

# Computer-Aided Detection and Diagnosis for prostate cancer based on mono and multiparametric MRI/MRSI: A review

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## Abstract

Prostate cancer is reported to be the second most diagnosed cancer of men all over the world. In the last decades, new imaging techniques based on MRI have been developed improving the diagnosis task of radiologists. In practise, diagnosis can be affected by multiple factors reducing the chance to detect potential lesions. Computer-aided detection and computer-aided diagnosis have been designed to answer to these needs and provide help to radiologists in their daily duties. Research on computer-aided systems specifically focused for prostate cancer is a young technology and part of a dynamic field for the last ten years. This survey aimed to provide an overview of the researches carried out in this lapse of time and more precisely a comprehensive review of all the different stages composing the work-flow of computer-aided system. We also provide a comparison between these studies and potential avenues for future research are also discussed.

*Keywords:* computer-aided detection, computer-aided diagnosis, CAD, magnetic resonance imaging, magnetic resonance spectroscopy imaging, computer vision

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## 1. Introduction

During the last century, physicists focused on constantly innovating in terms of imaging techniques assisting radiologists to overcome different tasks as cancer detection and diagnosis. However, human diagnosis still suffers from low repeatability,

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5 synonymous with erroneous detection or interpretations of abnormalities throughout  
6 clinical decisions (Giger et al. (2008), Hambrock et al. (2013)). These errors are  
7 driven by two majors causes (Giger et al. (2008)). On the one hand, observer lim-  
8 itations (e.g., constrained human visual perception, fatigue or distraction) are the  
9 principal human issues. On the other hand, the second reason is linked to the clinical  
10 cases themselves, for instance due to unbalanced data (number of healthy cases more  
11 abundant than malignant cases) or overlapping structures resulting from limitations  
12 of imaging techniques.

13 Computer vision has given rise to many promising solutions, but, instead of  
14 focusing on fully automatic computerized systems, researchers have aimed at provid-  
15 ing computer image analysis techniques to aid radiologists in their clinical decisions  
16 (Giger et al. (2008)). In fact, these investigations brought about both concepts of  
17 computer-aided detection (CADe) and computer-aided diagnosis (CADx) grouped  
18 under the acronym CAD. Since those first steps, evidence has shown that CAD sys-  
19 tems enhance the diagnosis performance of radiologists. Chan et al. (1999) reported  
20 a significant 4 % improvement in breast cancer detection, in accordance with later  
21 studies (Dean and Ilvento (2006)). Similar conclusions were drawn in the case of lung  
22 nodule detection (Li et al. (2004)), colon cancer (Petrick et al. (2008)) and prostate  
23 cancer (CaP) as well (Hambrock et al. (2013)). Chan et al. (1999) also hypothesized  
24 that CAD systems will be even more efficient assisting inexperienced radiologists to  
25 senior radiologists. That hypothesis was tested by Hambrock et al. (2013) and was  
26 confirmed in case of CaP detection. In this particular study, inexperienced radiolo-  
27 gists obtained equivalent performance to senior radiologists, both with the help of a  
28 CAD system whereas the accuracy of their diagnosis was significantly poorer without  
29 this assistance.

30 In the late eighties, the first CAD systems were developed to detect anomalies on  
31 chest radiographies and mammograms (Chan et al. (1987), Doi et al. (1990), Giger  
32 et al. (1988)). In the past twenty years, extensive investigations were conducted in  
33 the advancement of CAD systems, migrating from intensive time consuming algo-  
34 rithms performed on reduced number of cases to “fast” processing on a large medical  
35 dataset. These works were focused on diverse organ cancer diagnosis making use of  
36 numerous imaging modalities: micro-calcification detection in breast mammography  
37 (Elter and Horsch (2009), Rangayyan et al. (2007)) and ultrasound (US) imaging  
38 (Cheng et al. (2010)), lung nodules detection based on computer tomography (CT)  
39 (Chan et al. (2008), Suzuki (2012)), colon tumours detection (Suzuki (2012)) and  
40 melanoma detection using dermoscopy imaging (Korotkov and Garcia (2012)). Not-  
41 ing the abundance of diverse CAD systems, these fields achieved a certain maturity  
42 which can be explained by the imaging techniques employed. Indeed, x-rays, US as

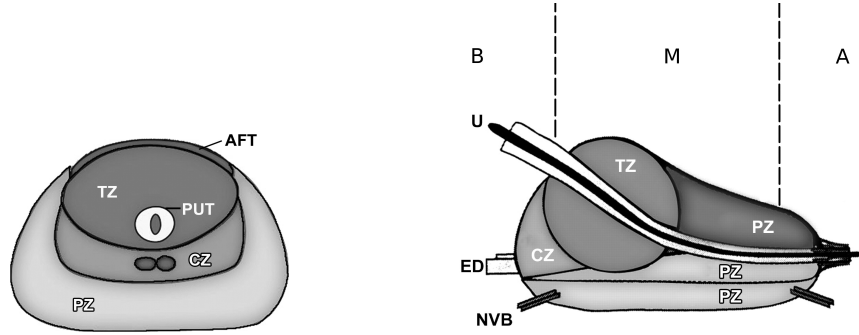
well as CT are medical imaging techniques developed all before the 1970s and were subject to intensive research.

In contradiction with the aforementioned statement, CaP detection using CAD is a young technology due to the fact that magnetic resonance imaging (MRI) is the keystone medical imaging technique (Hegde et al. (2013)). Four distinct MRI modalities are employed in CAD for CaP and were mainly developed after the mid-1990s: (i)  $T_2$  Weighted ( $T_2$ -W) MRI (Hricak et al. (1983)), (ii) dynamic contrast-enhanced (DCE) MRI (Huch Boni et al. (1995)), (iii) magnetic resonance spectroscopy imaging (MRSI) (Kurhanewicz et al. (1996)) and (iv) diffusion weighted (DW) MRI (Scheidler et al. (1999b)). It can be noted that these techniques came into existence relatively recently mainly due to technological progress. In addition, the increase of magnetic field strength and the development of endorectal coil, both improved image spatial resolution (Swanson et al. (2001)) needed to perform more accurate diagnosis. It is for this matter that development of CAD for CaP is lagging behind the other fields stated above.

The first study using MRI as inputs of CAD system was published ten years ago by Chan et al. (2003). Despite this, no less than fifty studies have been reviewed for this survey since that seminal work. To the best of our knowledge, there is no review in the literature regarding the advancement of CAD systems devoted specifically to CaP detection and diagnosis. Thus, our aim with this survey is threefold: (i) provide an overview of developed CAD systems for CaP detection and diagnosis based on MRI modalities (ii) assess the different work and (iii) pointing out avenues for future work.

As discussed further in Sect. 2.3.3, CAD systems share a common framework. Stages involved in CAD work-flow can be categorized into six distinctive processes: (i) pre-processing, (ii) segmentation, (iii) registration, (iv) feature detection, (v) feature selection and extraction and (vi) classification. The first three stages are used to enhance data as well as to extract regions of interest and, in the case of multi-modal sources, to merge information of those heterogeneous sources in a joint reference system. The last three categories deal with pattern recognition, machine learning and data mining notions and more precisely with the data classification problem. First, information is detected from the different data sources and a subset of relevant features is selected and/or extracted. Then, this meaningful data will then be classified in order to provide the probability of malignancy of the area of interest and will assist radiologists in their diagnosis decisions (see Fig. 2.3.2).

This paper is organized as follows: Sect. 2 deals with general information about human prostate and background about CaP. Methods regarding CaP screening and imaging techniques used are also presented as well as an introduction on the CAD



(a) Transverse anatomy of the prostate.

(b) Sagittal anatomy of the prostate.

Figure 1: Prostate anatomy with division in different zones. *AFT*: anterior fibromuscular tissue, *CZ*: central zone, *ED*: ejaculatory duct, *NVB*: neurovascular bundle, *PUT*: tissue, *PZ*: peripheral zone, *U*: urethra, *TZ*: transitional zone, *B*: base, *M*: median, *A*: apex (copyright by Choi et al. (2007)).

framework. Sections 3 - 4 review techniques used in different steps involved in a CAD work-flow which will be our main contribution. Image regularization framework including pre-processing (Sect. 3.1), segmentation (Sect. 3.2) and registration (Sect. 3.3) will be covered as well as the image classification framework comprising of feature detection (Sect.4.2), feature selection and extraction (see Sect. 4.3) and feature classification (Sect. 4.4). Results and discussion are reported in Sect. 5 followed by a concluding section.

## 2. Background

This section provides an overview of CaP and its detection and diagnosis. We start with a summary of the prostate anatomy and a brief overview of different CaPs. Subsequently a discussion of the current screening strategy for CaP and its drawbacks is presented. MRI plays an important role in improving the current strategy and a more detailed description of MRI modalities is given. These different techniques are used as inputs to the CAD system which is finally discussed.

### 2.1. The human prostate

The prostate is an exocrine gland of the male reproductive system having an inverted pyramidal shape. It measures approximately three centimetres in height by two and half centimetres in depth and its weight is estimated to be between seven and sixteen grams for an adult (Leissner and Tisell (1979)). The prostate size

100 increases at two distinct stages during physical development: initially at puberty to  
101 reach its normal size, then again after sixty years of age leading to benign prostatic  
102 hyperplasia (BPH) (Parfait (2010)).

103 A zonal classification of the prostate, depicted in Fig. 1, was suggested by McNeal  
104 (McNeal (1981)). Subsequently, this categorization was widely accepted in the lit-  
105 erature (cf., Coakley and Hricak (2000), Hricak et al. (1987), Parfait (2010), Villers  
106 et al. (1991)) and is used in all medical examinations (e.g., biopsy, MRI screening).  
107 The classification is based on dividing the gland into three distinct regions: (i) central  
108 zone (CZ) accounting for 20-25% of the whole prostate gland, (ii) transitional zone  
109 (TZ) standing for 5% and (iii) peripheral zone (PZ) representing the 70%. In MRI  
110 images, tissues of CZ and TZ are difficult to distinguish and are usually merged into  
111 a common region, denominated central gland (CG). As part of this classification,  
112 the prostate can be divided in three longitudinal portions depicted in Fig. 1(b): (i)  
113 base, (ii) median gland and (iii) apex.

## 114 2.2. Prostate carcinoma

115 CaP has been reported on a worldwide scale to be the second most frequently  
116 diagnosed cancer of men accounting for 13.6% (Ferlay et al. (2010)). Statistically,  
117 in 2008, the number of new diagnosed cases was estimated to be 899,000 with no  
118 less than 258,100 deaths (Ferlay et al. (2010)). In United States, aside from skin  
119 cancer, CaP was declared to be the most commonly diagnosed cancer among men,  
120 implying that approximately one in six men will be diagnosed with CaP during their  
121 lifetime and one in thirty-six will die from this disease causing CaP to be the second  
122 most common cause of cancer death among men (Siegel et al. (2013), American  
123 Cancer Society (2013)).

124 Despite active research to determine the causes of prostate cancer, a fuzzy list of  
125 risk factors has arisen (American Cancer Society (2010)). The etiology was linked to  
126 the following factors (American Cancer Society (2010)): (i) family history (Giovan-  
127 nucci et al. (2007), Steinberg et al. (1990)), (ii) genetic factors (Agalliu et al. (2009),  
128 Amundadottir et al. (2006), Freedman et al. (2006)), (iii) race-ethnicity (Giovannucci  
129 et al. (2007), Hoffman et al. (2001)), (iv) diet (Alexander et al. (2010), Giovannucci  
130 et al. (2007), Ma and Chapman (2009)), (v) obesity (Giovannucci et al. (2007), Ro-  
131 driguez et al. (2007)). This list of risk factors alone cannot be used to diagnose CaP  
132 and in this way, screening enables early detection and treatment.

133 CaP growth is characterized by two main types of evolution (Strum and Pogliano  
134 (2005)): slow-growing tumours, accounting for up to 85 % of all CaPs (Lu-Yao  
135 et al. (2009)), progress slowly and usually stay confined to the prostate gland. For  
136 such cases, treatment can be substituted with active surveillance. In contrast, the

second variant of CaPs develops rapidly and metastasises from prostate gland to others organs, primarily the bones (Oster et al. (2013)). Bone metastases, being an incurable disease, significantly affects the morbidity and mortality rate (Ye et al. (2007)). Hence, the results of the surveillance have to be trustworthy in order to distinguish aggressive from slow-growing CaP.

CaP is more likely to come into being in specific regions of the prostate. In that respect, around 70-80 % of CaPs originate in PZ whereas 10-20 % in TZ (Carrol et al. (1987), McNeal et al. (1988), Stamey et al. (1998)). Only about 5 % of CaPs occur in CZ (Cohen et al. (2008), McNeal et al. (1988)). However, those cancers appear to be more aggressive and more likely to invade other organs due to their location (Cohen et al. (2008)).

### *2.3. CaP screening and imaging techniques*

#### *2.3.1. Current CaP screening*

Current CaP screening consists of three different stages. First, prostate-specific antigen (PSA) control is performed to distinguish between low and high risk CaP. Then, for confirmation, samples are taken during prostate biopsy and finally analysed to evaluate the prognosis and the stage of CaP. In this section, we present a detailed description of the current screening as well as its drawbacks.

Since its introduction in mid-1980s, PSA is widely used for CaP screening (Etzioni et al. (2002)). A higher-than-normal level of PSA can indicate an abnormality of the prostate either as a BPH or a cancer (Hoeks et al. (2011)). However, other factors can lead to an increased PSA level such as prostate infections, irritations, a recent ejaculation or a recent rectal examination (Parfait (2010)). PSA can be found in the bloodstream in two different forms: free PSA (about 10%), and linked to another protein (about 90%). A level of PSA higher than  $10 \text{ ng.mL}^{-1}$  is considered to be at risk (Parfait (2010)). If the PSA level is between  $10 \text{ ng.mL}^{-1}$  and  $4 \text{ ng.mL}^{-1}$ , the patient is considered as suspicious (Barentsz et al. (2012)). In that case, the ratio of free PSA to total PSA is computed; if the ratio is higher than 15%, the case is considered as pathological (Parfait (2010)).

A transrectal ultrasound (TRUS) biopsy is carried out for cases which are considered as pathological. At least six different samples are taken randomly from the right and left parts of three different zones: apex, median and base. These samples are further evaluated using the Gleason grading system (Gleason (1977)). The scoring scheme to characterize the biopsy sample is composed of five different patterns which correspond to grades ranging from 1 to 5. Higher grades are associated with poor prognosis (Epstein et al. (2005)). Then, in the Gleason system, two scores are assigned corresponding to (i) the grade of the most present tumour

174 pattern, and (ii) the grade of the second most present tumour pattern (Epstein et al.  
175 (2005)). A higher Gleason score (GS) indicates a more aggressive tumour (Epstein  
176 et al. (2005)). Also, it should be noted that biopsy is an invasive procedure which can  
177 result in serious infection or urine retention (Chou et al. (2011), Hara et al. (2005)).

178 Although PSA screening has been shown to improve early detection of CaP (Chou  
179 et al. (2011)), its lack of reliability motivates further investigations using MRI-CAD.  
180 Two reliable studies, carried out in the United States (Andriole et al. (2009)) and  
181 in Europe (Hugosson et al. (2010), Schröder et al. (2012)), have attempted to assess  
182 the impact of early detection of CaP, with diverging outcomes (Chou et al. (2011),  
183 Heidenreich et al. (2013)). The study carried out in Europe<sup>1</sup> concluded that PSA  
184 screening reduces CaP-related mortality by 21-44% (Hugosson et al. (2010), Schröder  
185 et al. (2012)), while the American<sup>2</sup> trial found no such effect (Andriole et al. (2009)).  
186 However, both studies agree that PSA screening suffers from low specificity, with an  
187 estimated rate of 36 % (Schroder et al. (2008)). Both studies also agree that over-  
188 treatment is an issue: decision making regarding treatment is further complicated by  
189 difficulties in evaluating the aggressiveness and progression of CaP (Delpierre et al.  
190 (2013)).

191 Hence, new screening methods should be developed with improved specificity of  
192 detection as well as more accurate risk assessment (aggressiveness and progression).  
193 Current research is focused on identifying new biological markers to replace PSA-  
194 based screening (Bourdounis et al. (2010), Brenner et al. (2013), Morgan et al.  
195 (2011)). Until such research comes to fruition, these needs can be met through  
196 active-surveillance strategy using multi-parametric MRI techniques (Hoeks et al.  
197 (2011), Moore et al. (2013)). An MRI-CAD system, which is an area of active  
198 research and forms the focus of this paper, can be incorporated into this screening  
199 strategy allowing a more systematic and rigorous follow-up.

200 Another weakness of the current screening strategy lies in the fact that TRUS  
201 biopsy does not provide trustworthy results. Due to its “blind” nature, there is  
202 a chance of missing aggressive tumours or detecting microfocal “cancers”, which  
203 influences the aggressiveness-assessment procedure (Noguchi et al. (2001)). As a  
204 consequence, over-diagnosis is estimated at up to 30 % (Haas et al. (2007)), while  
205 missing clinically significant CaP is estimated at up to 35 % (Taira et al. (2010)).  
206 In an effort to solve both issues, alternative biopsy approaches have been explored.

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<sup>1</sup>The European Randomized Study of Screening for Prostate Cancer (ERSSPC) started in the 1990s in order to evaluate the effect of PSA screening on mortality rate.

<sup>2</sup>The Prostate Lung Colorectal and Ovarian (PLCO) cancer screening trial is carried out in the United States and intends to ascertain the effects of screening on mortality rate.

MRI/US-guided biopsy has been shown to outperform standard TRUS biopsy (De-longchamps et al. (2013)). There, multimodal MRI images are fused with US images in order to improve localization and aggressiveness assessment to carry out biopsies. Human interaction plays a major role in biopsy sampling which can lead to low repeatability; by reducing potential human errors at this stage, the CAD framework can be used to improve repeatability of examination.

CaP detection and diagnosis benefit from the use of CAD and MRI techniques. In the following sections, these techniques will be presented in addition to an overview of CAD for CaP.

### 2.3.2. Imaging techniques: MRI - MRSI

MRI provides promising imaging techniques to overcome the previous mentioned drawbacks. Unlike TRUS biopsy, MRI examination is a non-invasive protocol and has been shown to be the most acute and harmless technique available currently (Turkbey and Choyke (2012)). In this section, we review different MRI techniques developed for CaP detection and diagnosis. Features strengthening each modality, will receive particular attention together with their drawbacks. Commonly, these features form the basis for developing analytic tools and automatic algorithms. However, we refer the reader to Sect. 4.2 for more details on automatic feature detection methods since they are part and parcel of the CAD framework. Table 2.3.2 provides an overview of the following discussion.

- **$T_2$ -W MRI:**  $T_2$ -W MRI was the first MRI-modality used to perform CaP diagnosis using MRI (Hricak et al. (1983)). Nowadays, radiologists make use of it for CaP detection, localization and staging purposes. This imaging technique is well suited to render zonal anatomy of the prostate (Barentsz et al. (2012)).

This modality relies on a sequence based on setting a long repetition time (TR), reducing the  $T_1$  effect in nuclear magnetic resonance (NMR) signal measured, and fixing the echo time (TE) to sufficiently large values in order to enhance the  $T_2$  effect of tissues. Thus, PZ and CG tissues are well perceptible in these images. The former is characterized by an intermediate/high-SI while the latter is depicted by a low-SI (Hricak et al. (1987)). An example of a healthy prostate is shown in Fig. 3(a).

In PZ, round or ill-defined low-SI masses are synonymous with CaPs (Hricak et al. (1983)) as shown in Fig. 3(b). Detecting CaP in CG is more challenging. In fact both normal CG tissue and malignant tissue, have a low-SI in  $T_2$ -W MRI reinforcing difficulties to distinguish between them. However, CaPs in CG appear often as homogeneous mass possessing ill-defined edges with lenticular or “water-drop” shapes (Akin et al. (2006), Barentsz et al. (2012)) as depicted in Fig. 3(c).



Table 1: Overview of the features associated with each MRI-MRSI. Acronyms: prostate cancer (CaP) - signal intensity (SI) - Gleason score (GS).

Modality	Significant features	CaP	Healthy tissue	GS correlation
T <sub>2</sub> -W MRI	SI	low-SI	intermediate to high-SI	+
T <sub>2</sub> map	SI	low-SI	intermediate to high-SI	+
DCE MRI	Semi-quantitative features: – wash-in – wash-out – integral under the curve – maximum signal intensity – time-to-peak enhancement	faster faster higher higher faster	slower slower lower lower slower	0 0 0 0 0
	Quantitative features (Tofts' parameters): – $k_{ep}$ – $K^{trans}$	higher higher	lower lower	0 0
DW MRI	SI	higher-SI	lower-SI	+
ADC map	SI	low-SI	high-SI	+
MRSI	Metabolites: Citrate (2.64 ppm) Choline (3.21 ppm) Spermine (3.11 ppm)	lower concentration higher concentration lower concentration	higher concentration lower concentration higher concentration	+

Notes:

+ = significantly correlated.

0 = no correlation.

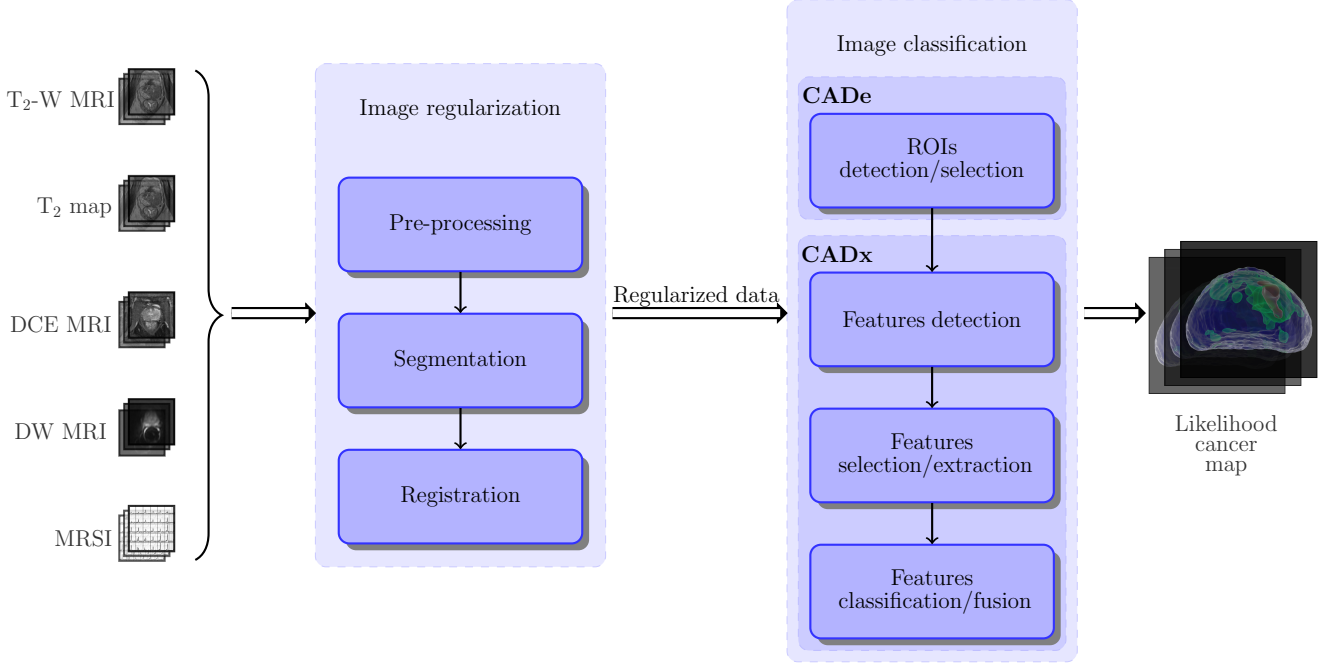
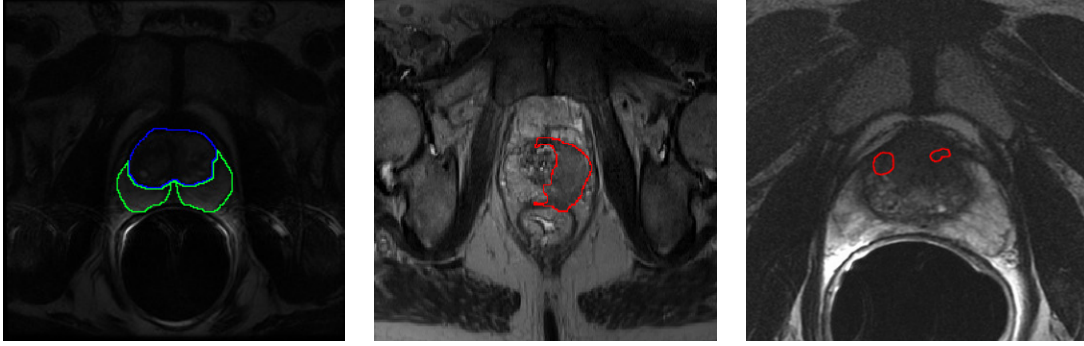


Figure 2: CAD framework using MRI images. Multiparametric MRI images are provided as inputs. These data arise from heterogeneous sources and need to be regularized. Some studies do not consider this stage as mandatory and do not implement or only partly those processes (see Tab. 2). A pre-processing stage is usually applied to standardize the intensity of images, reduce noise and artefacts. Then, in the image set, the prostate organ has to be segmented to focus the next processing stages only on that particular ROI. Moreover, prostate location can vary depending of the modality chosen. Therefore, the images are registered so that all segmented images will be in the same reference frame. Once the image regularisation performed, image classification can be carried out. First, a strategy defining ROIs to focus on is decided. Then, distinctive features are extracted before to be post-processed to select the most salient features. Finally, these salient features will feed a classifier previously trained which will provide a likelihood cancer map associated with either CaP detection or diagnosis.



