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Research Article

Application of Multiple Criteria Decision-Making approach for ranking Lentil genotypes

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ABSTRACT

The conception of the multiple criteria decision-making (MCDM) approach was applied to lentil genotypes under study to rank their performances. The study was conducted in University Research Farm, BCKV, West Bengal, during 2020-2021 and 2021-2022. The identification of 16 cultivars was performed using the above approach based on 7 different growth and yield attributing parameters. The concept of entropy was employed to assign suitable weights to the recorded characters for their relative importance in the assessment and ranking process. Considering 7 parameters (criteria), the variety L1112-7 ranked first. While the variety L1112-16 ranked the last. It was also observed that this approach was very robust as it can accommodate many alternatives for comparison with multiple numbers of characters or Alternatives.

Keywords: MCDM, TOPSIS, Entropy, Lentil

INTRODUCTION

Lentil is one of the important pulse crops worldwide for its nutritional value, market demands, affordability, nitrogen fixation, and drought resistance ability (Shrestha et al., 2023). Selection of location and agro-climatic condition-oriented genotypes is crucial for achieving this job. Several genotypes are available in different agro-climatic conditions. Decision-making is crucial in such situations. Multiple criteria decision-making (MCDM) is a usual technique in agriculture and other industries. Filar et al. (2003) applied the MCDM method, namely, the Technique for order of preference by similarity to ideal solution (TOPSIS) for multiple indicators of environmental evaluation. It has long been practiced to produce intercrops of products such as pineapples, sweet corn, shallots, papaya, and so on, and to grow two or more crops of these varied plants concurrently and combined in the same field. There have been many approaches available for solving MCDM problems, as summarized by Hwang and Yoon in 1981, but some of the methods were criticized as being ad hoc, and others have been thought to be, to some extent, inappropriate in theoretical or empirical grounds, as indicated by Stewart in 1992. The TOPSIS method was used by Filar et al. (2003) for environmental assessment based on several indicators. However, in general, MCDM methods are highly effective in helping decision-making in various conditions. Recently, Biswas et al. (2024) reported a successful application of the TOPSIS method in an experiment on a rice-based wheat cropping system under conservation agriculture to rank the fifteen tillage-based alternatives. However, the Analytic hierarchic process (AHP) method derived the criteria weights.

The present research looked at the application of MCDM approaches to the agricultural field, such as ranking crop varieties based on their performance. The application of MCDM to the agricultural sector did not get much attention in the past; it should be useful in decision support systems. For many years, several authors have attempted to identify a group of varieties suitable for a specific zone by either using;

i) The ANOVA model for selecting the better performers for each character under study or

ii) Clustering the varieties using Euclidean distance matrix and dendrogram, simultaneously considering multiple characters under study.

It can be shown that no performance evaluation method considering all the characters by a single index has yet been used on a large scale. Therefore, developing a single index that represents the entire set of traits under consideration is required to evaluate overall varietal performance fully and easily. Typically, such an index can be constructed as a function of the entire collection of varietal characteristics. Statistical techniques can be utilized to assess a single integrated indicator with appropriate robustness features for scientific judgment about the performance of various types. In the current study, the above-mentioned MCDM approach was used to evaluate 16 cultivars of lentil based on 7 growth and yield-attributing characters, including Primary branches per plant, Number of pods per plant, 100 seeds weight, Yield (Kg/ha), Days to 50% flowering, Days to maturity and Plant Height (cm).

MATERIALS AND METHODS

The experiment was conducted in Kalyani, West Bengal, India (220 56' N and 880 32' E) at the University Research Farm of the Bidhan Chandra Krishi Viswavidyalaya over the summer seasons of 2020–2021 and 2021–2022. The investigation was conducted using the average values for the aforementioned seasons. In the current study, the aforementioned MCDM approach has been used to assess sixteen cultivars of lentil on seven growth and yield-attributing traits: primary branches per plant, number of pods per plant, 100 seed weight, yield (kg/ha), days to 50% flowering, days to maturity and plant height (cm).

Database

Sixteen lentil cultivars were used for investigation. Each of the sixteen cultivars was noticed with the aforementioned seven characters. To make the cultivars easier to understand and for simplicity, let's use the abbreviations S1, S2,…and S16. We also focus on the seven characters for each variety, which are marked as C_1, C_2,… and C_7.

