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LINGUISTIC CHARACTERISATIONS OF INFLAMMATORY SYNDROMES AND FUZZY MATCHING MEASURES.

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ABSTRACT

It is proposed a linguistic model of inflammatory syndroms-proteins relationships, an important and complex problem frequently encountered in Internal Medicine. The linguistic pattern has been translated into a fuzzy sets pattern expressing relative variations of serum protein levels. Four indexes or measures (possibility measure, necessity measure, neartude grade and "truth-possibility" index) have been used for patient-pattern matching purposes. Finally from separation powers yielding non fuzzy partitions, patients are assigned diagnoses corresponding to their condition.

I - INTRODUCTION

In internal medicine, many diseases are associated with an inflammatory syndrom. Given an inflammatory syndrom (I.S.) observed on a patient, it is difficult to assign a right diagnosis, based on specific protein variations. The main reason is that some I.S. are "typical" but, unfortunately most of the I.S. are "non typical". In a typical I.S., proteins are all increased in similar proportions and in the same way, as it is the case for severe infections and septicemias. In a non typical I.S. like vasculitis and collagen diseases, protein variations are dissociated, for example two or three protein levels are increased while some others are normal or decreased.

II - MEDICAL KNOWLEDGE : PATTERN OF INFLAMMATORY SYNDROMS

We have characterized seric levels (determined by nephelometric methods) of the five most important proteins involved in biological inflammatory reactions. The five proteins are : C3 (C3-Complement Fraction), A1 AT (alpha-1-AntiTrypsine), Orosomucoid, Haptoglobin, C.R.P. (C-Reactive Protein). Our protein-I.S. pattern contains eight groups : six inflammatory syndroms (Infection, Vasculitis, Nephrosis, Intravascular Hemolysis with inflammation, Collagen diseases neither Lupus nor infection, and Lupus), Normal condition and Intravascular Hemolysis without Inflammation.

In the protein-I.S. model, uncertainty is not of probabilistic nature, as pointed out in [6]. What really matters is relative variations of serum level proteins. Moreover, thresholds cannot be defined with precision to allow a classification of patients in the pattern of I.S. Finally, these variations are easily interpreted in linguistic terms by internists, so that the protein-I.S. pattern is very appropriated to a fuzzy sets representation.

For example, Lupus is characterised by :

The C3-Complement Fraction is DECREASED
AND
The A1-Antitrypsine is SLIGHTLY INCREASED OR INCREASED
AND
The Orosomucoid is SLIGHTLY INCREASED OR INCREASED
AND
The Haptoglobin is NORMAL or SLIGHTLY DECREASED
AND
The C-Reactive Protein is NORMAL

Linguistic descriptions have been established for the eight groups (Normal condition, six I.S. and Hemolysis without Inflammation), they are reported in Table 1. This linguistic pattern expresses the relative protein variations among the I.S. . It applies to young adults and does not depend on Age and Sex as shown by previous studies.

III - FUZZY SET INTERPRETATIONS

The linguistic information conveyed by the pattern is treated by conjunctions of fuzzy propositions of the form :

X is F,

where the variable X represents one of the five proteins and F is a fuzzy subset of the universe of discourse of the corresponding

protein. For example, in the description of Lupus, we have :

Orosomuroid (X) is SLIGHTLY-INCREASED-OR-INCREASED (F)

The fuzzy set F which expresses a relative variation compared to the Normal condition (basic levels) is depicted in Figure 1.