(a) T<sub>2</sub>-W-mri slice of an healthy prostate acquire with a 1.5 Tesla MRI. The blue contour represents the CG while the PZ corresponds to the green contour.

(b) T<sub>2</sub>-W-mri slice of a prostate with a CaP highlighted in the PZ using a 3.0 Tesla MRI scanner.

(c) T<sub>2</sub>-W-mri slice of a prostate with a CaP highlighted in the CG using a 3.0 Tesla MRI scanner.

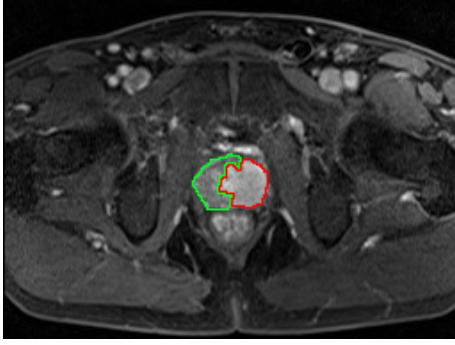
Figure 3: Rendering of T<sub>2</sub>-W-MRI prostate image with both 1.5 and 3.0 Tesla MRI scanner.

CaP aggressiveness was shown to be inversely correlated with SI. Indeed, CaPs assessed with a GS of 4-5 implied lower SI than the one with a GS of 2-3 (Wang et al. (2008)).

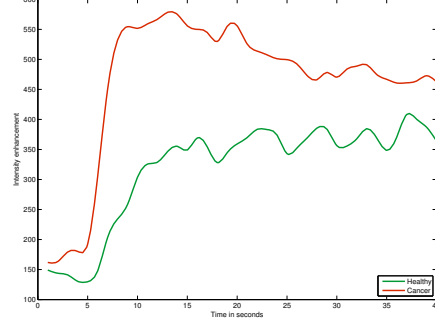
In spite of the availability of these useful and encouraging features, the T<sub>2</sub>-W modality lacks reliability (Hoeks et al. (2011), Kirkham et al. (2006)). Sensitivity is affected by the difficulties in detecting cancers in CG (Kirkham et al. (2006)) while specificity rate is highly affected by outliers (Barentsz et al. (2012)). In fact, various conditions emulate patterns of CaP such as BPH, post-biopsy haemorrhage, atrophy, scars and post-treatment (Barentsz et al. (2012), Cruz et al. (2002), Hricak et al. (1987), Quint et al. (1991), Scheidler et al. (1999b)). These issues can be partly addressed using more innovative and advanced modalities.

- **T<sub>2</sub> Map:** As previously mentioned, T<sub>2</sub>-W MRI modality shows low sensitivity. Moreover, T<sub>2</sub>-W MRI images are a composite of multiple effects (Hegde et al. (2013)). However, T<sub>2</sub> values alone have been shown to be more discriminative (Liu et al. (2011)) and highly correlated with citrate concentration, a biological marker in CaP (Liney et al. (1996b, 1997)).

T<sub>2</sub> values are computed using the characteristics of transverse relaxation.



(a) T<sub>1</sub>-W-MRI image where the cancer is delimited by the red contour. The green area was still not invaded by the CaP



(b) Enhancement curve computed during the DCE-MRI analysis. The red curve is typical from CaP cancer while the green curve is characteristic of healthy tissue.

Figure 4: Illustration of typical enhancement signal observed in DCE-MRI analysis collected with a 3.0 Tesla MRI scanner.

261 Transverse relaxation is formalized as:

$$M_{x,y}(t) = M_{x,y}(0) \exp\left(-\frac{t}{T_2}\right), \quad (1)$$

262 where  $M_{x,y}(0)$  is the initial value of  $M_{x,y}(t)$  and  $T_2$  is the relaxation time.

263 By rearranging Eq. 1,  $T_2$  map is computed performing a linear fitting on the  
264 model in Eq. 2 using several TE,  $t = \{TE_1, TE_2, \dots, TE_m\}$ .

$$\ln \left[ \frac{M_{x,y}(t)}{M_{x,y}(0)} \right] = -\frac{t}{T_2}. \quad (2)$$

265 The Fast Spin-Echo (FSE) sequence has been shown to be particularly well  
266 suited in order to build a  $T_2$  map and obtain accurate  $T_2$  values (Liney et al.  
267 (1996a)).

268 Similar to  $T_2$ -W MRI,  $T_2$  values associated with CaP are significantly lower  
269 than those of healthy tissues (Gibbs et al. (2001), Liney et al. (1996b)).

270 – **DCE MRI:** DCE MRI is an imaging technique which exploits the vascular-  
271 ity characteristic of tissues. Contrast media, usually gadolinium-based, is in-  
272 jected intravenously into the patient. The media extravasates from vessels to  
273 extravascular-extracellular space (EES) and is the released back into the vascu-  
274 lature before being eliminated by the kidneys (Gribbestad et al. (2005)). Further-

more, the diffusion speed of the contrast agent may vary due to several parameters: (i) the permeability of the micro-vessels, (ii) their surface area and (iii) the blood flow (Padhani (2002)).

Healthy PZ is mainly made up of glandular tissue, around 70 % (Choi et al. (2007)), which implies a reduced interstitial space restricting exchanges between vessels and EES (Buckley et al. (2004), van Niekerk et al. (2009)). Normal CG has a more disorganised structure, composed of mainly fibrous tissue (Choi et al. (2007), Hoeks et al. (2011)), which facilitates the arrival of the contrast agent in EES (van Niekerk et al. (2013)). To understand the difference between contrast media kinetic in malignant tumours and the two previous behaviours mentioned, one has to focus on the process known as angiogenesis (Carmeliet and Jain (2000)). In order to ensure growth, malignant tumours produce and release angiogenic promoter substances (Carmeliet and Jain (2000)). These molecules stimulate the creation of new vessels towards the tumour (Carmeliet and Jain (2000)). However, the new vessel networks in tumours differ from those present in healthy tissue (Gribbestad et al. (2005)). They are more porous due to the fact that their capillary walls have a large number of “openings” (Choi et al. (2007), Gribbestad et al. (2005)). In contrast to healthy cases, this increased vascular permeability results in increased contrast agent exchanges between vessels and EES (Verma et al. (2012)).

By making use of the previous aspects, DCE MRI is based on an acquisition of a set of  $T_1$ -W MRI images over time. the Gadolinium-based contrast agent shortens  $T_1$  relaxation time enhancing contrast in  $T_1$ -W MRI images. The aim is to post-analyse the pharmacokinetic behaviour of the contrast media concentration in prostate tissues (Verma et al. (2012)). The image analysis is carried out in two dimensions: (i) in the spatial domain on a pixel-by-pixel basis and (ii) in the time domain corresponding to the consecutive images acquired with the MRI. Thus, for each spatial location, a signal linked to contrast media concentration is measured as shown in Fig. 4(b) (Tofts (2010)).

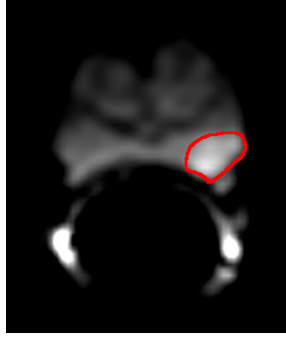
By taking the previous remarks regarding medical aspects and signal theory into account, CaPs are characterized by a signal having an earlier and faster enhancement and an earlier wash-out (cf., the rate of the contrast agent flowing out of the tissue) (see Fig. 4(b)) (Verma et al. (2012)). Three different approaches exist to analyse these signals with the aim of tagging them as corresponding to either normal or malignant tissues. Qualitative analysis is based on assessment of the signal shape (Hoeks et al. (2011)). Quantitative approaches consist of inferring pharmacokinetic parameter values (Tofts (2010)). Those parameters are part of mathematical-pharmacokinetic models which are directly based on physiological

exchanges between vessels and EES. Several pharmacokinetic models were proposed such as the Kety model (Kety (1951)), the Tofts model (Tofts (1997)) and mixed models (Larsson et al. (1996), St Lawrence and Lee (1998)). The last family of methods mixed both approaches and are grouped together under the heading of semi-quantitative methods. They rely on shape characterization using mathematical modelling to extract a set of parameters such as wash-in gradient, wash-out, integral under the curve, maximum signal intensity, time-to-peak enhancement and start of enhancement. These parameters will be discussed in a later section (see Fig. 17) (Hoeks et al. (2011), Verma et al. (2012)). It was shown that semi-quantitative and quantitative methods improve localization of CaP when compared with qualitative methods (Rosenkrantz et al. (2013)). Section 4.2.2 provides a full description of quantitative and semi-quantitative approaches.

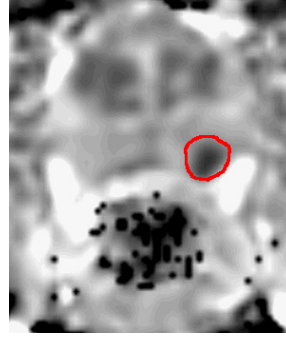
DCE MRI combined with T<sub>2</sub>-W MRI has shown to enhance sensitivity compared to T<sub>2</sub>-W MRI alone (Jager et al. (1997), Kim et al. (2005), Schlemmer et al. (2004), Zelhof et al. (2009)). Despite this fact, DCE MRI possesses some drawbacks. Due to its “dynamic” nature, patient motions during the image acquisition lead to spatial misregistration of the image set (Verma et al. (2012)). Furthermore, it has been suggested that malignant tumours are difficult to distinguish from prostatitis located in PZ and BPH located in CG (Hoeks et al. (2011), Verma et al. (2012)). These pairs of tissues tend to have similar appearances. Later studies have shown that CaPs in CG do not always manifest in homogeneous fashion. Indeed, tumours in this zone can present both hypo-vascularization and hyper-vascularization which illustrates the challenge of CaP detection in CG (van Niekerk et al. (2013)).

— **DW MRI:** As previously mentioned in the introduction, DW MRI is the most recent MRI imaging technique aiming at CaP detection and diagnosis (Scheidler et al. (1999b)). This modality exploits the variations in the motion of water molecules in different tissues (Koh and Collins (2007), Le Bihan et al. (1988)).

From a physiological point of view, the following facts can be claimed. On the one hand, PZ, as previously mentioned, is mainly glandular and tubular in structure allowing water molecules to move freely (Choi et al. (2007), Hoeks et al. (2011)). On the other hand, CG is made up of muscular or fibrous tissue causing the motion of the water molecules to be more constrained and heterogeneous than in PZ (Hoeks et al. (2011)). Then, CaP growth leads to the destruction of normal glandular structure and is associated with an increase in cellular density (Hoeks et al. (2011), Koh and Collins (2007), Somford et al. (2008)). Furthermore, these factors both have been shown to be inversely correlated with water diffusion



(a) DW-MRI image acquired with a 1.5 Tesla MRI scanner. The cancer corresponds to the high SI region highlighted in red.



(b) ADC map computer after acquisition of DW-MRI iages with a 1.5 Tesla MRI scanner. The cancer corresponds to the low SI region highlighted in red.

Figure 5: Illustration of of DW-MRI and ADC map. The signal intensity corresponding to cancer are inversely correlated on these two types of imaging techniques.

(Koh and Collins (2007), Somford et al. (2008)): higher cellular density implies a restricted water diffusion. Thus, water diffusion in CaP will be more restricted than both healthy PZ and CG (Hoeks et al. (2011), Koh and Collins (2007)).

From the NMR principle side, DW MRI sequence produces contrasted images due to variation of water molecules motion. The method is based on the fact that the signal in DW MRI images is inversely correlated to the degree of random motion of water molecules (Huisman (2003)). In fact, gradients are used in DW MRI modality to encode spatial location of nuclei temporarily. Simplifying the problem in only one direction, a gradient is applied in that direction, dephasing the spins of water nuclei. Hence, the spin phases vary along the gradient direction depending of the gradient intensity at those locations. Then, a second gradient is applied aiming at cancelling the spin dephasing. Thus, the immobile water molecules will be subject to the same gradient intensity as the initial one while moving water molecules will be subject to a different gradient intensity. Thus, spins of moving water molecules will stay dephased whereas spins of immobile water molecules will come back in phase. As a consequence, a higher degree of random motion results in a more significant signal loss whereas a lower degree of random motion is synonymous with lower signal loss (Huisman (2003)). Under

368 these conditions, the MRI signal is measured as:

$$M_{x,y}(t, b) = M_{x,y}(0) \exp\left(-\frac{t}{T_2}\right) S_{\text{ADC}}(b) , \quad (3)$$

$$S_{\text{ADC}}(b) = \exp(-b \times \text{ADC}) , \quad (4)$$

369 where  $S_{\text{ADC}}$  refers to signal drop due to diffusion effect, ADC is the apparent  
 370 diffusion coefficient and  $b$  is the attenuation coefficient depending only on gradient  
 371 pulses parameters: (i) gradient intensity and (ii) gradient duration (Le Bihan et al.  
 372 (1986)).

373 By using this formulation, image acquisition with a parameter  $b = 0 \text{ s.mm}^{-2}$   
 374 corresponds to a  $T_2$ -W MRI acquisition. Then, increasing the attenuation coef-  
 375 ficient  $b$  (cf., increase gradient intensity and duration) enhances the contrast in  
 376 DW MRI images.

377 To summarize, in DW MRI images, CaPs are characterized by high-SI com-  
 378 pared to normal tissues in PZ and CG as shown in Fig. 5(a) (Barentsz et al.  
 379 (2012)). However, some tissues in CG can look similar to CaP with higher SI  
 380 (Barentsz et al. (2012)).

381 Diagnosis using DW MRI combined with  $T_2$ -W MRI has shown a significant  
 382 improvement compared with  $T_2$ -W MRI alone and provides highly contrasted  
 383 images (Choi et al. (2007), Padhani (2011), Shimofusa et al. (2005)). As draw-  
 384 backs, this modality suffers from poor spatial resolution and specificity due to  
 385 false positive detection (Choi et al. (2007)).

386 With a view to eliminate these drawbacks, radiologists are extracting quanti-  
 387 tative maps from DW MRI. This imaging technique is presented next.

388 – **ADC Map:** The NMR signal measured for DW MRI images is not only affected  
 389 by diffusion as shown in Eq. (3). However, the signal drop (Eq. (4)) is formulated  
 390 such that the only variable is the acquisition parameter  $b$  (Le Bihan et al. (1986)).  
 391 The ADC is considered as a “pure” diffusion coefficient and can be extracted to  
 392 build a quantitative map.

393 From Eq. (3), it is clear that performing multiple acquisitions only varying  $b$   
 394 will not have any effect on the term  $M_{x,y}(0) \exp\left(-\frac{t}{T_2}\right)$ . Thus, Eq. (3) can be  
 395 rewritten as:

$$S(b) = S_0 \exp(-b \times \text{ADC}) . \quad (5)$$

396 To compute the ADC map, a minimum of two acquisitions are necessary: (i)  
 397 for  $b_0 = 0 \text{ s.mm}^{-2}$  where the measured signal is equal to  $S_0$ , and (ii)  $b_1 > 0$



398 s.mm<sup>-2</sup> (typically 1000 s.mm<sup>-2</sup>). Then, the ADC map can be computed as:

$$\text{ADC} = -\frac{\ln\left(\frac{S(b_1)}{S_0}\right)}{b_1} . \quad (6)$$

399 More accurate computation of the ADC map can be obtained by performing  
400 several acquisitions with different values for the parameter  $b$  and performing a  
401 semi-logarithmic linear fitting using the model presented in Eq. (5).

402 Regarding the appearance of the ADC maps, it was previously stated that by  
403 increasing the value of  $b$ , the signal of CaP tissue increases significantly. From Eq.  
404 (6), it can be shown that tissue appearance in the ADC map will be the inverse  
405 of DW MRI images. Then, CaP tissue is associated with low-SI whereas healthy  
406 tissue appears brighter as depicted in Fig. 5(b) (Barentsz et al. (2012)).

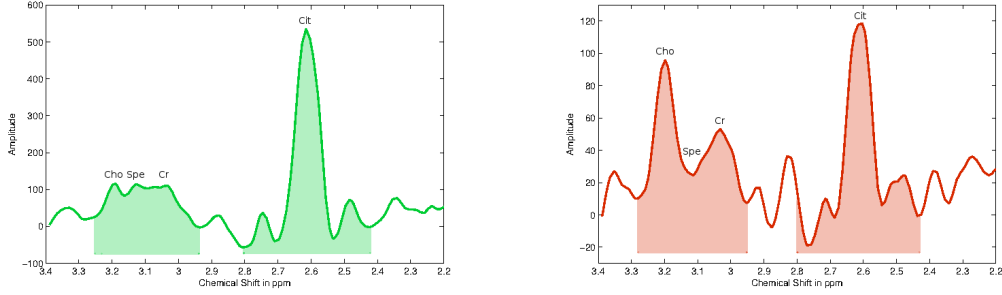
407 Similar to the gain achieved by DW MRI, diagnosis using ADC map combined  
408 with T<sub>2</sub>-W MRI significantly outperforms T<sub>2</sub>-W MRI alone (Choi et al. (2007),  
409 Doo et al. (2012)). Moreover, it has been shown that ADC is correlated with GS  
410 (Hambrock et al. (2011), Itou et al. (2011), Peng et al. (2013)).

411 However, some tissues of the CG zone mimic CaP with low-SI (Kirkham et al.  
412 (2006)) and image distortion can arise due to haemorrhage (Choi et al. (2007)).  
413 It has also been noted that a high variability of the ADC occurs between different  
414 patients making it difficult to define a static threshold to distinguish CaP from  
415 non-malignant tumours (Choi et al. (2007)).

416 – **MRSI:** CaP induces metabolic changes in the prostate compared with healthy  
417 tissue. Thus, CaP detection can be carried out by tracking changes of metabo-  
418 lite concentration in prostate tissue. MRSI is an NMR-based technique which  
419 generates spectra of relative metabolite concentration in a ROI.

420 In order to track changes of metabolite concentration, it is important to know  
421 which metabolites are associated with CaP. To address this question, clinical stud-  
422 ies identified three biological markers: (i) citrate, (ii) choline and (iii) polyamines  
423 composed mainly of spermine, and in less abundance of spermidine and putrescine  
424 (Awwad et al. (2012), Costello and Franklin (2006), Giskeodegard et al. (2013)).

425 Citrate is involved in the production and secretion of the prostatic fluid, and  
426 the glandular prostate cells are associated with a high production of citrate en-  
427 abled by zinc accumulation by these same cells (Costello and Franklin (2006)).  
428 However, the metabolism allowing the accumulation of citrate requires a large  
429 amount of energy (Costello and Franklin (2006)). In contrast, malignant cells  
430 do not have high zinc levels leading to lower citrate levels due to citrate oxyda-



(a) Illustration of an MRSI spectrum of a healthy voxel acquired with a 3.0 Tesla MRI. (b) Illustration of an MRSI spectrum of a cancerous voxel acquired with a 3.0 Tesla MRI.

Figure 6: Illustration of an MRSI spectrum both healthy and cancerous voxel with a 3.0 Tesla MRI. The highlighted areas corresponds to the related concentration of the metabolites which is computed by integrating the area under each peak. Acronyms: Choline (Cho), Spermine (Spe), Creatine (Cr) and Citrate (Cit).

tion (Costello and Franklin (2006)). Furthermore, this change results in a more energy-efficient metabolism enabling malignant cells to grow and spread (Costello and Franklin (2006)).

An increased concentration of choline is related to CaP (Awwad et al. (2012)). Malignant cell development requires epigenetic mechanisms resulting in metabolic changes and relies on two mechanisms: DNA methylation and phospholipid metabolism which both result in choline uptake, explaining its increased level in CaP tissue (Awwad et al. (2012)).

Spermine is also considered as a biological marker in CaP (Giskeodegard et al. (2013), van der Graaf et al. (2000)). In CaP, reduction of the ductal volume due to shifts in polyamine homeostasis might lead to a reduced spermine concentration (van der Graaf et al. (2000)).

To determine the concentration of these biological markers, one has to focus on the MRSI modality. In theory, in presence of a homogeneous magnetic field, identical nuclei precesses at the same operating frequency known as the Larmor frequency (Haacke et al. (1999)). However, MRSI is based on the fact that identical nuclei will slightly precess at different frequencies depending on the chemical environment in which they are immersed (Haacke et al. (1999)), a phenomenon known as the chemical shift effect (CSE) (Parfait (2010)). Given this property, metabolites can be identified and their concentrations can be determined. In this regard, the Fourier transform is used to obtain the frequency spectrum of the

452 NMR signal (Haacke et al. (1999), Parfait (2010)). In this spectrum, each peak is  
453 associated with a particular metabolite and the area under each peak corresponds  
454 to the relative concentration of this metabolite (see Fig. 6) (Parfait (2010)).

455 Two different quantitative approaches are used to decide or whether not the  
456 spectra of a ROI is associated with CaP classified either as relative quantification  
457 or absolute quantification (Lemaître (2011)). In relative quantification, the ratio  
458 of choline-polyamines-creatine to citrate is computed. The integral of the signal  
459 is computed from choline (cf., 3.21 ppm) to creatine (cf., 3.02 ppm) because the  
460 peaks in this region can be merged at clinical magnetic field strengths (see Fig.  
461 6) (van der Graaf et al. (2000), Hoeks et al. (2011)). Considering the previous  
462 assumption that choline concentration rises and citrate concentration decreases  
463 in the presence of CaP, the ratio computed should be higher in malignant tissue  
464 than in healthy tissue.

465 Two different quantitative approaches are used to decide or not the spectra  
466 of a ROI is associated with CaP classified either as relative quantification or  
467 absolute quantification (Lemaître (2011)). In relative quantification, the ratio of  
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470 peaks in this region can be merged at clinical magnetic field strengths (see Fig.  
471 6) (van der Graaf et al. (2000), Hoeks et al. (2011)). Considering the previous  
472 assumption that choline concentration rises and citrate concentration decreases  
473 in the presence of CaP, the ratio computed should be higher in malignant tissue  
474 than in healthy tissue.

475 In contrast with relative quantification, absolute quantification measures mo-  
476 lar concentrations by normalizing relative concentrations using water as reference  
477 (Lemaître (2011)). In this case, “true” concentrations are directly used to differ-  
478 entiate malignant from healthy tissue. However, this method is not commonly  
479 used as it requires an additional step of acquiring water signals, inducing time  
480 and cost acquisition constraints.

481 MRSI allows examination with high specificity and sensitivity compared to  
482 other MRI modalities (Choi et al. (2007)). Furthermore, it has been shown that  
483 combining MRSI with MRI improves detection and diagnosis performance (Kaji  
484 et al. (1998), Scheidler et al. (1999a), Vilanova et al. (2009)). Citrate and spermine  
485 concentrations are inversely correlated with the GS allowing us to distinguish low  
486 from high grade CaPs (Giskeodegard et al. (2013)). However, choline concentra-  
487 tion does not provide the same properties (Giskeodegard et al. (2013)).

488 Unfortunately, MRSI also presents several drawbacks. First, MRSI acquisition  
489 is time consuming which prevents this modality from being used in daily clini-

cal practise (Barentsz et al. (2012)). In addition, MRSI suffers from low spatial resolution due to the fact that signal-to-noise (SNR) is linked to the voxel size. However, this issue is addressed by developing new scanners with higher magnetic field strengths such as 7.5 T (Giskeodegard et al. (2013)). Finally, a high variability of the relative concentrations between patients was observed (Choi et al. (2007)). The same observation was made depending on the zones studied (cf., PZ, CG, base, mid-gland, apex) (Lemaître (2011), Walker et al. (2010)). Due to this variability, it is difficult to use a fixed thresholds in order to differentiate CaP from healthy tissue.

### 2.3.3. Computer-aided systems for CaP: CAdE - CAdx

As previously mentioned in the introduction (see Sect. 1), CADs are developed to advise and backup radiologists in their tasks of CaP detection and diagnosis; CADs are not aimed to provide fully automatic decisions (Giger et al. (2008)). CADs can be divided into two different sub-groups either as CAdE, with the purpose to highlight probable lesions in MRI images, or CAdx, which focuses on differentiating malignant from non-malignant tumours (Giger et al. (2008)). Moreover, an intuitive approach, motivated by developing a framework combining detection-diagnosis, is to mix both CAdE and CAdx by using the output of the former mentioned as a input of the latter named. Although the outcomes of these two systems should differ, the framework of both CAD systems is similar. The CAD work-flow is presented in Fig. 2.3.2.