MCDM method

MCDM involves constructing and resolving multiple-criteria decision and planning problems. The goal is to assist decision-makers who are facing these issues. Assume K's total choices must be evaluated before choosing the best one. Assign the possibilities to the letters $S_1, S_2, ..., S_K$. N criteria are also identified to evaluate the options, represented by $C_1, C_2, ..., C_N$. The k^{th} alternative's value on the n^{th} criteria is derived as x_{kn}, and we write $S_k = (x_{k1}, x_{k2}, ..., x_{kN})$ and $Cn = (x_{1n}, x_{2n}, ..., x_{kn})$; k = 1,2,….,K and n = 1,2,…..,N.

The TOPSIS method and related topics

This method of compensatory aggregation examines a group of alternatives by determining weights for each criterion, normalizing scores for each criterion, and computing the geometric separation between each alternative and the ideal alternative (which is the alternate with the best score in each criterion) as well as negative ideal alternative (which is the alternate with the worst score in each criterion). TOPSIS presupposes that the criteria are monotonically rising or decreasing. Normalization is required when the factors are recorded with inconsistent dimensions and scales. Trade-offs between criteria are possible using compensatory approaches like TOPSIS, where a strong performance in one criterion can offset a weak performance in another. This gives a more realistic kind of modeling than non-compensatory techniques, which include or exclude alternate solutions based on strict cut-offs. TOPSIS's key principle is that the optimal option should be the closest to the ideal alternatives and far away from the negative ideal alternative, which is both intuitive and crucial.

The Ideal Solution

Define the positive ideal alternative (excessive performance on each criterion) and the negative ideal alternative (opposite extreme performance on each criterion). The ideal positive solution maximizes the benefit criterion while minimizing the cost criteria, whereas the negative ideal solution maximizes the cost criteria while minimizing the benefit criteria. The positive ideal $S^+ = (x^+_1, x^+_2, ..., x^+_N)$ and the negative ideal $S^- = (x^-_1, x^-_2, ..., x^-_N)$ is created by taking all the best values reached on each criterion by some alternatives and all the worst values attained on each criterion by some alternatives, respectively.

The TOPSIS procedure

With the aforementioned notation and explanation, the TOPSIS technique for evaluating the ranking of the K options based on their values on the N criteria may be expressed as follows;

The normalized form of the n^{th} criteria vector Cn is TCn. As a result, the k^{th} alternative vector S_k, the positive ideal solution S^+, and the negative ideal solution S^- are also changed to TS_k, TS^+, and TS^-, respectively.

Next, $d(S_k, S^+)$ is defined as the weighted Euclidean distance of TS_k from TS^+.;

$d(S_k, S^+) = \| w \bullet (TS_k - TS^+)\|$, where ($\bullet$) is the vector product and w is the weight.

$=\sqrt{\left(\sum_{n=1}^{N}(Wn(t_{kn} - t_{+n}))^2\right)}$

Similarly,

$d(S_k, S^-)$ is defined as,

$d(S_k, S^-) =\sqrt{\left(\sum_{n=1}^{N}(Wn(t_{kn} - t_{-n}))^2\right)}$

The K alternatives are evaluated in order of performance by their proximity to the ideal solution S^+, which is given for the k^{th} alternatives;

$r(S_k, S^+) = d(S_k, S^+)/ [d(S_k, S^+) + d(S_k, S^-)]$.

TOPSIS's evaevaluation criteria are founded on the idea that the smaller the value of $r(S_k, S^+)$, the more preferable the option.

Choice of weights

The entropy concept has been used to determine the internal importance or weights. It is a criterion for the amount of information (or uncertainty) conveyed by a discrete probability distribution, $p_1, p_2, ..., p_k$. Shannon (1948) created this level of information as $E(p_1, p_2, \dots, p_k) = -\phi_k \sum_{k=1}^{K} p_k \ln(p_k)$, where $\phi_k = 1/\ln(k)$ is a positive constant ranging from 0 to 1. Now assuming that $p_{kn} = x_{kn} / X_n$, where $X_n = x_{k1}+ x_{k2} +\dots+ x_{kN}$ as the probability distribution of C_n on the K alternatives, we may similarly define the entropy of Cn as $E(Cn) = -\phi_k \sum_{k=1}^{K} p_k \ln(p_k) = -\phi_k \sum_{k=1}^{K}(xkn /Xn) \ln(xkn/Xn)$, n = 1,2,…, N and define the weights as $Wn = (1-E(Cn)) / \sum_{j=1}^{N}(1 - E(Cj))$, n = 1,2,…,N. and k = 1,2,…..K.