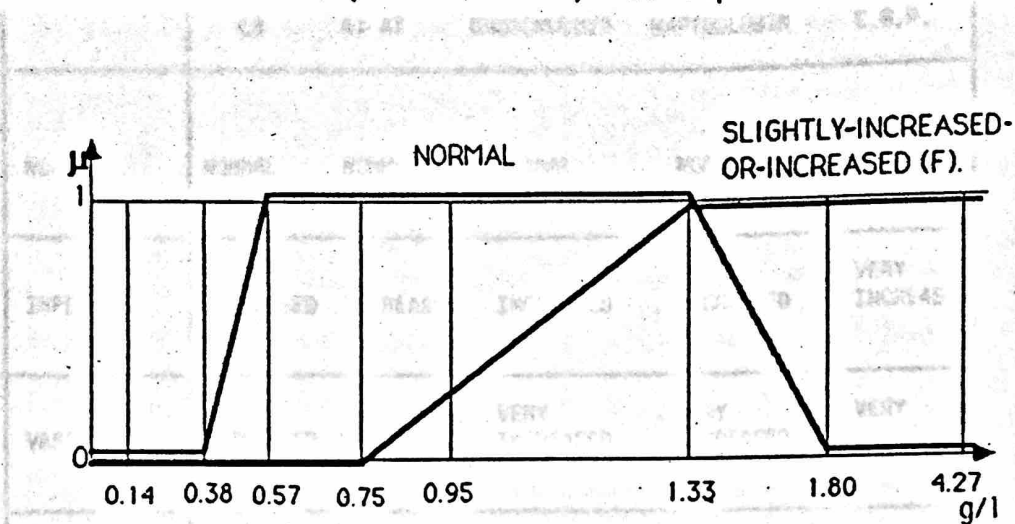


Fig.1 : Illustration of : "Orosomuroid is slightly increased or increased".

In order to compare different protein variations in various syndroms, it is customary to represent these variations in a relative scale. For example, NORMAL Orosomuroid is centered on value "0.95 g/l" (mean value evaluated from a reference population of normal subjects), which is now assigned reference value "1" (normalized value). Hence, 1.33 g/l will be assigned value 1.40 (i.e. $1.33/0.95$), etc. So that the two fuzzy sets of the example are now expressed according to their new relative variations (see Figure 2).

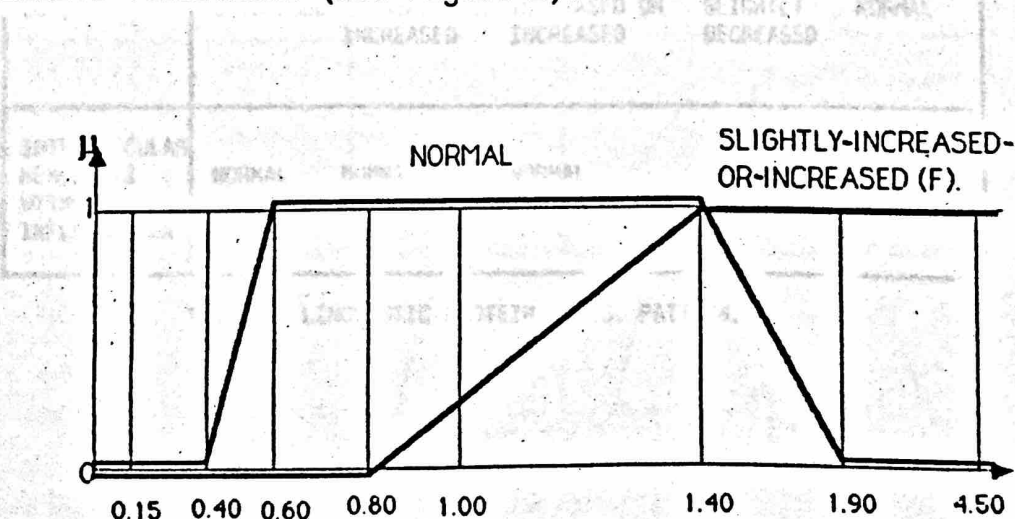


Fig.2 : Normalized values issued from Fig.1.

GROUPS	PROTEINS				
	C3	A1 AT	OROSOMUCOID	HAPTOGLOBIN	C.R.P.
NORMAL	NORMAL	NORMAL	NORMAL	NORMAL	NORMAL
INFECTION	INCREASED	INCREASED	INCREASED	INCREASED	VERY INCREASED
VASCULITIS	DECREASED	DECREASED	VERY INCREASED	VERY INCREASED	VERY INCREASED
NEPHROSIS	NORMAL OR DECREASED	NORMAL	NORMAL OR DECREASED	SLIGHTLY INCREASED OR INCREASED	SLIGHTLY INCREASED
INTRAVASCULAR HEMOLYSIS WITH INFECTION	NORMAL OR DECREASED	INCREASED	INCREASED	NORMAL OR VERY DECREASED	VERY INCREASED
COLLAGEN DISEASES WITHOUT LUPUS WITHOUT INFECTION	DECREASED	SLIGHTLY INCREASED OR INCREASED	SLIGHTLY INCREASED OR INCREASED	NORMAL OR SLIGHTLY DECREASED OR INCREASED	SLIGHTLY INCREASED OR INCREASED
LUPUS	DECREASED	SLIGHTLY INCREASED OR INCREASED	SLIGHTLY INCREASED OR INCREASED	NORMAL OR SLIGHTLY DECREASED	NORMAL
INTRAVASCULAR HEMOLYSIS WITHOUT INFLAMMATION	NORMAL	NORMAL	NORMAL	DECREASED	NORMAL

TABLE 1. LINGUISTIC PROTEIN - I.S. PATTERN.

