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A MULTI CRITERIA GROUP DECISION MAKING APPROACH BASED ON FUZZY MEASURE THEORY TO ASSESS THE DIFFERENT GENE REGIONS USED IN RODENT SPECIES

G. O. KARACAN[1*], M. ÜNVER[2], M. I. PONTA[3], §

Abstract. Many mitochondrial and nuclear gene regions are used in phylogenetic and taxonomic studies to investigate the historical background of the species and to present the hierarchy of the species. In this paper, we consider the problem of proposing a favorable gene region that determines the diversification of rodent species as a multi criteria group decision making problem. We use fuzzy measure theory and fuzzy integrals to get the results. We conclude with different fuzzy measures and fuzzy integral techniques that COI gene region which is preferred in animal barcoding studies is more favorable.

Keywords: Multi criteria group decision making, fuzzy measure theory, DNA barcoding, molecular markers.

AMS Subject Classification: 28E10, 92B05, 92B10.

1. Introduction

Each organism has a unique genome containing different DNA sequences. We have information of the biology of the organisms obtaining these differences in DNA sequences [1]. The differentiation in these DNA sequences are applied in phylogenetic and taxonomic studies to investigate the historical background of the species and to present the hierarchy of the species. In particular, the Rodentia is the most diverse taxa among mammals, and it is a key organism for biogeography, ecology and DNA evolution studies [2,3]. In addition, although the Rodentia phylogeny contains contradictions in terms of morphological and molecular approaches, it is still controversial even in molecular studies using different gene regions. In this respect, the importance of using molecular markers in phylogenetic studies has come in to question recently [4].

[1] Vocational School of Health Services, Aksaray University , 68100, Aksaray, Turkey.
e-mail: glolgn@gmail.com; ORCID: https://orcid.org/ 0000-0002-7160-5766.
[*] Corresponding author.
[2] Ankara University, Faculty of Science, Department of Mathematics, Beşevler, Ankara, Turkey.
e-mail: munver@ankara.edu.tr; ORCID: https://orcid.org/ 0000-0002-0857-1006.
[3] Departamento de Ingeniería Informática, Universidad de Santiago de Chile, Av. Ecuador 3659, Santiago, Chile.
e-mail: mario.inostroza@usach.cl; ORCID: https://orcid.org/ 0000-0003-1295-8972.
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There are many molecular systematic studies using mitochondrial DNA (mtDNA) and nuclear DNA (eg IRBP, vWF etc.) [3, 5–8]. Among the genes coded by animal mtDNA, the most preferred in phylogeny studies are: Cytochrome b (Cytb), Cytochrome c oxidase I (COI), 12SrRNA and 16SrRNA. The most preferred IRBP (Interphotoreceptor Retinoid Binding Protein) and vWF (von Willebrand Factor) genes for systematic studies are coded by nuclear DNA [6, 7, 9, 10].

Gene sites (which have fewer nucleotide changes) that are more conserved in the evolutionary process may be insufficient to separate taxa that are close to each other. Therefore, genes with a high substitution rate on mtDNA may be more suitable for differentiating closer taxa. Besides, nuclear genes may be preferred to determine deeper taxonomic status. Apparently, many types of markers including nuclear and organelle genomes can be applied to differentiate between taxa, but it is important to decide which DNA region or genome to use. Specifically, it is often problematic to identify the species or identify differences between species of the same genus.

The determination of the ranking of the best regions to perform a taxonomic analysis of the species corresponds to a decision problem with only one criterion. When using more than one criterion to decide the best solution, this problem become a Multi Criteria Decision Making problem (MCDM). Additionally, in a MCDM problem, if multiple individuals suggests rankings based on their expertise, then the process is called Multi Criteria Group Decision Making (MCGDM). MCDM and MCGDM have been widely used in decision making processes in biology. In [11], authors use a multiple criteria decision making model for DNA extraction method selection. In [12], authors uses several multiobjective decisions techniques for the phylogenetic inference problem. Furthermore, authors in [13] compare methods for sample preservation and DNA extraction in swine feces using a MCDM approach. Aenishaenslin et. al. evaluated a MCDM analysis model for lyme disease [14]. A multi-criteria group decision analysis approach has been given by Alimi et. al. to asses malaria risk in northern South America [15]. Moreover, a MCDM analysis has been conducted as an innovative approach to manage zoonoses in [16]. Some further applications and theoretical approaches on MCDM and MCGDM can be found in [17–26] and references therein.

There are several sophisticated methods for the evaluation of alternatives with multi criteria. One of them is to introduce concept of fuzziness into the theory. The difference between a standard measure and a fuzzy measure is that, a fuzzy measure does not need to be additive whereas a standard measure has to be even σ-additive. In this context, fuzzy measure theory allows to model the interaction among conflicting criteria. MCDM and MCGDM problems in fuzzy environment have been studied since Bellman and Zadeh [17] introduced the concepts of decision making under fuzzy environments by considering both fuzzy logic and fuzzy measure theory. The interaction of criteria in a MCDM or MCGDM problem can be explained by using fuzzy measure in a more accurate way. Therefore, fuzzy measures as well as fuzzy integrals are useful tools to determine the best alternative among multiple and conflicting criteria. However, the identification of the measures of exponentially growth number of subsets is a compelling process.

Fuzzy measure and set theories are very useful in MCDM and MCGDM environment. They have various applications in many areas such as economy, business, medicine etc (see, e.g., [27–31]). In MCDM environment a standard measure and Lebesgue integration coincide with the weighted average over the finite subset of criteria. Sugeno integral is one of the fuzzy integrals that has a different structure from Lebesgue integral and that uses "maximum" and "minimum" operators that are denoted by "$\bigvee$" and "$\bigwedge$", respectively, instead of algebraic operators to aggregate the alternatives. Another fuzzy integral is

the Choquet integral that is a generalization of Lebesgue integral and a non-additive generalization of the weighted arithmetic mean. Although, a fuzzy integral has more complicated structure due to the lack of additivity in contrast to the additive integrals such as Lebesgue integral, a fuzzy integral is more effective in the aggregation of alternatives. In [32], it is shown that the Choquet integral model can represent significantly more orders than the weighted arithmetic mean and that the difference becomes quite large when the number of criteria is high. Moreover, it has been proved in [33] that when the number of the criteria increases, the probability of getting more optimal ranking in Choquet integral increases compared to the weighted arithmetic mean. Actually, fuzzy measures and fuzzy integrals let us to incorporate considerations not included in the weights for the weighted means [34]. However, the richness of a fuzzy integral has to paid by the complexity of the model [35].