RESULTS AND DISCUSSIONS

Table 1 shows the average values of various growth and yield contributing features. For each character, the maximum and lowest values are indicated using red and green, respectively. The hypothetical alternative genotype prepared from the recorded data is listed as S^+ in the last row of Table 3.1 with all maximum values. Similarly, the fictitious alternative genotype with all minimum values generated as S^- is listed in the last row of Table 1.

Table 1. Average Yield and yield attributing characters of lentil for the years 2020-21 and 2021- 22:

Genotypes	Primary branches per plant	Number of pods per plant	100 seeds weight	Yield (Kg/ha)	Days to 50% flowering	Days to maturity	Plant Height (cm)
L1112-6	4.3	146.7	1.57	1626.24	84	120.5	49.1
L1112-7	3.6	145.9	2.14	1907.08	84	118.5	48.09
L1112-8	2.7	87.2	3.01	1652.49	71	119	41.26
L1112-9	2.1	86.4	1.59	1375.83	87	118.5	34.13
L1112-10	2.8	84	2.09	872.91	47.5	93	34.5
L1112-11	2.6	55.6	1.6	802.08	53	106	32.25
L1112-12	3	98	2.31	1031.25	53.5	110	33.67
L1112-13	2.6	52.2	2.15	859.16	46	102.5	29.65
L1112-14	2.6	76.8	2.29	1430.83	63	110	36.76
L1112-15	2.3	74.9	2.01	1541.24	74.5	116	45.23
L1112-16	2.2	38.9	2.87	329.58	52.5	91	33.2
L1112-17	2.3	73.1	2.79	1301.25	68	116.5	35.3
L1112-18	3.6	68.1	2.06	842.91	45.5	92.5	33.89
L1112-19	2.9	90.8	2.65	1481.66	76	117	38.58
L1112-20	2.1	72.8	2.23	1370	81	116.5	45.07
Subrata	2.8	80.4	1.67	1852.08	75	111.5	43.75
*S^+	4.3	146.7	3.01	1907.08	87	120.5	49.1
*S^-	2.1	38.9	1.57	329.58	45.5	91	29.65
* S^+ and S^- are positive Ideal and Negative Ideal solutions							

Table 2 computed the square root of the sum of the squares of the various characters in Table 1. This table was used for deriving the normalized values for each genotype shown in Table 1.

Table 2. Square root of the sum of square of different characters of Table 3.1:

[C_1]	[C_2]	[C_3]	[C_4]	[C_5]	[C_6]	[C_7]
11.371	351.232	8.936	5343.188	271.472	441.493	155.440

Table 3 presents the normalized values for each studied criterion-.

Table 3. Transformed Table with normalized values of Table 1:

Transformed Genotypes	TC_1	TC_2	TC_3	TC_4	TC_5	TC_6	TC_7
TS_1	0.3781	0.4177	0.1757	0.3044	0.3094	0.2729	0.3159
TS_2	0.3166	0.4154	0.2395	0.3569	0.3094	0.2684	0.3094
TS_3	0.2374	0.2483	0.3368	0.3093	0.2615	0.2695	0.2654
TS_4	0.1847	0.2460	0.1779	0.2575	0.3205	0.2684	0.2196
TS_5	0.2462	0.2392	0.2339	0.1634	0.1750	0.2106	0.2220
TS_6	0.2286	0.1583	0.1791	0.1501	0.1952	0.2401	0.2075
TS_7	0.2638	0.2790	0.2585	0.1930	0.1971	0.2492	0.2166
TS_8	0.2286	0.1486	0.2406	0.1608	0.1694	0.2322	0.1907
TS_9	0.2286	0.2187	0.2563	0.2678	0.2321	0.2492	0.2365
TS_{10}	0.2023	0.2132	0.2249	0.2884	0.2744	0.2627	0.2910
TS_{11}	0.1935	0.1108	0.3212	0.0617	0.1934	0.2061	0.2136
TS_{12}	0.2023	0.2081	0.3122	0.2435	0.2505	0.2639	0.2271
TS_{13}	0.3166	0.1939	0.2305	0.1578	0.1676	0.2095	0.2180
TS_{14}	0.2550	0.2585	0.2966	0.2773	0.2800	0.2650	0.2482
TS_{15}	0.1847	0.2073	0.2496	0.2564	0.2984	0.2639	0.2900
TS_{16}	0.2462	0.2289	0.1869	0.3466	0.2763	0.2526	0.2815

