A Comparative Study of Various Methods for Identification of Isomorphism in Kinematic Chains

Rashmi Arora
Mechanical Engg. Deptt.
Thapar University
Patiala, India
rashmi_arora@thapar.edu

S.P. Nigam
Mechanical Engg. Deptt.
Thapar University
Patiala, India
spnigam@thapar.edu

***Abstract*—Study of isomorphism of kinematic chains has found a lot of attention on the part of kinematicians during last couple of decades. Isomorphism identification is very important with a view point in saving time and doing correct synthesis and analysis of mechanisms. A lot of methods are available in literature for the identification of isomorphism among chains and inversions but each method has its own shortcomings. Some of the existing methods for identification of isomorphism among kinematic chains and among inversions of given kinematic chain have been critically studied and applied for identification of various structural properties. These methods have been compared with the illustrations of Watt and Stephenson Chain and rating factor from 0 to 5 has been given from the point of view of various attributes, in order to select the best method for identification of isomorphism among chains and inversions of a chain. The final rating for different methods is presented graphically and from this rating, it has been concluded that the method with the highest total rating may be considered as the best method for isomorphism identification. Also, the inner relationship between different methods compared has also been established.**

***Keywords—Isomorphism, kinematic chains, kinematics*.**

I. INTRODUCTION

During last couple of decades, study of isomorphism has found a lot of attention on the part of kinematicians. For doing analysis and synthesis of a kinematic chain, a designer would require a thorough knowledge of the concept of isomorphism and inversions. Comparison of all chains from the point of view of structural similarity is termed as isomorphism identification among chains and inversions of a kinematic chain. Therefore, identification of isomorphism is necessary to avoid unnecessary duplication of mechanisms and to avoid omission of a potentially useful chain.

A number of important methods have been proposed till now for detection of isomorphism among kinematic chains and these are --- Linkage Characteristic Polynomials Method, Hamming Number Technique *, Degree Code Method, Link Adjacency Table Method, Distance Concept *, Neural Network Approach, Fuzzy Logic Approach, Loop Based Detection Method *, Genetic Algorithm Approach *, Spanning Tree Method, Adjacency Matrix Method *, Joint-Joint Matrix Method * etc.

Three methods namely A Genetic Algorithm Approach, Adjacency Matrix Method and Joint-Joint Matrix Method have already been compared [1] by the authors. But in this paper, three more methods along with those three methods (* marked out of above) have been compared in detail with the illustrations of Watt and Stephenson Chain. Rating factor from 0 to 5 has been given from the point of view of attributes such as reliability, computational ease, computational time, detection of inversions, applicability to structural properties and other features, in order to select the best method for identification of isomorphism among chains and inversions of a chain. The Final rating for different methods is also presented graphically in the end for more clarity. The inner relationship between these methods has also been established, which is very important to see that the different methods compared are also related to each other.

II. CRITICAL COMPARISON OF VARIOUS METHODS

To develop the most reliable and most efficient method for identification of isomorphism in kinematic chains, many researchers have devoted a lot of time and effort [11] and work is continuing in this field from a long time. For comparing the methods, important aspects are simplicity in calculation, quick response time and reliability of results. Six important methods have been compared in this work. An attempt has been made to quantify the applicability of these methods by providing a rating factor R* to them based on certain definable attributes like reliability of results, simplicity, time, applicability, detection of inversions etc. This rating would enable one to compare these methods and to detect the best method of isomorphism identification among chains and inversions of a chain. From this rating, it is concluded that the method with the highest total rating may be considered as the best method for isomorphism identification among kinematic chains and inversions of a chain.

The comparison is made easier and clearly illustrated with the six links one degree of freedom Watt chain and Stephenson chain 1 and 2, as shown in Fig. 1, 2 and 3.

