

# A boosting approach for prostate cancer detection using multi-parametric MRI

Guillaume Lemaître<sup>a,c</sup> and Joan Massich<sup>a</sup> and Robert Martí<sup>c</sup> and Jordi Freixenet<sup>c</sup>  
and Joan C. Vilanova<sup>d</sup> and Paul M. Walker<sup>b</sup> and Désiré D. Sidibé<sup>a</sup> and  
Fabrice Mériaudeau<sup>a</sup>

<sup>a</sup>LE2I-UMR CNRS 6306, Université de Bourgogne, 12 rue de la Fonderie, 71200 Le Creusot, France;

<sup>b</sup>LE2I-UMR CNRS 6306, Université de Bourgogne, Avenue Alain Savary, 21000 Dijon, France;

<sup>c</sup>ViCOROB, Universitat de Girona, Campus Montilivi, Edifici P4, 17071 Girona, Spain;

<sup>d</sup>Department of Magnetic Resonance, Clinica Girona, Lorenzana 36, 17002 Girona, Spain

## ABSTRACT

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**Keywords:** Gradient boosting, multi-parametric MRI, prostate cancer, computer-aided diagnosis

## 1. INTRODUCTION

On a worldwide scale, prostate cancer (PCa) has been reported as the second most frequently diagnosed men cancers accounting for 13.6 %.<sup>1</sup> Statistically, the estimated number of new diagnosed cases was 899,000 with no less than 258,100 estimated deaths.<sup>1</sup> In United States, aside from skin cancer, PCa was declared to be the most commonly diagnosed cancer among men, implying that around one in seven men will be diagnosed with PCa during their lifetime.<sup>2</sup>

Since its introduction in mid-1980s, prostate-specific antigen (PSA) is widely used for PCa screening<sup>3</sup> and has shown to improve early detection of PCa.<sup>4</sup> However, several trials conducted in Europe and United States conclude that PSA screening suffers from low specificity.<sup>5–7</sup> Thus, current research focus on developing new screening methods to improve PCa detection. In this perspective, Magnetic resonance imaging (MRI) techniques have recently shown promising results for PCa detection. Furthermore, three different modalities are currently investigated: (i) T<sub>2</sub> Weighted (T<sub>2</sub>-W) MRI, (ii) Dynamic Contrast-Enhanced (DCE) MRI and (iii) Diffusion Weighted (DW) MRI.

Several researches have been carried out in order to investigate the contributions of machine learning classifiers for PCa detection using the three aforementioned 3T multi-parametric MRI such as Support Vector Machines (SVM),<sup>8–12</sup> probabilistic boosting tree<sup>13</sup> or probabilistic neural network.<sup>13</sup> However, these studies use different datasets and evaluation statistics to report their results leading to an impossibility to give rise to a fair comparison.

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Further author information: (Send correspondence to G.L.)  
G.L.: E-mail: guillaume.lemaitre@udg.edu

In this research, we investigate the performance of gradient boosting for PCa detection using 3T multi-parametric MRI. Two different features extraction strategies have been chosen in order to feed the classifier: (i) voxel-based and (ii) 3D texton-based. An evaluation of both strategies as well as the contribution of each modality is provided. Furthermore, the dataset used for this experimentation is part of our future benchmarking platform I2CVB available at <http://visor.udg.edu/i2cvb/> and are available for future comparisons.

## 2. MATERIAL AND METHODS

### 2.1 Data

The multi-parametric MRI was acquired from a cohort of patients with higher-than-normal level of PSA. The acquisition was performed using a 3T whole body MRI scanner (Siemens Magnetom Trio TIM, Erlangen, Germany) using sequences to obtain T<sub>2</sub>-W MRI, DCE MRI and DW MRI. Aside of the MRI examination, these patients also underwent a guided-biopsy. Finally, the dataset was composed of a total of 20 patients of which 18 patients had biopsy proven PCa and 2 patients were “healthy” with negative biopsies. The prostate organ as well as the prostate zones (i.e., peripheral zone (PZ) and central gland (CG)) and PCa were manually segmented by an experienced radiologist. Therefore, 13 patients had a PCa in the PZ, 3 patients had PCa in the CG, 2 patients had invasive PCa in both PZ and CG and finally 3 patients were considered as “healthy”.

