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Performance Comparison of Fuzzy Clustering and Hard Clustering (K-Means) Methods for Grouping of Wheat Genotypes

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ABSTRACT

In data clustering, partition based clustering algorithms are widely used clustering algorithms. Among various partition algorithms, fuzzy algorithms, Fuzzy c-Means (FCM) and non-fuzzy algorithm, k-means (KM) are most popular methods. k-means and Fuzzy c-Means use standard Euclidian distance measure. In this work, a comparative study of these algorithms with Secondary data on growth and yield attributes of 67 genotypes of wheat is presented. The performance of the two algorithms is analyzed based on the clustering output criteria. The results were compared with the results obtained from the both methods. The results showed that Fuzzy c-means clustering method provides better group separation for wheat genotypes whereas k-means provides more compact clusters.

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Email: pooniahemant80@gmail.com *Corresponding author **Keywords** Fuzzy c-means, K-means, Data clustering, Wheat genotypes.

INTRODUCTION

Many organizations generate and store large volume of data in their databases. The methods to extract the most useful knowledge from the databases are known as Data mining or knowledge discovery in databases (KDD). Data mining is an analytic process of discovering valid, unsuspected relationships among datasets and transforms the data into a structure that are both understandable and useful to the users. Data analysis contains several techniques and tools for handling the data. Classification or clustering is well known method in data analysis. It is a multivariate analysis technique to partition the dataset into groups (classes or clusters) in a dataset such that the most indiscernible objects belong to the same group while the discernible objects in different groups. Clustering methods are used as a common technique in many fields such as pattern recognition, machine learning, image segmentation, medical diagnostics and bioinformatics (Jain et al. 1999).

The two important features in clustering are partition based clustering and hierarchical-based clustering. Partition based clustering algorithms have the capable of discovering underlying structures of clusters by using appropriate objective function (Velmurugan and Santhanam 2011). The algorithms k-means (KM) and Fuzzy c-Means (FCM) clustering

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algorithms are widely used partition-based clustering algorithms. The algorithms k-means and Fuzzy c-Means are proposed based on Euclidean distance measure. Yin et al. (2014) analyzed the performance of k-means and Fuzzy c-Means algorithms and reported that the k-means method is preferable to FCM for Arterial Input Function (AIF) detection using both clinical and simulated data. Velmurugun (2012) has compared the clustering performance of k-means and Fuzzy c-Means algorithms using different shapes of arbitrary distributed data points and reported that the k-means performs better than FCM. Wang and Garibaldi (2005) have compared the performance of k-means and Fuzzy c-Means algorithms on Infrared spectra collected from auxiliary lymph node tissue section. Bora and Gupta (2014) evaluated the performance between k-means and Fuzzy c-Means algorithms based on time complexity. Gosh and Dubey (2013) evaluated the clustering performance of k-means and Fuzzy c-Means algorithms on the basis of the efficiency of the clustering output and the computational time and reported that k-means is superior to FCM. Jipkate and Gohokar (2012) compared the color image segmentation performance between k-means and Fuzzy c-Means algorithms. Cebeci and Yildiz (2015) compared the k-means (KM) and the Fuzzy c-means (FCM) algorithms for their computing performance and clustering accuracy on different shaped cluster structures which are regularly and irregularly scattered in two dimensional space. By advancing an adaptive algorithm for the entropy weight of the feature weight of FCM, Huang et al. (2016) focused on the influence of the feature weight on a clustering algorithm. Kapoor and Singhal (2017) discussed the partition-predicted clustering techniques, such as k-Means, k-Means++ and object predicted Fuzzy c-Means clustering algorithm and proposed a method for getting better clustering result by application of sorted and unsorted data into the algorithms. Hassan et al. (2020) investigated in KM and FCM performance and which of them has better ability to construct balanced clusters, in order to enable the researchers to choose the appropriate algorithm for the purpose of improving network lifespan.

