A Reliable Neighbor-Based Method for Identifying Essential Proteins by Integrating Gene Expressions, Orthology, and Subcellular Localization Information

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Abstract: Essential proteins are those necessary for the survival or reproduction of species and discovering such essential proteins is fundamental for understanding the minimal requirements for cellular life, which is also meaningful to the disease study and drug design. With the development of high-throughput techniques, a large number of Protein-Protein Interactions (PPIs) can be used to identify essential proteins at the network level. Up to now, though a series of network-based computational methods have been proposed, it is still a challenge to improve the prediction precision as the high false positives in PPI networks. In this paper, we propose a new method GOS to identify essential proteins by integrating the Gene expressions, Orthology, and Subcellular localization information. The gene expressions and subcellular localization information are used to determine whether a neighbor in the PPI network is reliable. Only reliable neighbors are considered when we analyze the topological characteristics of a protein in a PPI network. We also analyze the orthologous attributes of each protein to reflect its conservative features, and use a random walk model to integrate a protein’s topological characteristics and its orthology. The experimental results on the yeast PPI network show that the proposed method GOS outperforms the ten existing methods DC, BC, CC, SC, EC, IC, NC, PeC, ION, and CSC.

Key words: essential protein; reliable neighbors; GOS; orthology; subcellular localization information

1 Introduction

Proteins are the products of gene expressions and indispensable for cells life which play important roles for various biological activities[1]. Essential proteins are the products of essential genes which can lead to cell death or infertility if one of them has been removed. The identification of essential proteins and their functions[2] not only can help researchers to understand the basic needs of life, but also can provide useful information for disease study and drug design[3, 4].

In the previous studies, biological researchers generally use gene knockouts[5], RNA interference[6] or conditional knockouts[7] to predict essential proteins on a special condition. Such biological experiments are relatively tedious, time consuming, and expensive. In the past decades, many computational approaches have been proposed as complementary and alternative methods for predicting essential proteins. Especially with the development of high-throughput technologies, such as yeast two-hybrid, tandem affinity purification, and mass spectrometry, a large number of Protein-Protein Interactions (PPIs) are available, which makes
it possible for us to discover new essential proteins at a network level\cite{8–11}. Of course, there are also some other non-network-based methods which use different biological information. For example, Gustafson et al.\cite{12} identified essential proteins by using targeted genome sequencing with the basic idea that proteins whose corresponding genes have longer sequences of Open Reading Frames (ORF) tend to be essential\cite{13}. However, the network-based approaches are the most popular ones in literature.

Generally, the network-based methods for essential protein discovery can be grouped into three categories: neighborhood-based methods, path-based methods, and iterative refinement methods. The neighborhood-based methods investigate a protein’s essentiality by considering its neighbors. The simplest one of neighborhood-based methods is Degree Centrality (DC) proposed by Jeong et al.\cite{1}, which is also known as “centrality-lethality” principle. DC counts the number of neighbors for each protein and ranks all the proteins in a non-increased order according to the number of their neighbors. The studies of Jeong et al.\cite{1} show that the most highly connected proteins in the cell are the most important for its survival. Although there are some controversies\cite{14, 15} whether or why highly connected proteins tend to be essential, most of the researchers confirmed the relationship between degree centrality and protein essentiality\cite{11, 15–18}. For most species, there exist a number of highly connected proteins which are not essential. In our previous studies, by analyzing the highly connected non-essential proteins in yeast, we found that a few of their neighbors interact with each other and proposed a local connectivity-based method LAC\cite{15} to determine a protein’s essentiality by evaluating the relationship between a protein and its neighbors. We also used Edge Clustering Coefficient (ECC) to describe the closeness of two connected proteins by counting their common neighbors and proposed an essential protein discovery method NC\cite{14} by calculating the sum of ECC values among proteins and their neighbors. What’s more, topology potential of PPI networks was investigated to predict essential proteins\cite{16}.

