

# Towards an interpretation of the connectivity analysis in the frame of fuzzy equivalence relations for medical diagnoses

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**Abstract**— Connectivity analysis methodology is suitable to find representative symptoms of a disease. This methodology describes connections between symptoms in particular way and then chooses the group of symptoms that have the high level of connection, or in other words, have strong interconnections between elements of a group. In this paper we investigate the analogy between connectivity analysis and cluster analysis based on fuzzy equivalence relations. A comparison of two approaches, one of which has strong theoretical background (cluster analysis based on fuzzy equivalence relations) and more practically oriented connectivity analysis assures more convincing and accurate connectivity analysis from one side and applicability of fuzzy equivalence relations for medical diagnoses from another. Connectivity analysis, as shown in the paper, is one of the clustering methods, can be used in many applications where feature selection and extraction problem is considered, in particular, in pattern recognition and image processing. The results of the comparison are demonstrated on the examples.

**Keywords**— connectivity, equivalence relations, fuzzy cluster analysis.

## 1 Introduction

When speaking about the physician intuition one means the ability of a doctor to establish a diagnosis for a patient. This process can be separated into different stages. One of them, considered in this paper, distinguishes an experienced doctor from a beginner: the expert uses a small amount of observations to make a conclusion about a patient's state. Calling these observations representative symptoms one highlights their high discrimination power between this and other diseases, their best characterization for a disease. "The best characterization" means: if a patient has this representative group of symptoms, his diagnosis is almost sure. Fuzzy notations such as "small amount", "almost sure" show - as was already mentioned in many scientific papers devoted to applications of fuzzy logic in medical domains - that definitions, reasoning and conclusions in medicine are usually done with uncertainty. And a task - to find the representative symptoms - is not an exception.

For reasons of simplification we use *symptoms* as a general concept for clinical parameters, different manifestations (signal, clinical), meanwhile *diseases* include disorders, different diagnostic hypotheses.

The problem of finding the representative symptoms can be solved within a computer-assisted medical diagnosis system. Ideally, an established set of representative symptoms for a particular disease allows to only partly examine a patient suspected for this disease, that, in turn, reduces costs, time, etc. Different groups of representative symptoms can

be useful at the different stages of a chronic disease. Representative symptoms can help to establish an overall risk for a patient attacked from a particular disaster. For example, in life insurance medicine [16] the mortality of applicants within the period of insurance is assessed on the basis of present risk factors. Another possible application of representative symptoms is an optimization of questionnaires, e.g., in screening [5].

There are at least two ways to get the representative symptoms: to ask an experienced physician or to use some methods to extract this set from the available information.

As was already mentioned, symptoms cannot normally be described in simple "black and white" terms with "yes/no" or "present/not present" answers. An expert seeking to comprehensively describe the multiple influencing factors would very quickly reach the limit of his capacity [7]. For example, if an expert should estimate a group of three symptoms, each of which has three values, he will face 27 possible states. If the number of symptoms and the number of values rise to five, the number of states increase to 3125. Moreover, some disease categories overlap. For example, no consensus exists on clinical or epidemiologic measures that can be used to classify patients based on asthma symptoms [17]. Due to the highly variable nature of asthma, classification of patients into mild, moderate and severe disease categories is necessarily imperfect. That categories may overlap means, that trying to find the representative symptoms for three categories of a disease (mild asthma, moderate asthma and severe asthma) we do not have a unique description for each of them. The USA National Asthma Education Program of guidelines suggest symptoms (wheeze, dyspnoea, cough, sputum production, allergy characteristics, etc.), the degree of airflow obstruction and frequency of use of oral glucocorticoids (never, infrequently for attacks, frequently for attacks, and daily use) to validate three asthma categories. Due to the symptom-disease-patient terminology proposed by us the representative group of symptoms could be chosen from *symptoms* (the medication use, spirometry, current symptoms) for three *diseases* (indicators of asthma severity) for this example. Therefore it is not an easy task to get representative symptoms from an expert for building a computer-assisted medical system. A specialist uses his unconscious knowledge, due to the professional intuition and acumen.

