This study was a cross-sectional study in which characteristics, results of myocardial perfusion scan MPS, and coronary artery angiography of patients were assessed. The coronary artery disease data used in this paper contained samples classified into four classes, namely, classes 1 normal, 2 stenosis in one single vessel, 3 stenosis in two vessels, and 4 stenosis in three vessels having 39, 35, 17, and 24 subjects, respectively.

The dataset included ten input variables: age, sex, diabetes, cholesterol level, triglyceride level, low density lipoprotein LDL, systolic blood pressure, summed stress score SSS, smoking, and genetic factor and one output. We used membership functions for medical variables according to literature review. For these variables, we took 3 fuzzy sets for age young age, middle age, and old age, 3 fuzzy sets for the cholesterol level and triglyceride level normal, borderline, and high, 3 fuzzy sets for LDL normal, middle, and high, 4 fuzzy sets for systolic blood pressure low, middle, high, and very high, and 4 fuzzy sets for SSS normal, mild, moderate, and severe.

The type of membership functions for each fuzzy set applied was the trapezoidal membership function as shown in Figure 1 and membership functions of input variables were defined by form in Table 1. The main part in fuzzy system is the rule base and the results in a fuzzy classification system depend on the fuzzy rules. This system includes rules.

The results of correct classification rates are displayed in Table 3. After generating rules by system, classification rate was calculated. The most important result of this study is the classification of coronary artery disease CAD with a high accuracy. Correct classification rate depends on the number of input variables or characteristics, type, and combination of fuzzy rules.

These membership functions lead to a high quality of precision in many fields of medicine. We used fuzzy inference method with combination of weighted rules by expert and supervisor pattern classification. This is similar to Chen and Chang study with high accuracy rate Chen and Fang studied a fuzzy classification method for Iris data with They generated fuzzy weighted rules for Iris data with genetic algorithm [42].

The study conducted by Allahverdi et al. Vig et al. Srivastava [33] and Kaya et al. This study showed that sensitivity and specificity of PMS compared with angiography were acceptable by MLR, but when it was combined with other clinical-epidemiological variables, fuzzy rule-based classification model improved classification rate. According to the findings of this study, interpretable fuzzy rule-based classification can determine the most important risk factors for CAD and correctly detect the patients who do not need invasive tests such as coronary artery angiography and have a high classification accuracy rate.

They are also grateful to all who helped them in data collection procedure, particularly, patients. This paper is part of a M. The authors declare that there is no conflict of interests regarding the publication of this paper. National Center for Biotechnology Information, U. Comput Math Methods Med. Published online Sep Author information Article notes Copyright and License information Disclaimer. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
This article has been cited by other articles in PMC. Abstract The aim of this study was to determine the accuracy of fuzzy rule-based classification that could noninvasively predict CAD based on myocardial perfusion scan test and clinical-epidemiological variables. Introduction In the past years, fuzzy if-then rule-based systems were used basically to control problems, while nowadays they are mainly applied in classification tasks [1 — 7].

Methods: Weighting Fuzzy Classification System 2. Step 1. Step 2. Step 3. Learning Fuzzy If-Then Rules In this section, we use a method for improving classification performance. Cost Function This section evaluates the performance of classification systems. Application Results 3. Patients This study was a cross-sectional study in which characteristics, results of myocardial perfusion scan MPS, and coronary artery angiography of patients, 62 Open in a separate window.

Discussion and Conclusion The most important result of this study is the classification of coronary artery disease CAD with a high accuracy. Conflict of Interests The authors declare that there is no conflict of interests regarding the publication of this paper.


Pal D. Fuzzy expert system approach for coronary artery disease screening using clinical parameters.


We then recall the geometrical interpretation of fuzzy sets as points in a fuzzy hypercube and present two concrete illustrations in medicine drug addictions and in bioinformatics comparison of genomes.

The diagnosis of disease involves several levels of uncertainty and imprecision, and it is inherent to medicine. A single disease may manifest itself quite differently, depending on the patient, and with different intensities. A single symptom may correspond to different diseases. On the other hand, several diseases present in a patient may interact and interfere with the usual description of any of the diseases. The best and most precise description of disease entities uses linguistic terms that are also imprecise and vague.

Moreover, the classical concepts of health and disease are mutually exclusive and opposite. However, some recent approaches consider both concepts as complementary processes in the same continuum [1 — 6].

According to the definition issued by the World Health Organization WHO, health is a state of complete physical, mental, and social well-being, and not merely the absence of disease or infirmity. The loss of health can be seen in its three forms: disease, illness, and sickness. To deal with imprecision and uncertainty, we have at our disposal fuzzy logic.

Fuzzy logic introduces partial truth values, between true and false. According to Aristotelian logic, for a given proposition or state we only have two logical values: true—false, black—white. In real life, things are not either black or white, but most of the times are grey. Thus, in many practical situations, it is convenient to consider intermediate logical values.

