

TWO NEW MODIFICATIONS OF THE INTERCRITERIA  
ANALYSIS

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**Abstract**

In the present work two modifications of the InterCriteria Analysis are proposed in order to extend its theoretical foundation. The results obtained from the application of these methods over real data (from patients with prostate carcinoma) have been analyzed to determine the reliability of the calculated consonance and dissonance.

The similarity scores obtained by the modified versions of the InterCriteria Analysis are close to those given by the classical InterCriteria Analysis, as well as to the values of the correlation coefficients between the considered criteria. This shows the reliability of the proposed modification with respect to determining the consonance and dissonance between criteria in different problems.

**Key words:** InterCriteria Analysis, prostate cancer, index matrix, intuitionistic fuzzy pairs, correlation

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**1. Introduction.** Solving real-world decision-making tasks in various fields of science and practice often necessitates the development and implementation of formal procedures using and combining mathematical, statistical and logical approaches and techniques. However, their implementation is made harder due to both the large number of criteria and the intrinsically complex formal decision-making frameworks [1]. The first step towards solving such problems is to reduce the number of criteria on the basis of which the decision is to be made. The recently developed *InterCriteria Analysis* (ICrA) has proven itself to be a reliable approach for solving the above problem in various scientific fields [2-4]. ICrA determines, on the basis of pairwise comparisons of the object/criteria the so-called degrees of consonance between the particular pairs of criteria, and ignores criteria that have sufficiently high degrees of consonance [5,6]. As a result the number of criteria is reduced.

The current work extends the theoretical framework of ICrA based on a modification, which permits the reduction of the degree of indeterminacy when assessing the consonance and dissonance between the criteria. The main objective that the authors have focused on is to determine, based on the obtained results, the likelihood of the evaluated consonance and dissonance. The reduction of the number of criteria as a result of the proposed method will be an object of further research.

The developed algorithm has been applied to real healthcare data, namely – on data of patients with prostate carcinoma. The data selection was guided by the following principles:

- The decision making in healthcare is a complex problem, since it frequently requires weighing compromises between many oftentimes conflicting goals. The utilization of structured approaches, including many criteria, is the key to improving the quality of the decisions made [7]. The importance of the problem is emphasized by the fact that in May 2014 Health Science Policy Council of The Professional Society for Health Economics and Outcomes Research (ISPOR) recommended to the Board of Directors to create a workgroup, which would look at the healthcare practices based on multiple criteria decision analysis (MCDA) and provide good practice guidelines for conducting MCDA.

- Prostate carcinoma is at second place for malignant neoplasms, affecting males and is ranked second as a cause of death after lung carcinoma in them [8]. At the current moment, there exists no standardized prognostic model for the calculation of the lifetime expectancy. The published retrospective analyses aim at the systematization of the factors with greatest contribution for the determination of 10-year-long survivability [9,10] in patients with prostate carcinoma. The research in this direction will serve a step in the development of prognostic model to objectify the decisions regarding potential concepts for curative definitive therapy in patients with prostate carcinoma, which could impact the treatments results and the quality of life.

**2. Materials and methods. 2.1. Theoretical background of the classical InterCriteria Analysis.** In order to simplify the exposition we will briefly remind some of the main components involved in the description and calculation of ICRA.

*Intuitionistic fuzzy pair* (IFP) is an object of the form  $\langle a, b \rangle$ , with  $a \geq 0, b \geq 0$  and  $a + b \leq 1$ .

Let  $I$  be a set of indices and  $L, K \subset I$ . Then the *index matrix* (IM) is an object of the form [6]

$$[K, L, \{a_{k_i, l_j}\}] \equiv \begin{array}{c|cccc} & l_1 & l_2 & \dots & l_n \\ \hline k_1 & a_{k_1, l_1} & a_{k_1, l_2} & \dots & a_{k_1, l_n} \\ k_2 & a_{k_2, l_1} & a_{k_2, l_2} & \dots & a_{k_2, l_n} \\ \dots & \dots & \dots & \dots & \dots \\ k_m & a_{k_m, l_1} & a_{k_m, l_2} & \dots & a_{k_m, l_n} \end{array},$$

where  $k_i \in K, l_j \in L$  and  $a_{k_i, l_j}$  is an object of some type (real numbers, logical variables, IFPs, etc.).