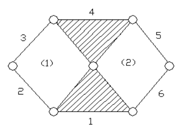

Fig.1 Watt Chain

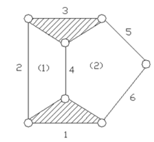

Fig.2 Stephenson Chain 1

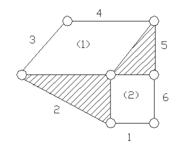

Fig.3 Stephenson Chain 2

The calculations for a genetic algorithm approach [5] , adjacency matrix method [6] and joint-joint matrix method [7] have already been reported [1] so they are not shown here.

A. Hamming Number Technique [2]

1) Evaluation of Parameters for Watt Chain

TABLE I. HAMMING MATRIX

H =

Link → **Link ↓**	**1**	**2**	**3**	**4**	**5**	**6**	**Link Hamming No. (L.H.N.)**
1	0	5	1	6	1	5	18
2	5	0	4	1	4	2	16
3	1	4	0	5	2	4	16
4	6	1	5	0	5	1	18
5	1	4	2	5	0	4	16
6	5	2	4	1	4	0	16

TABLE II. LINK HAMMING STRING (L.H.S.)

Link	**Link Hamming String**
1	18, 1200021
2	16, 0120111
3	16, 0120111
4	18, 1200021
5	16, 0120111
6	16, 0120111

∑L.H.N. = Chain Hamming No.(C.H.N.) = 100

Chain Hamming String (C.H.S.) = 100; 18, 1200021; 18, 1200021; 16, 0120111; 16, 0120111; 16, 0120111; 16, 0120111

TABLE III

Links	**Adjacent Links**	**L.H.S.**	**Link Neighbourhood Strings**
1	2, 4, 6	18, 1200021	16, 0120111; 18, 1200021; 16, 0120111
2	3, 1	16, 0120111	16, 0120111; 18, 1200021
3	2, 4	16, 0120111	16, 0120111; 18, 1200021
4	3, 1, 5	18, 1200021	16, 0120111; 18, 1200021; 16, 0120111
5	4, 6	16, 0120111	16, 0120111; 18, 1200021
6	1, 5	16, 0120111	16, 0120111; 18, 1200021

2) Evaluation of Parameters for Stephenson Chain 1

TABLE IV. HAMMING MATRIX

Link → **Link ↓**	**1**	**2**	**3**	**4**	**5**	**6**	**L.H.N.**
1	0	5	2	5	3	5	20
2	5	0	5	0	2	2	14
3	2	5	0	5	5	3	20
4	5	0	5	0	2	2	14
5	3	2	5	2	0	4	16
6	5	2	3	2	4	0	16

TABLE V. LINK HAMMING STRING (L.H.S.)

Link	**Link Hamming String**
1	20, 0301101
2	14, 0200202
3	20, 0301101
4	14, 0200202
5	16, 0111201
6	16, 0111201

∑L.H.N.= C.H.N. = 100

C.H.S. = 100; 20, 0301101; 20, 0301101; 16, 0111201; 16, 0111201; 14, 0200202; 14, 0200202

TABLE VI

Links	**Adjacent Links**	**L.H.S.**	**Link Neighbourhood Strings**
1	2, 4, 6	20, 0301101	14, 0200202; 14, 0200202; 16, 0111201
2	3, 1	14, 0200202	20, 0301101; 20, 0301101
3	2, 4, 5	20, 0301101	14, 0200202; 14, 0200202; 16, 0111201
4	3, 1	14, 0200202	20, 0301101; 20, 0301101
5	3, 6	16, 0111201	20, 0301101; 16, 0111201
6	1, 5	16, 0111201	20, 0301101; 16, 0111201

3) Evaluation of Parameters for Stephenson Chain 2

TABLE VII. HAMMING MATRIX

Link → **Link ↓**	**1**	**2**	**3**	**4**	**5**	**6**	**L.H.N.**
1	0	5	2	4	1	4	16
2	5	0	5	1	6	1	18
3	2	5	0	4	1	4	16
4	4	1	4	0	5	2	16
5	1	6	1	5	0	5	18
6	4	1	4	2	5	0	16

TABLE VIII. LINK HAMMING STRING (L.H.S.)