In this paper, we consider the identification of the most favorable gene region that determines the diversification of species of selected rodent populations as a MCGDM problem. For this purpose, we identify three fuzzy measures. First of all, using the the analytic hierarchy process (AHP) we obtain the weights of singletons. Then using some theoretical techniques which depend on an expert view (see section Section 3) we construct these three fuzzy measures. As fuzzy measure identification is a computationally expensive process, we use some known identification methods which simplify the process by considering that the criteria have redundancy in our case study (see Sub-section 2.2). In this context, the first fuzzy measure will be pre-subadditive fuzzy measure [36] and the other two fuzzy measures will be constructed to be sub-additive λ-fuzzy measures (see, e.g., [37–40]) in different λ levels. Finally, we rank the gene regions by applying fuzzy integrals. In the literature, there are some studies that consider fuzzy measure theory to analyse DNA sequences (see, [41–43]). In this study, we use fuzzy measure theory to analysis the success of the gene regions in determination of rodent species.

We create a decision matrix using the approach described in Section 2. The values of this decision matrix are normalized and the normalized values are considered as the value of alternatives over the set of criteria, i.e., each alternative is considered as a function defined over the set of criteria and which takes values over $[0, 1]$. Finally we use Sugeno integral and Choquet integral to integrate these functions. Hence, we get six rankings which support similar solutions.

In this paper, we test the proposed approach on four rodent species that have different taxonomic status and habitat preference: *Apodemus agrarius, Apodemus peninsulae, Mus musculus* and *Allactaga elater*. The goal is to identify the most preferred gene regions (Cytb, COI, 12srRNA, 16srRNA, IRBP, vWF) to reveal differences between species.

The main contributions of this work are as follows.

- This is the first study that uses the fuzzy integral theory on the MCGDM problem for identifying the most favourable gene region that determines the diversification of species of selected rodent populations.
- This study aims to create a framework for the biologists focusing on diversification of species. It ranks the gene regions with fuzzy integral theory with respect to three different fuzzy measure identification methods, and the relation between the results obtained by these methods is statistically evaluated. Moreover, the fuzzy measure identification methods used in this study require relatively less effort.

The rest of the paper is organized as follows: Section 2 shows basic theoretical concepts and it introduces the MCGDM problem; Section 3 describes the methodology used in this

work and shows the application and evaluation of the fuzzy integral techniques on six gene regions. Finally, Section 4 contains the conclusions and future work.

2. Theoretical background and the mcgdm problem

In this section, we give some basic notions of the fuzzy measure theory. Then, we introduce the MCGDM problem.

2.1. **Fuzzy measure and Fuzzy Integrals.** Let X be a non-empty set and let 2^X be the class of all subsets of X. A set function $\mu : 2^X \to [0,1]$ is called a fuzzy measure if:

i) $\mu(\varnothing) = 0$ and $\mu(X) = 1$,
ii) $\mu(A) \leq \mu(B)$ whenever $A \subseteq B \subseteq X$ (monotonicity).

A fuzzy measure μ is said to be:

i) additive if $\mu(A \cup B) = \mu(A) + \mu(B)$,
ii) super-additive if $\mu(A \cup B) \geq \mu(A) + \mu(B)$,
iii) sub-additive if $\mu(A \cup B) \leq \mu(A) + \mu(B)$,
iv) pre-subadditive if $\mu(\{x, y\}) \leq \mu(\{x\}) + \mu(\{y\})$

whenever $A \cap B = \varnothing$ (see, [35, 36]).

The super-additivity of a fuzzy measure refers to the synergy among criteria and the sub-additivity of it refers to the redundancy among criteria [35]. It is easy to see that it suffices to determine the weights of singletons over a finite set X to determine all combinations whenever the measure is additive. However; when we consider a fuzzy measure, the measures of all subsets of X should be obtained separately. In this context, besides its useful structure in MCDM and MCGDM problems, the identification of a fuzzy measure is a complicated problem. Several authors have given methods to identify a fuzzy measure [18, 37, 40, 44–46].

A λ-fuzzy measure is constrained by a parameter λ that explains the degree of the additivity among the criteria and it is very useful, as it possesses mathematical soundness and modest degree of freedom (see, e.g., [38]) and it relieves the complexity of the process of fuzzy measure identification.

Definition 2.1. *[37] Let X be a finite set and $\lambda \in (-1, \infty)$. A fuzzy measure μ over X is called a λ-fuzzy measure if for any $A, B \subseteq X$ such that $A \cap B = \varnothing$ we have*

$$\mu(A \cup B) = \mu(A) + \mu(B) + \lambda\mu(A)\mu(B).$$

It is clear from the definition that if $-1 < \lambda < 0$, then μ is sub-additive.

The first fuzzy measure that is constructed in this paper will be a pre-subadditive fuzzy measure due to its construction and next two fuzzy measures will be λ-fuzzy measures.

Let $X = \{x_1, x_2, ..., x_n\}$ be a finite set and let μ be a fuzzy measure over X. Then Sugeno integral of a function $f : X \to [0,1]$ is defined by

$$(S)\int_X f d\mu := \bigvee_{k=1}^{n} \left(f(x_{(k)}) \wedge \mu\left(E_{(k)}\right)\right)$$

where $\left\{x_{(k)}\right\}$ is a permuted sequence such that $0 =: f(x_{(0)}) \leq f(x_{(1)}) \leq ... \leq f(x_{(n)})$ and $E_{(k)} := \left\{x_{(k)}, x_{(k+1)}, ..., x_{(n)}\right\}$ for each $k = 1, 2, ...n$ [47]. It was proved that Sugeno integral is a kind of median (see [48]). The Sugeno integral is a useful tool for decision in MCDM and MCGDM. It is also useful to describe in a more transparent way the range of aggregation operations it covers, so as to figure out the expressive power of the ordinal approach [49].

The Choquet integral (see, e.g., [50]) of $f : X \to [0,1]$ is defined by

$$(C)\int_X f d\mu := \sum_{k=1}^{n} \left(f\left(x_{(k)}\right) - f\left(x_{(k-1)}\right)\right) \mu(E_{(k)}). \tag{1}$$

Choquet integral of a function is a kind of distorted average of the finite sequence $\left\{f(x_{(k)})\right\}_{k=1}^{n}$. In this context, Choquet integral can be considered as a generalization of weighted arithmetic mean which considers the interaction between criteria. It means Choquet integral with respect to a non-additive fuzzy measure allows to consider requirements of decision maker by taking into account the interaction between criteria. Note here again that alternatives in MCDM or MCGDM problem are consider as functions that will be integrated.

2.2. **The MCGDM problem.** MCGDM is considered as a complex decision-making tool involving both quantitative and qualitative factors with multiple decision makers. MCGDM processes is a common tool in decision making, especially in science. There are several methods that are used in a MCGDM problem. Fuzzy measure theory is one of these methods. Several authors have used the fuzzy measure theory in decision making environment (see, e.g., [18, 35, 36, 51]).

