Detection of Isomorphism in Kinematic Chains: A Review on Methods Applied

Vimalkumar P. Palsanawala[1]

[1]Lecturer-Mechanical Engineering, Dr. S. & S. S. Ghandhy College of Engineering & Technology, Surat, Gujarat-India

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Abstract:- *Mechanisms have fascinated engineers and researchers, throughout the recorded history of innovations. Search is still on to explore some facts on unknown and unexplored mechanisms. The linkage type mechanisms are simple mechanisms those can be designed to perform some complex tasks such as non-linear motion and force transmission. Due to its simplicity of design along with ability to perform variety of tasks, kinematic chains play vital role in the design of robots and many more automates. A mechanism is obtained by fixing one of the links in a kinematic chain. All the mechanisms that can be obtained from a given kinematic chain form kinematic inversions of the chain. However, with the raising number of links in a chain, the no of inversions become cumbersome to be listed, especially when number of links is 8 or more and among them again there may be duplication of mechanisms in the listed inversions. Thus to avoid duplication it is important to detect isomorphism among the mechanisms. Much more work has been done by researchers to identify the isomorphism among the kinematic chains. The paper is an attempt to review the contribution by various researchers in the said field.*

Key Words: *algorithm, graph theory, hamming number, isomorphism, kinematic chain, link-path code, matrices, topological graph, vertices*

1. INTRODUCTION

Structural analysis and synthesis of mechanism is very important for the invention and innovation of mechanisms used extensively in robot design. Isomorphism identification of mechanism kinematic chain is an essential step in kinematic mechanism synthesis. Undetected isomorphism results in duplicate solutions and an unnecessary effort along with wastage of precious time. Falsely detected isomorphism eliminates possible candidates for new mechanisms, on the other hand. Many researchers have presented systematic methods to detect the isomorphism for the kinematic mechanisms / chains. These methods can broadly be categorized under a) method based on loop algebra and topological graph b) method based on neural network c) methods based on matrices d) method based on hybrid algorithm e) other methods.

2. SOME METHODS APPLIED BY RESEARCHERS

(a)Method based on loop algebra and topological graph:

Freudenstein and Dobrjanskyj (1964) introduced the graph theory for representing the topological structure of kinematic chains for the first time. Based on the concept of loops and the novel topological representation of kinematic chains, Huang Zhen & Ding Hua Feng (2007) proposed the algebra representation and operation of loops, and established the theorem framework of the loop algebra of kinematic chains. The concept of loop set was proposed by them. On the basis of loop analysis the perimeter topological graph, the characteristic perimeter topological graph and the characteristic adjacency matrix were also presented. The one-to-one correspondence between the diagram, the characteristic perimeter topological graph and the characteristic adjacency matrix were established for mechanism / kinematic chains. Here, for the structure synthesis of mechanisms, a kinematic chain has been represented by a graph whose vertices correspond to links of the chain and whose edges to joints. The graph is called the topological graph. Two 12-bar kinematic chains A and B are shown in Fig- 1(a) and (c) respectively. Their characteristic perimeter topological graphs are shown in Fig-1(b) and (d) and characteristic adjacency matrices are as follows:
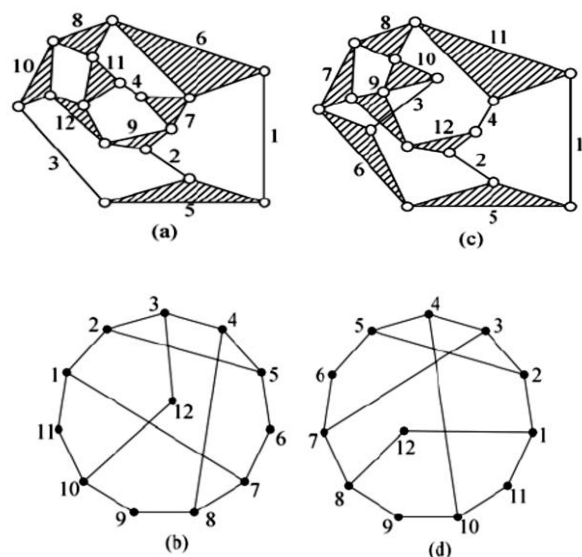

Fig-1 characteristic perimeter topological graph

$$CAM(A) = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 1 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \end{bmatrix},$$

$$CAM(B) = \begin{bmatrix} 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 \\ 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \end{bmatrix}.$$

$CAM(A) \neq CAM(B)$, so the two kinematic chains are non-isomorphic.