MRI modalities mentioned in Sect. 2.3.2 are used as inputs of CAD for CaP. It can be noted that ADC map is not considered as an input since it is a feature derived from the DW MRI images. The images acquired from the different modalities show a large variability between patients: the prostate organ can be located at different positions in images (e.g., patient motion, variation of acquisition plan), and the SI can be corrupted with noise or artefacts during the acquisition process (eg., magnetic field inhomogeneity, use of endorectal coil). To address these issues, the first stage of CAD is to pre-process multiparametric MRI images to reduce noise, remove artefacts and standardize the SI. Then, it is important to mention that most of the later processes would be only focused on the prostate. Thus, it is necessary to segment the prostate in each MRI-modality to define it as a ROI. However, data suffers of misalignment due to patient motions or different acquisition plan. Therefore, a registration step is performed so that all the previously segmented MRI images will be in the same reference frame.

Some studies do not fully apply the methodology depicted in Fig. 2.3.2. Details about those can be found in Tab. 2. Some studies preferred to work directly with raw data in order to demonstrate the robustness of their approaches to noise or artefacts.

528 In some cases, prostate segmentation is performed manually as well as registration.  
529 It is also sometimes assumed that no patient motions occur during the acquisition  
530 procedure, removing the need of registering the multiparametric MRI images.

531 Once the data are regularized, it becomes possible to extract features and classify  
532 the data to obtain the probabilistic maps. We referred this stage to image classifi-  
533 cation where CADe and CADx are the main components.

534 In a CADe framework, possible lesions will be segmented automatically and fur-  
535 ther used as input of CADx. We also included in CADe studies, the methods using  
536 voxel-based delineation in which the final results will highlight the boundaries of the  
537 lesions. On the other hand, manual lesions segmentation are not considered to be  
538 part of a CADe. The output of the CADe is used as input of the CADx.

539 CADx is composed of the processes allowing to distinguish malignant from non-  
540 malignant tumours. We divided CADx into three different stages. First, salient  
541 features are extracted, in an pixel-based or region-based manner, from MRI images  
542 to characterize the lesion. Of course, more discriminative features will be associated  
543 with a robust and accurate likelihood cancer map. Frequently, the number of features  
544 extracted can be large resulting in redundant or insufficient discriminative features  
545 which will negatively affect the performances of the further classification. Therefore,  
546 a step consists of selecting the best features or/and reducing the number of dimen-  
547 sions is commonly used. Then, this modified feature vector is finally classified using  
548 different pattern recognition approaches.

549 As pointed out in the introduction, performance of CaP detection and diagnosis  
550 are affected by observer interpretation and limitations (Giger et al. (2008), Hambrock  
551 et al. (2013)). CAD offers a possible solution in order to reduce this variability. As  
552 mentioned in the introduction, the effects of CAD on the observer performance has  
553 been studied (Hambrock et al. (2013)), with results showing that CADs benefit to  
554 less-experienced radiologist to perform similarly as experienced radiologist in their  
555 tasks (Hambrock et al. (2013)).

#### 556 2.4. Literature classification

Table 2: Overview of the different studies reviewed with their main characteristics. Acronyms: number (#) - image regularization (Img. Reg.).

Index	Study	# patients	MRI-modality				Strength of field		Studied zones		CAD stages		
			T <sub>2</sub> -W MRI	DCE MRI	DW MRI	MRSI	1.5 T	3.0 T	PZ	CG	Img. Reg.	CADe	CADx
[1]	Ampeliotis et al. (2007)	25	✓	✓	✗	✗	✓	✗	✓	✗	✓!	✗	✓
[2]	Ampeliotis et al. (2008)	25	✓	✓	✗	✗	✓	✗	✓	✗	✓!	✗	✓
[3]	Antic et al. (2013)	53	✓	✗	✓	✗	✓	✗	✓	✓	✗	✗	✓
[4]	Artan et al. (2009)	10	✓	✓	✓	✗	✓	✗	✓	✗	✗	✓	✓
[5]	Artan et al. (2010)	21	✓	✓	✓	✗	✓	✗	✓	✗	✓!	✓	✓
[6]	Chan et al. (2003)	15	✓	✗	✓	✗	✓	✗	✓	✗	✗	✗	✓
[7]	Giannini et al. (2013)	10	✓	✓	✓	✗	✓	✗	✓	✗	✓	✓	✓
[8]	Kelm et al. (2007)	24	✗	✗	✗	✓	✓	✗	✓	✓	✓!	✓	✓
[9]	Langer et al. (2009)	25	✓	✓	✓	✗	✓	✗	✓	✗	✓!	✗	✓
[10]	Litjens et al. (2011)	188	✓	✓	✓	✗	✗	✓	✓	✗	✓!	✓	✓
[11]	Litjens et al. (2012b)	288	✓	✓	✓	✗	✗	✓	✓	✓	✓!	✓	✓
[12]	Liu et al. (2009)	11	✓	✓	✓	✗	✓	✗	✓	✗	✓!	✓	✓
[13]	Liu et al. (2013)	54	✓	✓	✓	✗	✗	✓	✓	✓	✓!	✗	✓
[14]	Lopes et al. (2011)	27	✓	✗	✗	✗	✓	✗	✓	✗	✓!	✓	✓
[15]	Lv et al. (2009)	55	✓	✗	✗	✗	✓	✗	✓	✗	✓!	✗	✓
[16]	Matulewicz et al. (2013)	18	✗	✗	✗	✓	✗	✓	✓	✓	✗	✓	✓
[17]	Mazzetti et al. (2011)	10	✗	✓	✗	✗	✓	✗	✓	✗	✓!	✓	✓
[18]	Niaf et al. (2011)	23	✓	✓	✓	✗	✓	✗	✓	✗	✓!	✗	✓
[19]	Niaf et al. (2012)	30	✓	✓	✓	✗	✓	✗	✓	✗	✓!	✗	✓
[20]	Ozer et al. (2009)	20	✓	✓	✓	✗	✓	✗	✓	✗	✓!	✓	✓
[21]	Ozer et al. (2010)	20	✓	✓	✓	✗	✓	✗	✓	✗	✓!	✓	✓
[22]	Parfait et al. (2012)	22	✗	✗	✗	✓	✗	✓	✓	✓	✓!	✓	✓
[23]	Peng et al. (2013)	48	✓	✓	✓	✗	✗	✓	✓	✓	✗	✗	✓
[24]	Puech et al. (2009)	100	✗	✓	✗	✗	✓	✗	✓	✓	✗	✗	✓
[25]	Sung et al. (2011)	42	✗	✓	✗	✗	✗	✓	✓	✓	✗	✓	✓
[26]	Tiwari et al. (2007)	14	✗	✗	✗	✓	✓	✗	✓	✓	✓!	✓	✓
[27]	Tiwari et al. (2008)	18	✗	✗	✗	✓	✓	✗	✓	✓	✓!	✓	✓
[28]	Tiwari et al. (2009a)	18	✗	✗	✗	✓	✓	✗	✓	✓	✓!	✓	✓
[29]	Tiwari et al. (2009b)	15	✓	✗	✗	✓	✓	✗	✓	✓	✓!	✓	✓
[30]	Tiwari et al. (2010)	19	✓	✗	✗	✓	✓	✗	✓	✓	✓!	✓	✓
[31]	Tiwari et al. (2012)	36	✓	✗	✗	✓	✓	✗	✓	✓	✗	✓	✓
[32]	Tiwari et al. (2013)	29	✓	✗	✗	✓	✓	✗	✓	✓	✓!	✓	✓
[33]	Viswanath et al. (2008b)	16	✓	✗	✗	✓	✓	✗	✓	✓	✗	✓	✓
[34]	Viswanath et al. (2008a)	6	✓	✓	✗	✗	✗	✓	✓	✓	✓!	✓	✓
[35]	Viswanath et al. (2009)	6	✓	✓	✗	✗	✗	✓	✓	✓	✓	✓	✓
[36]	Viswanath et al. (2011)	12	✓	✓	✓	✗	✗	✓	✓	✓	✓!	✓	✓
[37]	Viswanath et al. (2012)	22	✓	✗	✗	✗	✗	✓	✓	✓	✓	✓	✓
[38]	Vos et al. (2008a)	29	✓	✓	✗	✗	✓	✗	✓	✗	✓!	✗	✓
[39]	Vos et al. (2008b)	29	✗	✓	✗	✗	✓	✗	✓	✗	✓!	✗	✓
[40]	Vos et al. (2010)	29	✓	✓	✗	✗	✓	✗	✓	✗	✓!	✗	✓
[41]	Vos et al. (2012)	NA	✓	✓	✓	✗	✗	✓	✓	✗	✓!	✓	✓

Notes:  
✗: not used or not implemented.  
✓!: partially implemented.  
✓: used or implemented.

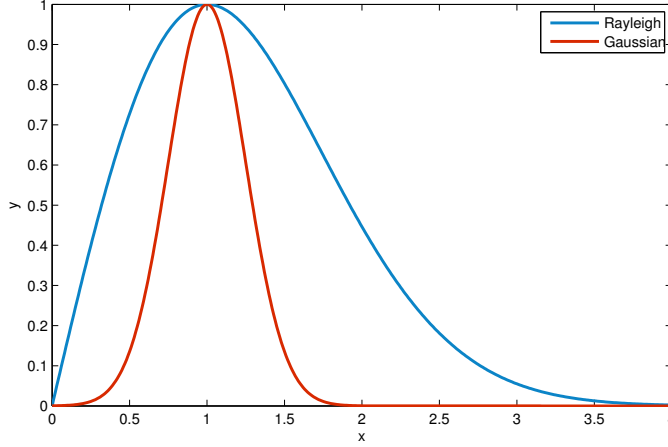


Figure 7: Illustration of a Gaussian distribution ( $\mu = 1, \sigma = 0.25$ ) and a Rayleigh distribution ( $\sigma = 2$ ). It can be seen that the Rayleigh distribution is suffering of a bias term when compared with the Gaussian distribution.

557 The CAD review is organized using the methodology presented in Fig. 2.3.2.  
 558 Methods embedded in the image regularization framework are presented before to  
 559 focus on the image classification framework, the later being divided into CADe and  
 560 CADx. Table 2 summarizes the different CAD studies reviewed in this paper. Char-  
 561 acteristics related to MRI acquisition as well as CAD strategies are reported. Only  
 562 methods used in CAD system are discussed.

### 563 3. Image regularization framework

564 This section provides a review of the methods used in CADs in order to regularize  
 565 input images. We start with pre-processing methods presented in Sect. 3.1, focusing  
 566 mainly on the reduction of noise level and artefacts as well as standardization of  
 567 SI. Sections 3.2 and 3.3 will be dedicated to segmentation methods, so that later  
 568 methods only operate on the segmented prostate, and registration to align segmented  
 569 images from different MRI-modalities in the same reference frame.

#### 570 3.1. Pre-processing

##### 571 3.1.1. MRI images pre-processing

572 Three different groups of pre-processing methods are commonly applied to images  
 573 as initial stage in CAD.

Table 3: Overview of the pre-processing methods used in CAD systems.

Pre-processing operations	References
<i>MRI pre-processing:</i>	
Noise filtering:	
Median filtering	[20-21]
Wavelet-based filtering	[1-2,14]
Bias correction:	
Parametric methods	[15-35]
Non-parametric methods	[36]
Standardization:	
Statistical-based normalization:	[3-4,15,20-21,35,37]
Organ SI-based normalization	[18-19]
<i>MRSI pre-processing:</i>	
Phase correction	[22]
Water and lipid residuals filtering	[8]
Baseline correction	[22,31]
Frequency alignment	[31]
Normalization	[22]



574 – **Noise filtering:** The NMR signal measured and recorded in the k-space dur-  
575 ing an MRI acquisition is affected by noise. This noise obeys a complex Gaussian  
576 white noise mainly due to thermal noises in the patient area (Nowak (1999)). Fur-  
577 thermore, MRI images visualized by radiologists are in fact the magnitude images  
578 resulting from the complex Fourier transform of the k-space data. The complex  
579 Fourier transform, being a linear and orthogonal transform, does not affect the  
580 Gaussian noise characteristics (Nowak (1999)). However, the function involved  
581 in the magnitude computation is a non-linear transform (i.e., the square root of  
582 the sum of squares of real and the imaginary parts), implying that the noise dis-  
583 tribution is no longer Gaussian; it indeed follows a Rician distribution making  
584 the denoising task harder. Briefly, a Rician distribution can be characterized as  
585 follows: in low-SI region (low SNR), it can be approximated with a Rayleigh  
586 distribution while in high-SI region (high SNR), it is similar to a Gaussian distri-  
587 bution (see Fig. 7) (Manjon et al. (2008)). Reviews of all denoising methods can  
588 be found in the work of Buades et al. (2005) and Mohan et al. (2014).

589 Median filtering is the simplest approach used to address the denoising issue in  
590 MRI images (Ozer et al. (2009, 2010)). In both studies, Ozer et al. used a square  
591 kernel of size  $5 \times 5$  pixels with the image resolutions ranging from  $320 \times 256$   
592 (cf., T<sub>2</sub>-W MRI) to  $256 \times 128$  (cf., T<sub>2</sub> map, DCE and DW MRI) and a field of  
593 view (FOV) ranging from 14 cm (cf, T<sub>2</sub>-W and DW MRI) to 20 cm (cf, T<sub>2</sub> map  
594 and DCE MRI). However, from a theoretical point of view, this simple filtering  
595 method is not well formalized to address the noise distribution in MRI images.

596 More complex approaches were proposed to overcome this problem. A com-  
597 mon method used to denoise MRI images is based on wavelet-based filtering. This  
598 filtering exploits the sparsity property of the wavelet decomposition. The projec-  
599 tion of a noisy signal from the spatial-domain to the wavelet-domain implies that  
600 only few wavelet coefficients contribute to the “signal-free noise” while all wavelet  
601 coefficients contribute to the noise (Donoho and Johnstone (1994)). Therefore,  
602 denoising is performed by thresholding/attenuating the insignificant wavelet coef-  
603 ficients to enforce the sparsity in the wavelet-domain. Investigations focus on the  
604 strategies to perform the most adequate coefficient shrinkage method (e.g., using  
605 thresholding, singularity property or Bayesian framework) (Pizurica (2002)).

606 Ampeliotis et al. (2007, 2008) performed wavelet shrinkage to denoise magni-  
607 tude MRI images (cf., T<sub>2</sub>-W-MRI and DCE-MRI) using thresholding techniques  
608 (Mallat (2008)). However, since the wavelet transform is an orthogonal transform,  
609 the Rician distribution of the noise is preserved in the wavelet-domain. Hence,  
610 for low SNR, the wavelet and scaling coefficients still suffer from a bias due to  
611 this specific noise distribution (Nowak (1999)).

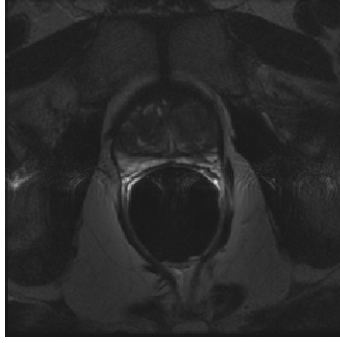


Figure 8: Example of artefacts with high SI due to perturbation from the endorectal coil which create inhomogeneity.

Lopes et al. (2011) used a technique proposed by Pizurica et al. (2003) to denoise T<sub>2</sub>-W-MRI. Pizurica et al. (2003) proposed a filtering technique based on joint detection and estimation theory (Middleton and Esposito (1968)). The wavelet coefficients “free-of-noise” are estimated from the noisy wavelet coefficients using a maximum *a posteriori* (MAP) estimate. Furthermore, the estimator designed takes spatial context into account by including both local and global information in the prior probabilities. The different probabilities needed by the MAP are empirically estimated by using mask images representing the locations of the significant wavelet coefficients. These mask images are computed by thresholding the detail images obtained from the wavelet decomposition. To remove the bias from the wavelet and scaling coefficients, the squared magnitude MRI image used instead of the magnitude MRI image as proposed by Nowak (1999). This involves changing the Rician distribution to a scaled non-central Chi-square distribution. It implies that the wavelet coefficients are also unbiased estimators and the scaling coefficients are unbiased estimators but up to a constant  $C$  as defined in Eq. (7) which needs to be subtracted from each scaling coefficient,

$$C = 2^{(J+1)}\hat{\sigma}^2, \quad (7)$$

where  $J$  is the number of levels of the wavelet decomposition and  $\hat{\sigma}$  is an estimate of the noise standard deviation.

- **Bias correction:** Besides being corrupted by noise, MRI images are also affected by the inhomogeneity of the MRI field commonly referred to as bias field (Styner et al. (2000)). This bias field results in a smooth variation of the SI through the image. When an endorectal coil is used, an artefact resulting of an hyper-

intense signal can be observed around the coil on the images (see Fig. 8). As a consequence, the SI of identical tissues varies depending on their spatial location in the image making further processes such as segmentation or registration harder (Jungke et al. (1987), Vovk et al. (2007)). A review of bias correction methods can be found in Vovk et al. (2007).

The model of image formation is usually formalized such that:

$$s(\mathbf{x}) = o(\mathbf{x})b(\mathbf{x}) + \eta(\mathbf{x}) , \quad (8)$$

where  $s(\mathbf{x})$  is the corrupted SI at the pixel for the image coordinates  $\mathbf{x} = \{x, y\}$ ,  $o(\mathbf{x})$  is the “noise-free signal” ,  $b(\mathbf{x})$  is the bias field function and  $\eta(\mathbf{x})$  is an additive white Gaussian noise.

Hence, the task of bias correction involves estimating the bias function  $b(\mathbf{x})$  in order to infer the “signal-free bias”  $o(\mathbf{x})$ .

Viswanath et al. (2009) performed bias correction on T<sub>2</sub>-W-MRI using a parametric Legendre polynomial model proposed by Styner et al. (2000) and available in the Insight Segmentation and Registration Toolkit (ITK) library<sup>3</sup>. Styner et al. (2000) chose to model the bias field by using a linear combination of Legendre polynomials as:

$$\hat{b}(\mathbf{x}, \mathbf{p}) = \sum_{i=0}^{m-1} p_i f_i(\mathbf{x}) = \sum_{i=0}^l \sum_{j=0}^{l-i} p_{ij} P_i(x) P_j(y) , \quad (9)$$

where  $\hat{b}$  is the bias estimation with the image coordinates  $\mathbf{x} = \{x, y\}$  and the  $m$  coefficients of the linear combination  $\mathbf{p} = p_{11}, \dots, p_{ij}$  ;  $m$  can be defined as  $m = (l+1)\frac{(l+2)}{2}$  where  $l$  is the degree of Legendre polynomials chosen and  $P_i(\cdot)$  denotes a Legendre polynomial of degree  $i$ .

This family of functions allows us to model the bias as a smooth inhomogeneity function across the image. To estimate the set of parameters  $\mathbf{p}$ , a cost function is defined which relies on the following assumptions: (i) an image is composed of  $k$  regions with  $\mu_k$  being the mean SI and a variance  $\sigma_k^2$  of each particular class, and (ii) each noisy pixel belongs to one of the  $k$  regions with its SI value close to the class mean  $\mu_k$ . Hence, the cost function is defined as:

$$C(\mathbf{p}) = \sum_{\mathbf{x}} \prod_k \rho_k(s(\mathbf{x}) - \hat{b}(\mathbf{x}, \mathbf{p}) - \mu_k) , \quad (10)$$

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<sup>3</sup>The ITK library is available at: <http://www.itk.org/>

$$\rho_k(x) = \frac{x^2}{x^2 + 3\sigma_k^2} , \quad (11)$$

660 where  $\rho_k(\cdot)$  is a M-estimator allowing estimations to be less sensitive to outliers  
 661 than usual square distance (Li (1996)).

662 Finally, estimation of the parameters  $\mathbf{p}$  results in finding the minimum of the  
 663 cost function  $C(\mathbf{p})$ . This optimization was performed using the non-linear (1 + 1)  
 664 Evolution Strategy (ES) optimizer (Styner and Gerig (1997)).

665 In a later publication, Viswanath et al. (2012) make use of the well known  
 666 N3 algorithm<sup>4</sup> to correct T<sub>2</sub>-W-MRI developed by Sled et al. (1998). To estimate  
 667 the bias function, Sled et al. (1998) proposed to estimate the probability density  
 668 functions (PDFs) of the signal and bias.

669 Recalling Eq. (8) and taking advantage of logarithm property, it implies that  
 670 this model becomes additive such that:

$$\begin{aligned} \log s(\mathbf{x}) &= \log b(\mathbf{x}) + \log \left( o(\mathbf{x}) + \frac{\eta(\mathbf{x})}{b(\mathbf{x})} \right) , \\ &\approx \log b(\mathbf{x}) + \log \hat{o}(\mathbf{x}) , \end{aligned} \quad (12)$$

671 where  $\hat{o}(\mathbf{x})$  is the signal only degraded by noise. Sled et al. (1998) shows that Eq.  
 672 (12) can be related to PDFs such that:

$$S(s) = B(s) * O(s) , \quad (13)$$

673 where  $S$ ,  $B$  and  $O$  are respectively the probability densities of  $s$ ,  $b$  and  $o$ .

674 Restoring the corrupted signal  $s$  is carried out by finding the multiplicative  
 675 field  $b$  which maximizes the frequency content of the distribution  $O$ . Sled et al.  
 676 (1998) argue that a search through all possible fields  $b$  and selection of the one  
 677 which maximizes the high frequency content of  $O$  could be carried out but results  
 678 in an exhaustive search. However, they show that the bias field distribution can  
 679 be assimilated to a near Gaussian distribution. Using this fact as *a priori*, it is  
 680 then possible to infer the distribution  $O$  using Wiener deconvolution given  $B$  and  
 681  $S$  and later estimate the corresponding smooth field  $b$ .

682 Lv et al. (2009) corrected the inhomogeneity in T<sub>2</sub>-W-MRI images by using  
 683 the method proposed by Madabhushi et al. (2006). In this method, the MRI im-  
 684 ages are corrected iteratively by successively detecting the image foreground via

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<sup>4</sup>The N3 algorithm implementation is available at: <http://www.bic.mni.mcgill.ca/software/N3/>

685 generalized scale ( $g$ -scale) and estimating a bias field function based on a second-  
686 order polynomial model. First the background of the MRI image is eliminated by  
687 thresholding. The threshold value is commonly equal to the mean SI of the consid-  
688 ered image. Then, in the seeded region growing algorithm is applied considering  
689 every thresholded pixel as a potential seed. However, pixels already assigned to  
690 a region will not be considered any more as seed. As in seeded region growing  
691 algorithm (Shapiro and Stockman (2001)), two criteria are taken into account to  
692 expand the region. First, the region will grow using a connected-neighbourhood,  
693 initially defined by the user. Then, the homogeneity of SI is based on a fuzzy  
694 membership function taking into account the absolute difference of the SIs of two  
695 pixels. Depending on the membership value (cf., a threshold has to be defined),  
696 the pixel considered is merged or not to the region. Once this segmentation is  
697 performed, the largest region  $R$  is used as a mask to select pixels of the origi-  
698 nal image and the mean SI,  $\mu_R$ , is computed. The background variation  $b(\mathbf{x})$  is  
699 estimated as:

$$b(\mathbf{x}) = \frac{s(\mathbf{x})}{\mu_R}, \quad \forall \mathbf{x} \in R, \quad (14)$$

700 where  $s(\mathbf{x})$  is the original MRI image.

701 Finally, a second order polynomial  $\hat{b}_\Theta(\mathbf{x})$  is fitted in a least-squares sense (Eq.  
702 (15)),

$$\hat{\Theta} = \arg \min_{\Theta} |b(\mathbf{x}) - \hat{b}_\Theta(\mathbf{x})|^2, \quad \forall \mathbf{x} \in R. \quad (15)$$

703 Finally, the whole original MRI image is corrected by dividing it by the es-  
704 timated bias field function  $\hat{b}_\Theta(\mathbf{x})$ . This process is repeated until the number of  
705 pixels in the largest region  $R$  does not change significantly between two iterations.

#### 706 – ***SI normalization/standardization:***

707 As discussed in the later section, segmentation or classification tasks are usu-  
708 ally performed by first learning from a training set of patients. Hence, one can  
709 emphasize the desire to perform MRI examinations with a high repeatability or  
710 in other words, one would ensure to obtain similar MRI images (cf., similar SIs)  
711 for patients of the same group (cf., healthy patients *vs.* patients with CaP), for a  
712 similar sequence.

713 However, it is a known fact that variability between patients occurs during the  
714 MRI examinations even using the same scanner, protocol or sequence parameters  
715 (Nyul and Udupa (1999)). Hence, the aim of normalization or standardization

of the MRI data is to remove the variability between patients and enforce the repeatability of the MRI examinations.

Approaches used to standardize MRI images can be either categorized as statistical-based standardization or organ SI-based standardization.

Artan et al. (2010, 2009) as well as Ozer et al. (2009, 2010) standardized T<sub>2</sub>-W, DCE and DW MRI images by computing the *standard score* (also called *z-score*) of the pixels of the PZ as:

$$I_s(\mathbf{x}) = \frac{I_r(\mathbf{x}) - \mu_{pz}}{\sigma_{pz}}, \quad \forall \mathbf{x} \in \text{PZ}, \quad (16)$$

where  $I_s(\mathbf{x})$  is the standardized SI with the image coordinates  $\mathbf{x} = \{x, y\}$ ,  $I_r(\mathbf{x})$  is the raw SI,  $\mu_{pz}$  is the mean-SI of the PZ and  $\sigma_{pz}$  is the SI standard deviation in the PZ.