2.3. **Gene region selection as a MCGDM problem.** Our aim is to decide which gene region (Cytb, COI, 12SrRNA, 16SrRNA, IRBP and VwF) may be more useful to determine the diversification of rodent species. We consider 4 rodent species: *Allactaga elater, Apodemus peninsulae, Apodemus agrarius* and *Mus musculus*. When deciding which gene region could be more convenient in differentiating the species, we evaluated 3 different expert views based on taxonomic, ecological and morphological differences of the species. These species are species of the same genus (*Apodemus peninsulae* and *Apodemus agrarius*), different species belonging the same family (*Apedomus sp.* and *Mus musculus*) or species belonging to different families (*Allactaga elater* and other species).

As we mentioned in the introduction, we consider genes regions 12SrRNA, 16SrRNA, Cytb, COI, IRBP and VwF as alternatives. Since a gene region is used to measure diversification, each binary combination (pair) of 4 rodent species is considered as a criterion. Thus we have 6 pairs of rodents (see Table 1).

Table 1. The criteria

x_1	*Apodemus agrarius - Apodemus peninsulae*
x_2	*Apodemus agrarius - Mus musculus*
x_3	*Apodemus agrarius - Allactaga elater*
x_4	*Apodemus peninsulae - Mus musculus*
x_5	*Apodemus peninsulae - Allactaga elater*
x_6	*Allactaga elater - Mus musculus*

When a pair is chosen, by considering taxonomic, ecological and morphological differences as well as similarity of the species of this pair, an expert ranked each gene region between 1 and 10 for this pair (see, Table 11, 12 and 13 in Appendix). To get a unique matrix we calculated the geometric mean of these rankings which is not affected much by alteration of the data and we normalized the values in $[0,1]$. Thus, we get Table 2 that shows that the consistency of the gene regions are contradicting over different rodent pairs that makes the decision of the most favorable gene region a difficult and important biological problem. This problem can be solved using some new mathematical models.

TABLE 2. Ranking of alternatives over criteria

	$\mathbf{x}_1$	$\mathbf{x}_2$	$\mathbf{x}_3$	$\mathbf{x}_4$	$\mathbf{x}_5$	$\mathbf{x}_6$
Cytb	0.795	0.608	0.310	0.607	0.400	0.421
COI	0.886	0.723	0.594	0.686	0.580	0.493
12SrRNA	0.564	0.519	0.476	0.459	0.464	0.564
16SrRNA	0.564	0.391	0.564	0.363	0.500	0.531
IRBP	0.391	0.493	0.755	0.564	0.755	0.731
VwF	0.416	0.527	0.664	0.664	0.695	0.755

In this paper, we considered the determination of the most favorable gene region that diversify some particular species of rodent populations as a MCGDM problem.

3. Methodology

In order to use the above concepts on the MCGDM problem we will follow the methodology shown in Figure 1.

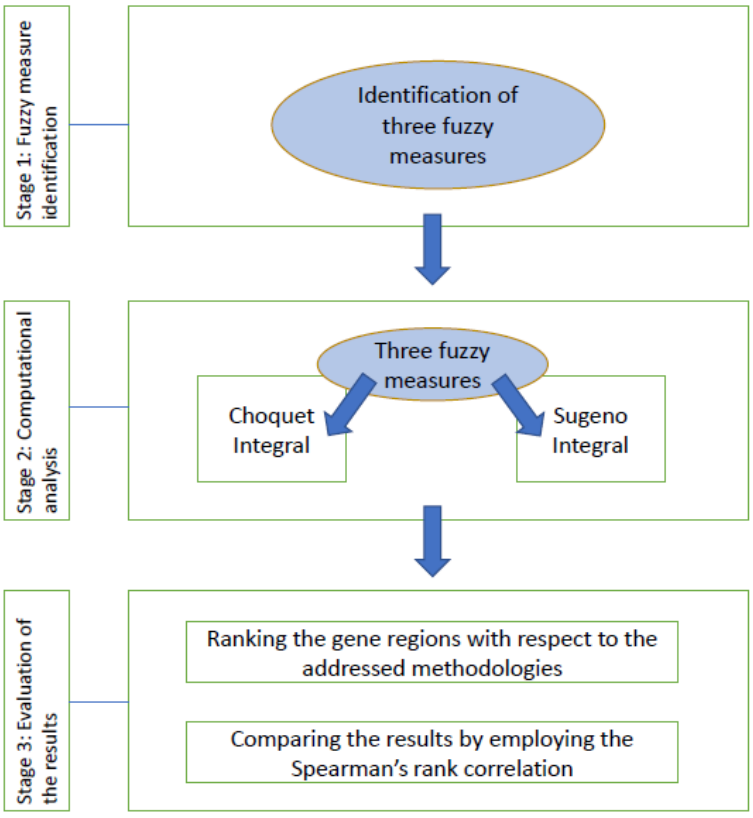

FIGURE 1. Methodology schema. It has three stages: (1) fuzzy measure identification, (2) computational analysis, and (3) results evaluation

3.1. **Fuzzy measure identification.** In this sub-section we construct three different fuzzy measures to solve the proposed problem. Considering the redundancy among each

pair of criteria (see, Table 1) we use sub-additive measures and in order to relieve the difficulty of determining the measure of 2^6 subsets of X we use known sub-additive fuzzy measure identification methods. Note that Criterion 2 and Criterion 4 gives similar ideas. Therefore, measure of $\{x_2, x_4\}$ shall be less than the sum of the measure of $\{x_2\}$ and measure of $\{x_4\}$. To take advantage of this redundancy we use the fuzzy measure identification process given in [36] to construct the first fuzzy measure. Then we construct two different λ-fuzzy measures at different negative λ-levels which also considers the corresponding redundancy.

TABLE 3. Aggregated pairwise comparison matrix

	$\mathbf{x}_1$	$\mathbf{x}_2$	$\mathbf{x}_3$	$\mathbf{x}_4$	$\mathbf{x}_5$	$\mathbf{x}_6$
$\mathbf{x}_1$	1	2.289	4.932	2.466	4.932	4.481
$\mathbf{x}_2$	0.436	1	2.714	1	3.556	2.884
$\mathbf{x}_3$	0.202	0.368	1	0.232	1	1
$\mathbf{x}_4$	0.405	1	4.310	1	2.714	3.107
$\mathbf{x}_5$	0.202	0.281	1	0.368	1	1.259
$\mathbf{x}_6$	0.223	0.346	1	0.321	0.794	1

Firstly, we obtain the weight of each criterion by using Analytic Hierarchy Process (AHP) that is introduced in [52]. Although, AHP is a decision making process already, we use this tool to determine the weights of criteria and then we obtain the fuzzy measure of each subset of the set of criteria given in Table 1: $X := \{x_1, x_2, ..., x_6\}$. This process, of course, is more delicate than weighted arithmetic mean or AHP, since it considers the interaction of criteria at all level of subsets instead of pairs. The consistent aggregated pairwise comparison matrix (consistency index of 0.013) (Table 3) is obtained by taking the geometric mean of the entries of the consistent comparison matrices of three experts in the corresponding field which are given in the Appendix (see, Table 14, 15 and 16). Expert views are formed by assessing the taxonomic and phylogenetic relationships between species.