(b)Methods based on artificial neural network:

Yang et al.(2007), very first time, used "Ant algorithm" to improve the isomorphism identification efficiency and reliability for epicyclical gear mechanism. On the basis of mapping property between graphs, the isomorphism identification problem can be converted into a matrix operation problem. Two graphs must be in isomorphism if the two matrices of the two graphs can be induced as a same matrix by exchanging their certain rows and columns. In the other words, two graphs must not be in isomorphism if the two matrices of the two graphs cannot be induced as a same matrix by exchanging their certain rows and columns. A mixed model was developed for isomorphism identification by integrating the ant algorithm and mapping property between graphs. The gratifying results can be achieved while parameters are selected in appropriate situation by using the model. The researchers developed a computer program in Visual C++. Some cases confirm the validity of the model. The work has been considered as a reliable isomorphism identification algorithm for intelligent CAD of epicyclical

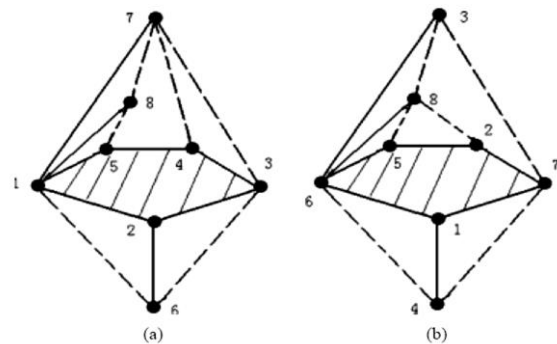gear mechanism. The two examples are shown in Fig-2 and Fig-3.

Fig-2 Two structure graphs of eight vertexes epicyclic gear mechanism
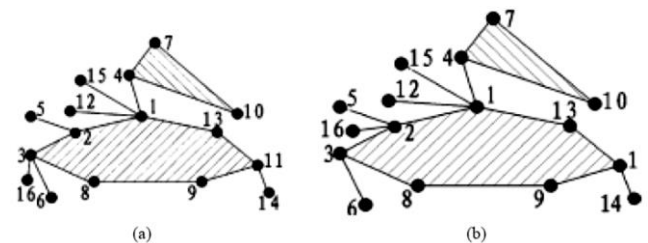

Fig-3 Two structure graphs of sixteen vertexes epicyclic gear mechanisms

Method based on artificial immune algorithm: Zeng et al. (2008) proposed an artificial immune algorithm to search the optimal solution for mechanism / kinematic chain isomorphism identification. AIS have recently emerged as a computational intelligence approach. Inspired by the complexity of the immune system, computer scientists have created systems that in some way mimic or capture certain computationally appealing properties of the immune system, with the aim of building more robust and adaptable solutions. It had been known from many materials that application areas of AIS techniques at least include learning, anomaly detection and optimization. Zeng applied clonal selection principle, which is one of the three basic theories of AIS, to solve the problem of isomorphism detection. When the researcher took the algorithm into simulation, he found that the algorithm have some limitations and need to be improvised. Then, the reasons for the limitations were explored and the algorithm was improvised by adding a process called saving and updating operator after refreshing operator. The improvised clonal selection artificial immune algorithm was taken into simulation and the results showed that the improvised algorithm had high robustness and effectiveness. The process of the CSAI algorithm for kinematic chain isomorphism identification can be described as following:

1) construction of the objective function

2) creation of 20 initial antibodies randomly as the initial population denoted by pop0, cycle number loop = 0

3) evaluation of the affinity of each antibody by affinity evaluation function; if F(x) = 100, then conclusion can be drawn that the two kinematic chains are isomorphic.

4) evaluation of the incentive degree of each antibody and selection of antibodies

5) Cloning of the selected antibodies; production of the interim population denoted by pop1

6) Mutation; production of the interim population pop2

7) Retention of N (N is the scale of initial population) antibodies whose affinity are higher than others; elimination of all the other antibodies; production of the interim population pop3

8) Refreshing pop3; production of the new population denoted by popnew for the next cycle;loop = loop + 1; if loop = 10,000, then the cycle is terminated and a conclusion can be drawn that the two kinematic chains be non-isomorphic; else skipping to step (3).