Let us have an IM with  $m$  row indices  $C_1, \dots, C_m$  and  $n$  column indices  $O_1, \dots, O_n$ :

$$M = \begin{array}{c|cccccc} & O_1 & \dots & O_k & \dots & O_l & \dots & O_n \\ \hline C_1 & a_{C_1, O_1} & \dots & a_{C_1, O_k} & \dots & a_{C_1, O_l} & \dots & a_{C_1, O_n} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots & \ddots & \vdots \\ C_i & a_{C_i, O_1} & \dots & a_{C_i, O_k} & \dots & a_{C_i, O_l} & \dots & a_{C_i, O_n} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots & \ddots & \vdots \\ C_j & a_{C_j, O_1} & \dots & a_{C_j, O_k} & \dots & a_{C_j, O_l} & \dots & a_{C_j, O_n} \\ \vdots & \vdots & \ddots & \vdots & \ddots & \vdots & \ddots & \vdots \\ C_m & a_{C_m, O_1} & \dots & a_{C_m, O_k} & \dots & a_{C_m, O_l} & \dots & a_{C_m, O_n} \end{array},$$

where:  $1 \leq i \leq j \leq m, 1 \leq k \leq l \leq n$ . Here,  $C_i$  denotes a criterion,  $O_k$  – an evaluated object (feature), and  $a_{C_i, O_k}$  is the value assigned to the  $k$ -th object by the  $i$ -th criterion.

The values of the criteria matrix are transformed into intuitionistic fuzzy pairs obtained on the basis of pairwise comparisons between each two rows over all evaluated objects. The type of relation between the respective elements (*greater than, equal, less than*) of each row are compared to the respective counterparts of the other rows.

As a result the input index matrix  $M$  generates another index matrix  $M^*$ , in which the relationships between the criteria are interpreted by intuitionistic fuzzy

pairs:

$$M^* = \begin{array}{c|ccc} & C_1 & \cdots & C_m \\ \hline C_1 & \langle \mu_{C_1, C_1}, \nu_{C_1, C_1} \rangle & \cdots & \langle \mu_{C_1, C_m}, \nu_{C_1, C_m} \rangle \\ \vdots & \vdots & \ddots & \vdots \\ C_m & \langle \mu_{C_m, C_1}, \nu_{C_m, C_1} \rangle & \cdots & \langle \mu_{C_m, C_m}, \nu_{C_m, C_m} \rangle \end{array}.$$

On the basis of this the degrees of “positive consonance”, “negative consonance” or “dissonance” are determined.

**2.2. Theoretical background of the modified version of the InterCriteria Analysis.** In these versions of ICrA each assigned object value is compared against the median of the values assigned by the criteria to this object. This comparison is used to estimate the similarity in behaviour between the criteria across all objects.

Further we provide a detailed description for both variants:

**Variant I. (Comparison to Median only).** For each pair of criteria  $(C_i, C_j)$  we compare the vectors with components  $a_{C_i, O_s} - Md_i$  and  $a_{C_j, O_s} - Md_j$  for  $1 \leq s \leq n$ . The number of places where they differ by sign is given by the Hamming distance, so the number of places where they coincide is given by the length of the vector reduced by this Hamming distance. After normalization, we obtain that the similarity in the assigned value by the criteria (with respect to the median value) is:

$$1 - \text{NormalizedHammingDistance}(V(a_{C_i, O_s} - Md_i), V(a_{C_j, O_s} - Md_j)).$$

This is the value assigned by the modified ICrA to  $\mu_{C_i, C_j}$  and may be viewed as level of agreement between the two criteria.