This transformation enforces the image PDF to have a zero mean and a unit standard deviation. In a similar way, Liu et al. (2013) normalized T<sub>2</sub>-W-MRI by making use of the median and interquartile range for all the pixels.

Lv et al. (2009) scaled the SI of T<sub>2</sub>-W-MRI images using the method proposed by Nyul et al. (2000) based on PDF matching. This approach is based on the assumption that MRI images from the same sequence should share the same PDF appearance. Hence, one can approach this issue by transforming and matching the PDFs using some statistical landmarks such as median and different quantiles. Using a training set, these statistical landmarks are extracted for  $N$  training images as for instance for the minimum, the 25<sup>th</sup> quantile, the median, the 75<sup>th</sup> quantile and the maximum:

$$\begin{aligned} \Phi_0 &= \{\phi_0^1, \phi_0^2, \dots, \phi_0^N\}, \\ \Phi_{25} &= \{\phi_{25}^1, \phi_{25}^2, \dots, \phi_{25}^N\}, \\ \Phi_{50} &= \{\phi_{50}^1, \phi_{50}^2, \dots, \phi_{50}^N\}, \\ \Phi_{75} &= \{\phi_{75}^1, \phi_{75}^2, \dots, \phi_{75}^N\}, \\ \Phi_{100} &= \{\phi_{100}^1, \phi_{100}^2, \dots, \phi_{100}^N\}, \end{aligned} \quad (17)$$

where  $\phi_{n^{\text{th}}}^{i^{\text{th}}}$  is the  $n^{\text{th}}$  quantile of the  $i^{\text{th}}$  training image.

Then, the mean of each quantile  $\{\bar{\Phi}_0, \bar{\Phi}_{25}, \bar{\Phi}_{50}, \bar{\Phi}_{75}, \bar{\Phi}_{100}\}$  is also calculated. Once this training stage is performed, a linear transformation by parts  $\mathcal{T}(\cdot)$  can be computed (Eq. (18)) for each test image  $t$  by mapping each statistical landmark  $\varphi_{(\text{cdot})}^t$  of this image with the pre-learned statistical landmarks  $\bar{\Phi}_{(\cdot)}$ . This linear

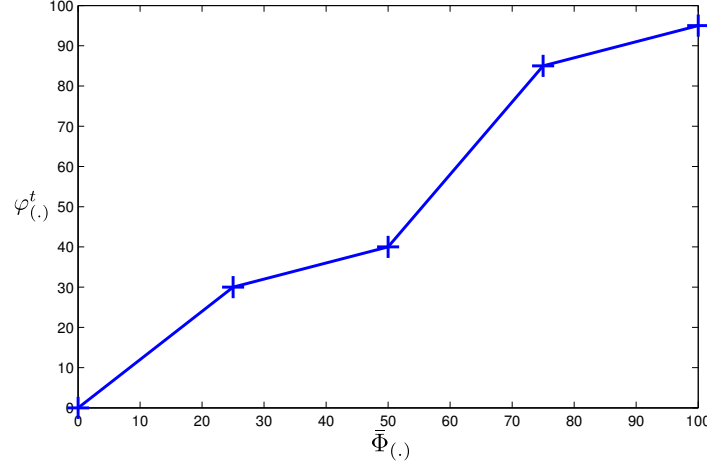


Figure 9: Example of linear mapping by parts as proposed by Nyul et al. (2000).

mapping is also depicted in Fig. 9.

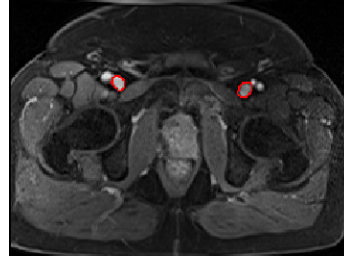
$$\mathcal{T}(s(\mathbf{x})) = \begin{cases} \lceil \bar{\Phi}_0 + (s(\mathbf{x}) - \varphi_0^t) \left( \frac{\bar{\Phi}_{25} - \bar{\Phi}_0}{\varphi_{25}^t - \varphi_0^t} \right) \rceil, & \text{if } \varphi_0^t \leq s(\mathbf{x}) < \varphi_{25}^t, \\ \lceil \bar{\Phi}_{25} + (s(\mathbf{x}) - \varphi_{25}^t) \left( \frac{\bar{\Phi}_{50} - \bar{\Phi}_{25}}{\varphi_{50}^t - \varphi_{25}^t} \right) \rceil, & \text{if } \varphi_{25}^t \leq s(\mathbf{x}) < \varphi_{50}^t, \\ \lceil \bar{\Phi}_{50} + (s(\mathbf{x}) - \varphi_{50}^t) \left( \frac{\bar{\Phi}_{75} - \bar{\Phi}_{50}}{\varphi_{75}^t - \varphi_{50}^t} \right) \rceil, & \text{if } \varphi_{50}^t \leq s(\mathbf{x}) < \varphi_{75}^t, \\ \lceil \bar{\Phi}_{75} + (s(\mathbf{x}) - \varphi_{75}^t) \left( \frac{\bar{\Phi}_{100} - \bar{\Phi}_{75}}{\varphi_{100}^t - \varphi_{75}^t} \right) \rceil, & \text{if } \varphi_{75}^t \leq s(\mathbf{x}) \leq \varphi_{100}^t, \end{cases} \quad (18)$$

Viswanath et al. (2011, 2009, 2012) use a variant of this previous approach presented in the work of Madabhushi and Udupa (2006) aiming to standardize the T<sub>2</sub>-W-MRI images. Instead of computing the PDF of an entire image, a pre-segmentation of the foreground is carried out via *g*-scale which was discussed in the bias correction section. Once the foreground is detected, the largest region is extracted and the same process than previously mentioned (see Eq. (18)) takes place in order to align PDFs of the foreground of the MRI images.

The methods described above were statistical-based methods. However, the standardization problem can be tackled by normalizing the MRI images using the SI of some known organs present in these images. Niaf et al. (2012, 2011) normalized T<sub>2</sub>-W-MRI images by dividing the original SI of the images by the mean SI of the bladder (see Fig. 10(a)). Likewise, Niaf et al. (2011) standardized the T<sub>1</sub>-W-MRI images using the arterial input function (AIF). They computed the AIF by taking the mean of the SI in the most enhanced part of the common



(a) Illustration and location of the bladder on a T<sub>2</sub>-W-MRI image acquired with a 3.0 Tesla MRI scanner



(b) Illustration and location of the femoral arteries on a T<sub>1</sub>-W-MRI image acquired with a 3.0 Tesla MRI scanner

Figure 10: Illustration of the two organs used by Niaf et al. (2012, 2011) to normalize T<sub>2</sub>-W and T<sub>1</sub>-W MRI images.

femoral arteries (see Fig. 10(b)) as proposed by Wiart et al. (2007).

### 3.1.2. MRSI spectra

Presented in Sect. 2.3.2, MRSI is a modality related to a one dimensional signal. Hence, specific pre-processing steps for this type of signals have been applied instead of standard signal processing methods.

— **Phase correction:** MRSI data acquired suffer from zero-order and first-order phase misalignments as shown in Fig. 11 (Chen et al. (2002), Osorio-Garcia et al. (2012)).

Parfait et al. (2012) used a method proposed by Chen et al. (2002) where the phase of MRSI signal is corrected based on entropy minimization in the frequency domain. The corrected MRSI signal  $o(\xi)$  can be expressed as:

$$\begin{aligned}\Re(o(\xi)) &= \Re(s(\xi)) \cos(\Phi(\xi)) - \Im(\xi) \sin(\Phi(\xi)) , \\ \Im(o(\xi)) &= \Im(s(\xi)) \cos(\Phi(\xi)) + \Re(\xi) \sin(\Phi(\xi)) , \\ \Phi(\xi) &= \phi_0 + \phi_1 \frac{\xi}{N} ,\end{aligned}\tag{19}$$

where  $\Re(\cdot)$  and  $\Im(\cdot)$  are the real and imaginary part of the complex signal respectively,  $s(\xi)$  is the corrupted MRSI signal,  $\phi_0$  and  $\phi_1$  are the zero-order and first-order phase correction terms respectively and  $N$  is the total number of samples of the MRSI signal.



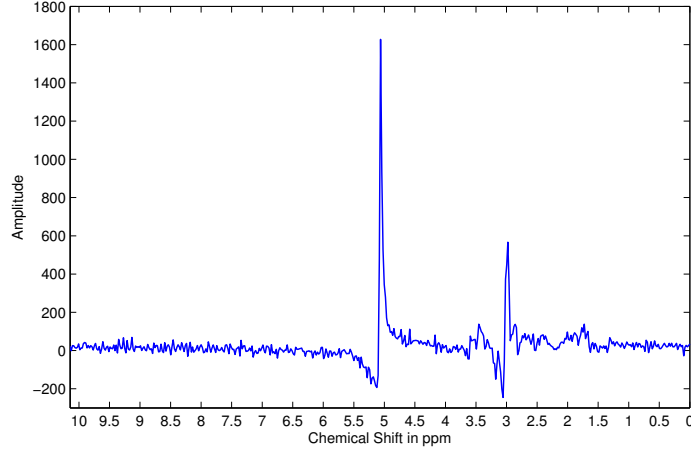


Figure 11: Illustration of phase misalignment in an MRSI spectra acquire with a 3.0 Tesla MRSI scanner. Note the distortion of the signal specially visible for the water and citrate peaks.

Chen et al. (2002) tackled this problem using an optimization framework where  $\phi_0$  and  $\phi_1$  had to be inferred. Hence, the simplex Nelder-Mead optimization method was used to minimize the following cost function based on the *Shannon entropy* formulation:

$$\hat{\Phi} = \arg \min_{\Phi} \left[ - \sum \Re(s'(\xi)) \ln \Re(s'(\xi)) + \lambda \|\Re(s(\xi))\|_2 \right], \quad (20)$$

where  $s'(\xi)$  is the first derivative of the corrupted signal  $s(\xi)$  and  $\lambda$  is a regularization parameter.

Once the best parameter  $\Phi$  is obtained, the MRSI signal is corrected using Eq. (19).

- **Water and lipid residuals filtering:** The water and lipid metabolites occur in much higher concentrations than the metabolites of interests (cf., choline, creatine and citrate) (Osorio-Garcia et al. (2012), Zhu et al. (2010)). Fortunately, specific MRSI sequences were developed in order to suppress water and lipid metabolites using pre-saturation techniques (Zhu et al. (2010)). However, these techniques do not perfectly remove water and lipids peaks and some residuals are still present in the MRSI spectra as shown in Fig. 12. Therefore, different post-processing methods have been proposed to enhance the quality of the MRSI spectra by removing these residuals.

Kelm et al. (2007) used the well known HSVD algorithm proposed by Pijnappel

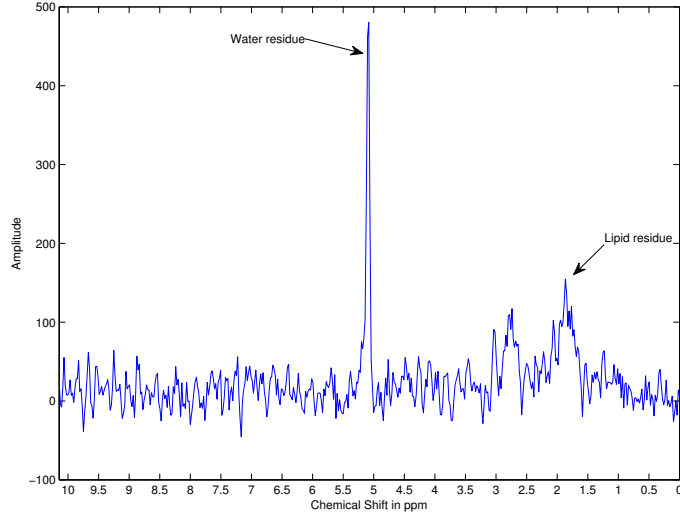


Figure 12: Illustration of the residues of water and fat even after their suppression during the acquisition protocol. The acquisition was carried out with a 3.0 Tesla MRI.

et al. (1992). In the time domain, a MRSI signal  $s(t)$  is modelled by a sum of  $K$  exponentially damped sinusoids such that:

$$s(t) = \sum_{k=1}^K a_k \exp(i\phi_k) \exp(-d_k + i2\pi f_k)t + \eta(t) , \quad (21)$$

where  $a_k$  is the amplitude proportional to the metabolite concentration with a resonance frequency  $f_k$ ,  $d_k$  represents the damping factor of the exponential,  $\phi_k$  is the first-order phase and  $\eta(t)$  is a complex white noise.

Pijnappel et al. (1992) showed that the “noise-free signal” can be found using the singular value decomposition (SVD) decomposition. First the noisy signal is reorganized inside a Hankel matrix  $H$ . It can be shown that if the signal considered would be a “noise-free signal”, the rank of  $H$  would be equal to rank  $K$ . However, due to the presence of noise,  $H$  is in fact a full rank matrix. Thus, to recover the “noise-free signal”, the rank of  $H$  can be truncated to  $K$  using its SVD decomposition. Hence, knowing the cut off frequencies of water (cf., 4.7 ppm) and lipid (cf., 2.2 ppm) metabolites, their corresponding peaks can be reconstructed and subtracted from the original signal (Laudadio et al. (2002)).

— **Baseline correction:** Sometimes, the problem discussed in the above section

regarding the lipid molecules is not addressed simultaneously with water residuals suppression. Lipids and macromolecules are known to affect the baseline of the MRSI spectra. They could cause errors during further fitting processes aiming to quantify the metabolites, especially regarding the citrate metabolite.

Parfait et al. (2012) made the comparison of two different methods to detect the baseline and correct the MRSI spectra which are based on the work of Lieber and Mahadevan-Jansen (2003) and Devos et al. (2004). Lieber and Mahadevan-Jansen (2003) addressed the problem of baseline detection in the frequency domain by fitting a polynomial of low degree  $p(x)$  (e.g., second or third degree) to the MRSI signal  $s(x)$  in a least-squares sense. Then, the values of the fitted polynomial are re-assigned as:

$$p_f(x) = \begin{cases} p(x) , & \text{if } p(x) \leq s(x) , \\ s(x) , & \text{if } p(x) > s(x) . \end{cases} \quad (22)$$

Finally, this procedure of fitting and re-assignment is iteratively repeated on  $p_f(x)$  until a stopping criterion is reached. The final polynomial function can be subtracted from the original signal  $s(x)$  to correct it.

Parfait et al. (2012) modified this algorithm by convolving a Gaussian kernel to smooth the MRSI signal instead of fitting a polynomial function, keeping the rest of the algorithm identical.

Unlike Lieber and Mahadevan-Jansen (2003), Devos et al. (2004) proposed to correct the baseline in the time domain by multiplying the MRSI signal by a decreasing exponential function as:

$$c(t) = \exp(-\beta t) , \quad (23)$$

Having a typical value for  $\beta$  of 0.15.

However, Parfait et al. (2012) concluded that the method proposed by Lieber and Mahadevan-Jansen (2003) outperforms the one of Devos et al. (2004). In the contemporary work of Tiwari et al. (2012), the authors detected the baseline using a local non-linear fitting method avoiding regions with significant peaks which were detected using a experimentally parametrised signal-to-noise ratio (i.e. a value larger than 5 dB).

- **Frequency alignment:** Due to variations of the experimental conditions, a frequency shift can be observed in the MRSI spectra as shown in Fig. 13 (Chen et al. (2002), Osorio-Garcia et al. (2012)).

Tiwari et al. (2012) correct the frequency shift by first detecting known metabolite peaks such as choline, creatine and citrate. The frequency shift is corrected by

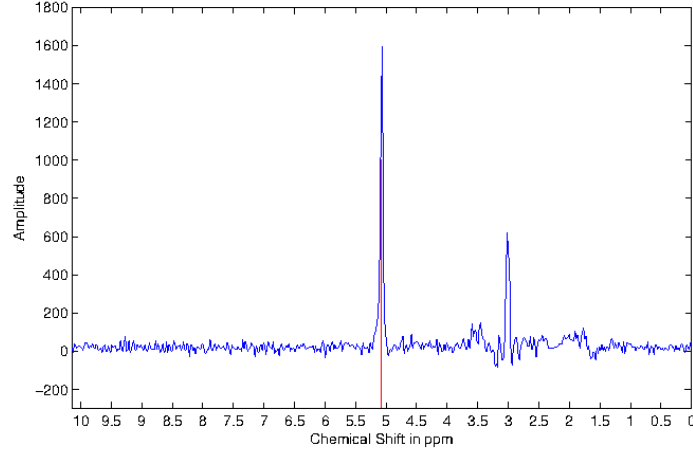


Figure 13: Illustration of frequency misalignment in an MRSI spectra acquired with a 3.0 Tesla MRSI scanner. The water peak is known to be aligned at 4.65 ppm. However, it can be seen that the peak on this spectra is aligned at around 5.1 ppm.

837 minimizing the frequency error between the experimental and theoretical values  
838 of each of these peaks.

839 – **Normalization:** Due to variations of the experimental conditions, the MRSI  
840 signal may also vary between patients.

841 Parfait et al. (2012) as Devos et al. (2004) compared two methods to nor-  
842 malize MRSI signal. In each method, the original MRSI spectra is divided by a  
843 normalization factor, similar to the intensity normalization described earlier.

844 The first approach to obtain the normalization factor is based on an estimation  
845 of the water concentration. It is required to have an additional MRSI sequence  
846 where the water metabolites are unsuppressed. Using this sequence, an estimation  
847 of the water concentration can be performed using the previously reported HSVD  
848 algorithm. The second approach to normalization is based on using the  $L_2$  norm  
849 of the MRSI spectra  $\|s(\xi)\|_2$ . It should be noted that both Parfait et al. (2012)  
850 and Devos et al. (2004) concluded that the  $L_2$  normalization was more efficient in  
851 their framework.

### 852 3.2. Segmentation

853 The segmentation task consists in delineating the prostate boundaries in the MRI.  
854 This procedure is of particular importance for focusing the posterior processing on the  
855 organ of interest (Ghose et al. (2012)). In this section, only the segmentation methods

Table 4: Overview of the segmentation methods used in CAD systems.

Segmentation methods	References
<i>MRI-based segmentation:</i>	
Manual segmentation	[4-5,16,18-21,24,38-40]
Region-based segmentation	[11]
Model-based segmentation	[10,34-36,41]
<i>MRSI-based segmentation:</i>	
Clustering	[28]

used in CAD systems are presented and summarized in Tab. 4. An exhaustive review of prostate segmentation methods in MRI can be found in Ghose et al. (2012).

### 3.2.1. MRI-based segmentation

— **Manual segmentation:** To highlight the importance of prostate segmentation task in CAD systems, it is interesting to note the large number of studies which segment manually the prostate organs (Artan et al. (2010, 2009), Matulewicz et al. (2013), Niaf et al. (2012, 2011), Ozer et al. (2009, 2010), Puech et al. (2009), Vos et al. (2008a,b)). In all the cases, the boundaries of the prostate gland is defined in order to limit the further processing to only this area. This approach ensure the right delineation of the organ nevertheless this procedure is highly time consuming and should be perform by a radiologist.

— **Region-based segmentation:** Litjens et al. (2012b) used a multi-atlas-based segmentation using multi-modal images (e.g., T<sub>2</sub>-W-MRI and ADC map) to segment the prostate with an additional pattern recognition method to differentiate CG and PZ as proposed in Litjens et al. (2012a). This method consists of three different steps: (i) the registration between each atlas and the multi-modal images, (ii) the atlas selection and finally (iii) the classification of the prostate segmented voxels in either CG or PZ.

The registration between each atlas and the MRI images is performed using two successive registrations: the first registration is a rigid registration to roughly align the atlases and the MRI images and the second is an elastic registration using B-spline transformation. The objective function to perform the registration is defined as the weighted sum of the metric of both T<sub>2</sub>-W-MRI and ADC map. The metric is based on mutual information (MI). We refer to the next section

for more details in regard to registration. Two strategies of atlas selection were performed by using either a majority voting approach or the simultaneous truth and performance level estimation (STAPLE) approach (Warfield et al. (2004)).

Subsequently, CG and PZ segmentation within the prostate region is achieved by classifying each voxel using a linear discriminant analysis (LDA) classifier. Three types of features were considered: (i) anatomy, (ii) intensity and (iii) texture. Regarding the anatomy, relative position and relative distance from the pixel to the border of the prostate were used. The intensity features consist of the intensity of the voxel in the ADC coefficient and the  $T_2$  map. The texture features were composed of five different features: homogeneity, correlation (Amadasun and King (1989)), entropy, texture strength (Li et al. (2005)) and local binary pattern (LBP) (Ojala et al. (1996)). Finally, morphological operations were applied to remove artefacts and the contours between the zones were smoothed using thin plate spline (TPS) (Bookstein (1989)).

- **Model-based segmentation:** Viswanath et al. (2008a, 2009) used the multi-attribute non-initializing texture reconstruction based active shape model (MANTRA) method as proposed by Toth et al. (2008). MANTRA is closely related to the active shape model (ASM) from Cootes et al. (1995). This algorithm consists of two stages: (i) a training stage where a shape and appearance model is generated and (ii) the actual segmentation performed based on the learned model.

For the training stage, a set of landmarks is defined and the shape model is generated as in the original ASM method (Cootes et al. (1995)). Then, to model the appearance, a set of  $K$  texture images  $\{I_1, I_2, \dots, I_k\}$  based on first and second order statistical texture features are computed. For a given landmark  $l$  with its given neighbourhood  $\mathcal{N}(l)$ , its feature matrix extracted can be expressed as:

$$f_l = \{I_1(\mathcal{N}(l)), I_2(\mathcal{N}(l)), \dots, I_k(\mathcal{N}(l))\}, \quad (24)$$

where  $I_k(\mathcal{N}(l))$  represents a feature vector obtained by sampling the  $k^{\text{th}}$  texture map using the neighbourhood  $\mathcal{N}(l)$ .

By generating multiple landmarks in the same fashion as ASM, principal components analysis (PCA) (Pearson (1901)) is applied to learn the appearance variations.

For the segmentation stage, the mean shape learned previously is initialised in the test image. The same associated texture images as in the training stage are computed. For each landmark  $l$ , a neighbourhood of patches are used to sample the texture images and a reconstruction is obtained using the appearance model

915 previously trained. The new landmark location will be defined as the position  
916 where the MI is maximal between the reconstructed and original values. This  
917 scheme is performed in a multi-resolution manner as in Cootes et al. (1995).

918 Subsequently, the same authors (Viswanath et al. (2012)) used the weighted  
919 ensemble of regional image textures for active shape model segmentation (WERITAS)  
920 method also proposed by Toth et al. (2009). As with the MANTRA method,  
921 WERITAS is based on the ASM formulation. In fact it is very close to the  
922 MANTRA itself. The same texture features are used to construct the appearance  
923 models, but instead of using MI between the landmarks and neighbour patches  
924 for adapting the landmark positions, it defines a metric based on the Mahalanobis  
925 distance. In the training stage, the Mahalanobis distance is computed between  
926 landmarks and neighbour patches for each of the features. Subsequently, a new  
927 metric is proposed as a linear weighted combination of those Mahalanobis dis-  
928 tances which maximises the correlation with the Euclidean distance between the  
929 patches and the true landmarks. In the segmentation step, this metric is then  
930 computed between the initialised landmarks and neighbouring patches in order  
931 to update landmark positions, in a similar fashion to other active contour model  
932 (ACM) models.

933 Litjens et al. (2011) and Vos et al. (2012) used an approach proposed by  
934 Huisman et al. (2010) in which the bladder, prostate and rectum are segmented  
935 tackling the segmentation task as an optimization problem. A probabilistic model  
936 is first trained by embedding the three following aspects: (i) the shape by defining  
937 each organ as an ellipse, (ii) the position by defining the distance and the angle  
938 between each organ center and (iii) the appearance using the PDFs of SI of each  
939 organ. Litjens et al. (2011) used only ADC map to encode the appearance whereas  
940 Vos et al. (2012) used both ADC and  $T_2$  maps. Then, during the optimization  
941 using a quasi-Newton optimizer, an objective function is minimized. This function  
942 is defined as the sum of the deviations from the above model learnt. This rough  
943 segmentation is then used inside a Bayesian framework to refine the segmentation.

### 944 3.2.2. MRSI-based segmentation

945 Tiwari et al. (2009a) localized the voxels corresponding to the prostate organ  
946 using a hierarchical spectral clustering. First, each MRSI spectrum is projected  
947 into a lower dimension space using graph embedding (Shi and Malik (2000)). To  
948 proceed, a similarity matrix  $W$  is computed using a Gaussian similarity measure

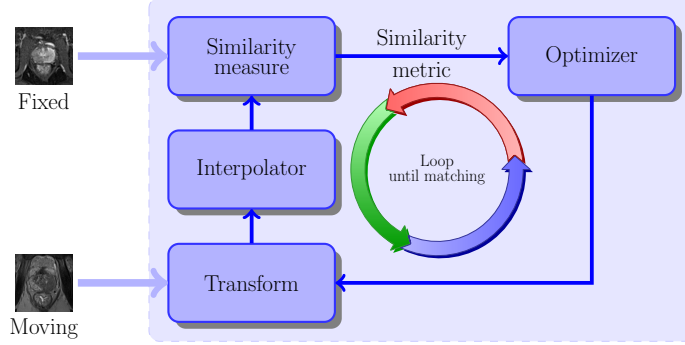


Figure 14: Typical framework involved to solve the registration problem.