Link	**Link Hamming String**
1	16, 0120111
2	18, 1200021
3	16, 0120111
4	16, 0120111
5	18, 1200021
6	16, 0120111

C.H.N. = 100

C.H.S. = 100; 18, 1200021; 18, 1200021; 16, 0120111; 16, 0120111; 16, 0120111; 16, 0120111

TABLE IX

Links	Adjacent Links	L.H.S.	Link Neighbourhood Strings
1	2, 6	16, 0120111	18, 1200021; 16, 0120111
2	3, 1, 5	18, 1200021	16, 0120111; 16, 0120111; 18, 1200021
3	2, 4	16, 0120111	18, 1200021; 16, 0120111
4	3, 5	16, 0120111	18, 1200021; 16, 0120111
5	2, 4, 6	18, 1200021	18, 1200021; 16, 0120111; 16, 0120111
6	1, 5	16, 0120111	16, 0120111; 18, 1200021

4) Summary - It is revealed that Watt Chain and Stephenson Chain 2 have same C.H.S. hence they are isomorphic. But C.H.S. of Watt Chain and Stephenson Chain 1 differ from each other considerably and hence they are non-isomorphic.

TABLE X: TOTAL DISTINCT INVERSIONS POSSIBLE BY HAMMING NUMBER TECHNIQUE

	IDENTICAL LINK NEIGHBOUHOOD STRINGS	TOTAL DISTINCT INVERSIONS
WATT CHAIN	[1, 4], [2, 3, 5, 6]	2
STEPHENSON CHAIN 1	[1, 3], [2, 4], [5, 6]	3
STEPHENSON CHAIN 2	[2, 5], [1, 3, 4, 6]	2

B. Modified Distance Concept [8] [9]

1) Evaluation of Parameters for Watt Chain

$$\text{Modified link-link distance matrix } M_D = \begin{array}{c} \text{Link} \\ 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \end{array} \begin{array}{c} \begin{array}{cccccc} 1 & 2 & 3 & 4 & 5 & 6 \end{array} \\ \begin{pmatrix} 0 & 7 & 11 & 8 & 11 & 7 \\ 7 & 0 & 6 & 11 & 15 & 11 \\ 11 & 6 & 0 & 7 & 11 & 15 \\ 8 & 11 & 7 & 0 & 7 & 11 \\ 11 & 15 & 11 & 7 & 0 & 6 \\ 7 & 11 & 15 & 11 & 6 & 0 \end{pmatrix} \end{array} \begin{array}{c} \text{Distance Ranks(DR)} \\ 44 \\ 50 \\ 50 \\ 44 \\ 50 \\ 50 \end{array}$$

Link	Identification Code for the Link				
1	152	152	140	140	138
2	146	140	140	136	135
3	146	140	140	136	135
4	152	152	140	140	138
5	146	140	140	136	135
6	146	140	140	136	135

Arranged sequence of modified total distance ranks of all the links (ASMTDRL) for this chain is: 50, 50, 50, 50, 44, 44

2) Evaluation of Parameters for Stephenson Chain 1

$$M_D = \begin{array}{c} \text{Link} \\ 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \end{array} \begin{array}{c} \begin{array}{cccccc} 1 & 2 & 3 & 4 & 5 & 6 \end{array} \\ \begin{pmatrix} 0 & 7 & 12 & 7 & 11 & 7 \\ 7 & 0 & 7 & 11 & 11 & 11 \\ 12 & 7 & 0 & 7 & 7 & 11 \\ 7 & 11 & 7 & 0 & 11 & 11 \\ 11 & 11 & 7 & 11 & 0 & 6 \\ 7 & 11 & 11 & 11 & 6 & 0 \end{pmatrix} \end{array} \begin{array}{c} \text{DR} \\ 44 \\ 47 \\ 44 \\ 44 \\ 46 \\ 46 \end{array}$$

The ASMTDRL for this chain is: 47, 47, 46, 46, 44, 44

Link	Identification Code for the Link				
1	148	145	145	136	134
2	139	139	137	136	136
3	148	145	145	136	134
4	139	139	137	136	136
5	146	144	137	137	135
6	146	144	137	137	135