And the saving and updating operator can be described as following:
For (i = 1; i <= N – 1; i++)
{
For (j = i + 1; j <= N; j++)
{
If unit$_i$ and unit$_j$ have the same alleles in the first three loci, then eliminate unit$_j$ and create a new antibody randomly to replace unit$_j$
}
}
After improvising the original algorithm, the statistic results of Fig-4 and Fig-5 are shown in Table I.
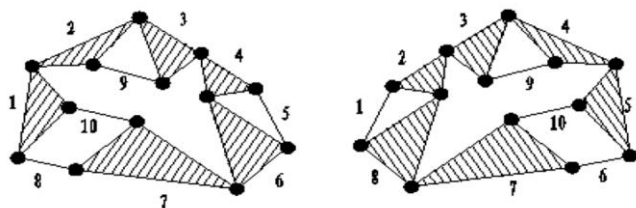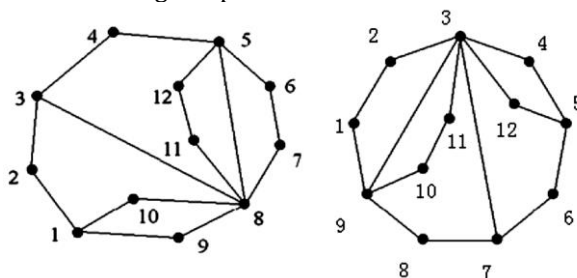

Fig-4 A pair of ten link chains

Fig-5 a pair of 12 vertices topological graphs

Table -1:

The simulation results obtained for solving isomorphic problems by using the improved CSAI algorithm

Average cycle number	Maximum cycle number	Average computation time/s	Maximum computation time/s
72	648	2.188	18.687
30	3,234	1.1975	8.531

(c) Methods based on matrices:

i) Hamming number technique:

Rao and Varada Raju (1991) considered the Hamming number technique from the information theory for detection of isomorphism among kinematic chains. The concept of Hamming number technique and its application to identify the isomorphism among kinematic chains has been already reported [Rao and Varada Raju, (1991), pp.55–75]. From hamming string value for each chain, the said method identifies the isomorphism. Kartik Pipalia, Dr.Anurag Verma and Satish Shah(2010) suggested MATLAB program for finding hamming strings for the kinematic chains to reduce the calculation efforts and errors. The researchers described connectivity matrix (fig-7), hamming number matrix (fig-8) and hamming string values for the said kinematic chain shown in fig-6.
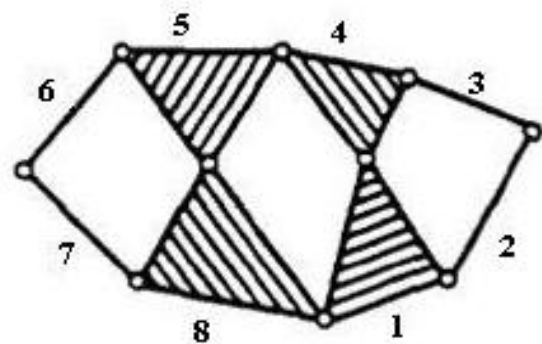

Fig-6- 8- link one degree of freedom

Fig-7 connectivity matrix

$$\begin{bmatrix} 0 & 5 & 1 & 6 & 2 & 5 & 3 & 6 \\ 5 & 0 & 4 & 1 & 5 & 4 & 4 & 3 \\ 1 & 4 & 0 & 5 & 3 & 4 & 4 & 5 \\ 6 & 1 & 5 & 0 & 6 & 3 & 5 & 2 \\ 2 & 5 & 3 & 6 & 0 & 5 & 1 & 6 \\ 5 & 4 & 3 & 5 & 0 & 5 & 4 & 1 \\ 3 & 4 & 4 & 5 & 1 & 4 & 0 & 5 \\ 6 & 3 & 5 & 2 & 6 & 1 & 5 & 0 \end{bmatrix} \quad \begin{matrix} 28 \\ 26 \\ 26 \\ 28 \\ 28 \\ 26 \\ 26 \\ 28 \\ \hline 216 \end{matrix}$$

Fig-8 hamming number matrix

216, 28,000220111, 26,000231011, 26,000231011, 28,000220111, 28,000220111, 26,000231011, 26,000231011

Fig-9 hamming string value

ii) Method based on Weighted Physical Connectivity Matrix (WPCM):

Ali Hasan, R. A. Khan, Ashok Kumar Dargar (2007) suggested WPCM based method to identify inversions and the isomorphism for given kinematic chains. The two structural invariants namely, sum of absolute characteristic polynomial coefficients [WPCMP] and Maximum absolute value of characteristic polynomial coefficient [WPCMPmax] are derived from [WPCM] matrix. These structural invariants can be calculated using Software MATLAB and are same for identical or structural equivalent kinematic chains /mechanism but different for distinct mechanism/ kinematic chains. Also Ali Hasan, Khan R.A., Aas Mohd(2007) designated the method as Joint Joint Method.

