Article

Finding fundamental circuits in the network: A Matlab program and application in tumor pathway

WenJun Zhang

School of Life Sciences, Sun Yat-sen University, Guangzhou 510275, China; International Academy of Ecology and Environmental Sciences, Hong Kong

E-mail: zhwj@mail.sysu.edu.cn, wjzhang@iaees.org

Abstract

In present article, I present full Matlab codes of the Paton algorithm for calculating fundamental circuit set and use it in tumor pathways.

Keywords network; Paton algorithm; fundamental circuits; Matlab.

1 Introduction

Following Zhang (2012), if k links of a network are naturally arranged and thus generates a finited sequence, the sequence is called a chain. The chain with distinct initial node and terminal node is an open chain, or else it is a closed chain. A chain without repeated links is a simple chain. An open simple chain without repeated nodes is defined as the elementary chain, or path. Moreover, if there is at least a chain starting from initial node u to terminal node v, then the elementary chain starting from u to v exists. Given that the two endpoints of an elementary chain are the same node, the chain becomes a circuit. A circuit with length k is called the k-circuit. In present article, I will present full Matlab codes of the Paton algorithm for calculating fundamental circuit set and use it in tumor pathways.

2 Algorithm

Assume there are totally n nodes in the network, and adjacency matrix of the network is $d=(d_{ij})$, i, $j=1,2,\ldots,n$, where $d_{ij}=d_{ji}$, $d_{ii}=0$, and if $d_{ij}=1$ or $d_{ji}=1$, there is a link (connection) between nodes i and j. The following is the algorithm of fundamental circuit set, developed by Paton (1969) (Chan et al., 1982; Zhang, 2012, 2016).

Suppose the node set of a network X is $V=\{1,2,\ldots, n\}$, the adjacency matrix is D, the set of the nodes already on the tree is T, and the set of the nodes to be tested is S. Let $1 \in T$, $S=V$, and the node 1 be the tree root, then

(1) If $T \cap S = \phi$, terminate calculation.

(2) If $T \cap S \neq \phi$, choose a node in $T \cap S$.

(3) Sequentially test every link associated with the node *v*; if there is not any link to be tested then remove *v* from *S*, and return to (1).

(4) If there exists a link (*v*, *w*) to be tested, test whether the node *w* is in *T* or not.

(5) If *w*∈*T*, find out the link (*v*, *w*) and the fundamental circuit generated by the unique path (in the tree) that links *v* and *w*; remove the link (*v*, *w*) from the network and return to (3).

(6) If *w*∉*T*, add the link (*v*, *w*) to the tree and the node *w* to *T*; remove the link (*v*, *w*) from the network and return to (3).

The Matlab codes for calculating fundamental circuit set, fundCircuit.m, are as follows

```
function [num,n,circuits]=foundCircuit(d)
% d: weighted adjacency matrix; num: total number of fundamental circuits; n: number of fundamental circuits containing each
node; circuits: string of all circuits
v=size(d,1);
l=zeros(1,v); vp=zeros(1,v); ts=zeros(1,v); circuit=zeros(1,v*(v-1)/2);
n=zeros(1,v);
num=0;
for i=1:v
l(i)=-1;
end
circuits='';
t=1;
while (v>0)
its=1;
ts(1)=t; l(t)=0;
while (v>0)
if (its==0) break; end
r=ts(its); lm=l(r)+1;
for w=1:v
if (d(r,w)<=0) continue; end
if ((d(r,w)>0) & ((l(w)+1)==0))
ts(its)=w;
its=its+1;
vp(w)=r; l(w)=lm;
d(r,w)=0; d(w,r)=0;
continue; end
num=num+1; a=vp(w);
m=1;
circuit(1)=r; j=r;
while (v>0)
j=vp(j);
m=m+1;
circuit(m)=j;
if (j==a) break; end
end
m=m+1;
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```
circuit(m)=w;
circuits=strcat(circuits,'Number of fundamental circuit: ',num2str(num),'\n');
circuits=strcat(circuits,'Fundamental circuit: ');
for j=1:m
circuits=strcat(circuits,num2str(circuit(j)),'->');
end
circuits=strcat(circuits,num2str(circuit(1)),'\n');
for i=1:v
for j=1:m
if (circuit(j)==i) n(i)=n(i)+1; break; end
end; end
d(r,w)=0; d(w,r)=0;
end
its=its-1;
end
la=0;
for t=t:v
if (l(t)==-1) la=1; break; end
end
if (la==1) continue; end
break;
end
```

3 Application

Use Paton algorithm and the adjacency matrix of tumor pathway p53 (Huang and Zhang, 2012; Li and Zhang, 2013), the calculated foundamental circuits in the p53 network are

Number of fundamental circuit:1
Fundamental circuit:47->26->50->24->47
Number of fundamental circuit:2
Fundamental circuit:47->26->50->51->52->48->47
Number of fundamental circuit:3
Fundamental circuit:37->47->35->37
Number of fundamental circuit:4
Fundamental circuit:16->18->50->51->52->48->16
Number of fundamental circuit:5
Fundamental circuit:31->29->16->18->50->51->52->48->31
Number of fundamental circuit:6
Fundamental circuit:49->51->52->48->49
Number of fundamental circuit:7
Fundamental circuit:28->52->4->28
Number of fundamental circuit:8
Fundamental circuit:2->14->52->8->2
Number of fundamental circuit:9

Fundamental circuit:2->14->52->10->2

Number of fundamental circuit:10

Fundamental circuit:2->14->52->12->2

Number of fundamental circuit:11

Fundamental circuit:5->2->14->52->4->5

Number of fundamental circuit:12

Fundamental circuit:5->2->14->52->7->5

Number of fundamental circuit:13

Fundamental circuit:9->52->7->9

References

Chan SB, et al. 1982. Graph Theory and Its Applications. Science Press, Beijing, China

Huang JQ, Zhang WJ. 2012. Analysis on degree distribution of tumor signaling networks. Network Biology, 2(3): 95-109

Li JR, Zhang WJ. 2013. Identification of crucial metabolites/reactions in tumor signaling networks. Network Biology, 3(4): 121-132

Paton K. 1969. An algorithm for finding a foundamental set of cycles of a graph. Communications of the ACM, 12(9): 514-518

Zhang WJ. 2012. Computational Ecology: Graphs, Networks and Agent-based Modeling. World Scientific, Singapore

Zhang WJ. 2016. Screening node attributes that significantly influence node centrality in the network. Selforganizology, 3(3): 75-86