3) Evaluation of Parameters for Stephenson Chain 2

$$M_D = \begin{array}{c} \text{Link} \\ 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \end{array} \begin{array}{c} \begin{array}{cccccc} 1 & 2 & 3 & 4 & 5 & 6 \end{array} \\ \begin{pmatrix} 7 & 11 & 15 & 11 & 6 & 0 \\ 0 & 7 & 11 & 8 & 11 & 7 \\ 7 & 0 & 6 & 11 & 15 & 11 \\ 11 & 6 & 0 & 7 & 11 & 15 \\ 8 & 11 & 7 & 0 & 7 & 11 \\ 11 & 15 & 11 & 7 & 0 & 6 \end{pmatrix} \end{array} \begin{array}{c} \text{DR} \\ 44 \\ 44 \\ 50 \\ 50 \\ 44 \\ 50 \end{array}$$

The ASMTDRL for this chain is: 50, 50, 50, 50, 44, 44

Link	Identification Code for the Link				
1	146	140	140	136	135
2	152	152	140	140	138
3	146	140	140	136	135
4	146	140	140	136	135
5	152	152	140	140	138
6	146	140	140	136	135

4) Summary - It can be seen that Watt Chain and Stephenson Chain 2 have same ASMTDRL hence they are isomorphic. But ASMTDRL of Watt Chain and Stephenson Chain 1 differ from each other considerably and hence they are non-isomorphic.

TABLE XI: TOTAL DISTINCT INVERSIONS POSSIBLE BY MODIFIED DISTANCE METHOD

	LINKS WITH IDENTICAL IDENTIFICATION CODES	TOTAL DISTINCT INVERSIONS
WATT CHAIN	[1, 4], [2, 3, 5, 6]	2
STEPHENSON CHAIN 1	[1, 3], [2, 4], [5, 6]	3
STEPHENSON CHAIN 2	[2, 5], [1, 3, 4, 6]	2

C. Loop Based Detection Method [4]

1) Evaluation of Parameters for Watt Chain

Links	Loop String of a Link (L.S.L.)	Loop Adjacency String of a Link (L.A.S.L.)
1	14-102	14-102, 14-102, 10-101, 10-101
2	10-101	10-101, 14-102, 10-101
3	10-101	10-101, 14-102, 10-101
4	14-102	14-102, 14-102, 10-101, 10-101
5	10-101	10-101, 14-102, 10-101
6	10-101	10-101, 14-102, 10-101

Joint Value of a Chain (JVC) = (1*4) + (4*3) + (2*2) = 20
Chain Loop String (CLS) = [14, (102), (14, 14, 10, 10, 10, 10), 20]

2) *Evaluation of Parameters for Stephenson Chain 1*

Links	L.S.L.	L.A.S.L.
1	14-021	14-021, 10-020, 9-011, 9-011
2	9-011	9-011, 14-021, 14-021
3	14-021	14-021, 10-020, 9-011, 9-011
4	9-011	9-011, 14-021, 14-021
5	10-020	10-020, 14-021, 10-020
6	10-020	10-020, 14-021, 10-020

JVC = (6*3) + (1*2) = 20
CLS = [14, (021), (14, 14, 10, 10, 9, 9), 20]

3) *Evaluation of Parameters for Stephenson Chain 2*

Links	L.S.L.	L.A.S.L.
1	10-101	10-101, 14-102, 10-101
2	14-102	14-102, 14-102, 10-101, 10-101
3	10-101	10-101, 14-102, 10-101
4	10-101	10-101, 14-102, 10-101
5	14-102	14-102, 14-102, 10-101, 10-101
6	10-101	10-101, 14-102, 10-101

JVC = (1*4) + (4*3) + (2*2) = 20
CLS = [14, (102), (14, 14, 10, 10, 10, 10), 20]

4) Summary - It is revealed that Watt Chain and Stephenson Chain 2 have same C.L.S. hence they are isomorphic. But C.L.S. of Watt Chain and Stephenson Chain 1 differ from each other considerably and hence they are non-isomorphic.