The work in this paper aimed to compare the performance of the two clustering techniques, k-means (KM) and Fuzzy c-means (FCM). These two methods are applied on secondary data on growth and yield attributes of 67 wheat genotypes and examined the performance of both clustering approach. It is observed that Fuzzy c-means clustering method provides better group separation for wheat genotypes whereas k-means provides more compact clusters.

MATERIALS AND METHODS

Clustering is an unsupervised data analysis which is used to partition a set of records or objects into clusters or classes with similar characteristics. The partition is done in such a fashion that most similar (or related) objects are placed together, while dissimilar (or unrelated) objects are placed in different classes or groups. The desired characteristics of clustering methods are ability to deal with different types of attributes with high dimensionality, effective handling of outliers and noise with minimum knowledge, ability to discover the underlying shapes and structures of the data, scalability, usability and interpretability. Clustering methods are categorized into five different methods: Partitioning method, hierarchical method, data density based method, grid based method and model based or soft computing methods. Among these five methods partition based methods, k-means (KM) and Fuzzy c-Means (FCM) clustering algorithms are implemented on secondary data on growth and yield attributes of 67 wheat genotypes to generate three clusters and six clusters.

RESULTS AND DISCUSSION

Secondary data on growth and yield attributes of 67 genotype wheat was used for examining the performance of fuzzy clustering approach. The experiment was conducted at the university farm with 6 row/entry and row length of 6 m. The detail of the genotypes and variables considered is given below:

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1	AL 1	24	AL 24	47	AL 47
2	AL 2	25	AL 25	48	AL 48
3	AL 3	26	AL 26	49	AL 49
4	AL 4	27	AL 27	50	HD3086
5	AL 5	28	AL 28	51	WH 1025
6	AL 6	29	AL 29	52	WH 542
7	AL 7	30	AL 30	53	WH 711
8	AL 8	31	AL 31	54	WH 1105
9	AL 9	32	AL 32	55	WH 1124

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
10 11 12 13 14 15 16 17	AL 10 AL 11 AL 12 AL 13 AL 14 AL 15 AL 16 AL 17	33 34 35 36 37 38 39 40	AL 33 AL 34 AL 35 AL 36 AL 37 AL 38 AL 39 AL 40	56 57 58 59 60 61 62 63	UP 2338 HD 2687 WH 1080 PBW 343 DPW621-50 PBW 550 DBW 17 HD 2967
18 19 20 21 22 23	AL 18 AL 19 AL 20 AL 21 AL 22 AL 23	41 42 43 44 45 46	AL 41 AL 42 AL 43 AL 44 AL 45 AL 46	64 65 66 67	HD 2851 RAJ 3765 PBW 373 PBW 590
 Biological yield (kg /plot) Harvest Index (%) Plant Height (cm) Spike length (cm) No. of tillers/ meter Grain weight (g/ spike) Flag leaf breath (cm) 			2. Grain y 4. No. of 6. 1000 8. Spike 10. Spik 12. Flag 14. Flag	ield (kg/p f days to ł grain weią let/spike e weight (leaf lengt leaf area	lot) neading ght (g) (g) h (cm) (cm ²)

 $\label{eq:table1} \textbf{Table 1.} Grouping of wheat genotypes into six clusters (k-means).$

Cluster	Cluster size	Wheat genotypes
Ι	6	AL 21, AL 28, AL 41, AL 43, HD2851, PBW373
Π	23	AL 1, AL 4, AL 9, AL 10, AL 11, AL 12, AL 13, AL 14, AL 15, AL 17, AL18, AL 23, AL 25, AL 27, AL 33, AL 34, AL 37, AL 39, WH1025, WH1124, HD2687, RAJ3765, PBW590
III	2	AL 32, AL 45
IV	6	AL 8, WH 711, UP 2338, PBW343, DBW17, HD2967
V	27	AL 2, AL 3, AL 5, AL 6, AL 7, AL 16, AL 20, AL 22, AL 26, AL 30, AL 31, AL 35, AL 36, AL 38, AL 40, AL 42, AL 44, AL 46, AL 47, AL 48, AL 49, HD3086, WH 542, WH 1105, WH1080, DPW621-50, PBW550
VI	3	AL 19, AL 24, AL 29