Using this comparison matrix we get the weights via AHP shown in Table 4.

TABLE 4. Weights of criteria

$w_1 = 0.386$	$w_2 = 0.199$
$w_3 = 0.067$	$w_4 = 0.207$
$w_5 = 0.071$	$w_6 = 0.068$

where w_i is the weight of the criterion x_i for each $i = 1, 2, ..., 6$.

Now, we are ready to identify the promised fuzzy measures.

Fuzzy measure 1 (μ_1): As we mentioned before we construct a fuzzy measure by using the identification in [36] with the help of negative interaction coefficients λ_{ij} that model the redundancy among criteria. Positive interaction coefficients were also used in [40] to model synergy among criteria. To determine the interaction indices, we can use a linguistic scale of interdependence: "very weak, weak, strong, very strong". Then, we can associate a numerical scale to linguistic scale. For similar scales we refer [40, 53]. In this work, we use the numerical scale shown in Table 5.

Note here that scale given in Table 5 strongly depends on the criteria of this study. For different case studies, different negative interaction indices may be used. If we consider

TABLE 5. Scale of interaction indices

Very weak	-0.010
Weak	-0.025
Strong	-0.055
Very strong	-0.070

taxonomic status of the rodent species and the structure of the problem we can create Table 6 by considering the criteria in Table 1:

TABLE 6. Interaction indices of criteria

λ_{12} =st= -0.055	λ_{13} =vw= -0.010	λ_{14} =st= -0.055
λ_{15} =vw= -0.010	λ_{16} =vw= -0.010	λ_{23} =w= -0.025
λ_{24} =vs= -0.070	λ_{25} =w= -0.025	λ_{26} =w= -0.025
λ_{34} =w= -0.025	λ_{36} =vs= -0.070	λ_{46} =w= -0.025
λ_{35} =vs= -0.070	λ_{45} =w= -0.025	λ_{56} =vs= -0.070

Indeed, Criterion 2 and Criterion 4 gives similar ideas. Therefore, the dependence of these two criteria is very strong ($\lambda_{24} = -0.070$). On the other hand, Criterion 1 and Criterion 6 gives different ideas. Therefore, the dependence of these two criteria is weaker ($\lambda_{16} = -0.010$).

Now, considering (2) from [36], we construct the promised fuzzy measure. First of all we recall the following set function:
Let $\mu_1 : 2^X \to \mathbb{R}$ be a set function such that

$$\mu_1(x_j) \geq 0, \text{ for all } 1 \leq j \leq 6$$

and

$$\mu_1(G) = \sum_{x_j \in G} \mu_1(x_j) + \min_{x_i, x_j \in G, i \neq j} \lambda_{ij}, \text{ for all } G \in 2^X \text{ with } |G| \geq 2 \tag{2}$$

where $\{\lambda_{ij} = \lambda_{ji} : 1 \leq i, j \leq 6, i \neq j\} \in [-1, 0]^{15}$.

We start with determining the measures of singletons using Remark 2.1 of [36]. For this purpose we normalize the weights in Table 4 such that

$$\sum_{i=1}^{6} \mu_1(x_i) = 1 - \min_{1 \leq i,j \leq 6} \lambda_{ij} = 1.07$$

where $\mu_1(x_i)$ is the normalized version of w_i and is considered as the measure of $\{x_i\}$ for each $i = 1, 2, ..., 6$.

TABLE 7. Measures of singletons with respect to μ_1

$\mu_1(x_1) = 0.414$	$\mu_1(x_2) = 0.213$
$\mu_1(x_3) = 0.072$	$\mu_1(x_4) = 0.222$
$\mu_1(x_5) = 0.076$	$\mu_1(x_6) = 0.073.$

The measures of singletons and interaction indices determine the set function μ_1 in (2). Before calculating the measures of each subset, we have to check the monotonicity of μ_1

by using Theorem 2.2 of [36] which yields that the function μ_1 given in (2) is monotone if and only if

$$\mu_1(x_i) + \lambda_{ij} \geq 0$$

for any $i = 1, 2, ..., 6$ and any $j \neq k$. As $\min_{1\leq i\leq 6} \mu_1(x_i) + \min_{1\leq i\neq j\leq 6} \lambda_{ij} = 0.072 - 0.070 > 0$, we immediately have that μ_1 is monotone. Hence, it is a fuzzy measure over X. Now, we are ready to calculate the measures of all subsets of X by using Table 6 and 7 (see, Appendix).

Fuzzy measure 2 and 3 (μ_2 and μ_3): Due to the redundancy among criteria (Table 1) we construct sub-additive λ-fuzzy measures by using negative λ values. As we mentioned before a λ-fuzzy measure is sub-additive whenever $0 < \lambda < 1$.

To identify a λ-fuzzy measure we have to be given either the value of λ and the weights of the singletons [39] or measures of singletons (see, e.g., Formula 2 of [40]). Considering the weights in Table 4 and negative λ values and using the input number standard method of Section 5 of [54], which is the English version of [39], we construct the promised λ-fuzzy measures. For $\lambda = -0.75$ and $\lambda = -0.98$ we can identify the fuzzy measures μ_2 and μ_3 given in the Appendix. Here, for the sake of completeness we keep the identification of $\mu_2(\{x_3\})$. As $1 + \lambda = 0.25$ we need the function $\phi_{0.25} : [0, 1] \to [0, 1]$ (see, [54]) that is defined by

$$\phi_{0.25}(u) := \frac{0.25^u - 1}{0.75}.$$

As

$$\mu_2(\{x_3\}) = \phi_{0.25}(w_3 = 0.067) = \frac{0.25^{0.067} - 1}{0.75}$$

we get $\mu_2(\{x_3\}) \cong 118264$ (see, [54]).

3.2. **Computational Studies.** In this sub-section, six solution approaches are generated by considering three different sub-additive fuzzy measures and two different fuzzy integral methods. We calculate the Sugeno integral and Choquet integral of the alternatives with respect to the fuzzy measures μ_1, μ_2 and μ_3 obtained in Sub-section 3.1. Thus, we get six different approaches (methods) $M_1 - M_6$ given in Table 8.