*TS^+	0.3781	0.4177	0.3368	0.3569	0.3205	0.2729	0.3159
*TS^-	0.1847	0.1108	0.1757	0.0617	0.1676	0.2061	0.1907

* TS^+ and TS^- are positive Ideal and Negative Ideal solutions.
The values of the cells in table 3.3 are $C_{ij}/[C_i]$, where i = 1, 2, 3,..., 7 and j = 1, 2, 3,..., 16. The cell values in Table 3.3 are now scale-free.

Then the sum for each column of Table 1 will be prepared in Table 4.

Table 4. Sum of each column of Table 3.1:

Column sum of table no. 1	X_1	X_2	X_3	X_4	X_5	X_6	X_7
Sum	44.50	1331.80	35.03	20276.59	1061.50	1759.00	614.43

These numbers will be used to create Table 5 with the probability values for each cell in Table 1.

Table 5. Probability matrix of Table 1:

P-Matrix	C_1	C_2	C_3	C_4	C_5	C_6	C_7
S_1	0.0966	0.1102	0.0448	0.0802	0.0791	0.0685	0.0799
S_2	0.0809	0.1096	0.0611	0.0941	0.0791	0.0674	0.0783
S_3	0.0607	0.0655	0.0859	0.0815	0.0669	0.0677	0.0672
S_4	0.0472	0.0649	0.0454	0.0679	0.0820	0.0674	0.0555
S_5	0.0629	0.0631	0.0597	0.0431	0.0447	0.0529	0.0561
S_6	0.0584	0.0417	0.0457	0.0396	0.0499	0.0603	0.0525
S_7	0.0674	0.0736	0.0659	0.0509	0.0504	0.0625	0.0548
S_8	0.0584	0.0392	0.0614	0.0424	0.0433	0.0583	0.0483
S_9	0.0584	0.0577	0.0654	0.0706	0.0593	0.0625	0.0598
S_{10}	0.0517	0.0562	0.0574	0.0760	0.0702	0.0659	0.0736
S_{11}	0.0494	0.0292	0.0819	0.0163	0.0495	0.0517	0.0540
S_{12}	0.0517	0.0549	0.0796	0.0642	0.0641	0.0662	0.0575
S_{13}	0.0809	0.0511	0.0588	0.0416	0.0429	0.0526	0.0552
S_{14}	0.0652	0.0682	0.0756	0.0731	0.0716	0.0665	0.0628
S_{15}	0.0472	0.0547	0.0637	0.0676	0.0763	0.0662	0.0734
S_{16}	0.0629	0.0604	0.0477	0.0913	0.0707	0.0634	0.0712

To find out the relative weights, we have to calculate the following value (ϕ).
Φ = 1/ ln (number of alternatives= 16); ln indicates log base 10 value.

ϕ =	0.3607

Table 6. Table for $E(C_i)$:

$E(C_i)$	$E(C_1)$=	$E(C_2)$=	$E(C_3)$=	$E(C_4)$=	$E(C_5)$=	$E(C_6)$=	$E(C_7)$=
Values	0.9924	0.9808	0.9926	0.9776	0.9914	0.9985	0.9957

Table 6 is prepared for the entropy value of characters. The values are estimated by
following the formula given as,
$E(Cn) = -\ \phi_k \sum_{k=1}^{K} p_k \ln(p_k) = -\ \phi_k \sum_{k=1}^{K} (xkn / Xn) \ln(xkn/ Xn)$, n = 1,2,…, N and define the weights as $Wn = (1- E(Cn)) / \sum_{j=1}^{N} (1 - E(Cj))$, n = 1,2,…,N. and k = 1,2,…..K.
Next prepare the Table 7 as 1- E(Ci)