The Apparent Diffusion Coefficient (ADC) maps were computed using the scanner software and the DW MRI. The DCE MRI sequence consist in a kinetic study composed of 40 samples over time. These DCE MRI sequences and ADC maps were resampled using the spatial information of the T<sub>2</sub>-W MRI sequence with dimensions of  $448 \times 360 \times 64$  and voxel spacing of  $0.68 \times 0.68 \times 1.25$  mm<sup>3</sup>. Linear interpolation was used to compute missing data during the up-sampling. The resampling was implemented in C++ using the Insight Segmentation and Registration Toolkit.<sup>14</sup>

Due to the large number of samples available at a voxel scale, the dataset was pre-processed in order to deal with a balanced dataset allowing to not bias the results. Therefore, all the positive samples (i.e., PCa voxels) were stored and an equal number of negative samples (i.e., “healthy” voxels) were randomly selected from the larger original pool. Thus, the total amount of positive and negative samples considered in our experiments accounted for 218,422 voxels.

### 2.2 Classification framework

#### 2.2.1 Feature extraction strategies

A summary of the features extracted as well as the strategies chosen are summarized in Table 1. Two main strategies are applied to extract features. In the voxel-based approach, at each voxel location, the intensities for the different MRI modalities are extracted as well as the membership of this voxel to belong to the PZ or CG. The 3D texton-based approach extend this extraction for a 3D window of size  $9 \times 9 \times 3$  around the central voxel. In both case, the vectors  $V(\cdot)$  and  $T(\cdot)$  extracted are scaled using min-max normalization.

Then, the different concatenation of the vectors  $V(\cdot)$  and  $T(\cdot)$  are summarized in Table 2. Different combinations are further tested in order to observe the contribution of each data feature.

Table 1: Overview of voxel features extracted in our classification framework.

| Extraction strategy | Name        | Size | Short description   |
|---------------------|-------------|------|---|
| Voxel-based         | $V_{T_2-W}$ | 1    | Intensity of a voxel in the $T_2$ -W MRI  |
|                     | $V_{ADC}$   | 1    | Intensity of a voxel in the ADC map   |
|                     | $V_{DCE}$   | 40   | Intensities of a voxel along the whole serie in the DCE MRI                                   |
|                     | $V_{PZ}$    | 1    | Boolean value of a voxel membership to the PZ   |
|                     | $V_{CG}$    | 1    | Boolean value of a voxel membership to the CG   |
| 3D texton-based     | $T_{T_2-W}$ | 243  | Intensities vector for a window of $9 \times 9 \times 3$ voxels in the $T_2$ -W MRI           |
|                     | $T_{ADC}$   | 243  | Intensities vector for a window of $9 \times 9 \times 3$ voxels in the ADC map                |
|                     | $T_{DCE}$   | 9720 | Intensities vector for a window of $9 \times 9 \times 3$ along the whole serie in the DCE MRI |
|                     | $T_{PZ}$    | 243  | Boolean vector of voxels memberships to the PZ for a window of $9 \times 9 \times 3$          |
|                     | $T_{CG}$    | 243  | Boolean vector of voxels memberships to the CG for a window of $9 \times 9 \times 3$          |

### 2.2.2 Gradient boosting

In this research, a gradient boosting classifier<sup>15</sup> originally proposed by Friedman<sup>16,17</sup> was used to implement our computer-aided detection and diagnosis (CAD) system for PCa. Gradient boosting is in fact a reformulation of the well-known AdaBoost<sup>18</sup> in which the problem of finding “boots” is tackled as a numerical optimization. In a greedy manner, a strong classifier is constructed by iteratively finding the best pair of real-valued weak learner function (e.g., regression trees) and its corresponding weight which minimize a given differentiable loss function. This minimization can be carried out via gradient descent or quadratic approximation.<sup>19</sup>

### 2.2.3 Validation model

k-cross validation

## 3. RESULTS

Include the two figures with one for voxel-based and the other one for texton-based and discuss briefly.

## 4. DISCUSSION

Discuss the results.