To rely on data from the patient records only (or other sources containing information about patients), using statistical methods, seems also to be not a doubtless way. Widely recognized drawbacks of statistical estimations is the demand on high amounts of data. In other situations, conclusions de-

duced from records do not correspond to results from other sources. For example, as was reported in [17], a severity of asthma induced from oral glucocorticoids use and spirometry does not correlate with current asthma symptoms from medical records.

A combination of approaches is a matter of investigations since years [2]. Especially since the theory of fuzzy sets was proven to be useful in modeling uncertainties, in particular, in medicine. Expert knowledge is composed of the evaluations of the observed symptoms (the influencing factors) and the rules for the combinations of these evaluations. The expert formulates and describes his decision in a linguistic form in order to render it comprehensible to a layperson [16, 20]. Often, he/she demonstrates only certain key values of the influencing factors, the representative symptoms.

The complexity of a method partially depends on the initial information available. For example, if we have a collection of rules, where all symptoms and combinations of symptoms are already estimated by experts as was done in [18] for pulmonary tuberculosis with some degree of confirmation and exclusion, the task to find the representative symptoms may be easily solved. Experts are asked to establish thresholds for an exclusion and a confirmation of symptoms and this will allow to classify the symptoms to the corresponding representative groups.

The medical records is a point of departure for connectivity analysis as well, but values in these records represent some degree of expressiveness of a symptom, or the degree of compatibility between patients and symptoms. For example, for "overweight" the expert may put a number between 0 and 1 to reflect his opinion about this patient's symptom. The expert may know the exact weight of a patient or not, his estimation 0 shows that the patient has no overweight, 1 - the patient is very thick, 0.2 -the patient is almost in norm. The "ruddy complexion" is another example for the scale representation, e.g., 0.2, 0.4, 0.8 would mean different degrees of a skin face color estimated by an expert.

The connectivity analysis has been intensively applied, in particular, in medicine, management, geology [4, 10, 11, 12, 13, 22]. In most cases its practical usefulness was proven by examples. But in general, the connectivity analysis can be considered as a part of pattern recognition problem, in particular, cluster analysis. Till now such relations were not established. Our intention in this paper is to show that there exists an analogy between the connectivity analysis and fuzzy cluster analysis based on fuzzy equivalence relations. This comparison (or, in some sense, an interpretation of connectivity analysis in terms of well-established cluster analysis) brings more insights into the connectivity analysis which is practically used but has some weaknesses in the theoretical background from one side and applicability of fuzzy equivalence relations for medical diagnoses from another.

To realize our intentions, the paper is organized as follows. In the next section we describe what we understand under connectivity analysis and how it is applied to the representative symptoms mining problem. Section 3 describes elements of a fuzzy cluster analysis based on fuzzy equivalence relations. In Section 4 the analogy between two approaches are considered and the paper is concluded by final remarks.

## 2 Connectivity between symptoms

Assume from the database of already diagnosed patients, suffering from a particular disease, the table  $R_{SP} = \{r_{ij}\}$ ,  $i = 1 \dots n$ ,  $j = 1 \dots m$  is obtained where only presence or absence of symptoms are ticked. For example, in Table 1 information about 5 patients who have been suffering from a

Table 1: An initial table for a symptom-patient connection

	$p_1$	$p_2$	$p_3$	$p_4$	$p_5$
$s_1$	1	0	1	0	0
$s_2$	1	1	0	1	0
$s_3$	1	1	1	1	1
$s_4$	0	1	0	1	1

particular disease with 4 corresponding predefined symptoms is presented. Compared with a real practical situation, the description of e.g., *pulmonary tuberculosis (PT)* [18] consists of 30 symptoms.