Once the links of the mechanism have been numbered from 1 to n, [PCM] is defined as a square symmetric matrix of order n. The elements of [PCM] are entered with either zero or the type of kinematic pair and defined as:

$$[PCM] = (\{P_{ij}\}nxn)\ldots\ldots\ldots\ldots1$$

Where, P_{ij} = Type of kinematic pair between ith link and jth link that are directly connected = 0, when ith and jth links are not connected directly. Off course; P_{ii} =0. The form of [PCM] matrix will be:

$$[PCM] = \begin{pmatrix} 0 & P_{12} & P_{13} & - & - & - & P_{1n} \\ P_{21} & 0 & P_{23} & - & - & - & P_{2n} \\ - & - & - & - & - & - & - \\ - & - & - & - & - & - & - \\ P_{n1} & P_{n2} & P_{n3} & - & - & - & 0 \end{pmatrix}$$

For increasing the discrimination power for detection of isomorphism and identification of degree matrix [DM], the mutual effect of Wij are introduced into each element of [PCM] matrix and so [WPCM] is defined as:

$$[WPCM]= (\{g_{ij}\}nxn)\ldots\ldots\ldots\ldots2$$

Where g_{ij} =(P_{ij}) x (W_{ij}), W_{ij} = ½ [v_i/v_j+v_j/v_i], V_i and v_j are the type of ith and jth links connected directly, V = [v_1 v_2 v_3 v_4 v_5 - - - - v_n].

The degree vector (V) represents the degree of individual link. The degree of link actually represents the type of link like binary, ternary, quaternary etc. Let d (v_i) =2, for binary link, d (v_i) =3, for ternary link, d (v_i) = 4, for quarter nary link, d (v_i) =k, for k-nary link.

The form of [WPCM] matrix will be:

$$[WPCM]= \begin{pmatrix} 0 & g_{12} & g_{13} & - & - & - & g_{1n} \\ g_{21} & 0 & g_{23} & - & - & - & g_{1n} \\ - & - & - & - & - & - & - \\ - & - & - & - & - & - & - \\ g_{n1} & g_{n2} & g_{n3} & - & - & - & 0 \end{pmatrix}$$

Considering 2 kinematic chains with 10- bars of class IV (h) as shown in Fig 10 and Fig 11 in which the binary (n2) and 5-nary (n5) links are same. WA and WB represent the [WPCM] matrices of chain 1(Fig-10) and chain 2(Fig-11) respectively.

WA=

$$\begin{pmatrix} 0 & 1.1 & 0 & 1.595 & 0 & 1.595 & 0 & 1.595 & 0 & 1.595 \\ 1.1 & 0 & 1.595 & 0 & 1.595 & 0 & 1.595 & 0 & 1.595 & 0 \\ 0 & 1.595 & 0 & 1.1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1.595 & 0 & 1.1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1.595 & 0 & 0 & 0 & 1.1 & 0 & 0 & 0 & 0 \\ 1.595 & 0 & 0 & 0 & 1.1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1.595 & 0 & 0 & 0 & 0 & 0 & 1.1 & 0 & 0 \\ 1.595 & 0 & 0 & 0 & 0 & 0 & 1.1 & 0 & 0 & 0 \\ 0 & 1.595 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1.1 \\ 1.595 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1. & 0 \end{pmatrix}$$