The places where the vectors  $V(a_{C_i, O_s} - Md_i)$  and  $V(a_{C_j, O_s} - Md_j)$  differ in sign (i.e. one is positive and the other negative, or vice versa), signify the opposite behaviour of the criteria  $C_i$  and  $C_j$ , and may be viewed as similar to negative correlation. The number of places once again normalized is assigned to  $\nu_{C_i, C_j}$ . The remaining value which complements the sum of  $\mu_{C_i, C_j}$  and  $\nu_{C_i, C_j}$  to 1 may be viewed as “unassignable” to either of the two values.

As an output of the modified ICrA we obtain an IM with values IFPs, which evaluate the degrees of agreement, opposition and uncertainty or indeterminacy. To interpret the results we use the concepts of positive consonance, negative consonance and dissonance.

**Variant II. (Pairwise comparison to the Median value).** For each pair of criteria  $(C_i, C_j)$  we construct the vectors of pairwise comparisons of  $a_{C_i, O_s}, a_{C_i, O_k}$  and  $Md_i$  versus  $a_{C_j, O_s}, a_{C_j, O_k}$  and  $Md_j$  for  $1 \leq s < k \leq n$ . For any comparison there are six possible cases:

- 1)  $Md_i \in (\min(a_{C_i, O_s}, a_{C_i, O_k}), \max(a_{C_i, O_s}, a_{C_i, O_k}))$
- 2)  $Md_i < \min(a_{C_i, O_s}, a_{C_i, O_k})$
- 3)  $Md_i > \max(a_{C_i, O_s}, a_{C_i, O_k})$

$$4) Md_i = \max(a_{C_i, O_s}, a_{C_i, O_k}) = \min(a_{C_i, O_s}, a_{C_i, O_k})$$

$$5) Md_i = \max(a_{C_i, O_s}, a_{C_i, O_k}) > \min(a_{C_i, O_s}, a_{C_i, O_k})$$

$$6) Md_i = \min(a_{C_i, O_s}, a_{C_i, O_k}) < \max(a_{C_i, O_s}, a_{C_i, O_k})$$

The places where the vectors  $V(a_{C_i, O_s}, a_{C_i, O_k}, Md_i)$  and  $V(a_{C_j, O_s}, a_{C_j, O_k}, Md_j)$  are the same in value can again be calculated as

$$1 - \text{NormalizedHammingDistance}(V(a_{C_i, O_s}, a_{C_i, O_k}, Md_i), V(a_{C_j, O_s}, a_{C_j, O_k}, Md_j)).$$

This is the value assigned by the modified ICRA to  $\mu_{C_i, C_j}$  and may be viewed as level of agreement between the two criteria.

We have considered the following to be bearers of the opposite behaviour of the criteria  $C_i$  and  $C_j$  in the respective  $V$  vectors:

**2) vs. 3) or 3) vs. 2)**

**1) vs. 2) or 2) vs. 1)**

**1) vs. 3) or 3) vs. 1)**

By counting their number and normalizing we obtain an evaluation of the opposite behaviour exhibited by the two criteria, which is denoted by  $\nu_{C_i, C_j}$ .

As an output of this modified ICRA variant we obtain an IM with values IFPs, which represent degrees of agreement, opposition and indeterminacy. To interpret the results we use the concepts of positive consonance, negative consonance and dissonance.

Two of the ICRA modifications, whose algorithms were described in the text prior, were implemented when analyzing the data of 277 patients with histologically verified prostate cancer. The patients were diagnosed at the Clinic of Urology and Andrology at the University Hospital "Queen Joanna – ISUL", Sofia, Bulgaria. The mean age of the patients was  $70.00 \pm 7.88$  years. The analyzed parameters included:

- Prostate-Specific Antigen (PSA).
- Digital rectal examination (DRE).
- *Prostate Cancer Risk Calculator* developed by the European Randomized Study of Screening for Prostate Cancer (ERSPC).
- Family history.
- Presence or absence of Lower Urinary Tract Symptoms or **LUTS**.
- Assessment of prostate cancer grade according to the Gleason scale – based on the architecture of the prostate glands and their relationship to the surrounding fibromuscular stroma. Two grades are assigned based on the two most commonly found patterns. The Gleason score itself is a summation of the two. If only one pattern is found, then it is doubled. This system is used in assessing the histological material from tru-cut prostate biopsy, transurethral resection of the prostate, laser enucleation of the prostate, open adenectomy, and radical prostatectomy.
- Tertiary grade of Gleason 5. Even a small component of Gleason pattern 5 is considered an independent bad prognostic factor.