TABLE XII: TOTAL DISTINCT INVERSIONS POSSIBLE BY HAMMING NUMBER TECHNIQUE

	IDENTICAL L.A.S.L.	TOTAL DISTINCT INVERSIONS
WATT CHAIN	[1, 4], [2, 3, 5, 6]	2
STEPHENSON CHAIN 1	[1, 3], [2, 4], [5, 6]	3
STEPHENSON CHAIN 2	[2, 5], [1, 3, 4, 6]	2

III. RESULTS AND DISCUSSION

The comparison of the three methods already done [1] were with respect to reliability, computational ease, computational time and applicability to structural properties. But in the present work, those three methods along with three more methods are compared from various aspects which include the older aspects and two more aspects such as detection of inversions and other features. The final table of comparison is shown in Table XIII. An attempt has been made in this work to assign ranks to different methods on the basis of various attributes to arrive at total rating factor so that overall ranking can be easily done.

A. *Evaluation of Rating Factor R**

1) Hamming Number Technique: Rating factor of 5 is assigned for reliability as reliability indicates the correctness of methods as applied to various types of chains and this method has been verified for all the chains of one, two and three degrees of freedom (d.o.f.) But it involves very difficult computations which involve very long manual calculations taking a lot of time. Hence for computational ease and time, rating factor assigned is 3. This method has the potential to disclose the number of structurally different inversions for a given chain so we can assign the rating factor 5 for this case. As this method cannot identify any structural property of a kinematic chain (KC) so it has been assigned 0 rating factor. Also no software dependence is there and all calculations are manual so rating factor is lowest for other features, i.e. 3.

2) Modified Distance Concept: Rating factor 5 can be assigned for reliability as it works well in all the cases of planar chains but the rating factor 4 is assigned as the result is obtained by feelings rather than by considering the facts, i.e. it is heuristic and intuitive in nature. The relation matrix in this method can be written easily and it is not very difficult to get final results so rating factor 4 is given in computational ease. The calculations are done by computer so for computational time, rating factor given is 5. Also it can identify inversions of a planar chain so we can give 5 rating for detection of inversions. But it fails to identify structural properties of a chain so here the rating factor is 0. For other features, it is noted that two computer aided methods are developed here so rating factor assigned is 4.

3) Loop Based Detection Method: For reliability, the rating factor given is 5 as this method has been tested for all the chains of one, two and three d.o.f. Computations are very easy and can be done manually so rating factor 5 is assigned in computational ease. As calculations are done manually without the use of any software so for computational time, rating factor 4 is given. Also it can detect isomorphism among inversions of a chain hence rating of 5 is given here. Moreover, it explores one property i.e. type of freedom in case of multi d.o.f. chains so rating factor assigned for structural properties is 3. In other features, it is seen that this method is unique as it has taken care of loops also whereas all other methods have considered only links and joints. Also, it is neither affected by relabeling or redrawing a chain. Therefore, it is assigned rating factor 5.

4) A Genetic Algorithm Approach: As this method works only for single d.o.f. chains and not for multi d.o.f. chains so it is assigned rating factor 3 for reliability. In computational ease, it is seen that the calculations are simple but lengthy hence rating factor 4 is given here. These calculations become very long in case of large KC so it takes some time and hence for computational time, rating factor 3 is assigned. As it can detect distinct inversions of a KC so rating factor here is 5. For structural properties, rating factor of 4 has been assigned as it identifies three properties but these are not of much importance as compared to the properties identified by adjacency matrix method. Also this method is unique in itself so rating factor of 5 is assigned for other features.

5) Adjacency Matrix Method: It has been assigned the rating factor of 5 as it covers all planar chains of one, two and three d.o.f. Only one input is necessary to get the final results and it takes few seconds to get results with the help of MATLAB software. Therefore, for computational ease and time, the rating factor assigned is 5. Also it can detect isomorphism among inversions of a given chain hence rating factor 5 has been assigned here. Moreover, it identifies two very important structural properties i.e. degeneration and type of freedom with regard to motion of the KC. So rating factor 5 is given for structural properties. For other features, rating factor 4 has been assigned as MATLAB software is used to get the final results quickly.