WB=

$$\begin{pmatrix} 0 & 0 & 0 & 1.595 & 0 & 1.595 & 0 & 1.595 & 1.595 & 1.595 \\ 0 & 0 & 1.595 & 0 & 1.595 & 0 & 1.595 & 0 & 1.595 & 1.595 \\ 0 & 1.595 & 0 & 1.1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1.595 & 0 & 1.1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1.595 & 0 & 0 & 0 & 1.1 & 0 & 0 & 0 & 0 \\ 1.595 & 0 & 0 & 0 & 1.1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1.595 & 0 & 0 & 0 & 0 & 1.1 & 0 & 0 & 0 \\ 1.595 & 0 & 0 & 0 & 0 & 1.1 & 0 & 0 & 0 & 0 \\ 1.595 & 1.595 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 1.595 & 1.595 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$
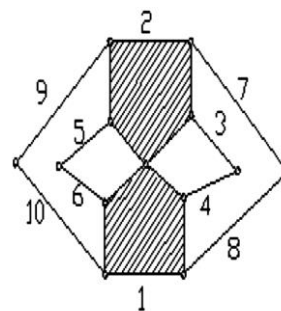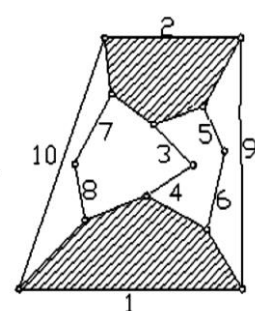

Fig-10 KC-1   Fig-11 KC-2

Structural Invariants of Kinematic Chains

The Structural Invariants (identification numbers) of KC1 and KC2 (using WA and WB matrices) are as follows:
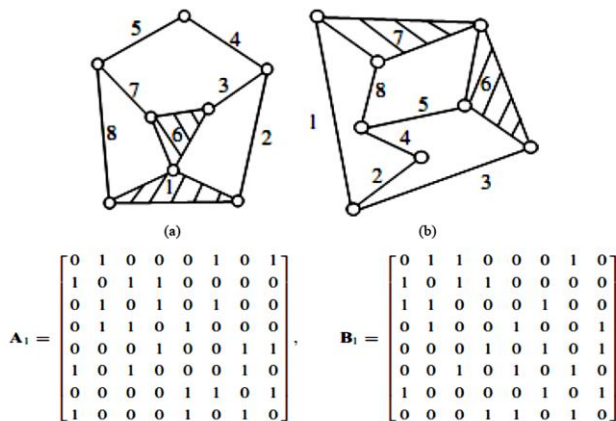
[WPCMP_] of WA (for KC1) = 1.1243e+003

[WPCMP_] of WB (for KC2) = 1.2763e+003

[WPCMPmax] of WA (for KC1) =393.6130

[WPCMPmax] of WB (for KC2) =397.7265

Method reports that chain 1 and 2 are non-isomorphic as the set of structural invariants [WPCMP] and [WPCMPmax] are different for both the KCs.

iii) Method based on eigenvectors and eigenvalues: Chang et al. (2002) introduced the method based on eigenvectors and eigenvalues. Cubillo and Wan (2005) furthered this idea. Kinematic chains were firstly represented by adjacent matrices. By comparing the eigenvalues and corresponding eigenvectors of adjacent matrices, the isomorphism of mechanism kinematics chain could easily be identified. The relationships in the mechanisms could also be obtained. The theory proposed by Chang et al. (2002) had been revised, after errors in the original theory were discovered. Subsequently, the necessary and sufficient conditions of the eigenvalues and eigenvectors of adjacent matrices for isomorphic kinematic chains had been proven rigorously. The new procedure was developed and presented by them to identify isomorphic chains. With this new procedure, it was only necessary to compare eigenvalues and several eigenvectors of adjacent matrices of isomorphic kinematic chains to detect the isomorphic chains. Some examples had been provided to demonstrate how to use the theory in paper published by the researchers (Cubillo and Wan, 2005) and (S.F.Patil and S.C.Pilli, 2007). Cubillo and Wan tested their theorem through an example and their adjacency matrices as shown in Fig-12.

(d) Method based on hybrid algorithm: Yang et al. (2007) presented a mixed algorithm based on a mapping property, a genetic algorithm and a simulated annealing algorithm for the isomorphism detection problem. A validity encoding scheme was developed by considering the mapping relationship between two graphs and some reset measures for the crossover and mutation operators were developed based on the characteristics in which the encoding cell could not be reiterated. A simulated annealing algorithm was introduced into the mixed algorithm to prevent premature convergence in resolution and some other measures were developed for improvising the efficiency, based on the parameter selection. An example demonstrated by the researchers showed that the mixed algorithm was a valid algorithm for the isomorphism identification of kinematic structure graphs in mechanism design. It was believed to be a reliable isomorphism identification algorithm for intelligent CAD and computer-aided manufacturing (CAM).

