**Three-Layer Heterogeneous Network based on the Integration of CircRNA information for MiRNA-Disease Association prediction**

Jia Qu1, Shuting Liu1, Han Li1, Jie Zhou2, Zekang Bian3, Zihao Song1, Zhibin Jiang2\*

1 School of Computer Science and Artificial Intelligence, Changzhou University, Changzhou, Jiangsu, China

2 School of Computer Science and Engineering, Shaoxing University, Shaoxing, Zhejiang, China

3 School of AI & Computer Science, Jiangnan University, Wuxi, Jiangsu, China

Corresponding Author:

Zhibin Jiang 2\*

No. 508 Huancheng West Road, Shaoxing, China, 312000

Email address: sxumeejzb@163.com

**Supplementary Material**

1.  and  defined in equations 26 and 27 in the main text will converge after normalization defined in the Proof.

**PROOF**

For a matrix  define function *normalize(),* which takes matrix  as input and  apply the following transformation to all its elements:

Let





Then equation 26 and 27 can be rewritten as:





Suppose the transformation step used in the proof of (Wang et al. 2013) as .







The eigenvalue of  is in the range of . Therefore, we have

We must prove that  is a contraction mapping on the domain . Apparently, for any given *,* we have . Because  is continuous, for any pair of vector  and  in the domain  , there is a .



Once we have  small enough, we can have . Therefore  is a contraction mapping and there is a fixed point for in . In fact, in our calculation, we have converged without any normalization on .

**Supplementary References**

Wang W, Yang S, and Li J. 2013. Drug target predictions based on heterogeneous graph inference. *Pac Symp Biocomput*:53-64.