With values normalized to "1", the fuzzy sets corresponding to our 11 protein patterns (Table 1) are represented in Table 2.

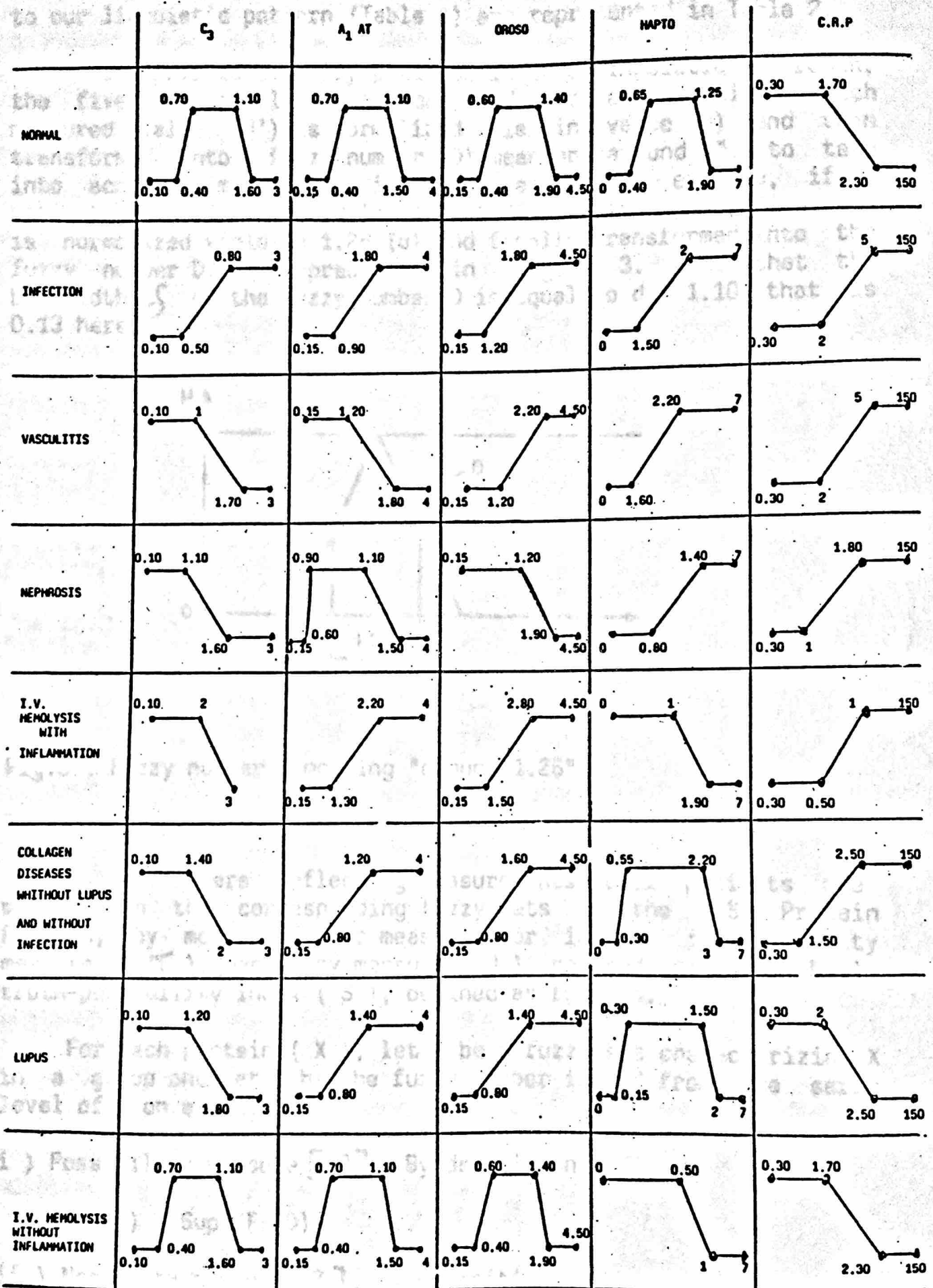


Table 2. FUZZY SETS TRANSLATION OF THE LINGUISTIC PROTEIN-IS PATTERN

where F' denotes the fuzzy complement of F ($F' = 1 - F$).

With values normalized to "1", the fuzzy sets corresponding to our linguistic pattern (Table 1) are represented in Table 2.