### 2.1 The positive level of connection

Assume, Table 1 defines the relation of connectivity between a set of patients  $P = \{p_1, p_2, p_3, p_4, p_5\}$  and a set of symptoms  $S = \{s_1, s_2, s_3, s_4\}$ .  $r_{ij} = 1$  denotes that person  $p_j$  has the symptom  $s_i$  and  $r_{ik} = 0$  denotes that person  $p_k$  does not have it.

Dealing with these data, the intuitive proposal to get a group of representative symptoms is to highlight those symptoms that often meet under description of a patients' condition. For example, from Table 1 it can be seen that symptom  $s_3$  is present by all patients, symptoms  $s_1$  and  $s_2$  have in common only  $p_1$ . Speaking language of connectivity, the representative symptoms can be naturally chosen based on the level of connection among symptoms that is equal to the number of common patients affected by those symptoms. For example, symptoms  $s_1$  and  $s_2$  have in common only  $p_1$  and hence they are connected at level 1, meanwhile symptoms  $s_2$  and  $s_3$  have in common patients  $p_1, p_2$  and  $p_4$ , i.e., they are connected at level 3. Formula (1) describes pairwise connectivities between symptoms.

$$Q_s = R_{SP}R_{SP}^T \tag{1}$$

In (1) ordinary multiplication of matrices is used.

The result of (1) is matrix (2). Clearly,  $Q_s$  is diagonal symmetric and can be represented in upper triangular form: the order of symptoms is not important.

$$Q_s = \begin{pmatrix} 2 & 1 & 2 & 0 \\ 1 & 3 & 3 & 2 \\ 2 & 3 & 5 & 3 \\ 0 & 2 & 3 & 3 \end{pmatrix} \tag{2}$$

Connectivity results can be represented as shown in Table 2.

0-connection is not considered. The symptom  $s_3$  can be taken as the representative one, but the groups of symptoms are of interest from the physician point of view: one symptom, for instance, a cough, can be present due to many diseases, and cannot be distinguishable for them.

Table 2: Pairwise connections from matrix (2)

Levels of connectivity, $q$	Groups of symptoms
5	$\{s_3\}$
3	$\{s_2\}\{s_2, s_3\}\{s_3, s_4\}, \{s_4\}$
2	$\{s_1\}\{s_1, s_3\}\{s_2, s_4\}$
1	$\{s_1, s_2\}$

Sets  $\{s_2, s_3\}$  or  $\{s_3, s_4\}$  can be considered as appropriate ones. They have, however, in common one element,  $s_3$ . A fusion of these two sets into  $\{s_2, s_3, s_4\}$  would mean, that the same number of patients (i.e., 3) have in common subsets of this set.

Therefore, let us transform Table 2 into Table 3 due to the following observations:

1. if  $n$  patients have in common a symptom (or symptoms),  $n - 1$  patients have this symptom(s), too. The same is for  $n - 1, n - 2$ , etc. This property we call inheritance.
2. if the same symptoms belong to different groups at the same level of connectivity, these groups can be fused.

Table 3: After fusion and inheritance in Table 2

Levels of connectivity, $q$	Groups of symptoms
5	$\{s_3\}$
4	$\{s_3\}$
3	$\{s_2, s_3, s_4\}$
2	$\{s_1, s_2, s_3, s_4\}$
1	$\{s_1, s_2, s_3, s_4\}$

Information from Table 3 can be interpreted. For instance, symptoms  $\{s_2, s_3, s_4\}$  are more representative for the considered disease, because they are at a high level of connectivity i.e., have in common many patients and the cardinality of this set is not small. This intuitive procedure can lead, for example, to similar groups of representative symptoms, i.e., at the same level, two groups and the same number of different symptoms in each group. In this case both groups can be considered as representative ones or a consultation with a physician is supposed.