Table 2.	Cluster means	(6-means)).
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Sl. No.	Character	Cluster		
		Ι	II	
1	Biological yield (kg /plot)	9.33	10.13	
2	Grain yield (kg/plot)	3.16	3.43	
3	Harvest index (%)	33.93	34.24	
4	No. of days to Heading	97.22	97.01	
5	Plant height (cm)	100.29	101.31	
6	1000 grain weight (g)	43.811	42.036	
7	Spike length (cm)	11.90	12.99	
8	Spikelet/spike	19.88	20.22	
9	No. of tillers/ meter	92.00	108.36	

Sl. No.	Character	Cluster		
		Ι	II	
10	Spike weight (g)	3.93	3.43	
11	Grain weight (g/ spike)	3.06	2.51	
12	Flag leaf length (cm)	28.8	28.6	
13	Flag leaf breath (cm)	2.25	2.24	
14	Flag leaf area (cm ²)	48.62	47.92	

Table 2. Continued.

Sl. No.	Character	Cluster		
		III	IV	
1	Biological yield (kg /plot)	9.50	10.32	
2	Grain yield (kg/plot)	2.92	3.61	
3	Harvest index (%)	30.78	35.19	
4	No. of days to heading	99.50	96.72	
5	Plant height (cm)	114.50	104.48	
6	1000 grain weight (g)	37.900	46.528	
7	Spike length (cm)	15.50	10.87	
8	Spikelet/spike	24.00	18.62	
9	No. of tillers/ meter	129.00	113.44	
10	Spike weight (g)	3.58	4.19	
11	Grain weight (g/ spike)	2.72	3.24	
12	Flag leaf length (cm)	29.8	23.1	
13	Flag leaf breath (cm)	2.45	2.11	
14	Flag leaf area (cm ²)	54.68	36.23	

Table 2. Continued.

Sl. No.	Character	Cluster		
		V	VI	
1	Biological yield (kg /plot)	9.92	10.25	
2	Grain yield (kg/plot)	3.54	3.46	
3	Harvest index (%)	35.71	33.91	
4	No. of days to heading	97.53	97.67	
5	Plant height (cm)	102.29	103.67	
6	1000 grain weight (g)	41.305	43.133	
7	Spike length (cm)	13.01	14.17	
8	Spikelet/spike	20.12	21.33	
9	No. of tillers/ meter	131.62	158.00	
10	Spike weight (g)	3.82	4.03	
11	Grain weight (g/ spike)	2.81	3.23	
12	Flag leaf length (cm)	25.5	27.5	
13	Flag leaf breath (cm)	2.32	2.53	
14	Flag leaf area (cm ²)	44.25	52.34	

Table 3. Distances	between cluster	centers	(6-means)).
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Clu- ster	1	2	3	4	5	6
1	12.58	16.588	41.097	26.007	40.178	66.270
2	16.588	12.54	26.525	15.240	23.826	49.955
3	41.097	26.525	5.71	29.683	18.548	31.932
4	26.007	15.240	29.683	12.79	21.002	47.932
5	40.178	23.826	18.548	21.002	11.77	27.873
6	66.270	49.955	31.932	47.932	27.873	11.30

 Table 4. Grouping of wheat genotypes in three different clusters (3-means).