949 from the Euclidean distance (Belkin and Niyogi (2001)) such that:

$$W(\mathbf{x}, \mathbf{y}) = \begin{cases} \exp\left(\frac{\|s(\mathbf{x}) - s(\mathbf{y})\|_2^2}{\sigma^2}\right) & , \text{ if } \|\mathbf{x} - \mathbf{y}\|_2 < \epsilon , \\ 0 & , \text{ if } \|\mathbf{x} - \mathbf{y}\|_2 > \epsilon , \end{cases} \quad (25)$$

950 where  $s(\mathbf{x})$  and  $s(\mathbf{y})$  are the MRSI spectra for the voxels  $\mathbf{x}$  and  $\mathbf{y}$  respectively,  $\sigma$  is  
 951 the standard deviation of the Gaussian similarity measure and  $\epsilon$  is a parameter used  
 952 to define an  $\epsilon$ -neighbourhood.

953 The MRSI spectra projection into the lower dimension space is approached as  
 954 a generalized eigenvector problem. Subsequently, a replicate k-means clustering  
 955 method is run defining two clusters. The data corresponding to larger cluster is  
 956 assumed to belong to the non-prostate voxels and these voxels will be eliminated  
 957 from the processing. The full procedure is repeated until the total number of voxels  
 958 left is inferior to a given threshold set experimentally.

### 959 3.3. Registration

960 The role of image registration is vital in CAD systems using multi-parametric  
 961 MRI images. As it will be discussed in Sect. 4, for the sake of an optimal classi-  
 962 fication, the features detected in each modality will be grouped depending of their  
 963 spatial locations. Hence, one has to ensure the perfect alignment of the multi-modal  
 964 MRI images ahead of performing any classification scheme.

965 Image registration is the procedure consisting of aligning an unregistered image  
 966 (also called moving image) into a template image (also called fixed image) via a  
 967 geometric transformation. This problem is usually addressed as presented in Fig. 14.  
 968 An iterative procedure takes place to infer the geometric transformation (parametric



Table 5: Classification of the different registration methods used in the CAD systems reviewed. Acronyms: gradient descent (GD), Nelder-Mead (NM).

Study index	Modality registered	Type	Geometric transform			Similarity measure			Optimizer		
			Rigid	Affine	Elastic	MSE	MI	CMI	GD	L-BFGS-B	NM simplex
[1-2]	T <sub>2</sub> -W - DCE	2D	—	✓	—	✓	—	—	—	—	—
[7]	T <sub>2</sub> -W - DW	2D	—	✓	✓	—	—	—	—	—	—
[7]	T <sub>2</sub> -W - DCE	2D	—	✓	✓	—	✓	—	✓	—	—
[34-35]	T <sub>2</sub> -W - DCE	2D	—	✓	—	—	✓	—	—	—	—
[36]	T <sub>2</sub> -W - DCE - DW	3D	—	✓	—	—	—	✓	✓	—	—
[38]	T <sub>2</sub> -W - DCE	3D	—	✓	—	—	✓	—	—	—	—
[40]	T <sub>2</sub> -W - DCE	3D	—	✓	✓	—	✓	—	—	✓	—

Notes:

—: not used or not mentioned.

✓: used or implemented.

or non-parametric) via an optimizer, which maximizes the similarity between the two images.

From Sect. 3.3.1 to 3.3.4, we individually review the different components of a typical registration framework (Fig 14). Section 3.3.5 will summarize the combinations of these components especially for the frameworks used in CAD systems. Exhaustive reviews covering all registration methods in computer science and medical fields can be found in Maintz and Viergever (1998) and Zitová and Flusser (2003).

### 3.3.1. Geometric transformation models

As previously mentioned, the registration problem is to align two images or volumes by finding the geometric transformation. Regarding the transformation, from all CAD systems reviewed, only parametric methods have been implemented.

Three different groups of parametric transformation models have been used, each of them are characterized by the degree of freedom that they offer.

The first type of transformation is usually referred to as rigid transformation. These transformations are only composed of rotation and translation transforms. Hence, for a 2D space where  $\mathbf{x} = (x, y) \in \mathbb{R}^2$  a rigid transformation  $\mathcal{T}_R$  is formalized as as:

$$\begin{aligned}
\mathcal{T}_R(\mathbf{x}) &= \begin{bmatrix} R & \mathbf{t} \\ \mathbf{0}^T & 1 \end{bmatrix} \mathbf{x} , \\
&= \begin{bmatrix} \cos \theta & -\sin \theta & t_x \\ \sin \theta & \cos \theta & t_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} ,
\end{aligned} \tag{26}$$

where  $\theta$  is the rotation angle and  $\{t_x, t_y\}$  represents the translation along  $\{x, y\}$  respectively.

In the case of 3D registration using volume, an additional component  $z$  has to be taken into account such that  $\mathbf{x} = (x, y, z)$ . Thus, the rotation matrix  $\mathbf{R}$  becomes of size  $3 \times 3$  whereas the translation vector  $\mathbf{t}$  consists of a vector of three elements. Hence, the geometric transformation  $\mathcal{T}_R(\cdot)$  is embedded into a matrix of size  $4 \times 4$ .

Affine transformations provide additional degrees of freedom managing rotations and translation as with the rigid transformations but also shearing and scaling. Hence, for a 2D space where  $\mathbf{x} = (x, y) \in \mathbb{R}^2$ , an affine transformation  $\mathcal{T}_A$  is formalized as:

$$\begin{aligned}
\mathcal{T}_A(\mathbf{x}) &= \begin{bmatrix} A & \mathbf{t} \\ \mathbf{0}^T & 1 \end{bmatrix} \mathbf{x} , \\
&= \begin{bmatrix} a_{11} & a_{12} & t_x \\ a_{21} & a_{22} & t_y \\ 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} x \\ y \\ 1 \end{bmatrix} .
\end{aligned} \tag{27}$$

Hence the four parameters  $\{a_{11}, a_{12}, a_{21}, a_{22}\}$  of the affine matrix and  $\{t_x, t_y\}$  of the translation encode an affine transformation.

Regarding volume registered, the same remark as previously mentioned can be applied in this case. Thus the geometric transformation  $\mathcal{T}_A(\cdot)$  is of size  $4 \times 4$  with nine parameters involved.

Finally, the last group of transformations is known as elastic transformations and offer the advantage to handle local distortions. In the reviewed CAD systems, the radial basis functions are used to formalize the local distortions such as:

$$\mathcal{T}_E(\mathbf{x}) = \frac{a_{11}x - a_{12}y + t_x + \sum_i c_i g(\|\mathbf{x} - p_i\|)}{a_{21}x + a_{22}y + t_y + \sum_i c_i g(\|\mathbf{x} - p_i\|)} , \tag{28}$$

where  $\mathbf{x}$  are the control points in both images and  $g(\cdots)$  is the actual radial basis function.

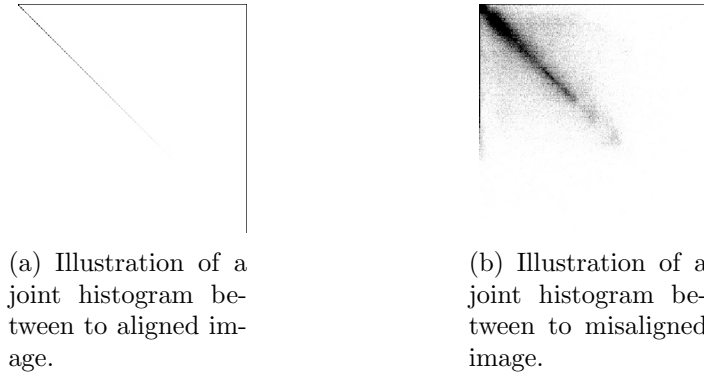


Figure 15: Difference observed in joint histogram between aligned and misaligned images. The joint measure will be more concentrated of the histogram in the case that the images are aligned and more randomly distributed in the case that both images are more misaligned.

Two radial basis functions are used: (i) the TPS and (ii) the B-splines. Apart from the formalism, these two approaches have a main difference. With B-splines, the control points are usually uniformly and densely placed on a grid where as with TPS, the control points correspond to detected or selected key points. By using TPS, Mitra et al. (2011) obtained more accurate and time efficient results than with the B-splines strategy (Mitra et al. (2012)).

It is reasonable to point out that usually only rigid or affine registrations are used to register multi-parametric images from a same protocol. Elastic registration methods are more commonly used to register multi-protocol images (e.g., histopathology with MRI images) (Toth et al. (2008, 2009)).

### 3.3.2. Similarity measure

During the registration procedure, a similarity criterion is computed in order to evaluate the quality of the alignment performed. Roughly speaking, this criterion will give the direction to take to the optimizer, in order to assign the most optimal values to the geometric transformation parameters.

The most naive similarity measure is the mean squared error (MSE) of the SI of MRI images. For a pair of images  $I$  and  $J$ , the MSE is formalized as:

$$\text{MSE} = \frac{1}{N} \sum_x \sum_y (I(x, y) - J(x, y))^2, \quad (29)$$

where  $N$  is the total number of pixels.

However, this metric is not well suited when multi-parametric images are involved due to the tissue appearance variations between the different modalities.

1026 In that regard, MI was introduced as a registration measure in the late 1990's by  
 1027 Pluim et al. (2003). The MI measure finds its foundation in the assumption that a  
 1028 homogeneous region in the first modality image should also appear as a homogeneous  
 1029 region in the second modality even if their SIs are not identical. Thus, those regions  
 1030 share information and the registration task can be achieved by maximizing this  
 1031 common information. Hence, MI of two images  $A$  and  $B$  is defined as:

$$MI(A; B) = S(A) + S(B) - S(A, B) , \quad (30)$$

1032 where  $S(A)$  and  $S(B)$  are the marginal entropies and  $S(A, B)$  is the joint entropy.

1033 Then, maximizing the MI is equivalent to minimizing the joint entropy. The joint  
 1034 entropy measure is related with the degree of uncertainty or dispersion of the data  
 1035 in the joint histogram of the images  $A$  and  $B$ . As shown in Fig. ??, the data in the  
 1036 joint histogram will be concentrated in the case of aligned images while will be more  
 1037 randomly distributed in the case of misaligned images. Regarding the computation  
 1038 of the entropies, an estimation of the PDFs have to be carried out. Histogram or  
 1039 Parzen window methods are a common way to estimate these PDFs.

1040 A generalized form of MI, CMI, was proposed by Chappelow et al. (2011). CMI  
 1041 encompasses interdependent information such as texture and gradient into the metric.  
 1042 Hence, for both of images  $A$  and  $B$ , the image ensembles  $\epsilon_n^A$  and  $\epsilon_m^B$  are generated  
 1043 and composed of  $n$  and  $m$  images based on the texture and gradient. Then, the CMI  
 1044 can be formulated such as:

$$CMI(\epsilon_n^A; \epsilon_m^B) = S(\epsilon_n^A) + S(\epsilon_m^B) - S(\epsilon_n^A, \epsilon_m^B) . \quad (31)$$

1045 From Eq. (31), it can be seen that CMI is estimated using high dimensional data  
 1046 and that histogram-based methods to estimate the PDFs are not suitable any more  
 1047 (Chappelow et al. (2011)). However, other approaches can be used such as the one  
 1048 employed by Staring et al. (2009) to compute the  $\alpha$ -MI (Hero et al. (2002)) which  
 1049 is based on the construction of entropic graphs using  $k$ -nearest neighbour ( $k$ -NN)  
 1050 inside the high dimensional feature space later used to estimate the MI.

### 1051 3.3.3. Optimization methods

1052 Registration is usually regarded as an optimization problem where the parame-  
 1053 ters of the geometric transformation model have to be inferred by minimizing the  
 1054 similarity measure. Iterative estimation methods are commonly used: Nelder-Mead  
 1055 simplex method (Nelder and Mead (1965)), L-BFGS-B quasi-Newton method (Byrd  
 1056 et al. (1995)) and gradient descent (Viola and Wells (1997)). During our review, we  
 1057 noticed that authors do not usually linger over optimizer choice.

#### 1058 3.3.4. Interpolation

1059 The registration procedure involves transforming an image, and pixels mapped  
1060 to non-integer points must be approximated using interpolation methods. As for the  
1061 optimization methods, we notice that little attention has been paid on the choice  
1062 of those interpolations methods. However, commonly used methods are bilinear,  
1063 nearest-neighbour, bi-cubic, spline and inverse-distance weighting method (Mitra  
1064 (2012)).

#### 1065 3.3.5. Review of the methods used in CAD system

1066 Studies presenting CAD pipeline incorporating an automatic registration proce-  
1067 dure are summarized in Tab. 5.

1068 Ampeliotis et al. (2007, 2008) did not use the framework as presented in Fig.  
1069 14 to register 2D T<sub>2</sub>-W and DCE images. By using image symmetries and the  
1070 MSE metric, they find the parameters of an affine transformation but not using a  
1071 common objective function. They are finding independently and consecutively the  
1072 scale factor, the rotation and finally the translation.

1073 Giannini et al. (2013) used also a in-house development registration method to  
1074 register 2D T<sub>2</sub>-W and DW images. To register both images using an affine transfor-  
1075 mation model, the bladder is first segmented in both modalities in order to obtain  
1076 its contours.

1077 Giannini et al. (2013) and also Vos et al. (2010) used the same framework (Rueck-  
1078 ert et al. (1999)) which is based on finding an affine transformation to register the  
1079 T<sub>2</sub>-W and DCE images using MI. Then, an elastic registration using B-spline takes  
1080 place using the affine parameters to initialize the geometric model with the same sim-  
1081 ilarity measure. However, the approaches differ regarding the choice of the optimizer  
1082 since Giannini et al. (2013) used a gradient descent and Vos et al. (2010) tackle the  
1083 optimization via a quasi-Newton method. Moreover, Giannini et al. (2013) performed  
1084 a 2D registration whereas Vos et al. (2010) registered 3D volumes.

1085 Viswanath et al. (2008a, 2009) as well as Vos et al. (2008a) performed an affine  
1086 registration using the MI as similarity measure to correct the misalignment between  
1087 T<sub>2</sub>-W and DCE images. The choice of the optimizer was not specified. Viswanath  
1088 et al. (2008a, 2009) focused on 2D registration while Vos et al. (2008a) performed  
1089 3D registration.

1090 Finally, Viswanath et al. (2011) performed a 3D registration with the three modal-  
1091 ities, T<sub>2</sub>-W and DCE and DW MRI, by using an affine transformation model com-  
1092 bined with the CMI similarity measure as presented in Chappelow et al. (2011).  
1093 Moreover, Chappelow et al. (2011) employed gradient descent to solve this problem  
1094 but suggested Nelder-Mead simplex and quasi-Newton method as other solutions.

Table 6: Overview of the CADe strategies employed in CAD systems.

CADe: ROIs selection strategy	References
All voxels-based approach	[4-5,7-8,12,14,16-17,20-22,25-37]
Lesions candidate detection	[10-11,41]

## 4. Image classification framework

### 4.1. CADe: ROIs detection/selection

As discussed in the introduction and shown in Fig. 2.3.2, the image classification framework is composed of eventually a CADe and a CADx. In this section, we will focus on studies embedding a CADe in their framework. Two approaches are considered to define a CADe (see Tab. 6): (i) voxel-based delineation and (ii) lesion segmentation.

The first strategy, which concerns the majority of the studies reviewed (see Tab. 6), is in fact linked to the nature of the classification framework. All voxels are considered as a possible threat and the output of the framework will be the lesions classified as cancerous.

The secondary group of methods is composed of method implementing a lesion segmentation algorithm to delineate potential candidates to further obtain a diagnosis through the CADx. This approach was borrowed from methodologies applied successfully in CADe for breast cancers.

Vos et al. (2012) highlighted lesion candidates by detecting blobs in the ADC map. These candidates were filter using some *a priori* criteria such as SI or diameter. As mentioned in Sect. 2.3.2 (see also Tab. 2.3.2), CaP can be interpreted as region of lower SI in ADC map. Hence, blob detectors are suitable to highlight these regions. Blobs are detected in a multi-resolution scheme by computing the three main eigenvalues  $\{\lambda_{\sigma,1}, \lambda_{\sigma,2}, \lambda_{\sigma,3}\}$  of the Hessian matrix for each voxel location of the ADC map at a specific scale  $\sigma$  as proposed by Li et al. (2003). The probability  $p$  of a voxel  $\mathbf{x}$  being a part of a blob at the scale  $\sigma$  is given by:

$$P(\mathbf{x}, \sigma) = \begin{cases} \frac{\|\lambda_{\sigma,3}(\mathbf{x})\|^2}{\|\lambda_{\sigma,1}(\mathbf{x})\|} , & \text{if } \lambda_{\sigma,k}(\mathbf{x}) > 0 \text{ with } k = \{1, 2, 3\} , \\ 0 , & \text{otherwise .} \end{cases} \quad (32)$$

1118 The fusion of the different scales is computed as:

$$L(\mathbf{x}) = \max P(\mathbf{x}, \sigma), \forall \sigma . \quad (33)$$

1119 The resulting map  $L(\mathbf{x})$  is then filtered depending on its appearance (cf. maxi-  
1120 mum of the likelihood of the region, diameter of the lesion) and their SI in ADC and  
1121 T<sub>2</sub>-W images. The detected regions are then used as inputs for the CADx.

1122 Litjens et al. (2011) used a pattern recognition approach in order to delineate  
1123 the ROIs. A blobness map was calculated in the same manner as previously men-  
1124 tioned using the multi-resolution Hessian blob detector on the ADC map, T<sub>2</sub>-W and  
1125 pharmacokinetic parameters maps (see Sect. 4.2 for details about those parameters).  
1126 Additionally, the position of the voxel  $\mathbf{x} = \{x, y, z\}$  was used as a feature as well as  
1127 the Euclidean distance of the voxel to the prostate center. Hence, the feature vectors  
1128 were composed of eight features and a support vector machines (SVM) classifier was  
1129 trained using a radial basis function (RBF) kernel (see Sect. 4.4 for more details).

1130 Subsequently, Litjens et al. (2012b) modified this approach by including only  
1131 features related to the blob detection on the different maps as well as the original  
1132 SIs of the parametric images. Two new maps were introduced based on texture.  
1133 Instead of a SVM classifier, a  $k$ -NN classifier was used. The candidate regions were  
1134 then extracted by performing a local maxima detection followed by post-processing  
1135 region-growing and morphological operations.

#### 1136 4.2. Feature detection

1137 Discriminative features which can be used to recognize CaP from healthy tissue  
1138 have to be first detected. This section will summarize the different strategies em-  
1139 ployed for this task. The feature type used is summarized in Tab. 7 while Tab. 8  
1140 sums up which strategies were used by the different studies reviewed.

Table 7: Overview of the feature detection methods used in CAD systems.

Feature detection methods	Indexes
<b>MRI image:</b>	
<i>Voxel-wise detection</i>	
Intensity-based	A
Edge-based	
Prewitt operator	B <sub>1</sub>
Sobel operator	B <sub>2</sub>
Kirsch operator	B <sub>3</sub>
Gabor filtering	B <sub>4</sub>
Texture-based	
Haralick features	C <sub>1</sub>
Fractal analysis	C <sub>2</sub>
Discrete cosine transform (DCT)	C <sub>3</sub>
Wavelet-based features	C <sub>4</sub>
Position-based	D
<i>Region-wise detection</i>	
Statistical-based	
Percentiles	E <sub>1</sub>
Statistical-moments	E <sub>2</sub>
Histogram-based	
PDF	F <sub>1</sub>
Histogram of oriented gradient (HOG)	F <sub>2</sub>
Shape context	F <sub>3</sub>
LBP	F <sub>4</sub>
Anatomical-based	G
<b>DCE signal:</b>	
Whole spectra approach	H
Semi-quantitative approach	I
Quantitative approach	
Toft model	J <sub>1</sub>
Brix model	J <sub>2</sub>
Weibull function	J <sub>3</sub>
Phenomenological universalities model	J <sub>4</sub>
<b>MRSI signal:</b>	
Whole spectra approach	K
Quantification approach	L
Wavelet-based approach	M



Table 8: Overview of the different features extracted by studies reviewed. The indexes of the features are presented in Tab. 7.

	A	B <sub>1</sub>	B <sub>2</sub>	B <sub>3</sub>	B <sub>4</sub>	C <sub>1</sub>	C <sub>2</sub>	C <sub>3</sub>	C <sub>4</sub>	D	E <sub>1</sub>	E <sub>2</sub>	F <sub>1</sub>	F <sub>2</sub>	F <sub>3</sub>	F <sub>4</sub>	G	H	I	J <sub>1</sub>	J <sub>2</sub>	J <sub>3</sub>	J <sub>4</sub>	K	L	M
[1]	△ --											△ --						✓								
[2]	△ --											△ --						✓								
[3]						△ --					-- ◇	-- ◇														
[4]	△ -- ◇																				✓!					
[5]	△ -- ◇																				✓!					
[6]	△ -- ◇							△ -- ◇		✓																
[7]	-- ◇																			✓		✓	✓			
[8]																								✓	✓	
[9]	△ -- ◇																			✓						
[10]	△ -- ◇									✓	△ • ◇	△ • ◇								✓						
[11]	△ -- ◇					△ • ◇				✓	△ • ◇	△ • ◇					✓			✓						
[12]	△ -- ◇																				✓					
[13]													△ • ◇	△ • ◇	△ • ◇	△ • ◇				✓!						
[14]							△ --																			
[15]							△ --																			
[16]																	✓								✓	
[17]																			✓	✓		✓	✓			
[18]	△ • ◇		△ • ◇	△ • ◇		△ • ◇					△ • ◇	△ • ◇							✓	✓						
[19]	△ • ◇		△ • ◇	△ • ◇		△ • ◇					△ • ◇	△ • ◇							✓	✓						
[20]	△ -- ◇																				✓!					
[21]	△ -- ◇																				✓!					
[22]																								✓	✓	
[23]										-- ◇	△ -- ◇									✓!						
[24]																			✓!							
[25]																			✓		✓					
[26]																								✓		
[27]																								✓		
[28]																								✓		
[29]		△ --	△ --	△ --		△ --						△ --												✓		
[30]		△ --	△ --	△ --		△ --						△ --												✓		
[31]					△ --																					✓
[32]		△ --	△ --	△ --		△ --						△ --												✓		
[33]		△ --	△ --	△ --	△ --	△ --						△ --												✓		
[34]																		✓								
[35]			△ --	△ --		△ --						△ --						✓								
[36]			△ --	△ --		△ • --						△ • --						✓								
[37]			△ --	△ --	△ --	△ --		△ --				△ --														
[38]	△ --																			✓						
[39]										-- • --										✓						
[40]										△ • --										✓						
[41]										△ • ◇										✓						

Notes:

△: implemented for T<sub>2</sub>-W-MRI images.

•: implemented for DCE-MRI images.

◇: implemented for DW-MRI images.

--: not used or not implemented.

✓: used or implemented.

✓!: partially implemented.

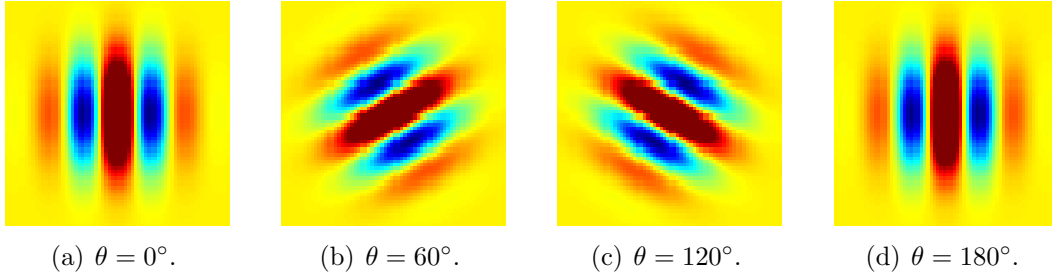


Figure 16: Illustration of four different Gabor filters varying their orientations  $\theta$ .

#### 4.2.1. Image-based features

This section will focus on image-based features detection. Two main strategies to detect features have been identified and used for the purpose of our classification: (i) voxel-wise detection and (ii) region-wise detection.

- **Voxel-wise detection:** This strategy refers to the fact that a feature is extracted at each voxel location of an image.

CaP as previously discussed (see Tab. 2.3.2) can be discerned due to SI changes. Hence, intensity-based features are one of the most common features used to build the feature vector which has to be classified (Ampeliotis et al. (2007, 2008), Artan et al. (2010, 2009), Chan et al. (2003), Langer et al. (2009), Liu et al. (2009), Niaf et al. (2012, 2011), Viswanath et al. (2011, 2008a)). This type of feature consists simply of the SI of each voxel of the different MRI modalities.

SI changes can be viewed as heterogeneous regions and edge-based features are used in that regard. Each feature is computed by convolving the original image with an edge operator. Three of these operators are used in CAD systems: (i) Prewitt operator (Prewitt (1970)), (ii) Sobel operator (Sobel (1970)) and (iii) Kirsch operator (Kirsch (1971)). Results obtained with these operators vary, due to their different kernels.