In order to classify patients in this linguistic approach, the five protein levels are measured over each patient. Each measured value (d') is normalized (yielding value d) and then transformed into a fuzzy number (D) meaning "around d ", to take into account imprecision in measurements. For example, if a patient has an Orosomucoid level of 1.20 g/l, this value (i.e. d') is normalized yielding 1.26 (d) and finally transformed into the fuzzy number D , as represented in Figure 3. Note that the bandwidth δ of the fuzzy number D is equal to $d \times 1.10$, that is 0.13 here.

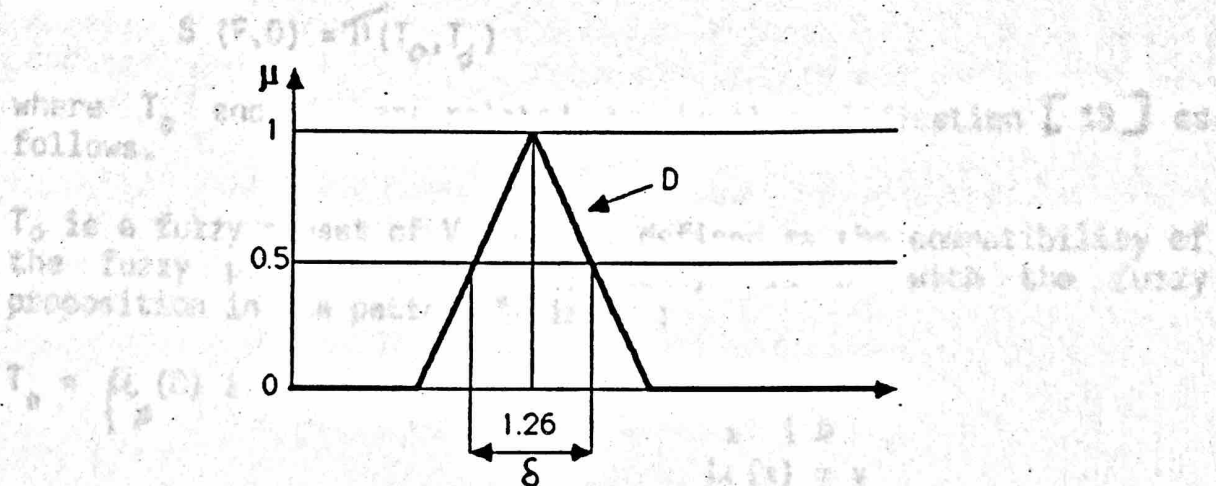


Fig.3 : Fuzzy number D meaning "around 1.26".

IV - MATCHING

Fuzzy numbers reflecting measurements over patients are matched to the corresponding fuzzy sets in the I.S.- Protein Pattern, by means of four measures or indexes : possibility measure (π), necessity measure (ν), nearitude grade (N), truth-possibility index (S), defined as follows.

For each protein (X), let F be a fuzzy set characterizing X in a group and let D be the fuzzy number issued from the seric level of X on a patient,

i) Possibility measure [13]. By definition,

$$\pi(F, D) = \sup (F \cap D)$$

ii) Necessity measure [3]. By definition,

$$\nu(F, D) = 1 - \pi(F', D)$$

where F' denotes the fuzzy complement of F ($F' = 1 - F$).

Note that

$$\nu(F,D) = 1 - \text{Sup} (F' \cap D) = \text{Inf} (F \cup D').$$

iii) Neartude grade [8] . By definition,

$$N(F,D) = \frac{1}{2} (\pi(F,D) + \pi(F',D')).$$

Note that

$$N(F,D) = \frac{1}{2} (\pi(F,D) + 1 - \nu(F,D')),$$

and that with the particular fuzzy sets in this study,
 $\pi(F',D') = 1$ so that, here, $N(F,D) = \frac{1}{2} \pi(F,D) + 0.5$

iv) Truth-possibility index [9,10] . By definition,

$$S(F,D) = \pi(T_0, T_1)$$

where T_0 and T_1 are related to truth-qualification [13] as follows.