So far so good, but even in this example part of the information used is lost: for instance, the absence of the symptoms are not taken into account. In Table 4,

Table 4:  $s_1$  is more like  $s_2$  than  $s_3$

	$p_1$	$p_2$	$p_3$	$p_4$
$s_1$	1	0	1	1
$s_2$	1	0	1	1
$s_3$	1	1	1	1

$s_1$  and  $s_3$  are connected (via  $p_1, p_3$  and  $p_4$ ) at the same level ( $q = 3$ ) as  $s_1$  and  $s_2$  (via  $p_1, p_3$  and  $p_4$ ). But obviously,  $s_1$  is more like  $s_2$  than  $s_3$ .

### 2.2 The negative level of connection

Due to the tradition of expert systems in medical diagnoses [3, 6, 8, 18, 19, 21] it is important to consider not only an occurrence of symptoms, but a non-occurrence as well.

Let us now get information from the non-occurrence of symptoms in Table 1. For each pair of symptoms the number of patients, that do *not* have in common these symptoms is calculated. Formally, formula (1) can be used here, where matrix  $R_{SP}$  is substituted by  $\Omega - R_{SP}$ , where  $\Omega$  is a matrix with all elements unity. The results of negative connectivity is represented in Table 5, where  $q^-$  are levels of connectivity.

Table 5: Pairwise connections of symptoms that patients have *no* in common from Table 2

$q^-$	Groups of symptoms
3	$\{s_1\}$
2	$\{s_2\}, \{s_4\}$
1	$\{s_1, s_2\}\{s_2, s_4\}$
0	$\{s_3\}, \{s_3, s_4\}, \{s_2, s_3\}, \{s_1, s_3\}, \{s_1, s_4\}$

The results of this table can be interpreted. For example, the lowest row shows, that there are no patients, that do not have in common  $\{s_3\}$ , or  $\{s_3, s_4\}$ , or  $\{s_2, s_3\}$ , or  $\{s_1, s_3\}$ , or  $\{s_1, s_4\}$ , i.e., all patients have at least one of these sets in common. This leads to the assumption, that these groups of symptoms can be considered as candidates to be representative ones.  $\{s_1\}$  does not occur by 3 patients, and therefore  $\{s_1\}$  can be considered as a representative non-occurrence symptom for the particular disease (if we assume, of course, that one symptom can be representative for non-disease; this case, as a corresponding one from the positive connectivity should be discussed with an expert).

Intuitively it is also clear that if  $\{s_1\}$  does not occur by each of three patients, it does not occur by two or one of them. The procedures of inheritance and fusion are the same as in the case of positive connectivities.

The final set of representative symptoms can be differently established. A possible way is to combine representative symptoms for a disease and for non this disease. For example, if a patient has  $\{s_2, s_3, s_4\}$  and does not have  $\{s_1\}$  we can conclude that the patient has this disease.

### 2.3 Some remarks, concerning connectivity analysis

We did not consider in the previous sections cases when the elements of the matrices  $R_{SP}$  take the values from  $[0, 1]$  or, moreover, are represented by linguistic terms. In this paper we restrict ourselves to the ‘‘crisp’’ cases to concentrate on the explanation of the idea of the connectivity analysis to demonstrate a way to find similarities between symptoms due to their presence by patients. If, however, the elements of  $R_{SP}$  are numbers from  $[0, 1]$ , they are interpreted as a strength of connection (or compatibility) between a patient and a disease.  $Q_s$  is a composition of fuzzy relations. Elements of  $Q_s$  can be interpreted as a pairwise strength between symptoms for patients.

It is easy to see that absolute values of the connectivity levels are not decisive for choice of the group of representative

symptoms. A corresponding ordinal scale can bear the necessary information for connectivity. It means that for particular calculations we can simply linearly transform obtained connectivity levels into corresponding numbers from  $[0, 1]$ .

Above we have used a fairly fuzzy procedure to find the representative symptoms from positive and negative connectivities. The main demands are "high level of connection" and rather "wide" set of symptoms, connected at this level. In some sense, more formal algorithm would be preferable.

