classifier.

3.3. Classification of the entire enhanced DCE-MRI signal

The quantification methods are extracting a minimal set of parameters which should characterized the enhancement DCE-MRI curves. However, this extraction could discard some information of the signal. This experiment attends to use the whole DCE-MRI signal to perform the classification. Therefore, the enhanced signal is classified using a RF classifier in a LOPO CV fashion. The ROC analysis and AUC are reported in Fig. 6. It can be note that the worst performance are achieved while data without normalization. However, normalizing the data, this classification strategy lead the best classification performance, outperforming any quantification method, showing the importance of our normalization algorithm.

4. Discussions

- Discuss about the T1 parameters in Tofts and say that we can do better probably.
- Compare the two approach for the AIF.

- Make a discussion about the detailed interpretation of individual feature classification. There is something to discuss about the semi-quantitative from wash-in to wash-out reversed performance. Something also about the PUN model.

- Explain the drawbacks of the whole signal classification (time).

5. Conclusions and future works

In this work, we presented a new method for normalizing/standardizing DCE-MRI data. Through different experiments, we show the benefit of such normalization. Furthermore, we show that using the whole DCE-MRI signal instead extracting parameters lead to the best classification performance.

As avenues for future research, this normalization has to be part of a mp-MRI CAD system, mixing T₂-W-MRI, DCE-MRI, DW-MRI, and MRSI.

Appendix A. Conversion from FLASH signal to media concentration

In this appendix, we show the demonstration used to extract the agent concentration from the MRI signal.

The signal equation in FLASH sequence (Haase et al., 1986) is defined as:

$$s(t) = S_{eq} \sin \alpha \cdot \frac{1 - \exp(-TR(R_{10} + r_1 c(t)))}{1 - \cos \alpha \cdot \exp(-TR(R_{10} + r_1 c(t)))}, \quad (\text{A.1})$$

where $s(t)$ is the MRI signal, S_{eq} is the maximum signal amplitude of the spoiled gradient at the TE which is proportional to the Proton Density (PD), α is the flip angle, TR is the Repetition Time (TR), R_{10} is the pre-contrast tissue relaxation time also equal to $\frac{1}{T_{10}}$, r_1 is the relaxativity coefficient of the contrast agent, and $c(t)$ is the media concentration.

Therefore, the pre-contrast signal prior to bolus injection of the media is defined as:

$$S_0 = S_{eq} \sin \alpha \cdot \frac{1 - \exp(-TR \cdot R_{10})}{1 - \cos \alpha \cdot \exp(-TR \cdot R_{10})}. \quad (\text{A.2})$$

To simplify the demonstration, let us define:

$$A = \exp(-TR \cdot R_{10}), \quad (\text{A.3})$$

$$B = \exp(-TR \cdot r_1 c(t)). \quad (\text{A.4})$$

330

Let us define:

$$S^* = \frac{S_0}{S_{eq} \sin \alpha}, \quad (\text{A.5})$$

$$= \frac{1 - A}{1 - A \cos \alpha}. \quad (\text{A.6})$$

Thus,

$$S^* \frac{s(t)}{S_0} = \frac{S_0}{S_{eq} \sin \alpha} \frac{s(t)}{S_0}, \quad (\text{A.7})$$

$$= \frac{1 - AB}{1 - AB \cos \alpha}. \quad (\text{A.8})$$

Now, let us define:

$$\frac{1 - \cos \alpha \cdot S^* \frac{s(t)}{S_0}}{1 - S^* \frac{s(t)}{S_0}} = \frac{1 - \cos \alpha \left(\frac{1 - AB}{1 - AB \cos \alpha} \right)}{1 - \frac{1 - AB}{1 - AB \cos \alpha}}, \quad (\text{A.9})$$

$$= \frac{1 - AB \cos \alpha - \cos \alpha (1 - AB)}{1 - AB \cos \alpha - (1 - AB)}, \quad (\text{A.10})$$

$$= \frac{1 - AB \cos \alpha - \cos \alpha + AB \cos \alpha}{1 - AB \cos \alpha - 1 + AB}, \quad (\text{A.11})$$

$$= \frac{1 - \cos \alpha}{AB(1 - \cos \alpha)}, \quad (\text{A.12})$$

$$= \frac{1}{AB}. \quad (\text{A.13})$$

Thus,

$$-TR \cdot R_{10} - TR \cdot r_1 c(t) = \ln \left(\frac{1 - \cos \alpha \cdot S^* \frac{s(t)}{S_0}}{1 - S^* \frac{s(t)}{S_0}} \right). \quad (\text{A.14})$$

Therefore,

$$c(t) = \frac{1}{TR \cdot r_1} \ln \left(\frac{1 - \cos \alpha \cdot S^* \frac{s(t)}{S_0}}{1 - S^* \frac{s(t)}{S_0}} \right) - \frac{R_{10}}{r_1}. \quad (\text{A.15})$$

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