T_0 is a fuzzy subset of $V = [0,1]$, defined as the compatibility of the fuzzy proposition "X (patient) is D" with the fuzzy proposition in the pattern "X is F" :

$$T_0 = \mu_F(D) \text{ i.e. for } v \text{ in } V, \mu_{T_0}(v) = \text{Sup}_x \mu_D(x) \text{ where } \mu_F(x) = v$$

T_0 is the truth-value of "X is F" relative to "X is D", so that $\mu_D(x) = \mu_{T_0}(\mu_F(x))$.

$$T_1 = (\mu_F(D'))' \text{ i.e. for } v \text{ in } V, \mu_{T_1}(v) = \text{Inf}_x \mu_D(x) \text{ where } \mu_F(x) = v$$

Given F and D, when no T exists such that $\mu_D(x) = \mu_T(\mu_F(x))$,

the following proposition [9] is particularly useful for applications :

$$\forall x \quad \mu_{T_1}(\mu_F(x)) \leq \mu_D(x) \leq \mu_{T_0}(\mu_F(x))$$

moreover T_1 is the greatest T such that $\mu_T(\mu_F(x)) \leq \mu_D(x)$

and T_0 is the least T such that $\mu_D(x) \leq \mu_T(\mu_F(x))$.

One has the semantic entailment :

$$(X \text{ is } F) \text{ is } T_1 \longrightarrow X \text{ is } D \longrightarrow (X \text{ is } F) \text{ is } T_0$$

With the particular fuzzy sets (F) and fuzzy numbers (D) in our model, one can show that the following ranking holds

$$\nu \leq S \leq \pi \leq N,$$

so that these indexes will be chosen according to optimistic or pessimistic considerations.

For each of the eight groups a patient's condition yields five (one for each protein) 4-uples (ν_i, S_i, π_i, N_i) , $i = 1, \dots, 5$, which are combined using "min" operators expressing conjunctions, yielding

$$(\nu, S, \pi, N) = (\min_i \nu_i, \min_i S_i, \min_i \pi_i, \min_i N_i)$$

Finally for each patient, one has four fuzzy sets f, g, h and l derived from ν, S, π, N , respectively, and such that for all groups (Γ) , one has $f(\Gamma) = \nu$, $g(\Gamma) = S$, $h(\Gamma) = \pi$ and $l(\Gamma) = N$.

The separating power $s(f)$ [4] allows to evaluate to which extend a fuzzy subset f of a universe of discourse E "separates" optimally E into a non fuzzy partition (A, A') , see [5]. A is defined as

$$s(f) = f \cdot A = \sup_{B \neq \emptyset} |f \cdot B| \quad (B: \text{subsets of } E)$$

$$\text{and } f \cdot B = \frac{|f_B|}{|B|} - \frac{|f_{B'}|}{|B'|}$$

where f_B denotes the restriction of μ_f to B and $|B| = \text{Card}(B)$,

$$|f_B| = \text{fuzzy Card}(f_B)$$

$$(\text{for example : } |f_B| = \sum_{x \in B} \mu_f(x)).$$

Applying the separating power to f, g, h, l , we associate to each fuzzy set the corresponding optimal partition (playing the role of (A, A') above)

$$f \rightarrow (F, F'), g \rightarrow (G, G'), h \rightarrow (H, H') \text{ and } l \rightarrow (L, L').$$

F, G, H and L are (non fuzzy) sets of diagnostic groups assigned to patients.

V - EXAMPLES OF PRACTICAL RESULTS

Patient G.D.	C3	A1 AT	OROSOM.	HAPTO.	CRP
raw data (g/l)	0.85	2.38	1.70	3.61	0.036
normalized data	0.97	0.95	1.79	1.80	6.0
F = COLLAGEN DISEASES (Min = 0.31) VASCULITIS (Min = 0.26)	s(f) = 0.26				
G = COLLAGEN DISEASES (Min = 0.38) VASCULITIS (Min = 0.34)	s(g) = 0.32				
H = COLLAGEN DISEASES (Min = 0.50) VASCULITIS (Min = 0.49)	s(h) = 0.42				
L = COLLAGEN DISEASES (Min = 0.75) VASCULITIS (Min = 0.75)	s(l) = 0.21				

Patient Ph.K.	C3	A1 AT	OROSOM.	HAPTO.	CRP
raw data (g/l)	0.79	3.40	1.83	5.23	0.087
normalized data	0.90	1.36	1.93	2.61	14.5
F = VASCULITIS (Min = 0.60)	s(f) = 0.48				
G = VASCULITIS (Min = 0.73)	s(g) = 0.58				
H = VASCULITIS (Min = 0.77) COLLAGEN DISEASES (Min = 0.61) INFECTION (Min = 0.58)	s(h) = 0.61				
L = VASCULITIS (Min = 0.89) COLLAGEN DISEASES (Min = 0.80) INFECTION (Min = 0.79)	s(l) = 0.31				

Due to lack of space, only two examples are reported here. During the conference, an extensive list will be presented and discussed.

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