TABLE 8. Approaches (methods)

M_1 : Sugeno integral with respect to μ_1
M_2 : Choquet integral with respect to μ_1
M_3 : Sugeno integral with respect to μ_2
M_4 : Choquet integral with respect to μ_2
M_5 : Sugeno integral with respect to μ_3
M_6 : Choquet integral with respect to μ_3

A fuzzy integral ranks alternatives by considering the interaction between conflicting criteria. More higher value in a fuzzy integral indicates more favorable alternative (see e.g., [55]). The rankings obtained by these approaches are showed in Table 9 and visualized in Figure 1. We conclude that gene region COI is the most favorable gene region that determines the diversification of species of rodent populations and Cytb is the second one in each approaches. We get close scores for the rest of the alternatives.

For the sake of completeness we keep the calculation of the Choquet integral (see, (1)) of $f =$**Cytb** with respect to μ_1. Firstly, we need the permuted values obtained in the Table 10.

TABLE 9. Scores of the fuzzy integrals

	M_1	M_2	M_3	M_4	M_5	M_6
Cytb	0.607	0.634296	0.608	0.686276	0.795	0.758633
COI	**0.686**	**0.745877**	**0.723**	**0.789616**	**0.827469**	**0.853264**
12SrRNA	0.519	0.520514	0.564	0.535812	0.564	0.55602
16SrRNA	0.500	0.477236	0.564	0.511201	0.564	0.549788
IRBP	0.493	0.504344	0.564	0.571198	0.603749	0.659413
VwF	0.527	0.538976	0.582075	0.594962	0.664	0.667087

TABLE 10. Values of function f and measures of permuted sets

$x_{(1)} = x_3$	$x_{(2)} = x_5$	$x_{(3)} = x_6$
$x_{(4)} = x_4$	$x_{(5)} = x_2$	$x_{(6)} = x_1$
$f\left(x_{(1)}\right) = 0.310$	$f\left(x_{(2)}\right) = 0.400$	$f\left(x_{(3)}\right) = 0.421$
$f\left(x_{(4)}\right) = 0.607$	$f\left(x_{(5)}\right) = 0.608$	$f\left(x_{(6)}\right) = 0.795$
$\mu_1(E_{(1)}) = 1$	$\mu_1(E_{(2)}) = 0.928$	$\mu_1(E_{(3)}) = 0.852$
$\mu_1(E_{(4)}) = 0.779$	$\mu_1(E_{(5)}) = 0.572$	$\mu_1(E_{(6)}) = 0.414.$

Considering the permuted values in Table 10 one can obtain

$$\begin{aligned}(C)\int_X f d\mu_1 &:= \sum_{k=1}^{6}\left(f\left(x_{(k)}\right) - f\left(x_{(k-1)}\right)\right)\mu_1(E_{(k)}) \\ &= 0.634296.\end{aligned}$$

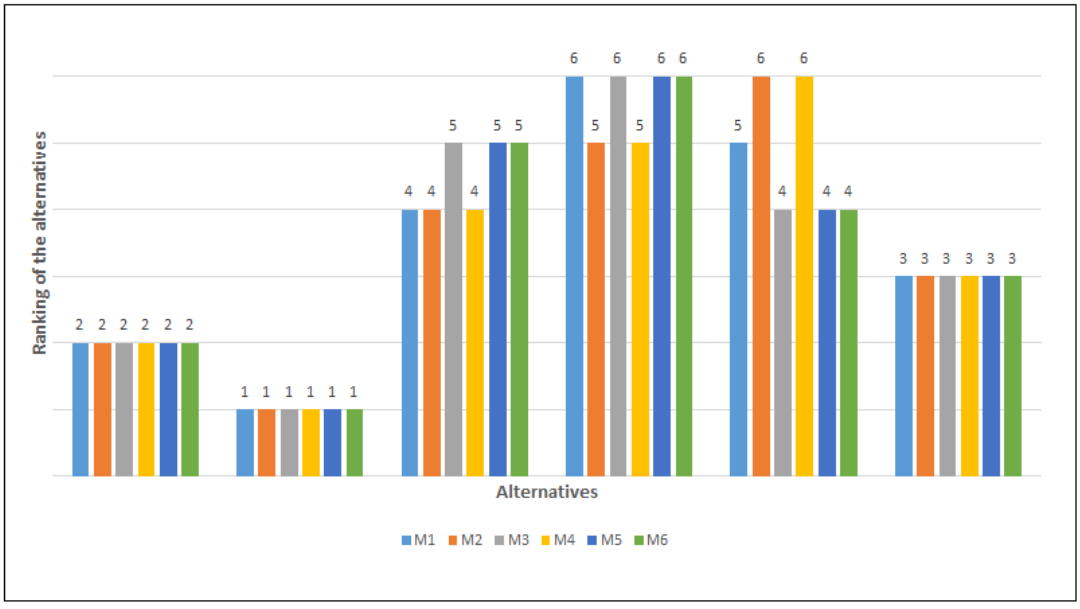

FIGURE 2. Visualization of the rankings of the alternatives according to six approaches

3.3. **Evaluation of the results.** The main findings are:

• In Figure 1 we can see all approaches indentify COI as the most favorable alternative.

• It is interesting that the gene region Cytb is obtained as the second most favorable alternative from all approaches.

• It is evaluated that the third most favorable alternative is found as the gene region VwF from all approaches.

• It is worth to note that close rankings are obtained for the rest of the remain alternatives.

To review the correlations of the approaches we employ the Spearman's rank correlation coefficients [56] which assesses the ordinal or ranked variables. $r(M_i, M_j)$ values are considered as highly valid range $r(M_i, M_j) \geq 0.71$ [56]. The values support strength of the results in terms of statistics. Figure 3 shows the Spearman's rank correlation coefficients which show the consistency of our results.

	M1	M2	M3	M4	M5	M6
M1	1	0,942857	1	0,828571	0,828571	0,828571
M2	0,942857	1	0,942857	0,942857	0,942857	0,942857
M3	1	0,942857	1	0,828571	0,828571	0,828571
M4	0,828571	0,942857	0,828571	1	1	1
M5	0,828571	0,942857	0,828571	1	1	1
M6	0,828571	0,942857	0,828571	1	1	1

FIGURE 3. The Spearman's rank correlation coefficients

4. CONCLUSION

In this paper, we present an interesting application of fuzzy integrals and fuzzy measure theory as tools for decision making in the context of choosing gene region. This study is the first one in this practical perspective.

The biomolecule based reconstruction of ancient phylogenetic history first requires the discovery and analysis of slowly evolving nucleotide or amino acid sequences. Not all genes or macromolecules are suitable phylogenetic markers and not all marker molecules are useful for the analysis of a given group of organisms [4].