These features are commonly incorporated in the feature vector for further classification in the CAD systems reviewed (Niaf et al. (2012, 2011), Tiwari et al. (2013, 2010, 2009b), Viswanath et al. (2011, 2008b)).

Gabor filters offer another approach to extract information related to edges and texture and were found to perform similar processing to that in the human visual system (Daugman (1985), Gabor (1946)). A Gabor filter is defined by the modulation of a Gaussian function with a sinusoid which can be further rotated.

1167 Hence, a Gabor filter  $g$  can be formalized as:

$$g(x, y; \theta, \psi, \sigma, \gamma) = \exp\left(-\frac{x'^2 + \gamma^2 y'^2}{2\sigma^2}\right) \cos\left(2\pi\frac{x'}{\lambda} + \phi\right) , \quad (34)$$

1168 with

$$\begin{aligned} x' &= s(x \cos \theta + y \sin \theta) , \\ y' &= s(-x \sin \theta + y \cos \theta) , \end{aligned}$$

1169 where  $\lambda$  is the wavelength of the sinusoidal factor,  $\theta$  represents the orientation of  
1170 the Gabor filter,  $\psi$  is the phase offset,  $\sigma$  is the standard deviation of the Gaussian  
1171 envelope,  $\gamma$  is the spatial aspect ratio and  $s$  is the scale factor.

1172 To perform Gabor analysis to extract features for a classification scheme, a  
1173 bank of Gabor filters is usually created with different angles, scale and dilatations  
1174 (see Fig. 16) and then convolved with the image. Viswanath et al. (2008a, 2012)  
1175 and Tiwari et al. (2012) integrated Gabor analysis in their feature vector.

1176 Texture-based features provide other characteristics discerning CaP from healthy  
1177 tissue. The most common texture analysis for image classification was proposed  
1178 by Haralick et al. (1973) and is commonly used in CAD systems (Antic et al.  
1179 (2013), Niaf et al. (2012, 2011), Tiwari et al. (2013, 2010, 2009b), Viswanath  
1180 et al. (2011, 2008a,b, 2012)). At each voxel, a neighbourhood is defined around  
1181 this center and a gray-level co-occurrence matrix is built by selecting a pair of  
1182 voxels based on a defined distance and angle. Then, using this co-occurrence  
1183 matrix, a set of features can be computed based on the statistics describing the  
1184 texture around each voxel. Computation of these features is presented in Tab. 9.

1185 Fractal analysis and more precisely a local estimation of the fractal dimension  
1186 (Benassi et al. (1998)) describing the texture roughness at a specific location  
1187 was used in Lopes et al. (2011). A wavelet-based method in a multi-resolution  
1188 framework was used to estimate the fractal dimension. Cancerous tissue were  
1189 characterized to have a higher fractal dimension than healthy tissue.

1190 Chan et al. (2003) aimed to describe the texture using the frequency signature  
1191 via the discrete cosine transform (DCT) (Ahmed et al. (1974)) defining a neigh-  
1192 bourhood of  $7 \times 7$  pixels for each of the modalities that they used.. The DCT  
1193 allows to decompose a portion of image into a coefficients space where few of these  
1194 coefficients encoded the visually significant information. The DCT coefficients are

Table 9: The fourteen statistical features for texture analysis commonly computed from the gray level co-occurrence matrix  $p$  as presented by Haralick et al. (1973).

Statistical features	Formula
Angular second moment	$\sum_i \sum_j p(i, j)^2$ .
Contrast	$\sum_{n=0}^{N_g-1} n^2 \{ \sum_{i=1}^{N_g-1} \sum_{j=1}^{N_g-1} p(i, j) \} ,  i - j  = n$ .
Correlation	$\frac{\sum_i \sum_j (ij) p(i, j) - \mu_x \mu_y}{\sigma_x \sigma_y}$ .
Variance	$\sum_i \sum_j (i - \mu)^2 p(i, j)$ .
Inverse difference moment	$\sum_i \sum_j \frac{1}{1+(i-\mu)^2} p(i, j)$ .
Sum average	$\sum_{i=2}^{2N_g} i p_{x+y}(i)$ .
Sum variance	$\sum_{i=2}^{2N_g} (i - f_s)^2 p_{x+y}(i)$ .
Sum entropy	$-\sum_{i=2}^{2N_g} p_{x+y}(i) \log p_{x+y}(i)$ .
Entropy	$-\sum_i \sum_j p(i, j) \log p(i, j)$ .
Difference variance	$\sum_{i=0}^{N_g-1} i^2 p_{x-y}(i)$ .
Difference entropy	$-\sum_{i=0}^{N_g-1} p_{x-y}(i) \log p_{x-y}(i)$ .
Info. measure of corr. 1	$\frac{S(X;Y) - S_1(X;Y)}{\max(S(X), S(Y))}$ .
Info. measure of corr. 2	$\sqrt{(1 - \exp[-2(H_2(X;Y) - H(X;Y))])}$ .
Max. corr. coeff.	$\sqrt{\lambda_2}$ , of $Q(i, j) = \sum_k \frac{p(i, k)p(j, k)}{p_x(i)p_y(k)}$ .

1195 computed such as:

$$C_{k_1, k_2} = \sum_{m=0}^{M-1} \sum_{n=0}^{N-1} p_{m,n} \cos \left[ \frac{\pi}{M} \left( m + \frac{1}{2} \right) k_1 \right] \cos \left[ \frac{\pi}{N} \left( n + \frac{1}{2} \right) k_2 \right] , \quad (35)$$

1196 where  $C_{k_1, k_2}$  is the DCT coefficient at the position  $k_1, k_2$ ,  $M$  and  $N$  are the di-  
 1197 mension of the neighbourhood and  $p_{m,n}$  is the pixel SI at the position  $p_{m,n}$ .

1198 In the same spirit, Viswanath et al. (2012) projected T<sub>2</sub>-W images into the  
 1199 wavelet space and used the coefficients obtained from the decomposition as fea-  
 1200 tures. The wavelet family used for the decomposition was the Haar wavelet.

1201 The position of a voxel within the prostate was also considered a possible  
 1202 feature. Litjens et al. (2011) computed the Euclidean distance from each voxel  
 1203 to the prostate center as well as the individual distance in the three directions  
 1204  $x$ ,  $y$  and  $z$ . Chan et al. (2003) embedded the same information but this time  
 1205 using cylindrical coordinate  $r$ ,  $\theta$  and  $z$  corresponding to the radius, azimuth and  
 1206 elevation respectively.

#### 1207 – *Region-wise detection:*

1208 Unlike the previous section, another strategy is to study an entire region and  
 1209 extract characteristic features corresponding to this region.

1210 The most common approach reviewed can be classified as statical methods.  
 1211 Full map corresponding to feature types presented in the previous section are  
 1212 computed. Then, ROIs are defined and statistics are extracted from each of these  
 1213 regions. The first type of statistic is based on percentiles and is widely used (Antic  
 1214 et al. (2013), Litjens et al. (2012b, 2011), Peng et al. (2013), Tiwari et al. (2013,  
 1215 2010, 2009b), Viswanath et al. (2011, 2008a,b, 2012), Vos et al. (2012, 2008a,  
 1216 2010, 2008b)). In fact, once that a ROI is defined, the features corresponding  
 1217 the  $n^{\text{th}}$  percentile is used as feature. This  $n$  can take any value between 0 and  
 1218 100. This threshold is usually manually determined observing the distribution and  
 1219 corresponds to the best discriminant value differentiating malignant and healthy  
 1220 tissue. in addition, statistic-moments such as mean, standard deviation, kurtosis  
 1221 and skewness are also used (Ampeliotis et al. (2007, 2008), Antic et al. (2013),  
 1222 Niaf et al. (2012, 2011), Peng et al. (2013)).

1223 Another subset of features are anatomic which were also used by Litjens et al.  
 1224 (2012b) and Matulewicz et al. (2013). Litjens et al. (2012b) computed the volume,  
 1225 compactness and sphericity related to the region to integrate it in their feature  
 1226 vector to later classify. Matulewicz et al. (2013) introduced four features corre-  
 1227 sponding to the percentage of tissue belonging to the regionsPZ, CG, periurethral

region or outside prostate region for the considered ROI.

In contrast to anatomical are histogram-based features. For instance, Liu et al. (2013) introduced four different types of histogram-based features. The first type corresponds to the histogram of the SI of the image. The second type is the histogram of oriented gradient (HOG) (Dalal and Triggs (2005)). HOG descriptor describes the local shape of the object of interest by using gradient directions distribution. This descriptor is extracted mainly in three steps. First the gradient image and its corresponding magnitude and direction are computed. Then, the ROI is divided into cells and an oriented-based histogram is generated for each cell. At each pixel location, the orientation of the gradient will vote for a bin of the histogram and this vote is weighted by the magnitude of the same gradient. Finally, The cells are grouped into block and each block is normalized. The third histogram-based type used by Liu et al. (2013) was shape context (Belongie et al. (2002)). The shape context is also a way to describe the shape of an object of interest. First, a set of points defining edges have to be detected and for each point of each edge, a log-polar-based histogram is computed using the relative points distribution. The last set of histogram-based feature extracted is based on the framework of Zhao et al. (2012) which is using the Fourier transform of the histogram created via local binary pattern (LBP) (Ojala et al. (1996)). LBP is generated by comparing the value of the central pixel with its 8-connected neighbours. Then, in the ROI, the histogram of the LBP distribution is computed. The discrete fourier transform (DFT) of the LBP histogram is used to make the feature invariant to rotation.

The last group of region-based feature is based on fractal analysis. The features proposed are based on estimating the fractal dimension which is a statistical index representing the complexity of what is analysed. Lv et al. (2009) proposed two features based on fractal dimension: (i) texture fractal dimension and (ii) histogram fractal dimension. The first feature is based on estimating the fractal dimension on the SI of each image. Hence, this feature is a statistical characteristic of the image roughness. The second fractal dimension is estimated in the PDF of each image and is characteristic of the complexity of the PDF. Lopes et al. (2011) proposed a 3D version to estimate the fractal dimension of a volume using wavelet decomposition.

#### *4.2.2. DCE-based features*

DCE-MRI is more commonly based on a SI analysis over time as presented in Sect. 2.3.2. The parameters extracted used in CAD system during the DCE-MRI analysis are presented

Table 10: Parameters used as features for a DCE semi-quantitative analysis in CAD systems.

Semi-quantitative features	Explanations
<i>Amplitude features:</i>	
$S_0$	Amplitude at the onset of the enhancement
$S_{\max}$	Amplitude corresponding to 95% of the maximum amplitude
$S_p$	Amplitude corresponding to the maximum amplitude
$S_f$	Amplitude at the final time point
<i>Time features:</i>	
$t_0$	Time at the onset of the enhancement
$t_{\max}$	Time corresponding to 95% of the maximum amplitude
$t_p$	Time corresponding to the maximum amplitude
$t_f$	Final time
$t_{tp}$	Time to peak which is the time from $t_0$ to $t_p$
<i>Derivatives and integral features:</i>	
$WI$	Wash-in rate corresponding to the signal slope from $t_0$ to $t_m$ or $t_p$
$WO$	Wash-out rate corresponding to the signal slope from $t_m$ or $t_p$ to $t_p$
$IAUC$	Initial area under the curve which is the area between $t_0$ to $t_f$

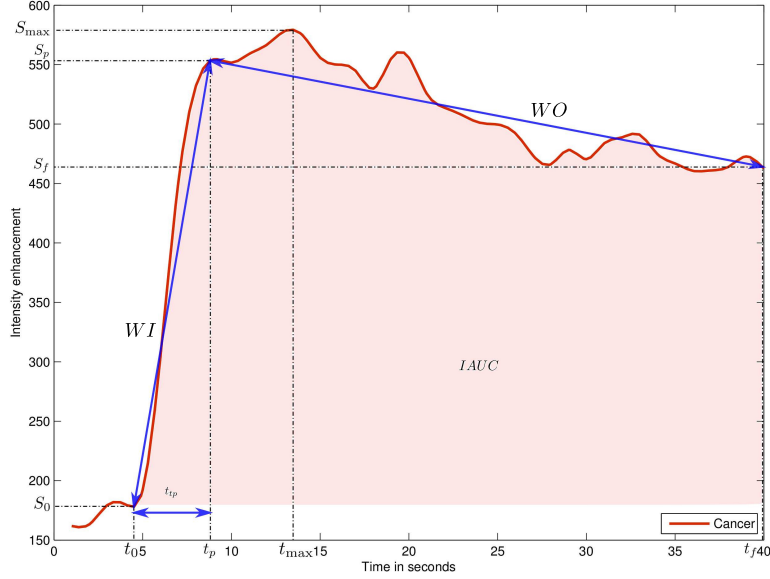


Figure 17: Graphical representation of the different semi-quantitative features used for DCE-MRI analysis.

- 1265 — **Whole-spectra approach:** Some studies are using the whole DCE time series  
1266 as feature vector such as Ampeliotis et al. (2007, 2008), Tiwari et al. (2012) and  
1267 Viswanath et al. (2008a,b). In some cases, the high-dimensional feature space is  
1268 reduced using dimension reduction methods as it will be presented in the next  
1269 section (see Sect. 4.3).
- 1270 — **Semi-quantitative approach:** Semi-quantitative approaches are based on mod-  
1271 elling mathematically the DCE time series. The parameters modelling the signal  
1272 are commonly used mainly due to the simplicity of their computation. Paramet-  
1273 ers included in semi-quantitative analysis are summarized in Tab. 10 and also  
1274 graphically depicted in Fig. 17. A set of time features corresponding to specific  
1275 amplitude level (start, maximum and end) are extracted. Then, derivative and in-  
1276 tegral features are also considered as discriminative and are commonly computed.
- 1277 — **Quantitative approach:** As presented in Sect. 2.3.2, quantitative approaches  
1278 correspond to mathematical-pharmacokinetic models based on physiological ex-  
1279 changes. Four different models have been used in CAD systems.  
1280 The most common model reviewed was the *Brix model* (Artan et al. (2010,



2009), Liu et al. (2009), Ozer et al. (2009, 2010), Sung et al. (2011)). This model is formalized such as:

$$\frac{S(t)}{S(0)} = 1 + Ak_{ep} \left( \frac{\exp(-k_{ep}t) - \exp(-k_{el}t)}{k_{el} - k_{ep}} \right) , \quad (36)$$

noindent where  $S(\cdot)$  is the DCE signal,  $A$  is the parameter simulating the tissue properties,  $k_{el}$  is the parameter related to the first-order elimination from the plasma compartment and  $k_{ep}$  is the parameter of the transvascular permeability. Thus, the parameters  $k_{ep}$ ,  $k_{el}$  and  $A$  are computed from the MRI data and used as features.

Thus, the parameters  $k_{ep}$ ,  $k_{el}$  and  $A$  are computed and used as features.

The Tofts model (Tofts (1997)) was used by Giannini et al. (2013), Langer et al. (2009), Mazzetti et al. (2011), Niaf et al. (2012, 2011). The DCE signal relative to the concentration is modelled as:

$$C_t(t) = v_p C_p(t) + K_{trans} \int_0^t C_p(\tau) \exp(-k_{ep}(t - \tau)) d\tau , \quad (37)$$

where  $C_t(\cdot)$  is the concentration of the medium,  $C_p(\cdot)$  is the AIF which have to be estimated apart,  $K_{trans}$  is the parameter related to the diffuse transport of media across the capillary endothelium,  $k_{ep}$  is the parameter related to the exchanges back into the vascular space and  $v_e$  is the extravascular-extracellular space fraction defined as  $v_e = 1 - v_p$ . Thus, the parameters  $K_{trans}$ ,  $k_{ep}$  and  $v_e$  are computed and used as features in this model.

Mazzetti et al. (2011) and Giannini et al. (2013) used the Weibull function empirically formalized as:

$$S(t) = At \exp(-t^B) , \quad (38)$$

where  $A$  and  $B$  are the two parameters which have to be inferred.

They also used another empirical model which is based on the West-like function and named the phenomenological universalities model (Castorina et al. (2006)) formalized as:

$$S(t) = \exp \left[ rt + \frac{1}{\beta} a_0 - r (\exp(\beta t) - 1) \right] , \quad (39)$$

where the parameters  $\beta$ ,  $a_0$  and  $r$  are inferred.

For all these models, the parameters are inferred using an optimization curve fitting approach.

### 4.2.3. MRSI-based features

— **Whole spectra approach:** As for the DCE analysis, one common approach is to incorporate the whole MRSI spectra in the feature vector for classification (Kelm et al. (2007), Matulewicz et al. (2013), Parfait et al. (2012), Tiwari et al. (2013, 2010, 2007, 2009a,b), Viswanath et al. (2008a)). Sometimes post-processing involving dimension reduction methods is performed to reduce the complexity during the classification as it will be presented in Sect. 4.3.

— **Quantification approach:** We can recall that in MRSI only few biological markers (cf., choline, creatine and citrate metabolites mainly) are known to be useful to discriminate CaP and healthy tissue. Then, quantification of these metabolites concentrations is considered as features which will be later classify. In order to perform this quantification, four different approaches have been used. The QUEST (Ratiney et al. (2005)), AMARES (Vanhamme et al. (1997)) and VARPRO (Coleman and Li (1993)) models were used by Kelm et al. (2007). They are all time-domain quantification methods varying by the type of pre-knowledge embedded and the optimization approaches used to solve the quantification problem. Unlike the previous method, Parfait et al. (2012) used the LcModel approach (Provencher (1993)) which solves the optimization problem in the frequency domain.

Once the different concentrations are computed, Kelm et al. (2007) calculated the relative concentrations (Eq. (40) and (41)) and used them as features. However, Parfait et al. (2012) used each metabolite concentrations individually.

$$R_1 = \frac{[\text{Cho}] + [\text{Cr}]}{[\text{Cit}]} . \quad (40)$$

$$R_2 = \frac{[\text{Cit}]}{[\text{Cho}] + [\text{Cr}] + [\text{Cit}]} , \quad (41)$$

where Cit, Cho and Cr are the concentration of citrate, choline and creatine respectively.

— **Wavelet decomposition approach:** Tiwari et al. (2012) performed a wavelet packet decomposition (Coifman and Wickerhauser (1992)) with the Haar wavelet basis function and used the coefficients of this decomposition as features for further classification.

### 4.3. Feature selection and feature extraction

As presented in the previous section, a wide variety of features can be computed (see Tab. 7). This often leads from multi-parametric MRI data to a high complexity

Table 11: Overview of the feature selection and extraction methods used in CAD systems.

Dimension reduction methods	References
<i>Feature selection:</i>	
Statistical test	[17-18,41]
MI-based methods	[18-19,37]
<i>Feature extraction:</i>	
Linear mapping	
PCA	[27-28,31]
Non-linear mapping	
Laplacian eigenmaps	[26,28-30,33,36]
LLE and LLE-based	[27-28,33-34]

feature space which might mislead or corrupt the classifier which used for training. Thus, it will be interesting to reduce the number of dimensions of the feature space before to proceed to any classification task. The strategy used can be grouped into two classes: (i) feature selection and (ii) feature extraction. Those methods used in CAD system are summarized in Tab. 11.

#### 4.3.1. Feature selection

The feature selection strategy is based on selecting the most discriminative feature dimension of the high-dimensional space. Thus, the low-dimensional space is then composed of a subset of the original features detected. In this section, methods employed in the studies reviewed will be briefly presented. More extensive review specific to feature selection can be found in Saeys et al. (2007).

Niaf et al. (2012, 2011) make use of the p-value by using the independent two-sample t-test with equal mean for each feature dimension. In this statistical test, it is assumed two classes, CaP against healthy. Hence, for each particular feature, the distribution of each class can be characterized by their means  $\bar{X}_1$  and  $\bar{X}_2$  and standard deviation  $s_{X_1}$  and  $s_{X_2}$ , respectively. Hence, the null hypothesis tested is based on the fact that these both distribution means are equal. Thus, the t-statistic related to verify the null hypothesis is then formalized such that:

$$t = \frac{\bar{X}_1 - \bar{X}_2}{s_{X_1X_2} \cdot \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}, \quad (42)$$

$$s_{X_1X_2} = \sqrt{\frac{(n_1 - 1)s_{X_1}^2 + (n_2 - 1)s_{X_2}^2}{n_1 + n_2 - 2}},$$

where  $n_1$  and  $n_2$  are the number of samples in each class.

From Eq. (42), it can be seen that the more the means of the class distribution diverge, the larger the  $t$ -statistic  $t$  will imply that this particular feature is more relevant and able to make the distinction between the two classes.

The  $p$ -value statistic can be deduced from the  $t$ -test and corresponds to the probability to obtain such an extreme test assuming that the null hypothesis is true (Goodman (1999)). Hence, smaller is the  $p$ -value, more likely is to reject the null hypothesis and more relevant the feature is likely to be.

Finally, the features can be ranked and the most significant features can be selected. However, this technique suffers from a main drawback since that it assumes that each feature is independent, which is unlikely to happen and introduces a high redundancy in the features selected.

Vos et al. (2012) employed a similar feature ranking approach but make use of the Fisher discriminant ratio to compute the relevance of each feature dimension. Taking the aforementioned formulation, the Fisher discriminant ratio is formalized as the ratio of the interclass variance to the intraclass variance as:

$$F_r = \frac{\bar{X}_1 - \bar{X}_2}{s_{X_1}^2 + s_{X_2}^2}. \quad (43)$$

Hence, a feature dimension can be seen as more relevant when the interclass variance is maximum and the intraclass variance in minimum. Once the features ordered, Vos et al. (2012) select the feature dimensions with the larger Fisher discriminant ratio.

MI can also be used to select the subset of feature dimension. Definition of the MI was presented in Sect. 3.3.2 and formalized in Eq. (30) and as previously mentioned, the computation of the entropies involves the estimation of some PDFs and the data being usually continuous variables, it is then necessary to estimate the PDFs using methods such as Parzen windows.

Peng et al. (2005) introduced two main criteria to select the feature dimensions: (i) maximal relevance and (ii) minimum redundancy.

1383 Maximal relevance criterion is based on the paradigm that the classes and the  
 1384 feature dimension which has to be selected have to share a maximal MI and can be  
 1385 formalized such that:

$$\arg \max Rel(\mathbf{x}, c) = \frac{1}{|\mathbf{x}|} \sum_{x_i \in \mathbf{x}} MI(x_i, c) , \quad (44)$$

1386 where  $\mathbf{x} = \{x_i, i = 1, \dots, d\}$  is a feature vector of  $d$  dimensions and  $c$  is the class  
 1387 considered.

1388 As in the previous method, using maximal relevance criterion alone will imply  
 1389 the independence between each feature dimension which is usually not true.

1390 Minimal redundancy criterion will force to select a new feature dimension which  
 1391 shares as less MI as possible with previously selected feature dimension. It can be  
 1392 formalized as:

$$\arg \min Red(\mathbf{x}) = \frac{1}{|\mathbf{x}|^2} \sum_{x_i, x_j \in \mathbf{x}} MI(x_i, x_j) . \quad (45)$$

1393 Combination of these two previous criteria is known as minimum redundancy  
 1394 maximum relevance (mRMR)<sup>5</sup> (Peng et al. (2005)) and can be computed such as a  
 1395 difference or a quotient of the Eqs. (44) and (45).

1396 Niaf et al. (2012, 2011) make use of maximal relevance criterion alone and also of  
 1397 both mRMR difference and quotient criterion. Viswanath et al. (2012) also reduced  
 1398 their feature vector via mRMR difference and quotient.

#### 1399 4.3.2. Feature extraction

1400 The feature extraction strategy is related to dimension reduction methods but not  
 1401 selecting discriminative features. Instead, these methods aim at mapping the data  
 1402 from the high-dimensional space into a low-dimensional space created to maximize  
 1403 the separability between the classes. The mapping can be performed a linear or a  
 1404 non-linear manner. Again, only methods employed in CAD system will be reviewed  
 1405 in this section. We refer the reader to the review of Fodor (2002) for a full review of  
 1406 feature extraction techniques.

1407 PCA is the most commonly used linear mapping method in CAD systems. PCA  
 1408 is based on finding the orthogonal linear transform mapping the original data into a  
 1409 low-dimensional space. The space is defined such that the linear combinations of the

---

<sup>5</sup>mRMR implementation can be found at: <http://penglab.janelia.org/proj/mRMR/>

1410 original data with the  $k^{th}$  greatest variances will lie on the  $k^{th}$  principal components  
1411 (Jolliffe (2002)).

1412 The principal components can then be computed by using the eigenvectors-  
1413 eigenvalues decomposition of the covariance matrix. Let's define the  $\mathbf{x}$  being the  
1414 data matrix. Then the covariance matrix is defined as:

$$\Sigma = \mathbf{x}^T \mathbf{x} . \quad (46)$$

1415 The eigenvectors-eigenvalues decomposition can be formalized as:

$$\mathbf{v}^{-1} \Sigma \mathbf{v} = \Lambda , \quad (47)$$

1416 where  $\mathbf{v}$  are the eigenvectors matrix and  $\Lambda$  is a diagonal matrix containing the eigen-  
1417 values.