- Clinical staging of prostate cancer is based on the TNM classification from 2009 and is based on the value of PSA, DRE, Transrectal ultrasound, CT scan, and MRI scan. Assessing the primary tumour “T” stage is as follows:

- TX: tumour cannot be assessed.
- T0: no evidence of tumour.
- T1: the tumour is too insignificant to be detected on a scan, or felt during examination of the prostate.
  - T1a: that tumour is in less than 5% of the examined tissue, resected during an unrelated operation (usually transurethral resection of benign prostate hyperplasia).
  - T1b: the tumour is an accidental find, but more than 5% of the resected tissue is involved.
  - T1c: the tumour is detected after a prostate biopsy, usually prompted after elevated PSA levels are found.
- T2: the tumour is detected during DRE, but confined in the prostate gland.
  - T2a: tumour involves less than one half of one lobe of the gland.
  - T2b: tumour involves more than one half of one gland, while the contralateral lobe remains uninvolved.
  - T2c: the tumour is found in both lobes.
- T3: tumour extends through the prostate capsule.
  - T3a: extracapsular tissue is involved.
  - T3b: tumour extends to the seminal vesicles.
- T4: tumour extends to other nearby organs – bladder, rectum, or the pelvic wall.

- The number of biopsy cores – the 12-core Gore protocol was used, which incorporates the 6-core Stamey protocol plus 6 cores from the lateral parts of the gland. Usually, the medial row of biopsy cores is represented by only 2 cores – base and apex (modified 10-core biopsy protocol). Any lesions suspected on DRE, Transrectal ultrasound, or MRI are also sampled. The number of cores can be modified depending on prostate size. If a cancer diagnosis is highly suspected – PSA over 50, highly suspected DRE, or when the patient has considerable comorbidities a 6 to 8 core biopsy is considered sufficient.

- The percentage of positive cores is an indirect and reliable assessment of the extent of prostate involvement. The percentage of positive cores has a strong, statistically significant, correlation with the levels of PSA.

- The percentage of involvement of each core – the percentage of involvement of each core by the neoplastic process gives indirect information about the size of the largest leading focus of adenocarcinoma.

- Presence of perineural invasion – the presence of perineural invasion is considered one of the prognostic markers for biological aggressiveness of the neoplastic processes. The presence of perineural invasion shows a significant correlation with

the pT stage and can be used as a prognostic sign for the tendency to local spread of cancer.

- D'Amico risk group (DRG) assessment – based on preoperative PSA, T-stage, and Gleason assessment after prostate biopsy, it divides patients into three risk groups according to the likelihood of disease progression:

- low-risk (PSA <10 ng/ml and cT1-cT2a and biopsy GS  $\leq$ 6);
- intermediate-risk (PSA 10–20 ng/ml or cT2b or bGS 7);
- high-risk (PSA >20 ng/ml or clinical stage  $\geq$  cT2c or GS  $\geq$ 8).

- Risk of extraprostatic spread – this is another major variable in the Partin tables, which gives the possibility of micro- or macroscopic extraprostatic spread through the gland capsule. This indicator is directly related to the frequency of positive resection lines.

Categorical variables are results of the digital rectal examination, family history, presence or absence of lower urinary tract symptoms, Ca, presence of Gleason 5 pattern, presence of perineural invasion, and risk of extraprostatic spread. Due to their representation in binary form, these were dropped from the scope of the present study, although they affect the values of the calculated criteria.

**3. Results and discussion.** The data were processed with the following procedures:

- Modified ICrA – Variant I (Table 1);
- Modified ICrA – Variant II (Table 2);
- ICrA (standard) (Table 3);
- Pearson correlation (Table 4).