Since mtDNA has a faster rate of evolution than nuclear genes, it is more preferred to detect phylogenetic differences between closer taxa [4, 57–59]. In this study, COI gene region on mtDNA was found to be the most effective marker to differentiate species. Furthermore, COI gene has a slower evolution rate than other mtDNA genes, and has a wide range of uses in molecular phylogeny [8, 60, 61]. COI is a gene region used in barcoding, especially for animals [62–67]. The DNA barcoding is a system which reveals species-specific DNA profiles, enables the identification of any organism at the species level according to the differences in DNA sequence in small parts of the genomes of organisms [68]. This study supports the effectiveness of COI as a barcode marker for rodent species. The other most effective marker was Cytb. Cytb is more preferred for the separation of relatively close taxa [4, 69–74]. Although the cytochrome b gene provides phylogenetically useful information, as the evolutionary depth increases, the efficiency of the gene may be

reduced [4]. In this case, it may be necessary to increase the reliability of studying the more conserved gene regions in the evolutionary process. In addition to the Cytb gene region, COI, ribosomal RNA or nuclear DNA gene regions are used in many phylogenetic studies. In this study, the 12SrRNA and 16SrRNA gene regions were not consistent to differentiate the species. These genes, which have similar structures and functions in all organisms ranging from bacteria to humans, also include numerous interspecies and intraspecies nucleotide variations [75–79]. Even if ribosomal RNA is considered as the best target for studying phylogenetic relationship because, it is universal and variable domains, rRNA genes are evolving more slowly and can be effective for the phylogenetic analysis of distantly related species [80–82]. Nuclear genes (IRBP and vWF) had the close scores with rRNA genes because they have less substitution rates, are generally used to detect deeper taxa (e.g. superordinal) [3, 83]. However, vWF was calculated as a more useful gene region to display interspecific differentiation. Further studies are need to show the segregation power of the nuclear genes in rodent species.

A fuzzy integral ranks alternatives by considering the interaction between conflicting criteria. More higher value in a fuzzy integral indicates more favorable alternative. In this study, we determine the most favorable gene region that determines the diversification of species of selected rodent populations. The problem is considered as a MCGDM problem. The pairs of rodent species given in Table 1 are considered as criteria and we use two different fuzzy integral methods (Sugeno integral and Choquet integral) with respect to three different fuzzy measures as aggregation tools. In six cases we get similar results. Consequently, this study is a reference for the marker choice in phylogenetic studies as it exposes that the effective markers to evaluate diversification among species are COI and Cytb. This study also supports that the marker COI which is still used as a barcode gene is the most effective marker for barcoding the rodent species.

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6. Appendix

Table 11. Ranking of alternatives over criteria for Expert 1

	$\mathbf{x}_1$	$\mathbf{x}_2$	$\mathbf{x}_3$	$\mathbf{x}_4$	$\mathbf{x}_5$	$\mathbf{x}_6$
Cytb	9	5	2	7	4	3
COI	6	9	6	4	7	5
12SrRNA	5	4	3	7	4	6
16SrRNA	5	4	4	4	5	6
IRBP	2	4	9	4	6	7
VwF	3	7	7	6	8	8

TABLE 12. Ranking of alternatives over criteria for Expert 2

	$\mathbf{x}_1$	$\mathbf{x}_2$	$\mathbf{x}_3$	$\mathbf{x}_4$	$\mathbf{x}_5$	$\mathbf{x}_6$
Cytb	8	5	3	8	4	5
COI	6	7	7	9	4	6
12SrRNA	6	7	6	5	5	6
16SrRNA	5	3	5	4	5	5
IRBP	6	5	8	5	8	8
VwF	4	3	7	7	6	9

TABLE 13. Ranking of alternatives over criteria for Expert 3

	$\mathbf{x}_1$	$\mathbf{x}_2$	$\mathbf{x}_3$	$\mathbf{x}_4$	$\mathbf{x}_5$	$\mathbf{x}_6$
Cytb	7	9	5	4	4	5
COI	9	6	5	9	7	4
12SrRNA	5	5	6	5	5	5
16SrRNA	6	5	5	3	5	5
IRBP	5	6	6	9	9	7
VwF	6	7	6	7	7	6

TABLE 14. Comparison matrix for Expert 1

	$\mathbf{x}_1$	$\mathbf{x}_2$	$\mathbf{x}_3$	$\mathbf{x}_4$	$\mathbf{x}_5$	$\mathbf{x}_6$
$\mathbf{x}_1$	1	1	4	1	4	3
$\mathbf{x}_2$	1	1	1	1	3	2
$\mathbf{x}_3$	0.25	1	1	0.25	1	1
$\mathbf{x}_4$	1	1	4	1	1	2
$\mathbf{x}_5$	0.25	0.33	1	1	1	1
$\mathbf{x}_6$	0.33	0.50	1	0.50	1	1

TABLE 15. Comparison matrix for Expert 2

	$\mathbf{x}_1$	$\mathbf{x}_2$	$\mathbf{x}_3$	$\mathbf{x}_4$	$\mathbf{x}_5$	$\mathbf{x}_6$
$\mathbf{x}_1$	1	3	5	2	5	5
$\mathbf{x}_2$	0.33	1	4	1	3	3
$\mathbf{x}_3$	0.20	0.25	1	0.25	1	1
$\mathbf{x}_4$	0.33	1	4	1	4	3
$\mathbf{x}_5$	0.20	0.33	1	0.25	1	1
$\mathbf{x}_6$	0.20	0.33	1	0.33	1	1

TABLE 16. Comparison matrix for Expert 3

	$\mathbf{x}_1$	$\mathbf{x}_2$	$\mathbf{x}_3$	$\mathbf{x}_4$	$\mathbf{x}_5$	$\mathbf{x}_6$
$\mathbf{x}_1$	1	4	6	5	6	6
$\mathbf{x}_2$	0.25	1	5	1	5	4
$\mathbf{x}_3$	0.16	0.20	1	0.20	1	1
$\mathbf{x}_4$	0.20	1	5	1	5	5
$\mathbf{x}_5$	0.16	0.20	1	0.20	1	2
$\mathbf{x}_6$	0.16	0.25	1	0.20	0.50	1

TABLE 17. μ_1 measures of sets of two elements

$\mu_1(x_1, x_2) = 0.572$	$\mu_1(x_1, x_3) = 0.476$	$\mu_1(x_1, x_4) = 0.581$
$\mu_1(x_1, x_5) = 0.480$	$\mu_1(x_1, x_6) = 0.477$	$\mu_1(x_2, x_3) = 0.260$
$\mu_1(x_2, x_4) = 0.365$	$\mu_1(x_2, x_5) = 0.264$	$\mu_1(x_2, x_6) = 0.261$
$\mu_1(x_3, x_4) = 0.269$	$\mu_1(x_3, x_5) = 0.078$	$\mu_1(x_3, x_6) = 0.075$
$\mu_1(x_4, x_5) = 0.273$	$\mu_1(x_4, x_6) = 0.270$	$\mu_1(x_5, x_6) = 0.079$