(e) Other methods:

(i) Link path code method: Yadav, Pratap and Agrawal(1995), suggested link path code method for the identification of inversions and isomorphism in mechanism/ kinematic chains. In the said method, a new invariant Link Path Code was defined for a link of a kinematic chain and the chain itself too. An algorithm was developed for determining the link-path code for all the links of a chain. The link-path code is used to identify structurally equivalent links in a chain, leading to detection of distinct mechanisms of chain. Algorithm is shown in Fig-13.
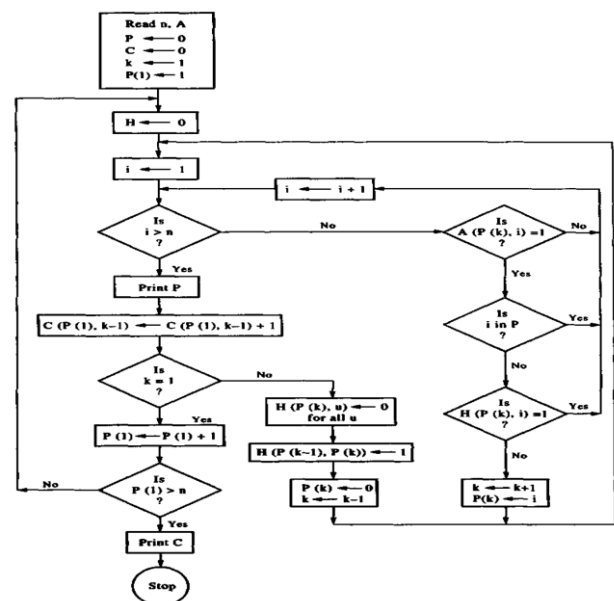

Fig-12 chains with their adjacency matrix

Fig-13 link-path code algorithm

3. CONCLUSION

The various approaches and methods discussed in the paper are effective in general in many of the cases .But no single method can be complete to deal with every case. The improvement may be needed and new method may be expected to be developed to detect the isomorphism among the mechanism- kinematic chain more effectively.

REFERENCES

1) T.S. Mruthyunjaya and H.R. Balasubramanian, Mech. Mac& Theory 22, 131-139 (1987).

2) J. J. Uicker and A. Raicu, Mech. Mac& Theory 10, 375 (1975).

3) T. S. Mruthyunjaya and M. R. Raghavan, J. Mech. Des. Trans. ASME 10l, 488 (1979).

4) H. S. Yah and A. S. Hall, J., Mech. Des. Trans. ASME 104, II (1982).

5) E. V. Krishnamurthy. CombinatoricJ and Graph Theory (Ed. S. B. Rao), p. 18. Springer, New York (1981).

6) H. R. Balasubramanian and K. R. Parthasarathy. Combinatorics and Graph Theory (Ed. S. B. Rao), p. 42. Springer, New York (1981).

7) H. S. Yan and W. M. Hwang, J. Mech. Transm. Automain Des. 105, 658 (1983).

8) R. K. Dube and A. C. Rao. ASME paper 86-DET-172 (1986).

9) A. C. Rao, Indian J. Tech.26, 105 (1988).

10) A.C. Rao, Indian J. Tech. 26, 155 (1988).

11) A.C. Rao, Raju D. Varada, Application of the hamming number technique to detect isomorphism among kinematic chain s and inversion, Mech. Mach. Theory 26 (1) (1991) 55-75.

12) A. G. Ambekar and V. P. Agrawal, Mech. Mac& Theory 22, 453-461 (1987)

13) A. G. Ambekar and V. P. Agrawal. ASME DET Conf. 86-DET-169, Columbus, Ohio, Oct. (1986).

14) A. C. Rao and C. Nageswara Rao. Indian J. Tech. 24, 773-776 (1986).

15) A. G. Ambekar and V. P. Agrawal, Mech. Mac& Theory 22, 453-461 (1987).

16) Ashok Dargar, Ali Hasan and R. A. Khan Identification Of Isomorphism Among Kinematic Chains And Inversions Using Link Adjacency Values IJMM E, Vol. 4 (2009), No. 3, 309-315.

17) Ding, H. and Huang, Z. (2007) 'A new theory for the topological structure analysis of kinematic chains and its applications', Mechanism and Machine Theory, Vol. 42, No. 10, pp.1264–1279.