



Mathematic model of node matching based on adjacency matrix and evolutionary solutions

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HIGHLIGHTS

- Presented the relations of adjacent matrixes for different node order of a same network.
- Established a mathematic model for the problem of node matching based on adjacent matrix.
- Proposed a genetic algorithm to solve the mathematic model.
- Applied the proposed method to different types of networks to measure its performance.

ARTICLE INFO

Article history:

Received 6 June 2014

Received in revised form 2 August 2014

Available online 16 September 2014

Keywords:

Complex network

Node matching

Adjacency matrix

Evolutionary algorithm

ABSTRACT

Research on complex networks is becoming a very hot topic in recent years, among which node matching problem is an important issue. The aim of node matching problem is to find out the corresponding relations between the individuals of associated networks. Traditional node matching problem of networks always hypothesize that a proportion of matching nodes are known. However, if the ratio of matched nodes is very small, the matching accuracy of the remaining nodes cannot be evaluated accurately. What is more, we may have not any matched nodes for reference at all. In view of this, this paper established the mathematic model of node matching problem based on the adjacency matrixes of networks, and presented an evolutionary algorithm to solve it. The experimental results show that the proposed method can achieve satisfactory matching precision in the absence of any matched nodes.

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1. Introduction

Research on complex networks is becoming a more and more hot topic in recent years. In many circumstances, there are often close association and interaction between different networks. A common interaction is that an individual may exist in several different networks at the same time (such an individual is called a multi-identity one) [1]. As the same concept has different expression in different languages, the same individual can play different roles in different social networks, such as: a phone number in the telephone network [2–4], an email address in the E-mail network [5], and a user ID in Blog or BBS [6,7].

For associated networks, a very important task is to find out the matching relations between their individuals, which is called the node matching problem. In fact, there are many similar matching problems for complex networks, such as alignment of biological networks [8,9], highway traffic network matching [10] and sub-graph matching in pattern recognition [11,12].

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Traditional node matching problem of networks always hypothesize that a proportion of matching nodes are known, and thus the matching accuracy of the remaining nodes can be evaluated using these matched nodes, so as to model the node matching problem as an optimal one. The matching of nodes can be obtained by solving the optimal problem using suitable methods.

However, if the ratio of matched nodes is very small, the matching accuracy of the remaining nodes cannot be evaluated accurately. What is more, we may have not any matched nodes for reference at all. In this circumstance, the existing methods will lose their effectiveness. How to solve the node matching problem in the absence of any matched nodes is a further worthy topic.

In view of this, this paper established the mathematic model of node matching problem based on the adjacency matrixes of networks, and presented an evolutionary algorithm to solve it. First, the objective function is constructed to evaluate the matching accuracy of two networks based on the similarity of their adjacency matrixes, and thus the node matching problem is transformed into an optimal one. Then, an evolutionary algorithm is proposed to solve the optimal problem. The experimental results show that the proposed method can achieve satisfactory matching precision in the absence of any matched nodes.

The main contributions of this paper are:

- (1) **Method:** Presented a mathematic model for the node matching problem based on adjacency matrix.
- (2) **Algorithm:** Proposed an evolutionary algorithm to solve the mathematic model.
- (3) **Experiment:** Applied the proposed method to different types of networks to evaluate its performance.

The rest of this paper is structured as follows. Section 2 gives the basic concepts and principles used in this paper. Section 3 proposes the mathematic model of node matching problem based on the adjacency matrixes of networks. An evolutionary algorithm is presented in Section 4 to solve the proposed optimal problem. Sections 5 and 6 are the experiments and conclusion, respectively.

2. Foundations

A network is an ordered triple $N = (V(N), A(N), \psi_N)$, where $V(N)$ is the set of nodes, $A(N)$ is the set of arcs, and function ψ_N associates each arc an ordered pair of nodes. If a is an arc and u and v are two nodes such that $\psi_N(a) = (u, v)$, then a is said to join u and v , u and v are the tail and head of a , respectively. For convenience, we abbreviate $N = (V, A)$.

A network H is called a sub network of N , if $V(H) \subseteq V(N), A(H) \subseteq A(N)$ and

$$\psi_H(e) = \psi_N(e), \quad e \in A(H).$$

Suppose that N is a network with $V(N) = \{v_1, v_2, \dots, v_n\}$, and $A(v_1, v_2, \dots, v_n) = (a_{ij})$ is a matrix of order n , where a_{ij} means the times of arcs joining nodes v_i and v_j . Then we call $A(v_1, v_2, \dots, v_n)$ the adjacency matrix of N in sequence of v_1, v_2, \dots, v_n .

It is convenient to represent a network with the adjacency matrix when we study its properties and implement calculations and processing with computers.

By the definition, we know that the elements in the adjacency matrix of a network are nonnegative integers. When the vertex sequence changes, the adjacency matrix of the network will change too, but different adjacency matrixes of the same network are all isomorphic. The following presents the relation between the adjacency matrixes of the same network.

Let e_i be the unit vector of dimension n with the i th component 1 and the other components 0. Suppose that r_1, r_2, \dots, r_n is an arrangement of $1, 2, \dots, n$, and P_{r_1, r_2, \dots, r_n} is the permutation matrix taking $e_{r_1}, e_{r_2}, \dots, e_{r_n}$ as columns, i.e. $P_{r_1, r_2, \dots, r_n} = [e_{r_1}, e_{r_2}, \dots, e_{r_n}]$. The transposed matrix of P_{r_1, r_2, \dots, r_n} is denoted as $P_{r_1, r_2, \dots, r_n}^T$.

Lemma 1 ([13]). Right multiplying a matrix A of order n with P_{r_1, r_2, \dots, r_n} can permute the r_i th column of A to i -column; left multiplying a matrix A of order n with $P_{r_1, r_2, \dots, r_n}^T$ can permute the r_i th row of A to i th row.

For example, let $n = 3, r_1 = 2, r_2 = 3, r_3 = 1$, and

$$A = \begin{bmatrix} 1 & 4 & 7 \\ 2 & 5 & 8 \\ 3 & 6 & 9 \end{bmatrix}$$

then

$$AP_{2,3,1} = \begin{bmatrix} 1 & 4 & 7 \\ 2 & 5 & 8 \\ 3 & 6 & 9 \end{bmatrix} \begin{bmatrix} 0 & 0 & 1 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{bmatrix} = \begin{bmatrix} 4 & 7 & 1 \\ 5 & 8 & 2 \\ 6 & 9 & 3 \end{bmatrix}$$

$$P_{2,3,1}^T A = \begin{bmatrix} 0 & 1 & 0 \\ 0 & 0 & 1 \\ 1 & 0 & 0 \end{bmatrix} \begin{bmatrix} 1 & 4 & 7 \\ 2 & 5 & 8 \\ 3 & 6 & 9 \end{bmatrix} = \begin{bmatrix} 2 & 5 & 8 \\ 3 & 6 & 9 \\ 1 & 4 & 7 \end{bmatrix}.$$

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