TABLE 18. μ_1 measures of sets of three elements

$\mu_1(x_1, x_2, x_3) = 0.644$	$\mu_1(x_1, x_2, x_4) = 0.779$
$\mu_1(x_1, x_2, x_5) = 0.648$	$\mu_1(x_1, x_2, x_6) = 0.645$
$\mu_1(x_1, x_3, x_4) = 0.653$	$\mu_1(x_1, x_3, x_5) = 0.492$
$\mu_1(x_1, x_3, x_6) = 0.489$	$\mu_1(x_1, x_4, x_5) = 0.657$
$\mu_1(x_1, x_4, x_6) = 0.654$	$\mu_1(x_1, x_5, x_6) = 0.493$
$\mu_1(x_2, x_3, x_4) = 0.437$	$\mu_1(x_2, x_3, x_5) = 0.291$
$\mu_1(x_2, x_3, x_6) = 0.288$	$\mu_1(x_2, x_4, x_5) = 0.441$
$\mu_1(x_2, x_4, x_6) = 0.438$	$\mu_1(x_2, x_5, x_6) = 0.292$
$\mu_1(x_3, x_4, x_5) = 0.300$	$\mu_1(x_3, x_4, x_6) = 0.297$
$\mu_1(x_3, x_5, x_6) = 0.151$	$\mu_1(x_4, x_5, x_6) = 0.301$

TABLE 19. μ_1 measures of sets of four elements

$\mu_1(x_1, x_2, x_3, x_4) = 0.851$	$\mu_1(x_1, x_2, x_3, x_5) = 0.705$	$\mu_1(x_1, x_2, x_3, x_6) = 0.702$
$\mu_1(x_1, x_2, x_4, x_5) = 0.870$	$\mu_1(x_1, x_2, x_4, x_6) = 0.852$	$\mu_1(x_1, x_2, x_5, x_6) = 0.706$
$\mu_1(x_1, x_3, x_4, x_5) = 0.714$	$\mu_1(x_1, x_3, x_4, x_6) = 0.711$	$\mu_1(x_1, x_3, x_5, x_6) = 0.565$
$\mu_1(x_1, x_4, x_5, x_6) = 0.715$	$\mu_1(x_2, x_3, x_4, x_5) = 0.513$	$\mu_1(x_2, x_3, x_4, x_6) = 0.510$
$\mu_1(x_2, x_3, x_5, x_6) = 0.364$	$\mu_1(x_2, x_4, x_5, x_6) = 0.514$	$\mu_1(x_3, x_4, x_5, x_6) = 0.373$

TABLE 20. μ_1 measures of sets of five elements

$\mu_1(x_1, x_2, x_3, x_4, x_5) = 0.927$	$\mu_1(x_1, x_2, x_3, x_4, x_6) = 0.924$
$\mu_1(x_1, x_2, x_3, x_5, x_6) = 0.778$	$\mu_1(x_1, x_2, x_4, x_5, x_6) = 0.928$
$\mu_1(x_1, x_3, x_4, x_5, x_6) = 0.787$	$\mu_1(x_2, x_3, x_4, x_5, x_6) = 0.586$

TABLE 21. μ_1 measures of entire set and empty set

$\mu_1(X) = 1,\ \mu_1(\varnothing) = 0$

TABLE 22. μ_2 measures of singletons

$\mu_2(x_1) = 0.553364$	$\mu_2(x_2) = 0.322013$
$\mu_2(x_3) = 0.118264$	$\mu_2(x_4) = 0.33319$
$\mu_2(x_5) = 0.125223$	$\mu_2(x_6) = 0.120178$

TABLE 23. μ_2 measures of sets of two elements

$\mu_2(x_1, x_2) = 0.741734$	$\mu_2(x_1, x_3) = 0.622678$	$\mu_2(x_1, x_4) = 0.748272$
$\mu_2(x_1, x_5) = 0.626616$	$\mu_2(x_1, x_6) = 0.623665$	$\mu_2(x_2, x_3) = 0.411888$
$\mu_2(x_2, x_4) = 0.574734$	$\mu_2(x_2, x_5) = 0.416993$	$\mu_2(x_2, x_6) = 0.413167$
$\mu_2(x_3, x_4) = 0.422071$	$\mu_2(x_3, x_5) = 0.232585$	$\mu_2(x_3, x_6) = 0.227989$
$\mu_2(x_4, x_5) = 0.42712$	$\mu_2(x_4, x_6) = 0.423336$	$\mu_2(x_5, x_6) = 0.234113$

TABLE 24. μ_2 measures of sets of three elements

$\mu_2(x_1, x_2, x_3) = 0.794309$	$\mu_2(x_1, x_2, x_4) = 0.88957$
$\mu_2(x_1, x_2, x_5) = 0.797295$	$\mu_2(x_1, x_2, x_6) = 0.795057$
$\mu_2(x_1, x_3, x_4) = 0.800265$	$\mu_2(x_1, x_3, x_5) = 0.689421$
$\mu_2(x_1, x_3, x_6) = 0.686732$	$\mu_2(x_1, x_4, x_5) = 0.803219$
$\mu_2(x_1, x_4, x_6) = 0.643109$	$\mu_2(x_1, x_5, x_6) = 0.690315$
$\mu_2(x_2, x_3, x_4) = 0.64215$	$\mu_2(x_2, x_3, x_5) = 0.498427$
$\mu_2(x_2, x_3, x_6) = 0.494941$	$\mu_2(x_2, x_4, x_5) = 0.645979$
$\mu_2(x_2, x_4, x_6) = 0.643109$	$\mu_2(x_2, x_5, x_6) = 0.499586$
$\mu_2(x_3, x_4, x_5) = 0.507654$	$\mu_2(x_3, x_4, x_6) = 0.504206$
$\mu_2(x_3, x_5, x_6) = 0.331799$	$\mu_2(x_4, x_5, x_6) = 0.5088$

TABLE 25. μ_2 measures of sets of four elements

$\mu_2(x_1, x_2, x_3, x_4) = 0.929006$	$\mu_2(x_1, x_2, x_3, x_5) = 0.844932$	$\mu_2(x_1, x_2, x_3, x_6) = 0.842892$
$\mu_2(x_1, x_2, x_4, x_5) = 0.931247$	$\mu_2(x_1, x_2, x_4, x_6) = 0.929568$	$\mu_2(x_1, x_2, x_5, x_6) = 0.84561$
$\mu_2(x_1, x_3, x_4, x_5) = 0.850329$	$\mu_2(x_1, x_3, x_4, x_6) = 0.848312$	$\mu_2(x_1, x_3, x_5, x_6) = 0.747459$
$\mu_2(x_1, x_4, x_5, x_6) = 0.851$	$\mu_2(x_2, x_3, x_4, x_5) = 0.707063$	$\mu_2(x_2, x_3, x_4, x_6) = 0.704448$
$\mu_2(x_2, x_3, x_5, x_6) = 0.57368$	$\mu_2(x_2, x_4, x_5, x_6) = 0.707933$	$\mu_2(x_3, x_4, x_5, x_6) = 0.582075$