6) Joint-Joint Matrix Method: This method has worked only in one and two d.of. chains so it is assigned a rating factor of 4 for reliability. Computations here are very easy and single input is used to get the final results which takes few seconds only hence rating 5 is given for computational ease and time. But it cannot detect the number of inversions of a chain so it has been assigned rating factor 0 here. Also structural properties of a chain cannot be identified by this method so in this aspect also, rating is 0. Whereas computer based MATLAB software is used to get the final results hence rating factor of 4 is given for other features.

B. Results

1) Detection of Best Method: In Table XIII, rating factors from 0-5 have been assigned to each of the methods compared for different attributes in brackets and then total rating factor is calculated at the end to detect the best method for isomorphism identification among kinematic chains. Overall ranking of various methods has also been given based on the total rating. As shown in Table XIII and Fig. 5, Adjacency Matrix Method has the highest rating factor of 29 so it can be said that this method is the best method among the six methods studied here for isomorphism identification among chains. Then second best method is Loop Based Detection Method with the rating factor of 27. Therefore, any one of these two methods can be used to detect isomorphism in kinematic chains.

2) Inner Relationship between Different Methods: The inner relationship between different methods compared in the paper has been established and is shown in Fig. 4. Here it can be seen that the calculations for the three methods namely Hamming Number Technique, A Genetic Algorithm Approach and Adjacency Matrix Method; start from one common matrix i.e. Adjacency Matrix. Also, the Hamming Matrix in Hamming Number Technique and first generation Fitness Matrix in Genetic Algorithm Approach are same. Similarly, Link Hamming Number and Fitness of link in these two methods respectively also come out to be the same.

Also, it is seen that Adjacency Matrix forms the basis for calculations in Joint-Joint Matrix Method. Moreover, same software MATLAB is used for final calculations in Adjacency Matrix Method and Joint-Joint Matrix Method.

Table XIII: Comparison of Various Methods

	HAMMING NUMBER TECHNIQUE	MODIFIED DISTANCE CONCEPT	LOOP BASED DETECTION METHOD	A GENETIC ALGORITHM APPROACH	ADJACENCY MATRIX METHOD	JOINT-JOINT MATRIX METHOD
1. RELIABILITY OF RESULTS	It has been verified for all six, eight and ten-bar chains with one d.o.f. as well as ten-bar chains with three d.o.f. **(5)**	It has worked well in all the known cases of planar chains with simple joints. But it is heuristic and intuitive in nature. **(4)**	All the 16 eight-bar single d.o.f. chains, 40 nine-bar two d.o.f. chains, 230 ten-bar single d.o.f. chains and 98 ten-bar three d.o.f. chains have been tested for isomorphism. **(5)**	All the 230 distinct ten-link single d.o.f. chains are tested for confirmation but it doesn't work for multi d.o.f. chains. **(3)**	It covers all planar chains of one, two and three d.o.f. **(5)**	All the simple jointed 1-F, 8-links 16 KC and 1-F, 10-links 230 KC along with 2-F, 9-links 40 KC have been tested successfully for their non-isomorphism. **(4)**
2. COMPUTATIONAL EASE	Computations are very long, especially in case of large KC. So it takes lot of effort to compute many things for single KC. **(3)**	The relation matrix can be written easily. So it is not very difficult to get results. **(4)**	This method is extremely simple in the formulation and execution stage. **(5)**	Computation is extremely simple as effort involved is very less. But these are lengthy. **(4)**	It has simplicity in its process and is very easy to get the final results. **(5)**	It is very simple as computations are very easy using MATLAB software. Also, the [JJ] matrix can be written with very little effort. **(5)**
3. COMPUTATIONAL TIME	It takes lot of time as calculations are very long. **(3)**	It is a computer aided method hence fast in calculations. **(5)**	The arithmetical computations made are very easy enough to be attempted by hand without the necessity of sophisticated algorithms. **(4)**	It takes some time as computations become very long in case of large KC. **(3)**	It takes few seconds to get results due to use of MATLAB software. **(5)**	It takes very less time as its not essential to determine both the composite invariants, only in case [∑JJ] is same then it is needed to determine [MJJ] for the KC. **(5)**
4. DETECTION OF INVERSIONS	It has the potential to disclose how many structurally different inversions can be obtained from a given chain. **(5)**	It can identify inversions of a planar chain. **(5)**	It can detect isomorphism among inversions of a of a given chain. **(5)**	It can detect distinct inversions of a given KC. **(5)**	It can detect isomorphism among inversions of a given chain. **(5)**	It can't be known by this method that how many distinct inversions can be obtained from a given chain. **(0)**
5. APPLICABILITY TO STRUCTURAL PROPERTIES	It can't identify any other property of a KC. **(0)**	Structural properties of a chain cannot be identified by this method. **(0)**	It explores only one property, i.e. type of freedom in case of multi d.o.f. chains. **(3)**	This method enables the selection of best chain, best inversion and best input links for a chain. **(4)**	It can identify structural properties as Degeneration and type of freedom ofa KC. **(5)**	Structural properties of a chain cannot be identified by this method. **(0)**
6. OTHER FEATURES	All calculations are manual. No software dependence is there. **(3)**	Two computer aided methods are developed here. **(4)**	This method is unique as it has taken care of all basic features of chain viz, links, joints and loops, whereas other methods have not considered loops. Also, it is neither affected by relabelling or redrawing a chain. **(5)**	Unlike other methods, this method fulfills both necessary and sufficient requirements, making it unique. **(5)**	Computer based MATLAB software is used to get final results. **(4)**	Computer based MATLAB software is used to get final results. **(4)**
TOTAL RATING FACTOR (R*)	19	22	27	24	29	18
OVERALL RANKING	5	4	2	3	1	6