1418 It is then possible to find the new low-dimensional space by sorting the eigen-  
1419 vectors using the eigenvalues and finally select the largest eigenvalues. The total  
1420 variation that is the sum of the principal eigenvalues of the covariance matrix (Fodor  
1421 (2002)), usually corresponds to the 95% to 98% of the cumulative sum of the eigenval-  
1422 ues. Tiwari et al. (2008, 2009a, 2012) used PCA in order to reduce the dimensionality  
1423 of their feature vector.

1424 Non-linear mapping was also used for dimension reduction. It is mainly based  
1425 on Laplacian eigenmaps and locally linear embedding (LLE) methods. Laplacian  
1426 eigenmaps<sup>6</sup> or also referred as spectral clustering in computer vision, aim to find  
1427 a low-dimensional space in which the proximity of the data should be preserved  
1428 from the high-dimensional space (Belkin and Niyogi (2001), Shi and Malik (2000)).  
1429 Thus, two adjacent data points in the high-dimensional space should also be close  
1430 in the low-dimensional space. In like manner, two far away data points in the high-  
1431 dimensional space also should be distant in the low-dimensional space. To compute  
1432 this projection, an adjacency matrix is defined as:

$$W(i, j) = \exp \|\mathbf{x}_i - \mathbf{x}_j\|_2 , \quad (48)$$

1433 where  $\mathbf{x}_i$  and  $\mathbf{x}_j$  are the two samples considered.

1434 Then, the low-dimensional space will be found by solving the generalized eigenvectors-  
1435 eigenvalues problem as:

$$(D - W)\mathbf{y} = \lambda D\mathbf{y} , \quad (49)$$

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<sup>6</sup>Laplacian eigenmap implementation is available at: <http://www.cse.ohio-state.edu/~mbelkin/algorithms/algorithms.html>

where  $D$  is a diagonal matrix such that  $D(i, i) = \sum_j W(j, i)$ .

Finally the low-dimensional space is defined by the  $k$  eigenvectors of the  $k$  smallest eigenvalues (Belkin and Niyogi (2001)). Tiwari et al. (2007, 2009a,b), Viswanath et al. (2008b) used this spectral clustering to project their feature vector into a low-dimensional space. The feature space in these studies is usually composed of features extracted from a single or multiple modalities and then concatenated before applying the Laplacian eigenmaps dimension reduction technique.

Tiwari et al. (2013, 2009a) used a slightly different approach by combining the Laplacian eigenmaps techniques with a prior multi-kernel learning strategy. First, multiple features were extracted for multiple modalities. The features of a single modality were then mapped to a higher dimensional space via the Kernel trick (Aizerman et al. (1964)) and more precisely using a Gaussian kernel. Then, each kernel associated with each modality was linearly combined to obtain a combined kernel  $K$ . Then, the computation of the adjacency matrix  $W$  took place and the same scheme as in Laplacian eigenmaps is performed. However, in order to use the combined kernel, Eq. (49) becomes:

$$K(D - W)K^T \mathbf{y} = \lambda K D K^T \mathbf{y} . \quad (50)$$

It can be solved as a generalized eigenvectors-eigenvalues problem as previously. Viswanath et al. (2011) used Laplacian eigenmaps inside a bagging framework in which multiple embeddings are generated by successively selecting feature dimensions.

LLE<sup>7</sup> is another common non-linear dimension technique broadly known firstly proposed by Roweis and Saul (2000). LLE is based on the fact that a data point in the feature space can be characterized by its neighbours. Thus, it was proposed to represent each data point in the high-dimensional space as the linear combination of its  $k$ -nearest neighbours. This can be expressed as:

$$\hat{\mathbf{x}}_i = \sum_j W(i, j) \mathbf{x}_j , \quad (51)$$

where  $\mathbf{x}_i$  and  $\mathbf{x}_j$  are the data point considered and its neighbours data points, respectively.

Hence, this problem which have to be solved at this stage is to estimate the weight matrix  $W$ . This problem can be tackled using a least square optimization scheme by optimizing the following objective function:

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<sup>7</sup>LLE implementation is available at: <http://www.cs.nyu.edu/~roweis/lle/code.html>

$$\begin{aligned} \hat{W} &= \arg \min_W \sum_i |\mathbf{x}_i - \sum_j W(i, j) \mathbf{x}_j|^2, \\ &\text{subject to } \sum_j W(i, j) = 1, \end{aligned} \quad (52)$$

Then, the essence of LLE is to project the data into a low-dimensional space keeping the data organization. Thus, the projection into the low-dimensional space can be seen as an optimization problem as:

$$\hat{\mathbf{y}} = \arg \min_{\mathbf{y}} \sum_i |\mathbf{y}_i - \sum_j W(i, j) \mathbf{y}_j|^2. \quad (53)$$

This optimization can be performed as an eigenvectors-eigenvalues problem by finding the  $k^{\text{th}}$  eigenvectors corresponding the  $k^{\text{th}}$  smallest eigenvalues of the sparse matrix  $(I - W)^T(I - W)$ . Tiwari et al. (2008, 2009a), Viswanath et al. (2008a,b) used LLE as dimension reduction technique to reduce the complexity of their feature vector.

Tiwari et al. (2008) used a modified version of the LLE algorithm in which they applied LLE in a bagging approach with multiple size of neighbourhood. The embedding obtained are then fused using the maximum likelihood estimation.

#### 4.4. Classification

##### 4.4.1. Classifier

Once that the feature vector has been extracted and eventually the complexity reduced, it is possible to make a decision and classify this feature vector to belong to CaP or healthy tissue. Classification methods used in CAD system to distinguish these two classes are summarized in Tab. 12. A full review of classification methods used in pattern recognition can be found in Bishop (2006).

##### — **Rule-based method:**

Lv et al. (2009) make use of a decision stump classifier to distinguish CaP and healthy classes.

Puech et al. (2009) detect CaP by implementing a given set of rules using a score medical decision making approach. The feature values are compared with a pre-defined threshold. Then, at each comparison, the final score is incremented or not, depending on the threshold and the final decision is taken depending of the final score.



Table 12: Overview of the classifiers used in CAD systems.

Classifier	References
<i>Rule-based method:</i>	[15,24]
<i>Clustering methods:</i>	
<i>k</i> -means clustering	[26-28,33-34]
<i>k</i> -NN	[11,18-19]
<i>Linear model classifiers:</i>	
LDA	[3,6,18-19,41]
Logistic regression	[8-9]
<i>Non-linear classifier:</i>	
QDA	[37]
<i>Probabilistic classifier:</i>	
Naive Bayes	[7,17-19]
<i>Ensemble learner classifiers:</i>	
AdaBoost	[14]
Random forest	[8,31-32,35]
Probabilistic boosting tree	[29-31,36]
<i>Kernel method:</i>	
Gaussian processes	[8]
<i>Sparse kernel methods:</i>	
SVM	[4-6,8,10-11,13-14,18-23,25,31,38-40]
RVM	[20-21]
<i>Neural network:</i>	
Multiple layer perceptron	[16,22]
Probabilistic neural network	[1-2,36]
<i>Graphical model classifiers:</i>	
Markov random field	[12,21]
Conditional random field	[4-5]

1492 – **Clustering methods:**

1493  $k$ -nearest neighbour ( $k$ -NN) is one of the simplest supervised machine learn-  
 1494 ing classification methods. In this method, a new unlabelled vector is assigned  
 1495 to the most represented class from its  $k$  nearest-neighbours in the feature space.  
 1496 The parameter  $k$  is usually an odd number in order to avoid any tie case.  $k$ -NN  
 1497 was one of the method used by Niaf et al. (2012, 2011) mainly to make a compar-  
 1498 ison with different machine learning techniques. Litjens et al. (2012b) used this  
 1499 method to roughly detect potential CaP voxels before performing a region-based  
 1500 classification.

1501  $k$ -means is an unsupervised clustering methods in which the data have to be  
 1502 partitioned into  $k$  clusters. The discovery of the clusters is an iterative procedure.  
 1503 First  $k$  random centroids are defined in the feature space and each data point  
 1504 is assigned to the nearest centroid. Then, the centroid position for each cluster  
 1505 is updated by computing the mean of all the data points belonging to this par-  
 1506 ticular cluster. Both assignment and updating are repeated until the centroids  
 1507 are stable. The number of clusters  $k$  is usually defined as the number of classes.  
 1508 This algorithm can also be used for “on-line” learning. In case that new data  
 1509 has to be incorporated, the initial centroid positions corresponds to the results  
 1510 of a previous  $k$ -means training and is followed by the assignment-updating stage  
 1511 previously explained.

1512 Tiwari et al. (2007, 2009a) used  $k$ -means in an iterative procedure. Three clus-  
 1513 ters were defined corresponding to CaP, healthy and non-prostate, respectively.  
 1514  $k$ -means was applied iteratively and the voxels corresponding to the larger cluster  
 1515 were excluded under the assumption that it is assigned to “non-prostate” cluster.  
 1516 The iteration stop until the number of voxels composing the clusters is smaller  
 1517 than a threshold.

1518 Tiwari et al. (2008), Viswanath et al. (2008a,b) used  $k$ -means in a repetitive  
 1519 manner to be less sensitive to the centroids initialisation. Thus,  $k$  clusters were  
 1520 generated  $T$  times. The final assignment was performed by majority voting using  
 1521 a co-association matrix as proposed by Fred and Jain (2005).

1522 – **Linear model classifiers:**

1523 Linear discriminant analysis (LDA) can be used as a classification method in  
 1524 which the optimal linear separation between two classes is found by maximizing  
 1525 the interclass variance and minimizing the intraclass variance (Friedman (1989)).  
 1526 The linear discriminant function is defined as:

$$\delta_k(\mathbf{x}_i) = \mathbf{x}_i^T \Sigma^{-1} \mu_k - \frac{1}{2} \mu_k^T \Sigma^{-1} \mu_k + \log(\pi_k) , \quad (54)$$

where  $\mathbf{x}_i$  is an unlabelled feature vector,  $\Sigma$  is the covariance matrix of the training data,  $\mu_k$  is the mean vector of the class  $k$  and  $\pi_k$  is the prior probabilities of class  $k$ .

To perform the classification, a sample  $\mathbf{x}_i$  will be assigned to the class which maximizes the discriminant function:

$$C(\mathbf{x}_i) = \arg \max_k \delta_k(\mathbf{x}_i) . \quad (55)$$

covariance matrix  $\Sigma_k$  specific at each class is computed Antic et al. (2013), Chan et al. (2003), Niaf et al. (2012, 2011), Vos et al. (2012) used LDA to classify their feature vectors defining two classes CaP *versus* healthy.

Logistic regression can be used to perform binary classification and can provide the probability of an observation to belong to a class. The posterior probability of one of the class  $c_1$  can be written as:

$$p(c_1|\mathbf{x}_i) = \frac{1}{1 + \exp(-\mathbf{w}^T \mathbf{x}_i)} , \quad (56)$$

with  $p(c_2|\mathbf{x}_i) = 1 - p(c_1|\mathbf{x}_i)$  and where  $\mathbf{w}$  is the vector of the regression parameters allowing to obtain a linear combination of the input feature vector  $\mathbf{x}_i$ .

Thus, an unlabelled observation  $\mathbf{x}_i$  will be assigned to the class which maximizes the posterior probability:

$$C(\mathbf{x}_i) = \arg \max_k p(C = k|\mathbf{x}_i) . \quad (57)$$

From Eq. (56), one can see that the key of classification using logistic regression model is to infer the set of parameters  $\mathbf{w}$  through a learning stage in the training set. This vector of parameters  $\mathbf{w}$  can be inferred by finding the maximum likelihood estimates. This step can be performed through an optimization scheme, using a quasi-Newton method (Byrd et al. (1995)), which iteratively seeks for the local minimum in the derivative of Eq. (56).

Kelm et al. (2007), Puech et al. (2009) used a logistic regression to create a linear probabilistic model in order to classify their feature vectors.

#### – ***Non-linear model classifier:***

Viswanath et al. (2012) used the most general quadratic discriminant analysis (QDA) instead of LDA. Unlike in LDA in which one assumes that the class covariance matrix  $\Sigma$  is identical for all the classes, in QDA, it is assumed that a

1554 covariance matrix  $\Sigma_k$  specific for each class is computed. Thus, Eq. (54) becomes:

$$\delta_k(\mathbf{x}_i) = \mathbf{x}_i^T \Sigma_k^{-1} \mu_k - \frac{1}{2} \mu_k^T \Sigma_k^{-1} \mu_k + \log(\pi_k) . \quad (58)$$

1555 The classification scheme in the case of the QDA is identical to Eq. (55).

1556 – ***Probabilistic classifier:***

1557 The most commonly used classifier is the naive Bayes classifier which is a  
1558 probabilistic classifier assuming the independence between each feature dimension  
1559 (Rish (2001)). This classifier is based on the Bayes' theorem:

$$p(C = k|\mathbf{x}) = \frac{p(C)p(\mathbf{x}|C)}{p(\mathbf{x})} , \quad (59)$$

1560 where  $p(C = k|\mathbf{x})$  is the posterior probability,  $p(C)$  is the prior probability,  $p(\mathbf{x}|C)$   
1561 is the likelihood and  $p(\mathbf{x})$  is the evidence.

1562 However, the evidence term is usually discarded since, it is not class dependent  
1563 and plays the role of a normalization term. Hence, in a classification scheme, an  
1564 unlabelled observation will be classified to the class which maximizes the posterior  
1565 probability such as:

$$C(\mathbf{x}_i) = \arg \max_k p(C = k|\mathbf{x}_i) , \quad (60)$$

$$p(C = k|\mathbf{x}_i) = p(C = k) \prod_{j=1}^n p(x_{ij}, |C = k) , \quad (61)$$

1566 where  $d$  is the number of dimensions of the feature vector  $\mathbf{x}_i = \{x_{i1}, \dots, x_{id}\}$ .

1567 Usually, a model includes both the prior and likelihood probabilities and it  
1568 is common to use an equal prior probability for each class or eventually a value  
1569 depending of the relative frequency derived from the training set. Regarding the  
1570 likelihood probability, it is common to choose a Normal distribution to character-  
1571 ize each class. Thus, each class will be characterized by two parameters: (i) the  
1572 mean and (ii) the standard deviation. These parameters can be inferred from the  
1573 training set by using the maximum likelihood (ML) approach.

1574 Giannini et al. (2013), Mazzetti et al. (2011), Niaf et al. (2012, 2011) used  
1575 the naive Bayes classifier to classify their feature vectors to either malignant or  
1576 healthy. The Normal distribution was used as the likelihood probability for that  
1577 model.

– **Ensemble learner classifiers:**

AdaBoost is an adaptive method based on an ensemble learner and was initially proposed by Freund and Schapire (1997). AdaBoost linearly combines several weak learners resulting into a final strong classifier. A weak learner is defined as a classification method performing slightly better than random classification. Popular choices regarding the weak learner methods are: decision stump, decision tree learners (cf., iterative dichotomiser 3 (ID3) (Quinlan (1986)), C4.5 (Quinlan (1993)), classification and regression tree (CART) (Breiman et al. (1984))).

AdaBoost is considered as an adaptive method in the way that the weak learners are selected. The selection is performed in an iterative manner. At each iteration  $t$ , the weak learner selected  $h_t$  corresponds to the one minimizing the classification error on a distribution of weights  $D_t$ , that is associated to the training sample. A weight  $\alpha_t$  is affected at each weak learner such that:

$$\alpha_t = \frac{1}{2} \ln \frac{1 - \epsilon_t}{\epsilon_t} , \quad (62)$$

where  $\epsilon_t$  corresponds to the classification error rate of the weak learner on the distribution of weight  $D_t$ .

Before performing a new iteration, the distribution of weight  $D_t$  is updated such that the weight associated with the misclassified samples by  $h_t$  will increase and the weights of well classified samples will decrease as shown in Eq. (63).

$$D_{t+1}(i) = \frac{D_t(i) \exp(-\alpha_t y_i h_t(\mathbf{x}_i))}{Z_t} , \quad (63)$$

where  $\mathbf{x}_i$  is the  $i^{\text{th}}$  sample corresponding to class  $y_i$  and  $Z_t$  is a normalization factor to impose that  $D_{t+1}$  to be a probability distribution.

This procedure allows to select a weak learner at the next iteration  $t+1$  which will classify in priority previous misclassified samples. Thus, after  $T$  iterations, the final strong classifier corresponds to the linear combination of the weak learners and the classification is performed such that:

$$C(\mathbf{x}_i) = \text{sign} \left( \sum_{t=1}^T \alpha_t h_t(\mathbf{x}_i) \right) . \quad (64)$$

Lopes et al. (2011) make use of the AdaBoost technique to perform their classification.

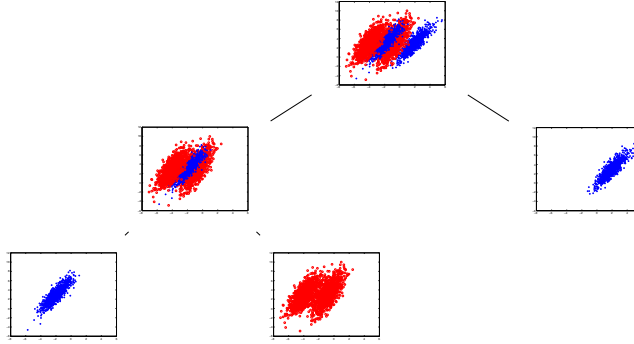


Figure 18: Representation of the capabilities of the probabilistic boosting tree algorithm to split at each node of the tree the positive and negative samples.

Random forest<sup>8</sup> is a classification method which is based on creating an ensemble of decision trees and was introduced by Breiman (2001). In the learning stage, multiple decision tree learners (Breiman et al. (1984)) will be trained. However, each decision tree will be trained with a different dataset. Each of these datasets corresponds to a bootstrap sample generated by randomly choosing  $n$  samples with replacement from the  $N$  samples available in the original set (Efron (1979)). Then, randomization is also part of the decision tree growth. At each node of the decision tree, from the bootstrap sample of  $D$  dimensions, a number of  $d \ll D$  dimensions will be randomly selected. Finally, the  $d^{\text{th}}$  dimension splitting the best the data will be used. This best splitting is often evaluated using MI (see Sect. 3.3.2). Finally, each tree is grown as much as possible without using any pruning procedure.

In the prediction stage, a sample is introduced in each tree and each of the tree will assign a class to this sample. Finally, it is common to use a majority voting approach to choose the final class label.

Kelm et al. (2007), Tiwari et al. (2013, 2012), Viswanath et al. (2009) make use of the random forest classifier to classify their feature vector.

Probabilistic boosting-tree is an ensemble classifier method which is sharing principles from AdaBoost but using them inside a decision tree (Tu (2005)). In the training stage, the probabilistic boosting-tree method grows a decision tree and at each node a strong classifier is learnt in an almost comparable scheme than

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<sup>8</sup>Random forest implementation can be found at: [http://www.stat.berkeley.edu/~breiman/RandomForests/cc\\_software.htm](http://www.stat.berkeley.edu/~breiman/RandomForests/cc_software.htm)

AdaBoost (see Eq. 64). Once the strong learner is trained, the training set will be split into two subsets which will be used to train the next strong classifiers in the next descending nodes. Thus, three cases are conceivable to decide which branch to propagate each sample  $\mathbf{x}_i$ :

- if  $q(+1, \mathbf{x}_i) - \frac{1}{2} > \epsilon$  then  $\mathbf{x}_i$  is propagated to the right branch set and a weight  $w_i = 1$  is assigned.
- if  $q(-1, \mathbf{x}_i) - \frac{1}{2} > \epsilon$  then  $\mathbf{x}_i$  is propagated to the left branch set and a weight  $w_i = 1$  is assigned.
- else  $\mathbf{x}_i$  will be propagated in both branches with  $w_i = q(+1, \mathbf{x}_i)$  in the right branch and  $w_i = q(-1, \mathbf{x}_i)$  in the left branch.

with  $\mathbf{w} = w_i, i = \{1, \dots, N\}$  corresponding to distribution of weights,  $N$  the number of samples as in AdaBoost and  $q(\cdot)$  is defined such as:

$$q(+1, \mathbf{x}_i) = \frac{\exp(2H(\mathbf{x}_i))}{1 + \exp(2H(\mathbf{x}_i))} , \quad (65)$$

$$q(-1, \mathbf{x}_i) = \frac{\exp(-2H(\mathbf{x}_i))}{1 + \exp(-2H(\mathbf{x}_i))} . \quad (66)$$

Employing such a scheme tends to divide the data in such a way that positive and negative samples are naturally split as shown in Fig. 18.

In the classification stage, the sample  $\mathbf{x}$  is propagated through the trees, where at each node, it will be classified by the strong classifier previously learned and where an estimation of the posterior distribution will be computed. The posterior distribution will correspond to the sum of the posterior distribution at each node of the tree.

Tiwari et al. (2010, 2009b, 2012), Viswanath et al. (2011) make use of the probabilistic boosting-tree classifier.

#### – **Kernel method:**

A Gaussian process<sup>9</sup> for classification is a kernel method in which it is assumed that the data can be represented by a single sample from a multivariate Gaussian distribution (Rasmussen and Williams (2005)). In the case of linear logistic regression for classification, the posterior probability can be expressed as:

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<sup>9</sup>Gaussian process implementation can be found at: <http://www.gaussianprocess.org/gpml/code/matlab/doc/index.html>

$$\begin{aligned} p(y_i|\mathbf{x}_i, \mathbf{w}) &= \sigma(y_i f(\mathbf{x}_i)) , \\ f(\mathbf{x}_i) &= \mathbf{x}_i^T \mathbf{w} , \end{aligned} \quad (67)$$

where  $\sigma(\cdot)$  is the logistic function and  $\mathbf{w}$  are the parameters of the model.

Thus, the classification using Gaussian processes is based on affecting a Gaussian process prior over the function  $f(\mathbf{x})$  which will be characterized by a mean  $\bar{f}$  and covariance functions  $K$ . Thus, in the training stage, the best mean and covariance functions have to be inferred in regard to our training data using a Newton optimization and a Laplacian approximation.

The prediction stage can be performed in two stages. First, for a new observation  $\mathbf{x}_*$ , the corresponding probability  $p(f(\mathbf{x}_*)|f(\mathbf{x}))$  can be computed such that:

$$\begin{aligned} p(f(\mathbf{x}_*)|f(\mathbf{x})) &= \mathcal{N}(K_* K^{-1} \bar{f}, K_{**} - K_*(K')^{-1} K_*^T) , \\ K' &= K + W^{-1} , \\ W &= \nabla \nabla \log p(\mathbf{y}|f(\mathbf{x})) , \end{aligned} \quad (68)$$

where  $K_{**}$  is the variance of the testing sample  $\mathbf{x}_*$ ,  $K_*$  is the covariance of training-testing samples  $\mathbf{x}$  and  $\mathbf{x}_*$ .

Then, the function  $f(\mathbf{x}_*)$  is squashed using the sigmoid function and the probability of the class membership can be defined such that:

$$C(\mathbf{x}_*) = \sigma \left( \frac{\bar{f}(\mathbf{x}_*)}{\sqrt{1 + \text{var}(f(\mathbf{x}_*))}} \right) . \quad (69)$$

Only the work of Kelm et al. (2007) used Gaussian process for classification in order to distinguish CaP in MRSI data.

#### – *Sparse kernel methods:*

In Gaussian process, when a prediction has to be performed, the whole training data will be used to assign a label to the new observations. That is why, this method is also called kernel method. Sparse kernel category is composed of methods which rely only on few labelled observations in order to label new observations (Bishop (2006)).

Support vector machines (SVM)<sup>10</sup> is a sparse kernel method based on finding the best linear hyperplane (non-linear separation is discussed further) which

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<sup>10</sup>SVM implementation can be found at: <http://www.csie.ntu.edu.tw/~cjlin/libsvm/>



separates two classes such as the margin between the two classes is maximized (Vapnik and Lerner (1963)). The margin is in fact the region defined by two hyperplanes splitting the two classes, such that no points lie in between. The distance between these two hyperplanes is equal to  $\frac{2}{\|\mathbf{w}\|}$  where  $\mathbf{w}$  is the normal vector of the hyperplane splitting the classes. Thus, maximizing the margin is equivalent to minimizing  $\|\mathbf{w}\|$ . Hence, This problem is solved by an optimization approach and formalized such that:

$$\begin{aligned} \arg \min_{\mathbf{w}} \quad & \frac{1}{2} \|\mathbf{w}^2\|, \\ \text{subject to} \quad & y_i(\mathbf{w} \cdot \mathbf{x}_i - b) \geq 1, \quad i = \{1, \dots, N\}, \end{aligned} \quad (70)$$

where  $\mathbf{x}_i$  is a training sample with is corresponding class label  $y_i$ .