Comparing the results, we can conclude that the four methods have very similar results. The results of these 4 methods find closeness between the same criteria/features and are almost analogous to the values by which the closeness is evaluated (respectively, similarity and correlation).

Prostate-specific antigen (PSA) is a widely used tumour marker for prostate cancer [11] although it is well known that PSA is organ-specific, and not a disease-specific biomarker. Both benign and malignant lesions of the prostate can cause an increase in serum PSA levels, but the chances of finding malignancy increase with rising values of PSA.

Since the ESRPC risk calculator incorporates age and PSA in its assessment, these factors are inherently linked to its value. In our investigation this relationship is categorically confirmed by the results of the two modified ICrA methods, while the original and the correlation analysis support it with significantly lower values.

The usefulness of PSA testing has been shown for early diagnosis, assessing the response of treatment, and determining tumour progression [12]. A strong correlation was found between the PSA level and tumour aggressiveness. Prostate cancer with Gleason score >7 is seen as more aggressive, i.e., more likely to grow faster and metastasize [13]. Prostate biopsy gives us the opportunity to assess not

Table 1

Results obtained from the implementation of modified ICrA – Variant I

MU	age	PSA	ERSPC	Gleason	“T” stage	% positive	% involvement	DRG
age	⟨1.00, 0.00⟩	⟨0.52, 0.42⟩	⟨0.51, 0.42⟩	⟨0.36, 0.31⟩	⟨0.37, 0.37⟩	⟨0.45, 0.49⟩	⟨0.35, 0.27⟩	⟨0.21, 0.14⟩
PSA	⟨0.52, 0.42⟩	⟨1.00, 0.00⟩	⟨0.99, 0.00⟩	⟨0.53, 0.19⟩	⟨0.54, 0.20⟩	⟨0.70, 0.30⟩	⟨0.45, 0.18⟩	⟨0.31, 0.00⟩
ERSPC	⟨0.51, 0.42⟩	⟨0.99, 0.00⟩	⟨1.00, 0.00⟩	⟨0.53, 0.19⟩	⟨0.54, 0.19⟩	⟨0.69, 0.30⟩	⟨0.45, 0.17⟩	⟨0.32, 0.00⟩
Gleason	⟨0.36, 0.31⟩	⟨0.53, 0.19⟩	⟨0.53, 0.19⟩	⟨1.00, 0.00⟩	⟨0.54, 0.10⟩	⟨0.59, 0.13⟩	⟨0.54, 0.09⟩	⟨0.39, 0.00⟩
“T” stage	⟨0.37, 0.37⟩	⟨0.54, 0.20⟩	⟨0.54, 0.19⟩	⟨0.54, 0.10⟩	⟨1.00, 0.00⟩	⟨0.66, 0.08⟩	⟨0.55, 0.04⟩	⟨0.50, 0.00⟩
% positive	⟨0.45, 0.49⟩	⟨0.70, 0.30⟩	⟨0.69, 0.30⟩	⟨0.59, 0.13⟩	⟨0.66, 0.08⟩	⟨1.00, 0.00⟩	⟨0.53, 0.09⟩	⟨0.26, 0.05⟩
% involvement	⟨0.35, 0.27⟩	⟨0.45, 0.18⟩	⟨0.45, 0.17⟩	⟨0.54, 0.09⟩	⟨0.55, 0.04⟩	⟨0.53, 0.09⟩	⟨1.00, 0.00⟩	⟨0.58, 0.01⟩
DRG	⟨0.21, 0.14⟩	⟨0.31, 0.00⟩	⟨0.32, 0.00⟩	⟨0.39, 0.00⟩	⟨0.50, 0.00⟩	⟨0.26, 0.05⟩	⟨0.58, 0.01⟩	⟨1.00, 0.00⟩