Table 7. Table for 1 - $E(C_i)$:

1-$E(C_1)$	1-$E(C_2)$	1-$E(C_3)$	1-$E(C_4)$	1-$E(C_5)$	1-$E(C_6)$	1-$E(C_7)$	SUM
0.0076	0.0192	0.0074	0.0224	0.0086	0.0015	0.0043	0.0709

The weights of each character under consideration are estimated using the tables (Tables 6 and 7). It's possible that not all of the characters being studied are equally significant, and the scale values may also have an impact on the study's eventual goal. Giving relative weight to the characters being studied is therefore a crucial component of decision-making studies in order to overcome these challenges.

Table 8. Table of weights using entropy:

Characters	W_1	W_2	W_3	W_4	W_5	W_6	W_7
Weight values	0.1076	0.2703	0.1043	0.3162	0.1208	0.0208	0.0600

The choice of weights is not original. The experimenter may select various weightage values according to the relative importance of the character. We may now move on to the study's last phase, which involves ranking each of the sixteen genotypes or cultivars of lentils being examined.

The Weighted Euclidean Distance from the ideal solution $d(S_k, S^+)$ is first calculated using the formula

$$d(S_k, S^+) = \sqrt{(\sum_{n=1}^{N} (Wn(t_{kn} - t_{+n}))^2)}$$

Similarly,

$$d(S_k, S^-) = \sqrt{\left(\sum_{n=1}^{N} (Wn(t_{kn} - t_{-n}))^2\right)}$$

The K alternatives are ranked according to how closely they adhere to the ideal solution S^+, which is provided for the k^{th} option, using the formula

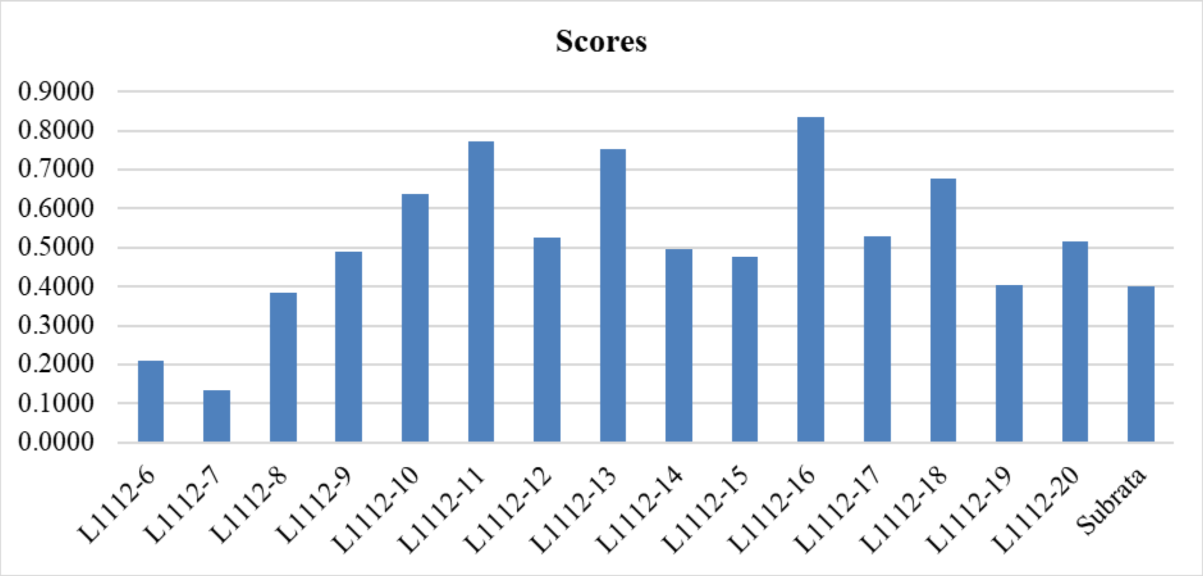
$$r(S_k, S^+) = d(S_k, S^+) / [d(S_k, S^+) + d(S_k, S^-)].$$

According to TOPSIS's evaluation criterion, the greater the favoured option is, the smaller the value of $r(S_k, S^+)$ must be.