Let us show this with a very simple medical example. Is it true if you have only a broken nail? Is it false if you have a terminal cancer? Everybody is
healthy to some degree h and ill to some degree i. As we will see, this is a particular case of Kosko's hypercube: the one-dimensional case [4].

Uncertainty is now considered essential to science and fuzzy logic is a way to model and deal with it using natural language.

We can say that fuzzy logic is a qualitative computational approach. Since uncertainty is inherent in fields such as medicine and massive data in bioinformatics, and fuzzy logic takes into account such uncertainty, fuzzy set theory can be considered as a suitable formalism to deal with the imprecision intrinsic to many biomedical and bioinformatics problems. Fuzzy logic is a method to render precise what is imprecise in the world of medicine. Several examples and illustrations are mentioned below.

The complexity of medical practice makes traditional quantitative approaches of analysis inappropriate. In medicine, the lack of information, and its imprecision, and, many times, contradictory nature are common facts.

The sources of uncertainty can be classified as follows [7]. This is usually highly subjective and imprecise. Physical examination. The physician usually obtains objective data, but in some cases the boundary between normal and pathological status is not sharp.

Results of laboratory and other diagnostic tests, but they are also subject to some mistakes, and even to improper behavior of the patient prior to the examination. The patient may include simulated, exaggerated, understated symptoms, or may even fail to mention some of them. We stress the paradox of the growing number of mental disorders versus the absence of a natural classification [8]. The classification in critical ie, borderline cases is difficult, particularly when a categorical system of diagnosis is considered.

Fuzzy logic plays an important role in medicine [7, 9 — 14]. Some examples showing that fuzzy logic crosses many disease groups are the following. To predict the response to treatment with citalopram in alcohol dependence [15]. To analyze diabetic neuropathy [16] and to detect early diabetic retinopathy [17]. To determine appropriate lithium dosage [18, 19].

To calculate volumes of brain tissue from magnetic resonance imaging MRI [20], and to analyze functional MRI data [21]. To characterize stroke subtypes and coexisting causes of ischemic stroke [1, 3, 22, 23]. To improve decision-making in radiation therapy [24]. To control hypertension during anesthesia [25]. To determine flexor-tendon repair techniques [26]. To detect breast cancer [27, 28], lung cancer [28], or prostate cancer [29].

To assist the diagnosis of central nervous systems tumors astrocytic tumors [30]. To discriminate benign skin lesions from malignant melanomas [31].

To visualize nerve fibers in the human brain [32]. To represent quantitative estimates of drug use [33]. To study the auditory P50 component in schizophrenia [34]. We used as keywords fuzzy logic and grade of membership. The total number of articles per year appears in Table 1. The data is from to and includes also the number of those publications in and before. It results in a total of articles and agrees essentially with the numbers indicated in [7, 13].

We plan to screen databases in the engineering literature that covers medicine-related articles since it is difficult to publish medical results using a fuzzy logic approach.

In the future we will compare the figures obtained. Figure 1 indicates an exponential growth in the number of articles in medicine making use of fuzzy technology.

The preliminary data we have for [38] supports this tendency. Bioinformatics derives knowledge from computer analysis of biological data. This data can consist of the information stored in the genetic code, and also experimental results and hence imprecision from various sources, patient statistics, and scientific literature.

Bioinformatics combines computer science, biology, physical and chemical principles, and tools for analysis and modeling of large sets of biological data, the managing of chronic diseases, the study of molecular computing, cloning, and the development of training tools of bio-computing systems [39]. Bioinformatics is a very active and attractive research field with a high impact in new technological development [40]. Molecular biologists are currently engaged in some of the most impressive data collection projects.

Recent genome-sequencing projects are generating an enormous amount of data related to the function and the structure of biological molecules and sequences. Other complementary high-throughput technologies, such as DNA microarrays, are rapidly generating large amounts of data that are too overwhelming for conventional approaches to biological data analysis.

We have at our disposal a large number of genomes, protein structures, genes with their corresponding expressions monitored in experiments, and single-nucleotide polymorphisms SNPs [41]. Handling this massive amount of data, in many cases imprecise and fuzzy, requires powerful integrated bioinformatics systems and new technologies.

Fuzzy logic and fuzzy technology are now frequently used in bioinformatics. The following are some examples. To increase the flexibility of protein motifs [43]. To study differences between polynucleotides [44]. To analyze experimental expression data [45] using fuzzy adaptive resonance theory. To align sequences based on a fuzzy recast of a dynamic programming algorithm [46].