From Eq. (70), it is important to notice that only few points from the set of  $n$  points have to be selected which will later define the hyperplane. This can be introduced in the optimization problem using Lagrange multipliers  $\alpha$ . All points which are not lying on the margin will be assigned a corresponding  $\alpha_i = 0$ . This can be formalized as:

$$\arg \min_{\mathbf{w}, b} \max_{\alpha \geq 0} \left\{ \frac{1}{2} \|\mathbf{w}\|^2 - \sum_{i=1}^n \alpha_i [y_i(\mathbf{w} \cdot \mathbf{x}_i - b) - 1] \right\}. \quad (71)$$

The different parameters can be inferred using quadratic programming. This version of SVM is known as hard-margin since that no point can lie in the margin area. However, this is highly probable to not find any hyperplane splitting the classes such as specified previously. Thus, a soft-margin optimization approach was proposed (Cortes and Vapnik (1995)), where points can lie into the margin but at the cost of penalty which will be minimized in the optimization process such that:

$$\arg \min_{\mathbf{w}, \xi, b} \max_{\alpha, \beta} \left\{ \frac{1}{2} \|\mathbf{w}\|^2 + C \sum_{i=1}^n \xi_i - \sum_{i=1}^n \alpha_i [y_i(\mathbf{w} \cdot \mathbf{x}_i - b) - 1 + \xi_i] - \sum_{i=1}^n \beta_i \xi_i \right\}. \quad (72)$$

The decision to assign the label to a new observation  $\mathbf{x}_i$  is taken such that:

$$C(\mathbf{x}_i) = \text{sign} \left( \sum_{n=1}^N \alpha_n (\mathbf{x}_n \cdot \mathbf{x}_i) + b_0 \right), \quad (73)$$

where  $\mathbf{x}_n | n = \{1, \dots, S\}$ ,  $S$  being the support vectors.

SVM can also be used as a non-linear classifier by performing a kernel trick Boser et al. (1992). The original data  $\mathbf{x}$  can be projected in an high-dimensional space in which it is assumed that a linear hyperplane will split the classes. Different kernels are popular such as the RBF kernel, polynomial kernels or Gaussian kernel.

In prostate CAD system, SVM is the most popular classification method and was used in a multitude of research works: Artan et al. (2010, 2009), Chan et al. (2003), Kelm et al. (2007), Litjens et al. (2012b, 2011), Liu et al. (2013), Lopes et al. (2011), Niaf et al. (2012, 2011), Ozer et al. (2009, 2010), Parfait et al. (2012), Peng et al. (2013), Sung et al. (2011), Tiwari et al. (2012), Vos et al. (2012, 2008a, 2010, 2008b).

Relevant vector machine (RVM) is a sparse version of Gaussian process previously presented and was proposed by Tipping (2001). RVM is identical to a Gaussian process with following covariance function (Quinonero-Candela et al. (2002)):

$$K_{RVM}(\mathbf{x}_p, \mathbf{x}_q) = \sum_{j=1}^M \frac{1}{\alpha_j} \Phi_j(\mathbf{x}_p) \Phi_j(\mathbf{x}_q) , \quad (74)$$

where  $\phi(\cdot)$  is a Gaussian basis function,  $\mathbf{x}_i | i = \{1, \dots, N\}$  are the  $N$  training points and  $\boldsymbol{\alpha}$  are the weights.

As mentioned in Quinonero-Candela et al. (2002), the sparsity regarding the relevance vector arises if  $j\alpha_j^{-1} = 0$ . The set of parameters  $\boldsymbol{\alpha}$  is inferred using the expectation maximization algorithm. Ozer et al. (2009, 2010) make use of RVM and make a comparison with SVM for the task of CaP detection.

#### – **Neural network:**

Multilayer perceptron is a feed-forward neural network considered as well as the most successful model of this kind in pattern recognition (Bishop (2006)). The most well spread model used is based on a two layers model where a prediction of an observation is computed as:

$$C(\mathbf{x}_n, w_{ij}^{(1)}, w_{kj}^{(2)}) = \sigma \left[ \sum_{j=0}^M w_{kj}^{(2)} h \left( \sum_{i=0}^D w_{ij}^{(1)} x_{in} \right) \right] , \quad (75)$$

where  $h(\cdot)$  and  $\sigma(\cdot)$  are two activation functions usually non-linear,  $w_{ij}^{(1)}$  and  $w_{kj}^{(2)}$  are the weights associated with the linear combination with the input feature  $\mathbf{x}_n$  and the hidden unit, respectively.

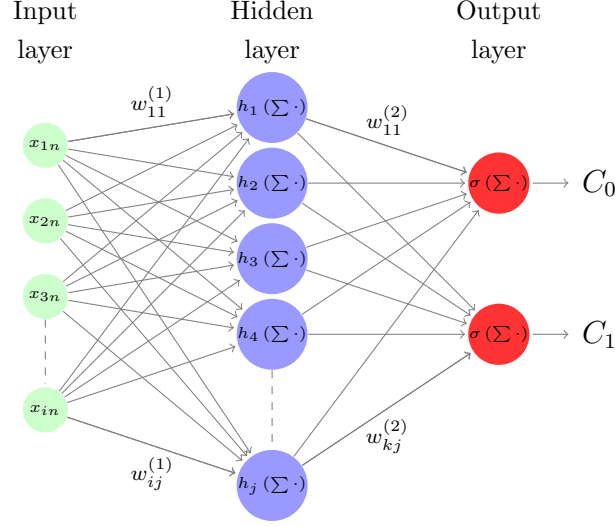


Figure 19: Representation of a neural network of the multilayer perceptron family.

A graphical representation of this network is presented in Fig. 19. Relating Fig. 19 with Eq. (75), it can be noted that this network is composed of some successive non-linear mapping of the input data. First, a linear combination of the input vector  $\mathbf{x}_i$  is performed into some hidden units through a set of weights  $w_{ij}^{(1)}$ . This combination becomes non-linear by the use of the activation function  $h(\cdot)$  which is usually chosen to be a sigmoid function. Then, a linear combination of these hidden units is performed into the output of the neural network through a set of weights  $w_{kj}^{(2)}$ . This combination is also mapped non-linearly using an activation function  $\sigma(\cdot)$  which is usually a logistic function.

Thus, the training of such a network resides in finding the best weights  $w_{ij}^{(1)}$  and  $w_{kj}^{(2)}$  which will model our data the best. The error of this model can be computed such that:

$$E(w_{ij}^{(1)}, w_{kj}^{(2)}) = \frac{1}{2} \sum_{n=1}^N \left( C(\mathbf{x}_n, w_{ij}^{(1)}, w_{kj}^{(2)}) - y(\mathbf{x}_n) \right)^2, \quad (76)$$

where  $\mathbf{x}_n | n = \{1, \dots, N\}$  are the  $N$  training vectors with their corresponding class label  $y(\mathbf{x}_n)$ .

Thus the best set of weights can be inferred in an optimization framework

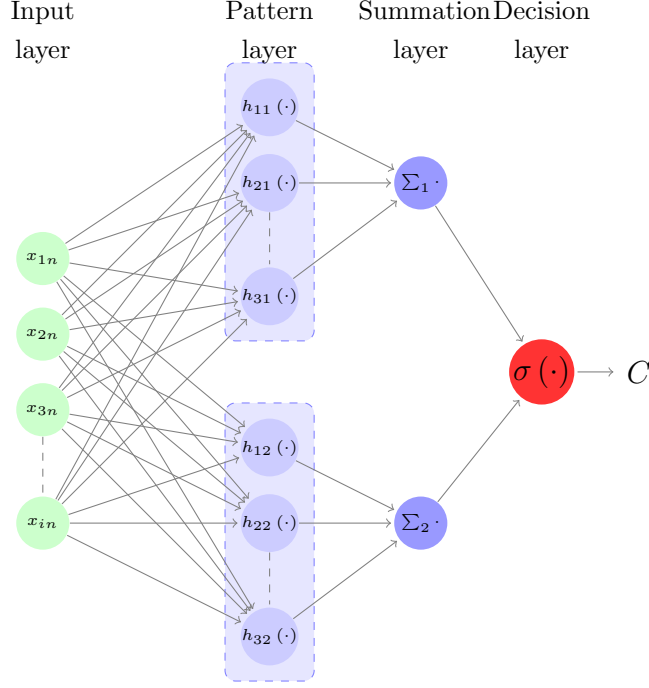


Figure 20: Representation of a neural network of the probabilistic neural network family.

such that:

$$\arg \min_{w_{ij}^{(1)}, w_{kj}^{(2)}} E(w_{ij}^{(1)}, w_{kj}^{(2)}) . \quad (77)$$

This optimization can be performed using a gradient descent method where the derivative of Eq. (76) can be computed using the backpropagation algorithm proposed by Rumelhart et al. (1988).

Matulewicz et al. (2013), Parfait et al. (2012) used this method to classify MRSI spectra.

Probabilistic neural networks are another type of feed-forward networks which can be derived from the multilayer perceptron case and was proposed by Specht (1988). This classifier can be modelled by changing the activation function  $h(\cdot)$  in Eq. (75) to an exponential function such that:

$$h(\mathbf{x}_n) = \exp \left( -\frac{(\mathbf{w}_j - \mathbf{x})^T (\mathbf{w}_j - \mathbf{x})}{2\sigma^2} \right) , \quad (78)$$

where  $\sigma$  is a free parameter.

1751 The other difference of the probabilistic neural network with the multilayer  
1752 perceptron resides in the architecture as shown in Fig. 20. This network is  
1753 formed by two hidden layers. The first hidden layer corresponds to the pattern  
1754 layer which is the mapping done using Eq. (78). This pattern layer is sub-divided  
1755 into groups corresponding to the class. The second hidden layer corresponds to the  
1756 summation layer which simply sums the output of each sub-group of the pattern  
1757 layer. This method was used by Ampeliotis et al. (2007, 2008), Viswanath et al.  
1758 (2011) in order to perform the classification of their feature vector.

1759 – **Graphical model classifiers:**

1760 Markov random fields can also be used as a lesion segmentation method to  
1761 detect CaP. First, we can define  $s$  as a pixel which will belong to a certain class  
1762 denoted by  $\omega_s$ . The labelling process can be noted as  $\omega = \{\omega_s, s \in I\}$  where  $I$  is  
1763 the set of all the pixels inside the image. The observations corresponding to SI  
1764 in the image are noted  $\mathcal{F} = \{f_s | s \in I\}$ . Thus, the image process  $\mathcal{F}$  represents  
1765 the deviation from the labelling process  $\omega$  (Kato and Pong (2001)). Hence, lesion  
1766 segmentation is equivalent to estimate to estimating the best  $\hat{\omega}$  which maximizes  
1767 the posterior probability  $p(\omega | \mathcal{F})$ . Thus, using a Bayesian approach, this can be  
1768 formulated such that:

$$p(\omega | \mathcal{F}) = \arg \max_{\omega} \prod_{s \in I} p(f_s | \omega_s) p(\omega) . \quad (79)$$

1769 It is generally assumed that  $p(f_s | \omega_s)$  follows a Gaussian distribution and that  
1770 the pixels classes  $\lambda = \{1, 2\}$  for a binary classification will be characterized by  
1771 their respective mean  $\mu_\lambda$  and standard deviation  $\sigma_\lambda$ . Then,  $\omega$  is supposed to be a  
1772 Markov random field thus:

$$p(\omega) = \frac{1}{Z} \exp(-U(\omega)) , \quad (80)$$

1773 where  $Z$  is a normalization factor to obtain a probability value,  $U(\cdot)$  is the energy  
1774 function.

1775 Thus the segmentation problem can be solved as an optimization problem  
1776 where the energy function  $U(\cdot)$  has to be minimized. There are different pos-  
1777 sibilities to define the energy function  $U(\cdot)$ . However, this is common to define  
1778 the energy function such that it combines two type of potential function: (i) a  
1779 local term relative to the pixel itself and (ii) a smoothing prior which embeds  
1780 neighbourhood information which will more or less penalizes the energy function  
1781 to obtain more or less homogeneous region. This optimization of such function

Table 13: Overview of the model validation techniques used in CAD systems.

Model validation techniques	References
LOOCV	[1-8,11,17-21,23,25,32,36,38-40]
$k$ -CV	[10,22,28-32,37,35,41]

can be performed with an algorithm such as iterated conditional modes (Kato and Pong (2001)).

Liu et al. (2009), Ozer et al. (2010) used Markov random fields as an unsupervised method to segment lesions in multi-parametric MRI images.

Artan et al. (2010, 2009) used conditional random fields instead of Markov random fields to segment their MRI images. The difference between these two methods reside in the fact that conditional probabilities are used such as:

$$p(\omega|\mathcal{F}) = \frac{1}{Z} \exp \left[ - \sum_{s \in I} V_{C1}(\omega_s|\mathcal{F}) - \sum_{\{s,r\} \in C} V_{C2}(\omega_s, \omega_r|\mathcal{F}) \right]. \quad (81)$$

$V_{C1}(\cdot)$  is the state (or partition) feature function and  $V_{C2}(\cdot)$  is the transition (or edge) feature function (Kato and Zerubia (2012)).

#### 4.4.2. Model validation

In pattern recognition, the use of model validation techniques to assess the performance of trained classifiers is quite important. Two techniques are broadly used in the development of CAD system and are summarized in Tab. 13.

The most popular technique used in CAD systems (see Tab. 13) is the leave-one-out cross-validation (LOOCV) technique. From the whole data, one patient is kept to validate and the other cases are used to train. This manipulation is repeated until each patient is used for validation. This technique is popular when working with medical data due to the restricted number of patients included in datasets. Thus, it allows to train on a fair number of patients even with a small dataset. However, this technique suffer from high variance and can considered as a non reliable estimate (Efron (1983)).

The other very well known technique used for assessing classifier is the  $k$ -fold cross-validation ( $k$ -CV) technique. This technique is based on splitting the dataset into  $k$  subsets where the samples are randomly selected. Then, one fold is kept for the validation and the remaining subsets for training. The classification is then repeated

Table 14: Overview of the evaluation metrics used in CAD systems.

Evaluation metrics	References
Accuracy	[4-5,12,25,31]
Sensitivity - Specificity	[4-5,7,12,14,17,20-23,25,27-28,33-34]
ROC - AUC	[2-3,6-9,13-19,23,29-32,35-40]
FROC	[10-11,41]
Dice's coefficient	[4-5,12,20]

as in the LOOCV technique. In our review, the typical values used for  $k$  were set to three and five. This technique is more appropriate than the previous one since that it does not suffer from large variance. However, the number of patients in the dataset needs to be large enough to apply such technique.

#### 4.4.3. Evaluation measure

Several metrics can be used in order to assess the performance of the classifier trained when tested on the test data. The techniques used for evaluation of the CAD system for CaP detection are summarized in Tab. 14.

Using the classification approach previously presented, each voxel in the MRI image will be classified into a class. Comparison with a ground-truth can give rise to a confusion matrix by counting true positive, true negative, false positive and false negative samples. From this analysis, different statistics can be extracted.

The first statistic used is the accuracy which computes the ratio of true detection over the number of samples. However, depending on the strategy employed in the CAD work-flow, this statistic can be highly biased by a high number of true negative samples which will boost the accuracy score and does not represent the actual performance of the classifier.

That is why, the most common statistic computed are sensitivity and specificity which are giving a full overview of the performance of the classifier trained. Sensitivity is also called the true positive rate and is equal to the ratio of the true positive samples over the true positive added with the false negative samples. Specificity is also named the true negative rate and is equal to the ratio of the true negative samples over the true negative added with the false positive samples.

These both statistics gave rise to the receiver operating characteristic (ROC)

analysis. This analysis represents graphically the sensitivity as a function of (1 - specificity), which is in fact the false positive rate, by varying the discriminative threshold of the classifier. By varying this threshold, more true negative samples will be found but at the cost to detect also more false negative. However, this fact is interesting in CAD since that it could be possible to obtain a high sensitivity and to ensure that no cancers were missed even if more false alarm will have to be investigated. A statistic derive from ROC analysis is the area under the curve (AUC) which corresponds to the area under the ROC and is a measure used to make comparison between models.

The previous method could have been classified on pixel-based evaluation method. However, a cancer can be also considered as a region. Free-response receiver operating characteristic (FROC) extends the ROC analysis but at region-based level. The same confusion matrix can be computed were the sample are not pixels any more but refer to a lesion. However, this is important to define what is a true positive sample in that case. Usually, a lesion is considered as a true positive sample if the region detected by the classifier and the one inside the ground-truth are overlapping “enough”. “Enough” is defined by each researcher and can correspond to one pixel only!!!

Finally, Dice’s coefficient is sometimes computed which is corresponding to the similarity of a lesion between the ground-truth and the output of the classifier. This coefficient corresponds to the ratio of twice the number of pixels in common over the sum of the pixels of the lesions in the ground-truth and the output of the classifier.

## 5. Discussion

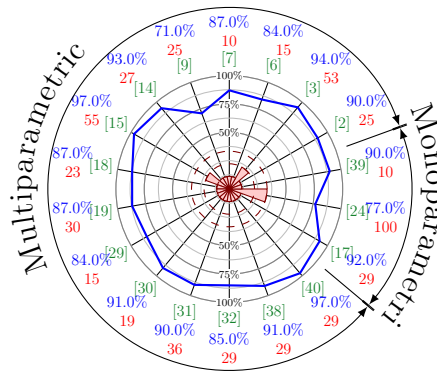
### 5.1. Brief comparison

As discussed previously in Sect. 4.4.3, different metrics have been used to report results. A comparison of the different methods reviewed is given depending on the metric used in each research and also the type of MRI scanner used (cf., 1.5 *versus* 3.0 Tesla). For each research, the experiment obtaining the best result was reported into these figures.

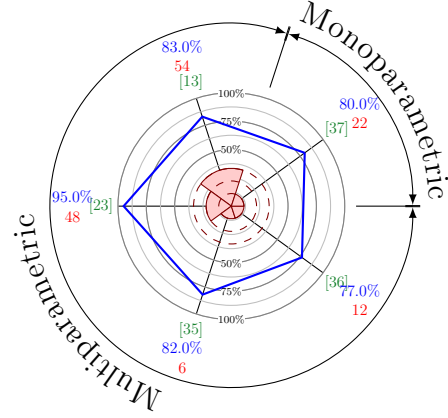
The results given in term of AUC-ROC are depicted in Fig. 21. The results vary between 77% and 95% for some experiments with a 1.5 MRI Tesla scanner and 77% and 95% with a 3.0 Tesla MRI scanner.

The results related with sensitivity and specificity are reported in Fig. 22. In the case that the data were collected with a 1.5 Tesla MRI scanner, the sensitivity is ranging from 74% and 100% and the specificity from 43% and 93%. For the experiments carried out with a 3.0 Tesla MRI scanner, the sensitivity is varying from 60% to 90% and the specificity from 66% to 99%.





(a) Comparison in term of AUC-ROC of the methods using data from 1.5 Tesla MRI scanner.



(b) Comparison in term of AUC-ROC of the methods using data from 3.0 Tesla MRI scanner.

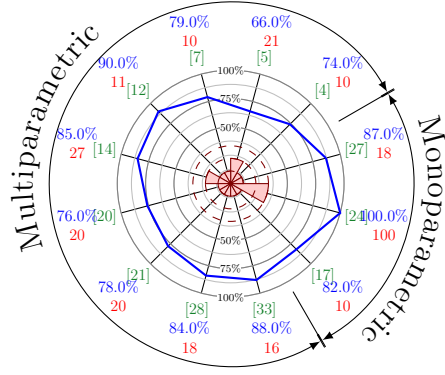
Figure 21: Comparison of the results in term of AUC for 1.5 and 3.0 Tesla MRI scanners. The blue value represents the metric and are graphically reported in the blue curve in the center of the figure. The red value and areas correspond to the number of patients in the dataset. The numbers between brackets in green correspond to the reference as reported in Tab. 2.

Three studies also use FROC analysis to report their results and are shown in Fig. 23. The results are ranging from 65% to 80%

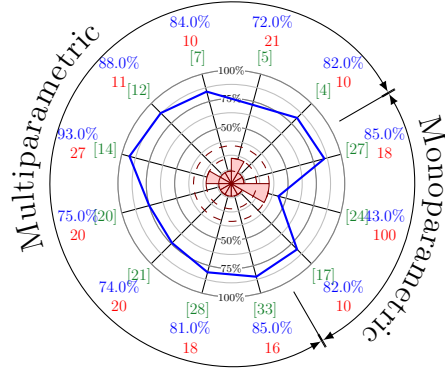
However, we would like to emphasize the fact that the results obtained from these different experiments cannot be fairly compared. Different datasets were used implying different complexity involved and set of input parameter during the data acquisition. To our mind, the only to provide a real and fair comparison would be to provide a common working dataset where those algorithms could be tested.

## 5.2. General discussion

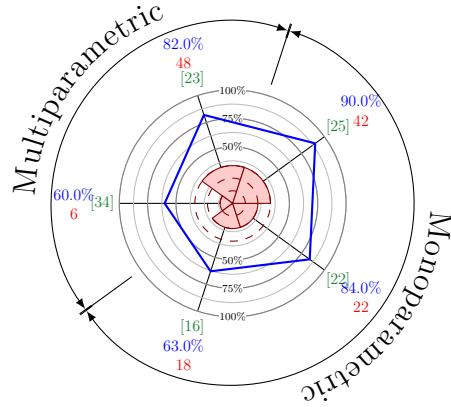
This review leads to some general discussions which could direct to future avenues for research. As previously mentioned, no open multi-parametric dataset is currently available. This fact leads to an impossibility to fairly compare the different algorithms designed over years. Also, the availability of a full multi-parametric dataset (cf., MRI and MRSI), could lead to the development of algorithms which use all the different modalities currently available. Recalling Tab. 2, it can be noted that none of the current works provide a solution using at the same time the four different modalities. We can also mention that all the algorithms are focused on one type of scanner only, either 1.5 Tesla and 3.0 Tesla. A dataset including both these types of imaging could allow to develop more generic algorithms.



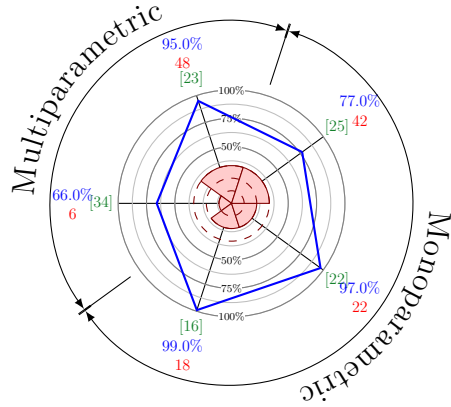
(a) Comparison in term of sensitivity of the methods using data from 1.5 Tesla MRI scanner.



(b) Comparison in term of specificity of the methods using data from 1.5 Tesla MRI scanner.



(c) Comparison in term of sensitivity of the methods using data from 3.0 Tesla MRI scanner.



(d) Comparison in term of specificity of the methods using data from 3.0 Tesla MRI scanner.

Figure 22: Comparison of the results in term of sensitivity (22(a),22(c)) and specificity (22(b),22(d)) 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. 2.

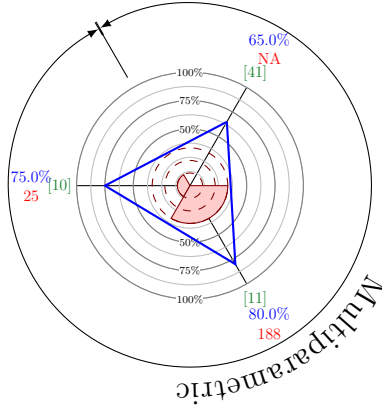


Figure 23: Comparison in term of FROC of the methods using data from 3.0 Tesla MRI scanner. The blue value represent the metric and are graphically reported in the blue curve in the center of the figure. The red value correspond to the number of patients in the dataset and is also reported in the center of the figure. The numbers between brackets correspond to the reference as reported in Tab. 2.

Then, by analysing the different stages of the CAD work-flow, it can be noticed that the actual CAD systems do not include all the different pre-processing steps. It could be interesting to evaluate the improvement using these pre-processing steps on the final results obtained after the classification. Regarding segmentation and registration of the prostate, CAD systems could highly benefit from specific research in these areas which could lead to a better automation of those system. Moreover, other methods specific to segmentation and registration which are not actually used in CAD systems could also perform better than the one currently used in CADs.

Regarding the classification framework, it seems that the current well-known pattern recognition methods have been widely studied. However, more investigations should be carried out regarding the feature detection stage. Lately, histogram-based features have shown good capabilities in the field of computer vision and could be further investigated. Only one study by Liu et al. (2013) used some of these features.

An important point allowing a fair comparison between methods resides in the fact that no universal evaluation model and metric has been defined by the research community allowing such comparison. Usually, it is quite common to choose an evaluation model which fits the dataset limitations, usually the size. Regarding the evaluation, the community would benefit from settling a standard metric which fairly represents the most performance of the algorithms designed.

Finally, we would like to focus the intention of the reader on the availability of a multi-parametric dataset from 1.5 and 3.0 Tesla MRI provided by the authors

1907 of this review. This dataset can be available at the following webpage address:  
1908 <http://visor.udg.edu/dataset>. The dataset is composed of the four modalities  
1909 discussed in this review with the corresponding ground-truth.

## 1910 6. Conclusion

1911 This review presented an overview and gave a staging of the research related  
1912 to CAD development for CaP using multi-parametric MRI and MRSI data. We  
1913 aimed at providing background information regarding multi-parametric MRI imaging  
1914 techniques. A work-flow describing the CAD stages were proposed. The methods  
1915 used in the literature for each of this stage were reviewed. The results of the available  
1916 CAD systems were briefly reviewed. Subsequently, an insight discussion were given  
1917 to conclude this survey.

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