TABLE 26. μ_2 measures of sets of five elements

$\mu_2(x_1, x_2, x_3, x_4, x_5) = 0.966979$	$\mu_2(x_1, x_2, x_3, x_4, x_6) = 0.96545$
$\mu_2(x_1, x_2, x_3, x_5, x_6) = 0.888953$	$\mu_2(x_1, x_2, x_4, x_5, x_6) = 0.967488$
$\mu_2(x_1, x_3, x_4, x_5, x_6) = 0.893864$	$\mu_2(x_2, x_3, x_4, x_5, x_6) = 0.763511$

TABLE 27. μ_2 measures of entire set and empty set

$\mu_2(X) = 1,\ \mu_2(\varnothing) = 0$

TABLE 28. μ_3 measures of singletons

$\mu_3(x_1) = 0.827469$	$\mu_3(x_2) = 0.590954$
$\mu_3(x_3) = 0.258675$	$\mu_3(x_4) = 0.605544$
$\mu_3(x_5) = 0.271836$	$\mu_3(x_6) = 0.261987$

TABLE 29. μ_3 measures of sets of two elements

$\mu_3(x_1, x_2) = 0.935464$	$\mu_3(x_1, x_3) = 0.874741$	$\mu_3(x_1, x_4) = 0.93813$
$\mu_3(x_1, x_5) = 0.877146$	$\mu_3(x_1, x_6) = 0.875347$	$\mu_3(x_2, x_3) = 0.698651$
$\mu_3(x_2, x_4) = 0.843067$	$\mu_3(x_2, x_5) = 0.70413$	$\mu_3(x_2, x_6) = 0.70003$
$\mu_3(x_3, x_4) = 0.709514$	$\mu_3(x_3, x_5) = 0.461062$	$\mu_3(x_3, x_6) = 0.45373$
$\mu_3(x_4, x_5) = 0.714804$	$\mu_3(x_4, x_6) = 0.710845$	$\mu_3(x_5, x_6) = 0.463485$

TABLE 30. μ_3 measures of sets of three elements

$\mu_3(x_1, x_2, x_3) = 0.955145$	$\mu_3(x_1, x_2, x_4) = 0.981537$
$\mu_3(x_1, x_2, x_5) = 0.956147$	$\mu_3(x_1, x_2, x_6) = 0.955397$
$\mu_3(x_1, x_3, x_4) = 0.95713$	$\mu_3(x_1, x_3, x_5) = 0.911727$
$\mu_3(x_1, x_3, x_6) = 0.910387$	$\mu_3(x_1, x_4, x_5) = 0.958097$
$\mu_3(x_1, x_4, x_6) = 0.957374$	$\mu_3(x_1, x_5, x_6) = 0.91217$
$\mu_3(x_2, x_3, x_4) = 0.886354$	$\mu_3(x_2, x_3, x_5) = 0.782913$
$\mu_3(x_2, x_3, x_6) = 0.77986$	$\mu_3(x_2, x_4, x_5) = 0.888557$
$\mu_3(x_2, x_4, x_6) = 0.886908$	$\mu_3(x_2, x_5, x_6) = 0.783922$
$\mu_3(x_3, x_4, x_5) = 0.79086$	$\mu_3(x_3, x_4, x_6) = 0.787913$
$\mu_3(x_3, x_5, x_6) = 0.603749$	$\mu_3(x_4, x_5, x_6) = 0.791834$

TABLE 31. μ_3 measures of sets of four elements

$\mu_3(x_1, x_2, x_3, x_4) = 0.989447$	$\mu_3(x_1, x_2, x_3, x_5) = 0.970544$	$\mu_3(x_1, x_2, x_3, x_6) = 0.969986$
$\mu_3(x_1, x_2, x_4, x_5) = 0.98985$	$\mu_3(x_1, x_2, x_4, x_6) = 0.989549$	$\mu_3(x_1, x_2, x_5, x_6) = 0.970728$
$\mu_3(x_1, x_3, x_4, x_5) = 0.971996$	$\mu_3(x_1, x_3, x_4, x_6) = 0.971458$	$\mu_3(x_1, x_3, x_5, x_6) = 0.937802$
$\mu_3(x_1, x_4, x_5, x_6) = 0.972174$	$\mu_3(x_2, x_3, x_4, x_5) = 0.920222$	$\mu_3(x_2, x_3, x_4, x_6) = 0.918995$
$\mu_3(x_2, x_3, x_5, x_6) = 0.84232$	$\mu_3(x_2, x_4, x_5, x_6) = 0.920627$	$\mu_3(x_3, x_4, x_5, x_6) = 0.84821$

TABLE 32. μ_3 measures of sets of five elements

$\mu_3(x_1, x_2, x_3, x_4, x_5) = 0.995637$	$\mu_3(x_1, x_2, x_3, x_4, x_6) = 0.995412$
$\mu_3(x_1, x_2, x_3, x_5, x_6) = 0.9814$	$\mu_3(x_1, x_2, x_4, x_5, x_6) = 0.995711$
$\mu_3(x_1, x_3, x_4, x_5, x_6) = 0.982477$	$\mu_3(x_2, x_3, x_4, x_5, x_6) = 0.944099$

TABLE 33. μ_3 measures of entire set and empty set

$\mu_3(X) = 1,\ \mu_3(\varnothing) = 0$

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Gül Olgun Karacan is an Assistant Professor in the Department of Medical Laboratory Techniques of Aksaray University Health Services Vocational School in Turkey. She completed her PhD and MSc in the field of Biology at Ankara University. Her research area includes population genetics, phylogeny, and micro-evolution and bioinformatics.

Mehmet Ünver earned his PhD degree in mathematics from Ankara University (Turkey). He worked as an assistant professor at Ankara University for about 2 years and currently, he has been working as an associate professor at Ankara University since 2017. His research interests are fuzzy measure theory, approximation theory and summability theory.

Mario Inostroza-Ponta is an Associate Professor in the Departamento de Ingeniería Informática of the Universidad de Santiago de Chile. He earned his PhD degree from the University of Newcastle, Australia, and his master's degree from the Universidad de Santiago de Chile. In 2008, he received the Prominent Professor Award at the Faculty of Engineering of the Universidad de Santiago de Chile. His research expertise includes bioinformatics, data mining, metaheuristics, combinatorial optimization and multiobjective optimization.