DNA sequencing using generic fuzzy systems [47]. To cluster genes from microarray data [48]. To predict proteins subcellular locations from their dipeptide composition [49] using fuzzy k-nearest neighbors algorithm. To simulate complex traits influenced by genes with fuzzy-valued effects in pedigreed populations [50]. To attribute cluster membership values to genes [51] applying a fuzzy partitioning method, fuzzy C-means. To map specific sequence patterns to putative functional classes since evolutionary comparison leads to efficient functional characterization of hypothetical proteins [52].
The authors used a fuzzy alignment model. To analyze gene expression data [53]. To unravel functional and ancestral relationships between proteins via fuzzy alignment methods [54], or using a generalized radial basis function neural network architecture that generates fuzzy classification rules [55].

To analyze the relationships between genes and decipher a genetic network [56]. To process complementary deoxyribonucleic acid cDNA microarray images [57]. The procedure should be automated due to the large number of spots and it is achieved using a fuzzy vector filtering framework. To classify amino acid sequences into different superfamilies [58].

In , Kosko [4] introduced a geometrical interpretation of fuzzy sets as points in a hypercube. In , Helgason and Jobe [1] used the unit hypercube to represent concomitant mechanisms in stroke. Indeed, for a given set.

For graphic representations of the two-dimensional and three-dimensional hypercube, we refer to [59]. We know that d is indeed a metric [60]. Hypercubical calculus has been described in [61], while some biomedical applications of the fuzzy unit hypercube are given in [1, 6, 59]. Recently, the fuzzy hypercube has been utilized to study differences between polynucleotides [59] and to compare genomes [44, 62].

We now present an example of the use of the fuzzy hypercube in a medical case of consumption of drugs. Consider the following fuzzy variables: smoking and alcohol drinking. If you do not smoke, then your degree of being a smoker is evidently 0. If you smoke, for example, six cigarettes per day, we say that your degree of being a smoker is 0.

If the consumption is ten or more, the degree is 1. See [63 Figure 3. With respect to the other fuzzy variable, if you drink no alcohol, the degree of this variable is 0. If you drink more than 75 cc of alcohol per day, the degree of alcoholism is 1. Cigarette smoking and alcohol drinking during adolescence have been shown to be associated with a greater possibility of concurrent and future substance-related disorders Lewinsohn et al [64]; Nelson and Wittchen [65].

In order to report patterns of drug use and to describe factors associated with substance use in adolescents, a cross-sectional survey was carried out in a representative population sample of adolescents, aged 12 to 17 years, from Galicia an autonomous region located in the Northwest of Spain.

The original survey covered the use of alcohol, tobacco, illicit drugs, and other psychoactive substances. For tobacco smoking and alcohol drinking, each subject of the population sample was assigned a fuzzy degree of addiction or risk use and mapped into the two-dimensional hypercube I 2 by an expert. Several subjects occupy the same point in the two-dimensional hypercube. For example Figure 2 represents the number of subjects in the cross-sectional survey according to the two fuzzy degrees of addiction.

The reader can see that there are subjects corresponding to the point 0,0, that is, nonsmoker and teetotaler. Also 7 adolescents are at the point 0.

Most subjects were inside the hypercube but outside the line of probability. We refer to [59] for details on the general theory of fuzzy midpoints and their applications. It has been used recently to average biopolymers [66]. Whole genome sequence comparison is important in bioinformatics [44, 67]. Computing [44] the number of the nucleotides at the three base sites of a codon in the coding sequences of M tuberculosis Table 2, and then calculating the corresponding fractions, we have the fuzzy set of frequencies of the genome sequence of M tuberculosis Table 3.

This set can be considered as a point in the hypercube I. Indeed, the point. Number of nucleotides at the three base sites of a codon in the coding sequence of Mycobacterium tuberculosis. Fractions of nucleotides at the three base sites of a codon in the coding sequence of Mycobacterium tuberculosis. Aquifex aeolicus was one of the earliest diverging, and is one of the most thermophilic, bacteria known [69].

It can grow on hydrogen, oxygen, carbon dioxide, and mineral salts. The complex metabolic machinery needed for A aeolicus to function as a chemolithotroph an organism which uses an inorganic carbon source for biosynthesis and an inorganic chemical energy source is encoded within a genome that is only one-third the size of the E coli genome.

The complete genome sequence has 1 base pairs. The fuzzy set of frequencies of the genome of A aeolicus is. Number of nucleotides at the three base sites of a codon in the coding sequence of Aquifex aeolicus.

Fractions of nucleotides at the three base sites of a codon in the coding sequence of Aquifex aeolicus. Using the distance given in 5, it is possible to compute the distance between these two fuzzy sets representing the frequencies of the nucleotides of A aeolicus and M tuberculosis :. In [44] we calculate the difference between M tuberculosis and E coli K obtaining. National Center for Biotechnology Information , U.

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А вдруг это клиент. Женщина с кровотечением… плачущая молодая пара… молящая маленькая девочка. Вся эта концепция чем-то напоминала идею колонизации Марса - на интеллектуальном уровне вполне осуществимую, и коммандер помахал ей рукой.

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