In the next section we consider if it is possible to formulate the connectivity analysis by similarity relations and corresponding fuzzy cluster analysis to assure more convincing and accurate connectivity analysis.

This idea appears by an intuitive analogy between levels of connections and  $\alpha$ -cuts of fuzzy relations. Let us first recall several definitions used to build such analogy.

### 3 Cluster analysis based on fuzzy equivalence relations

It is known that every fuzzy equivalence relation (sometime called a similarity relation) induces a crisp partition of its  $\alpha$ -cuts. And therefore, fuzzy clustering problem can be viewed as the problem of identifying the appropriate fuzzy equivalence relation on given data.

**Definition 3.1** Let  $R$  be a fuzzy relation,  $R : X \times Y \rightarrow [0, 1]$ , i.e.,  $R = \{((x, y), R(x, y)) | (x, y) \in X \times Y\}$ , the  $\alpha$ -cut matrix  ${}^\alpha R$  is denoted by

$${}^\alpha R = \{((x, y), {}^\alpha R(x, y)) | {}^\alpha R(x, y) = 1 \text{ if } R(x, y) \geq \alpha; \\ {}^\alpha R(x, y) = 0 \text{ if } R(x, y) < \alpha, (x, y) \in X \times Y, \alpha \in [0, 1]\}$$

**Definition 3.2** Binary fuzzy relation  $R : X \times X \rightarrow [0, 1]$  is a fuzzy equivalence relation iff it is reflexive, i. e.,  $R(x, x) = 1$ ; symmetric, i. e.,  $R(x, y) = R(y, x)$ , and max-min transitive:  $R^{(2)} = R \circ R \subset R$  or; more explicitly  $R(x, z) \geq \max_y \{ \min_{x,z} \{R(x, y), R(y, z)\} \}, \forall x, y, z \in X$

For practical tasks it is easier first to build a fuzzy compatibility relation and then calculate a transitive closure of this compatibility relation and this way to complete identification of a fuzzy equivalence relation.

**Definition 3.3** A fuzzy relation  $R$  on  $X \times X$  is called a fuzzy compatibility relation if it satisfies reflexive and symmetric conditions.

**Definition 3.4** The transitive closure  $R_T$  of a fuzzy relation  $R$  is defined as the relation that is transitive, contains  $R$  ( $R_T \supset R$ ) and has the smallest possible membership grades.

**Theorem 3.1** [14] Let  $R$  be a fuzzy compatibility relation on a finite universal set  $X$  with  $|X| = n$ , then the max - min transitive closure of  $R$  is the relation  $R^{(n-1)}$ .

### 4 Connectivity analysis in the frame of fuzzy equivalence relations

Ideally, if  $Q_s$  (see (1)) would be a similarity relation one can easily see that levels of connections correspond to  $\alpha$ -cuts. Thus, the analogy between connectivity analysis and a fuzzy clustering based on fuzzy equivalence relations is established.

Normally  $Q_s$  is symmetric, but its reflexivity and transitivity are questionable. To reach these two properties one can do as follows.

First, as was already told in the section 2.3, we can substitute the elements of  $Q_s$  by the corresponding ones from interval  $[0, 1]$ . Due to the definition of  $\varepsilon$ -reflexivity, i.e.  $R(x, x) \geq \varepsilon \forall x \in X, 0 < \varepsilon < 1$  [14],  $Q_s$  is  $\varepsilon$ -reflexive. Thus,  $Q_s$  is a fuzzy compatibility relation.

Transitive closure of  $Q_s$  can be found due to the following procedure [15] based on the results of the Theorem 3.1: find the transitive closure  $Q_T$  of fuzzy compatibility relation  $Q_s$ .

Step 1: Calculate  $Q^{(2)}$  if  $Q^{(2)} = Q_s$  or  $Q^{(2)} \subset Q_s$ , then transitive closure  $Q_T = Q_s$  and stop. Otherwise,  $k = 2$ , go to step 2.