Clu- ster	Cluster size	Wheat genotypes
T	17	AL 1 AL 9 AL 11 AL 14 AL 21 AL 25 AL
1	1,	27. AL 28. AL 33. AL 34. AL 39. AL 41. AL 43.
		PBW343, HD2851, PBW373, PBW590
II	44	AL 2, AL 3, AL 4, AL 5, AL 6, AL 7, AL 8, AL
		10, AL 12, AL 13, AL 15, AL 16, AL 17, AL 18,
		AL 20, AL 22, AL 23, AL 26, AL 31, AL 32, AL
		35, AL 37, AL 38, AL 40, AL 42, AL 44, AL
		45, AL 47, AL 48, AL 49, HD3086, WH1025,
		WH 542, WH 711, WH 1105, WH 1124, UP
		2338, HD2687, WH1080, DPW621-50,
		PBW550, DBW17, HD2967, RAJ3765
III	6	AL 19, AL 24, AL 29, AL 30, AL 36, AL 46

Table 5. 3-means cluster centers.

S1.	Character		Cluster	
No.		1	2	3
1	Biological yield (kg /plot)	9.57	10.11	10.17
2	Grain yield (kg/plot)	3.39	3.49	3.34
3	Harvest index (%)	35.70	34.66	32.95
4	No. of days to heading	97.24	97.21	98.33
5	Plant height (cm)	100.96	102.87	103.00
6	1000 grain weight (g)	42.583	42.177	41.600
7	Spike length (cm)	12.74	12.76	13.75
8	Spikelet/spike	20.11	20.01	21.50
9	No. of tillers/ meter	97.53	123.88	150.33
10	Spike weight (g)	3.58	3.83	3.43
11	Grain weight (g/ spike)	2.68	2.84	2.66
12	Flag leaf length (cm)	28.9	25.9	27.8
13	Flag leaf breath (cm)	2.23	2.28	2.45
14	Flag leaf area (cm ²)	48.49	44.13	51.09

Table 6. Distances between 3-means clusters.

Cluster	1	2	3	
1	12.49	26.975	53.043	
2	26.975	14.37	27.567	
3	53.043	27.567	11.98	

Table 7. Grouping of wheat genotypes in different clusters (Fuzzy 6-Means).

Cluster	Cluster size	Wheat genotypes
I	9	AL 2, AL 3, AL 5, AL 6, AL 7, AL 16, AL 20, AL 22, AL 26
II	14	AL 1, AL 4, AL 8, AL 9, AL 10, AL 11, AL 12, AL 13, AL 14, AL 15, AL 17, AL 18, AL 23, AL 25

Cluster	Cluster size	Wheat genotypes
III	9	AL 21, AL 27, AL 28, AL 33, AL 34, AL 37, AL 39, AL 41, AL 43
IV	15	AL 31, AL 32, AL 35, AL 38, AL 40, AL 42, AL 44, AL 45, AL 46, AL 47, AL 48, AL 49, HD3086, WH542, WH1105
V	15	WH1025, WH711, WH1124, UP2338, HD2687, WH1080, PBW343, DPW621-50, PBW550, DBW17, HD2967, HD2851, RAJ3765, PBW 373, PBW 590
VI	5	AL 19, AL 24, AL 29, AL 30, AL 36

Table 8. Euclidean distance matrix for clusters (Fuzzy 6-Means).

	Ι	II	III	IV	V	VI
I	12.01	20.39	42.05	33.18	51.3	28.87
II	20.39	10.63	27.72	39.02	47.75	45.06
III	42.05	27.72	11.46	37.95	33.2	55.14
IV	33.18	39.02	37.95	11.10	26.47	26.13
V	51.3	47.75	33.2	26.47	16.36	51.24
VI	28.87	45.06	55.14	26.13	51.24	12.23

Table 9. Grouping of wheat genotypes clusters (Fuzzy 3-Means).