Table 2

Results obtained from the implementation of modified ICrA – Variant II

MU	age	PSA	ERSPC	Gleason	“T” stage	% positive	% involvement	DRG
age	⟨1.00, 0.00⟩	⟨0.36, 0.52⟩	⟨0.35, 0.52⟩	⟨0.19, 0.27⟩	⟨0.20, 0.33⟩	⟨0.32, 0.56⟩	⟨0.16, 0.22⟩	⟨0.05, 0.06⟩
PSA	⟨0.36, 0.52⟩	⟨1.00, 0.00⟩	⟨0.97, 0.01⟩	⟨0.30, 0.22⟩	⟨0.31, 0.24⟩	⟨0.53, 0.47⟩	⟨0.21, 0.18⟩	⟨0.10, 0.00⟩
ERSPC	⟨0.35, 0.52⟩	⟨0.97, 0.01⟩	⟨1.00, 0.00⟩	⟨0.30, 0.22⟩	⟨0.31, 0.23⟩	⟨0.52, 0.46⟩	⟨0.22, 0.17⟩	⟨0.10, 0.00⟩
Gleason	⟨0.19, 0.27⟩	⟨0.30, 0.22⟩	⟨0.30, 0.22⟩	⟨1.00, 0.00⟩	⟨0.32, 0.10⟩	⟨0.36, 0.16⟩	⟨0.31, 0.08⟩	⟨0.17, 0.00⟩
“T” stage	⟨0.20, 0.33⟩	⟨0.31, 0.24⟩	⟨0.31, 0.23⟩	⟨0.32, 0.10⟩	⟨1.00, 0.00⟩	⟨0.44, 0.11⟩	⟨0.34, 0.04⟩	⟨0.27, 0.00⟩
% positive	⟨0.32, 0.56⟩	⟨0.53, 0.47⟩	⟨0.52, 0.46⟩	⟨0.36, 0.16⟩	⟨0.44, 0.11⟩	⟨1.00, 0.00⟩	⟨0.28, 0.10⟩	⟨0.07, 0.03⟩
% involvement	⟨0.16, 0.22⟩	⟨0.21, 0.18⟩	⟨0.22, 0.17⟩	⟨0.31, 0.08⟩	⟨0.34, 0.04⟩	⟨0.28, 0.10⟩	⟨1.00, 0.00⟩	⟨0.36, 0.01⟩
DRG	⟨0.05, 0.06⟩	⟨0.10, 0.00⟩	⟨0.10, 0.00⟩	⟨0.17, 0.00⟩	⟨0.27, 0.00⟩	⟨0.07, 0.03⟩	⟨0.36, 0.01⟩	⟨1.00, 0.00⟩



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Results obtained from the ICrA (standard)

MU	age	PSA	ERSPC	Gleason	“T” stage	% positive	% involvement	DRG
age	1.00, 0.00	⟨0.50, 0.43⟩	⟨0.46, 0.39⟩	⟨0.42, 0.36⟩	⟨0.38, 0.40⟩	⟨0.33, 0.32⟩	⟨0.37, 0.33⟩	⟨0.25, 0.23⟩
PSA	⟨0.50, 0.43⟩	1.00, 0.00	⟨0.89, 0.01⟩	⟨0.56, 0.23⟩	⟨0.57, 0.22⟩	⟨0.50, 0.16⟩	⟨0.51, 0.20⟩	⟨0.46, 0.04⟩
ERSPC	⟨0.46, 0.39⟩	⟨0.89, 0.01⟩	1.00, 0.00	⟨0.54, 0.21⟩	⟨0.56, 0.19⟩	⟨0.53, 0.15⟩	⟨0.51, 0.17⟩	⟨0.55, 0.04⟩
Gleason	⟨0.42, 0.36⟩	⟨0.56, 0.23⟩	⟨0.54, 0.21⟩	1.00, 0.00	⟨0.57, 0.14⟩	⟨0.56, 0.08⟩	⟨0.58, 0.10⟩	⟨0.53, 0.03⟩
“T” stage	⟨0.38, 0.40⟩	⟨0.57, 0.22⟩	⟨0.56, 0.19⟩	⟨0.57, 0.14⟩	1.00, 0.00	⟨0.66, 0.07⟩	⟨0.55, 0.11⟩	⟨0.50, 0.04⟩
% positive	⟨0.33, 0.32⟩	⟨0.50, 0.16⟩	⟨0.53, 0.15⟩	⟨0.56, 0.08⟩	⟨0.66, 0.07⟩	1.00, 0.00	⟨0.60, 0.04⟩	⟨0.58, 0.04⟩
% involvement	⟨0.37, 0.33⟩	⟨0.51, 0.20⟩	⟨0.51, 0.17⟩	⟨0.58, 0.10⟩	⟨0.55, 0.11⟩	⟨0.60, 0.04⟩	1.00, 0.00	⟨0.52, 0.04⟩
DRG	⟨0.25, 0.23⟩	⟨0.46, 0.04⟩	⟨0.55, 0.04⟩	⟨0.53, 0.03⟩	⟨0.50, 0.04⟩	⟨0.58, 0.04⟩	⟨0.52, 0.04⟩	1.00, 0.00