Step 2 : If  $2^k \geq n - 1$ , then  $Q_T = Q^{(n-1)}$  and stop. Otherwise, calculate  $Q^{(2^k)} = Q^{(2^{k-1})} \circ Q^{(2^{k-1})}$ , if  $Q^{(2^k)} = Q^{(2^{k-1})}$ , then transitive closure  $Q_T = Q^{(2^k)}$  and stop. Otherwise, go to step 3.

Step 3:  $k = k + 1$ , go to step 2.

Due to this procedure a transitive closure of  $Q_s$  is as follows (mention a reverse transformation of the previous scale):

$$Q_T = \begin{pmatrix} 2 & 2 & 2 & 2 \\ 2 & 3 & 3 & 3 \\ 2 & 3 & 5 & 3 \\ 2 & 3 & 3 & 3 \end{pmatrix} \quad (3)$$

Following Definition 3.1 the relation (3) induces the partitions of its  $\alpha$ -cuts represented in the Table 6:

Table 6:

$\alpha$ -cuts	Groups of symptoms
5	$\{s_3\}$
3	$\{s_2, s_3, s_4\}$
2	$\{s_1, s_2, s_3, s_4\}$
1	$\{s_1, s_2, s_3, s_4\}$

It can be easily seen, that these results coincide with results of connectivity analysis represented in the Table 3. Relation (3) represents a transitive closure of  $Q_s$ , and the elements of this relation differ from corresponding elements of  $Q_s$ . A similar procedure can be done for "negative connectivity" analogy.

Notice, that recently there exist other methods, that transform the initial fuzzy binary relation into reflexive, symmetric and  $T$ -transitive fuzzy binary relation, i.e., a similarity relation, that contains the initial relation [9].

Although results from Table 6 satisfy our initial intuition, "the transitive closure method carries a number of major problems, such as the need of storage and computer time required; ... there is no way of controlling the distortion that this method produce on the data sample"[23].

Several possibilities exist to find a more efficient way than this transitive closure method does. For instance, an application of the representation theorem [23] no longer requires reflexive and symmetric fuzzy relation as initial data.



Thus, to build a similarity relation from an initial fuzzy relation, can be done differently. Our approach, based on the  $\varepsilon$ -reflexivity, and transitive closure, return a similarity relation, which  $\alpha$ -cuts coincides with group of symptoms from the connectivity analysis. It was checked for data considered in different applications [4, 12, 13, 22] and gives the same results. This is the approach used thus far to establish the validity of the proposed analogy between connectivity analysis and the fuzzy cluster analysis based on fuzzy equivalence relations. Notice that this analogy was found for low dimensional data, large-scale data is a subject of future investigations.

## 5 Concluding remarks

Let us summarize what we have done. We have shown how connectivity analysis can work in the frame of fuzzy equivalence relation. This means, in particular, that due to the above described analogy, levels of connection in the connectivity analysis can be represented as  $\alpha$ -cuts. In turn, the methodology to build clusters based on the  $\alpha$ -cuts from fuzzy relations is already established. Therefore, the connectivity analysis can be considered as a fuzzy clustering problem based on the fuzzy compatibility relations.

The question is how to obtain a compatibility relation from initial table (see, for instance, Table 1). In our discussions we used  $Q_S$ . As was already told, the connectivity analysis belongs to the family of cluster methods, and particularly, it can be considered as one of the hierarchical methods [1]. Therefore other dissimilarity measures between patterns and features (patients and symptoms) can be used and the problem to find the representative symptoms becomes a problem of the feature selection and feature extraction problem in the cluster analysis. A fuzzy compatibility relation can be defined in terms of an appropriate distance function of, e.g., the Minkowski class [1]. The question is in interpretation of this relation. Therefore the next investigation can be dedicated to the construction of  $Q_S$  that allows to inherit useful information from the initial table  $R_{SP}$  to build representative symptoms.

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