Cluster	Cluster size	Wheat genotypes
Ι	22	AL 19, AL 20, AL 22, AL 24, AL 26, AL 29, AL 30, AL 31, AL 32, AL 35, AL 36, AL 38, AL 40, AL 42, AL 44, AL 45, AL 46, AL 47, AL 48, AL 49, HD3086, WH 542
II	23	AL 1, AL 2, AL 3, AL 4, AL 5, AL 6, AL 7, AL 8, AL 9, AL 10, AL 11, AL 12, AL 13, AL 14, AL 15, AL 16, AL 17, AL 18, AL 21, AL 23, AL 25, AL 27, AL 28
III	22	AL 33, AL 34, AL 37, AL 39, AL 41, AL 43, WH1025, WH 711, WH 1105, WH 1124, UP 2338, HD2687, WH1080, PBW343, DPW621-50, PBW550, DBW17, HD2967, HD2851, RAJ3765, PBW373, PBW590

 Table 10. Euclidean distance matrix for clusters (Fuzzy 3-Means).

Cluster Number	Ι	II	III
Ι	12.74	34.43	32.56
II	34.43	15.59	41.12
III	32.56	41.12	17.56

 Genotypes		Member	rship degi	ree (6-me	ans)		Member	ship degree		
Clust			Number					Cluster Number		
	Ι	II	III	IV	V	VI	Ι	II	III	
AL 1	0	1	0	0	0	0	0	1	0	
AL 2	0.99	0.01	0	0	0	0	0.01	0.99	0	
AL 3	0.99	0.01	0	0	0	0	0.01	0.99	0	
AL4	0	1	0	0	0	0	0	1	0	
AL 5	0.99	0.01	0	0	0	0	0	1	0	
AL 6	0.99	0	0	0	0	0	0.19	0.81	0	
AL 7	1	0	0	0	0	0	0.03	0.96	0	
AL 8	0.03	0.97	0	0	0	0	0	1	0	
AL9	0	1	0	0	0	0	0	1	0	
AL 10	0.06	0.94	0	0	0	0	0	1	0	
AL 11	0	1	0	0	0	0	0	1	0	
AL 12	0	1	0	0	0	0	0	1	0	
AL 13	0	1	0	0	0	0	0	1	0	
AL 14	0	1	0	0	0	0	0	1	0	
AL 15	0.01	0.99	0	0	0	0	0	1	0	
AL 16	0.8	0.2	0	0	0	0	0	1	0	
AL 17	0.02	0.98	0	0	0	0	0	1	0	
AL 18	0.01	0.99	0	0	0	0	0	1	0	
AL 19	0	0	0	0	0	1	0.99	0.01	0	
AL 20	1	0	0	0	0	0	0.93	0.07	0	
AL 21	0	0.07	0.93	0	0	0	0	0.97	0.03	
AL 22	0.82	0	0	0.01	0	0.17	1	0	0	
AL 23	0.39	0.6	0	0.01	0	0	0.01	0.98	0	
AL 24	0	0	0	0	0	1	1	0	0	
AL 25	0	0.8	0.19	0	0	0	0	1	0	
AL 26	0.79	0.03	0	0.17	0	0.02	0.96	0.04	0	
AL 27	0	0.01	0.99	0	0	0	0	0.96	0.03	
AL 28	0	0	1	0	0	0	0.01	0.79	0.2	
AL 29	0	0	0	0	0	1	1	0	0	
AL 30	0	0	0	0.02	0	0.98	1	0	0	
AL 31	0.05	0	0	0.93	0	0.02	1	0	0	
AL 32	0.05	0.01	0.01	0.84	0	0.09	0.99	0.01	0.01	
AL 33	0	0	1	0	0	0	0.02	0.4	0.59	
AL 34	0	0	1	0	0	0	0.02	0.32	0.66	
AL 35	0	0	0	1	0	0	1	0	0	
AL 36	0	0	0	0.02	0	0.98	1	0	0	
AL 37	0	0	0.99	0.01	0	0	0.02	0.04	0.94	
AL 38	0	0	0	1	0	0	1	0	0	
AL 39	0	0	1	0	0	0	0	0.01	0.98	
AL 40	0	0	0	1	0	0	1	0	0	
AL 41	0	0	1	0	0	0	0	0.01	0.99	
AL 42	0	0	0	1	0	0	1	0	0	
AL 43	0	0	1	0	0	0	0	0.02	0.98	
AL 44	0	0	0	1	0	0	0.92	0	0.08	
AL 45	0	0	0	1	0	0	0.99	0	0.01	
AL 46	0	0	0	0.99	0	0.01	1	0	0	
AL 47	0	0	0	1	0	0	1	0	0	
AL 48	0	0	0	1	0	0	1	0	0	
AL 49	0	0	0	1	0	0	0.95	0	0.05	
HD3086	0	0	0	1	0	0	0.89	0	0.11	
WH 1025	0	0	0.05	0.02	0.92	0	0	0	1	
WH 542	0	0	0	0.99	0.01	0	0.91	0	0.09	
 WH 711	0	0	0	0.01	0.99	0	0	0	1	