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Results obtained from the Pearson correlation

correlation	age	PSA	ERSPC	Gleason	“T” stage	% positive	% involvement	DRG
age	1.00	0.11	0.11	0.05	-0.03	0.00	0.04	0.01
PSA	0.11	1.00	0.80	0.42	0.48	0.47	0.44	0.54
ERSPC	0.11	0.80	1.00	0.47	0.55	0.52	0.45	0.74
Gleason	0.05	0.42	0.47	1.00	0.56	0.64	0.62	0.65
“T” stage	-0.03	0.48	0.55	0.56	1.00	0.72	0.57	0.59
% positive	0.00	0.47	0.52	0.64	0.72	1.00	0.69	0.61
% involvement	0.04	0.44	0.45	0.62	0.57	0.69	1.00	0.57
DRG	0.01	0.54	0.74	0.65	0.59	0.61	0.57	1.00

only the histological variant of cancer but also the extent of the gland involved – whether the process involves both lobes, for instance. In our investigation this relationship, although detected – the higher the PSA value the higher the likelihood of an advanced process, is not strong.

D’Amico Risk Classification for Prostate Cancer is developed to assess the 5-year risk of treatment failure based on clinical factors. Developed in 1998, it estimates the risk of prostate cancer recurrence (low, medium, or high) from PSA level, Gleason Score, and tumour stage. Ergo those factors are inherently linked to their value [14]. The two modifications of ICrA show weak consonance between D’Amico classification, PSA level and the Gleason score, while the original ICrA and the correlation analysis register moderate correlation/consonance.

Biopsy Gleason score has been shown to be less accurate than that obtained post radical prostatectomy. A concordance between the two has been described in about 55% of the cases, an under-staging of 34% and an over-staging of 11%. A well-differentiated tumour on prostate biopsy is a weak predictor of organ-confined disease. On the other hand, cancers with a high Gleason score on prostate biopsy are associated with extra-prostatic disease and with a poorly differentiated tumour as seen after radical prostatectomy [15].

Our results confirm the findings of BISMAR et al. [16] who discovered that the total percentage of cancer in biopsy cores was significantly related to the pathological T stage on multivariate analysis. The number of positive biopsy cores as an independent predictor of the risk of non-organ confined disease has also been reported [17]. Our investigation also proves that the greater the percentage of the gland involved in the tumour process, the greater the probability of the progression of the pathology.

**4. Conclusion.** The results of the four methods – the two proposed modifications of the ICrA, and the well-established classical ICrA, and the widely used correlation analysis, applied with the aim of finding the relationship between the considered criteria and its magnitude, are similar. The findings of these methods suggest closeness between one and the same criteria/features and the scores that evaluate the closeness (respectively, the consonance and the correlation) obtained by the methods are quite similar. This good agreement shows that the newly proposed methods are not only an appropriate extension of the theoretical background of the InterCriteria Analysis but they are a promising new tool for discovering potential relationships between criteria/features, which other methods may not indicate. Depending on the particular problem being considered these modifications may be used in combination with other methods to augment their ability to highlight potential relationships which, of course, would then have to be independently confirmed or rejected by other means.

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