Table 9. Ranking of Genotypes or cultivars of lentil

Genotypes /Cultivars	S_k	Distance from Ideal	Value	Distance from negative Ideal	Value	$r(S_k, S^+)$	Scores	Rank
L1112-6	S_1	$D(S_1,S^+)$	0.0600	$D(S_1,S^-)$	0.2271	$R(S_1,S^+)$	0.2089	2
L1112-7	S_2	$D(S_2,S^+)$	0.0376	$D(S_2,S^-)$	0.2415	$R(S_2,S^+)$	0.1348	1
L1112-8	S_3	$D(S_3,S^+)$	0.1057	$D\ (S_3,S^-)$	0.1703	$R(S_3,S^+)$	0.3831	3
L1112-9	S_4	$D(S_4,S^+)$	0.1353	$D(S_4,S^-)$	0.1415	$R(S_4,S^+)$	0.4888	7
L1112-10	S_5	$D(S_5,S^+)$	0.1631	$D(S_5,S^-)$	0.0925	$R(S_5,S^+)$	0.6382	12
L1112-11	S_6	$D(S_6,S^+)$	0.1983	$D(S_6,S^-)$	0.0585	$R(S_6,S^+)$	0.7721	15
L1112-12	S_7	$D(S_7,S^+)$	0.1348	$D(S_7,S^-)$	0.1212	$R(S_7,S^+)$	0.5267	10
L1112-13	S_8	$D(S_8,S^+)$	0.1970	$D(S_8,S^-)$	0.0645	$R(S_8,S^+)$	0.7535	14
L1112-14	S_9	$D(S_9,S^+)$	0.1328	$D(S_9,S^-)$	0.1347	$R(S_9,S^+)$	0.4965	8
L1112-15	S_{10}	$D(S_{10},S^+)$	0.1331	$D(S_{10},S^-)$	0.1464	$R(S_{10},S^+)$	0.4761	6
L1112-16	S_{11}	$D(S_{11},S^+)$	0.2437	$D(S_{11},S^-)$	0.0482	$R(S_{11},S^+)$	0.8348	16
L1112-17	S_{12}	$D(S_{12},S^+)$	0.1428	$D(S_{12},S^-)$	0.1264	$R(S_{12},S^+)$	0.5305	11
L1112-18	S_{13}	$D(S_{13},S^+)$	0.1765	$D(S_{13},S^-)$	0.0838	$R(S_{13},S^+)$	0.6781	13
L1112-19	S_{14}	$D(S_{14},S^+)$	0.1055	$D(S_{14},S^-)$	0.1564	$R(S_{14},S^+)$	0.4028	5
L1112-20	S_{15}	$D(S_{15},S^+)$	0.1417	$D(S_{15},S^-)$	0.1334	$R(S_{15},S^+)$	0.5151	9
Subrata	S_{16}	$D(S_{16},S^+)$	0.1191	$D(S_{16},S^-)$	0.1784	$R(S_{16},S^+)$	0.4004	4

Fig:1. Graphical Representation of Ranking Orders for Lentil Varieties



CONCLUSIONS

The study established that the genotype L1112- 7 (S_2) has the smallest $r(S_k, S^+)$ score meaning that it is the shortest distance away from the positive ideal genotype while also being the furthest distance away from the genotype of the negative ideal solution followed by L1112-6. As a result, L1112- 7 was the highest-ranking genotype when all seven characters were combined. Contrastingly, the genotype L1112- 16 (S_{11}) has the highest $r(S_k, S^+)$ score, indicating the furthest distance from the positive ideal option and the closest to the genotype of the negative ideal, the lowest ranking genotype when all seven traits were considered together. Our study established the application of the TOPSIS method in ranking agriculture alternative (s). However, including more conflicting criteria from diverse agriculture departments, for example, economics, crop protection, and energy criteria (i.e., fertilizers application, fuel, labor, machinery used, etc.), would give a better precision of the genotype ranking.

CONFLICT OF INTEREST

The author here declares that there is no conflict of interest in the publication of this article.

AUTHOR'S CONTRIBUTION

P.M (Principal author): employed the methodology, collected data and analysed the data; A.M: supervised the overall study and drafted the MS; P.M: collected and arranged the data and T.B: reviewed and edited the MS. All the authors read and approved the final version of the MS.

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