- Single modality is not working as good as multi-parametric

Table 2: Overview of the different concatenations tested for the classification.

| Name           | V <sub>T<sub>2</sub>-W</sub> | V <sub>ADC</sub> | V <sub>DCE</sub> | V <sub>PZ</sub> | V <sub>CG</sub> | T <sub>T<sub>2</sub>-W</sub> | T <sub>ADC</sub> | T <sub>DCE</sub> | T <sub>PZ</sub> | T <sub>CG</sub> |
|----------------|------------------------------|------------------|------------------|-----------------|-----------------|------------------------------|------------------|------------------|-----------------|-----------------|
| V <sub>1</sub> | ✗                            | ✗                | ✓                | ✗               | ✗               | ✗                            | ✗                | ✗                | ✗               | ✗               |
| V <sub>2</sub> | ✗                            | ✓                | ✗                | ✗               | ✗               | ✗                            | ✗                | ✗                | ✗               | ✗               |
| V <sub>3</sub> | ✗                            | ✓                | ✓                | ✗               | ✗               | ✗                            | ✗                | ✗                | ✗               | ✗               |
| V <sub>4</sub> | ✓                            | ✗                | ✗                | ✗               | ✗               | ✗                            | ✗                | ✗                | ✗               | ✗               |
| V <sub>5</sub> | ✓                            | ✗                | ✓                | ✗               | ✗               | ✗                            | ✗                | ✗                | ✗               | ✗               |
| V <sub>6</sub> | ✓                            | ✓                | ✗                | ✗               | ✗               | ✗                            | ✗                | ✗                | ✗               | ✗               |
| V <sub>7</sub> | ✓                            | ✓                | ✓                | ✓               | ✓               | ✗                            | ✗                | ✗                | ✗               | ✗               |
| T <sub>1</sub> | ✗                            | ✗                | ✗                | ✗               | ✗               | ✗                            | ✗                | ✓                | ✗               | ✗               |
| T <sub>2</sub> | ✗                            | ✗                | ✗                | ✗               | ✗               | ✗                            | ✓                | ✗                | ✗               | ✗               |
| T <sub>3</sub> | ✗                            | ✗                | ✗                | ✗               | ✗               | ✗                            | ✓                | ✓                | ✗               | ✗               |
| T <sub>4</sub> | ✗                            | ✗                | ✗                | ✗               | ✗               | ✓                            | ✗                | ✗                | ✗               | ✗               |
| T <sub>5</sub> | ✗                            | ✗                | ✗                | ✗               | ✗               | ✓                            | ✗                | ✓                | ✗               | ✗               |
| T <sub>6</sub> | ✗                            | ✗                | ✗                | ✗               | ✗               | ✓                            | ✓                | ✗                | ✗               | ✗               |
| T <sub>7</sub> | ✗                            | ✗                | ✗                | ✗               | ✗               | ✓                            | ✓                | ✓                | ✓               | ✓               |

- Which single modality is better.
- What is the increase of the zone information.
- Voxel-based vs texton-based

## 5. CONCLUSION

### 5.1 Future works

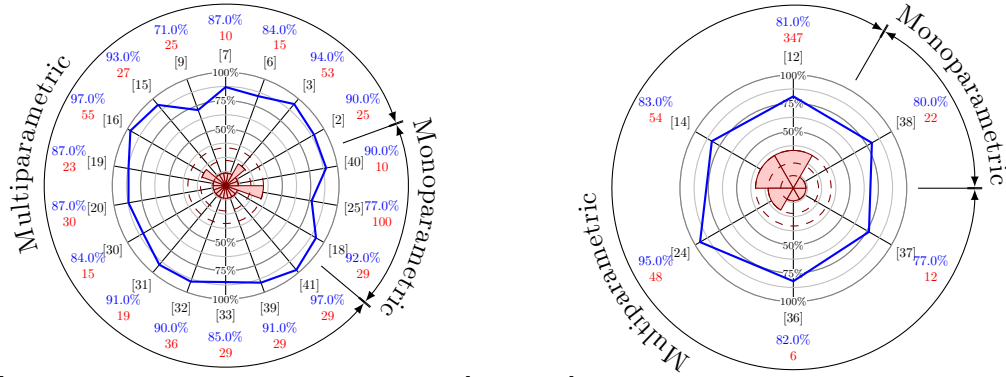
- Check the difference with other features usually extracted.
- Check the results difference with a registration of the three modalities.

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[caption] [caption2]  
Figure 1: Comparison of the results in terms of AUC for 1.5 and 3.0 Tesla MRI scanners. The blue value represents the metric and are graphically reported in the blue curve in the center of the figure. The red value and areas correspond to the number of patients in the dataset. The numbers between brackets in green correspond to the reference as reported in Tab. ??.

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