Table 11. Membership degree matrix for Fuzzy 6-Means and Fuzzy 3-Means methods.

Table 11. Continued.

Genotypes		Members	hip degree	(6-means)			Membershi (3-mea	p degree			
	Cluster Number							Cluster Number			
	Ι	II	III	IV	V	VI	Ι	II	III		
WH 1105	0	0	0	0.88	0.12	0	0.12	0	0.88		
WH 1124	0	0	0	0	1	0	0	0	1		
UP 2338	0	0	0	0.05	0.95	0	0.03	0	0.97		
HD 2687	0	0	0	0	1	0	0	0	1		
WH 1080	0	0	0	0.02	0.98	0	0.01	0	0.99		
PBW 343	0	0	0	0	1	0	0	0	1		
DPW621-50	0	0	0	0.4	0.6	0	0.16	0	0.84		
PBW 550	0	0	0	0.02	0.98	0	0	0	1		
DBW 17	0	0	0	0	1	0	0	0	1		
HD 2967	0	0	0	0	1	0	0	0	1		
HD 2851	0	0	0.01	0	0.99	0	0	0	1		
RAJ 3765	0	0	0	0.01	0.99	0	0	0	1		
PBW 373	0	0	0	0	1	0	0	0	1		
PBW 590	0	0	0.03	0	0.97	0	0	0	1		

 Table 12. Average inter and intra cluster distances for comparing k-means and Fuzzy c-Means methods.

Method	No. of clusters	Average distance		
		Inter	Intra	
k-means	6	32.18	11.12	
	3	35.86	12.95	
Fuzzy c-Means	6	37.70	12.30	
	3	36.04	15.30	

The k-means and Fuzzy c-means clustering methods with were tired with clusters sizes equal to 6 and 3 with Euclidean distance function as a measure separation. The clustering pattern of genotype for the 6-means clustering methods is given in Table1. The profile of the resulting clusters is given in Table 2 followed by inter and intra cluster distances in Table 3.

It was observed that tillers per meter and flag leaf area had considerable variations over the clusters whereas, a slight variation was observed for the remaining characters. Also two clusters (II and VI) had very low sizes suggesting less number of groups in the data. The similar results were also obtained from the 3-means clustering method (Table 4 - 6).

The genotypes were then grouped into clusters of sizes 6 and 3 using the Fuzzy c-means clustering method (Table 7 - 11). Average inter and intra cluster distances for comparing k-means and Fuzzy c-Means methods have been presented in Table 12.

CONCLUSIONS

It was observed that Fuzzy c-means clustering method provides more uniform distribution of the wheat genotype among various clusters as compared to the k-means method. Average inter cluster distance was observed to be more in Fuzzy c-Means clustering method than k-means indicating better group separation for wheat genotypes. C-means clustering method also indicated that some genotypes have high membership degree for two or more clusters. However, intra-cluster distance was observed to be less in case of k-means indicating that k-means clusters are more compact that Fuzzy c-means.

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