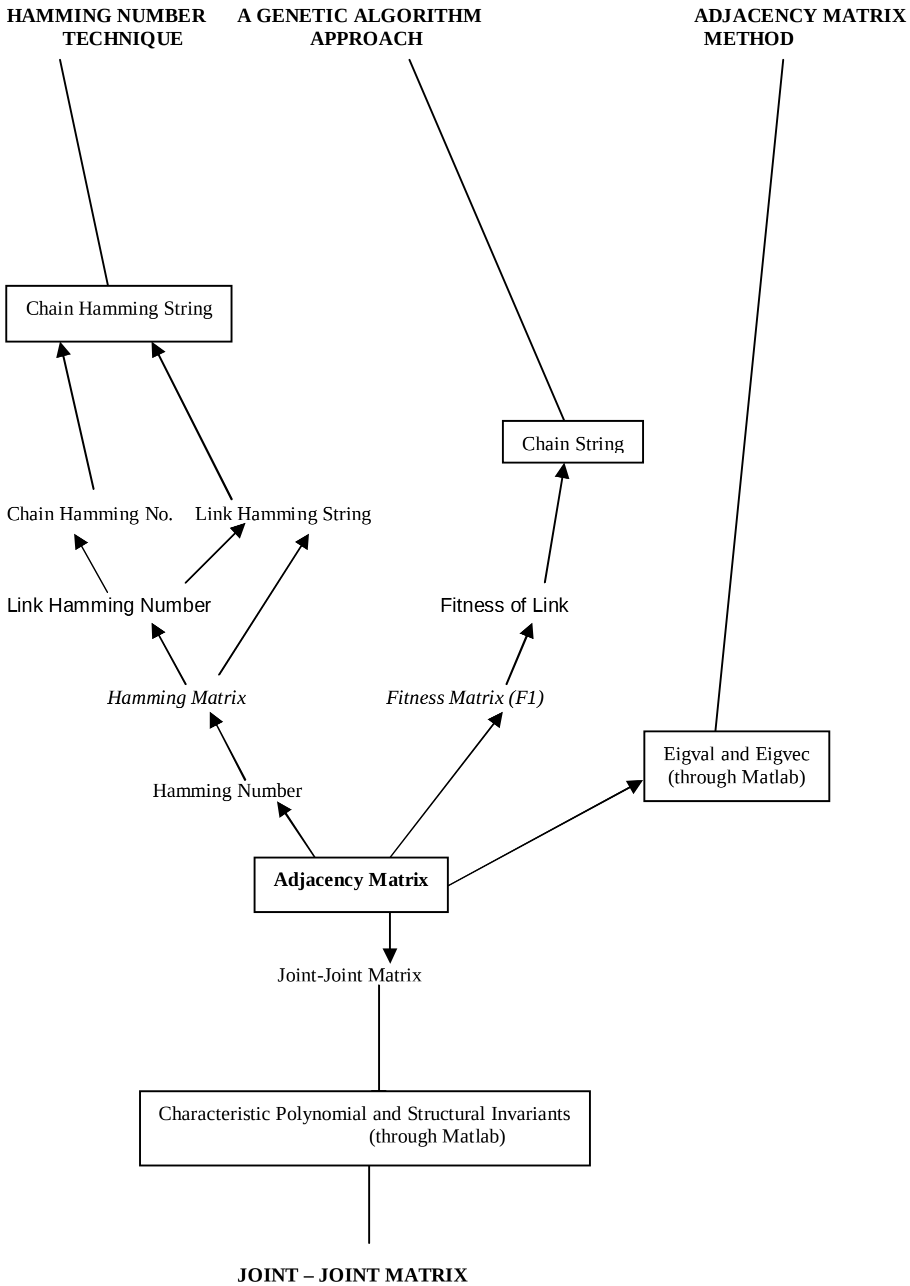

Fig. 4 Inner Relationship Between Different Methods

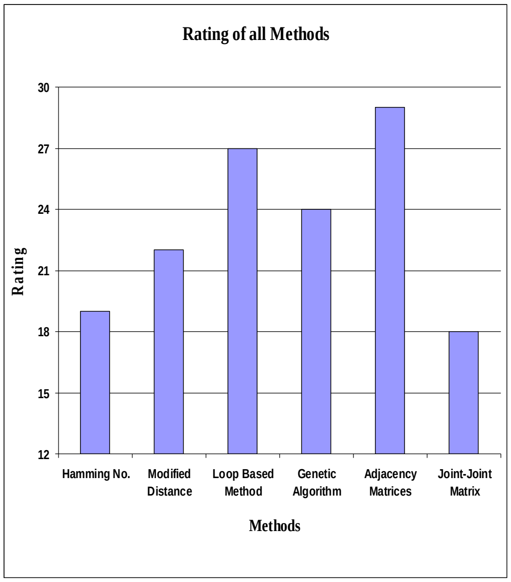

Fig. 5 Graph of Comparison of Various Methods

IV. CONCLUSIONS

Six important methods, developed by different kinematicians have been critically compared in the present work with respect to various attributes such as identification of structural properties, reliability, time, computational ease, detection of inversions and other features with the introduction of rating factor R* to rate a particular method and an inner relationship between these methods has also been established. Thus following conclusions are drawn on the basis of presented work:-

- Adjacency Matrix Method is the best method for the identification of Isomorphism among kinematic chains and inversions.

- Loop Based Detection Method can also be considered as a good method after Adjacency Matrices Method but it does not have capability to identify one of the structural properties of kinematic chains i.e. degeneration identification in kinematic chains.

- It is observed that most of the methods developed for identification of isomorphism are the offshoots of Adjacency Matrix. These are essentially same approaches but differ in the final outcome. It is therefore imperative to compare different methods available in literature on the basis of various attributes as discussed in the present work. This would enable a kinematician to rank and make use of a particular method according to his needs and requirements.

Summing up, the ranking of six methods which have been compared is as follows:

1. Adjacency Matrix Method
2. Loop Based Detection Method
3. A Genetic Algorithm approach
4. Modified Distance Concept
5. Hamming Number Technique
6. Joint-Joint Matrix Method

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