Different from the neighborhood-based methods, the path-based methods take into account the global topological characteristics such as Betweenness Centrality (BC)\cite{17, 18}, Closeness Centrality (CC)\cite{19}, Information Centrality (IC)\cite{20}, and Subgraph Centrality (SC)\cite{21}. For each protein in a given PPI network, BC\cite{17, 18} calculates the fraction of the shortest paths going through it. CC\cite{19} summarizes the distance between target protein and all the others and gets the inverse of the distance as their score so that the larger closeness of the protein can be more essential. IC\cite{20} measures the importance of a given protein by computing the information contained in all possible paths in the network from statistical estimation. SC\cite{21} evaluates the essentiality of a given protein by calculating the weighted sum of the numbers of all closed paths starting from and ending at it.

Besides the neighborhood-based methods and the path-based methods, the iterative refinement centralities are also popular for predicting essential proteins, such as Eigenvector Centrality (EC)\cite{22} that simulates a mechanism in which each node affects all of its neighbors. Moreover, some other approaches, such as Page-Rank algorithm\cite{23}, HITs\cite{24}, Leader-Rank\cite{25}, used in complex network analysis, could also be used to predict essential proteins. CytoNCA\cite{26}, a plug-in of cytoscape, has been developed to predict essential proteins by integrating eight network centralities for both weighted and unweighted networks.

Though great progresses have been made for the network-based essential protein discovery methods, its prediction precision highly depends on the reliability of the PPI network. Unfortunately, the protein-protein interactions, especially those generated by high-throughput technologies, include high false positives. To reduce the effect of noise in the PPI networks, some researchers began to introduce other biological data, such as domains, gene expressions, protein complexes, subcellular locations, and orthology, when they investigate the essential protein discovery methods. For example, Peng et al.\cite{27} proposed UDoNC by integrating domains and PPI networks. PeC\cite{28}, CEPPK\cite{10}, WDC\cite{29}, and CoEWC\cite{30} were developed to predict essential proteins by fusing gene expressions and topological characteristics of PPI networks. Kim\cite{31} proposed a machine learning method by using topological characters in GO-pruned PPI network. Harmonic Centrality (HC)\cite{32} integrates the information of protein complexes into SC, United complex Centrality (UC)\cite{33} uses protein complexes data to distinguish the contributions of different edge clustering coefficients between a pair of proteins. Of these methods, both the known complexes and the predicted complexes from different computational methods\cite{34–38} can be used.
LIDC\(^{39}\) was developed by the combination of Local Interaction Density and protein Complexes. CSC\(^{40}\) uses the in-degree of proteins in complexes. POEM\(^{41}\) measures the essentiality of a protein by determining the overlapping essential modules which the given protein belongs to. Localization-Specificity for Essential protein Detection (LSED)\(^{42}\) introduces subcellular localization information when predicting essential proteins and ION\(^{8}\) was developed by integrating orthologous information with the topological characteristics of PPI networks. SON\(^{43}\) integrates subcellular localization, orthology, and PPI networks. Zhong et al.\(^{44}\) collected 26 different biological and topological features and used SVM-RFE to select a feature space from them to predict essential proteins. Besides, some researchers constructed dynamic networks to reduce the effect of noise in the PPI networks by integrating dynamic gene expressions and PPI networks\(^{45–47}\). For example, Xiao et al.\(^{45}\) constructed an active PPI network and predicted essential proteins from the active PPI network by using different network centralities. In our previous work, we purified the PPI network by integrating gene expressions and subcellular localizations to construct a reliable network TS-PIN\(^{48}\). More network-based methods and other computational approaches can be seen in a comprehensive survey by Wang et al.\(^{49}\)

In this paper, we propose a new neighborhood-based method GOS to identify essential proteins by integrating Gene expressions, Orthology, and Subcellular localization information. The gene expressions and subcellular localization information are used to determine whether a neighbor in the PPI network is reliable. We think that it is the unreliable neighbors that affect the prediction precision of neighborhood-based methods. Hence, we investigate a protein’s topological characteristics only considering the reliable neighbors. We also analyze the orthologous attributes of each protein to reflect its conservative features, and use a random walk model to integrate a protein’s topological characteristics and its orthology. The experimental results on the yeast PPI network show that the proposed method GOS outperforms the ten existing methods DC\(^{11}\), NC\(^{14}\), BC\(^{17, \ 18}\), CC\(^{19}\), SC\(^{21}\), IC\(^{20}\), EC\(^{22}\), PeC\(^{28}\), ION\(^{8}\), and CSC\(^{40}\).

### 2 Method

The basic idea of our proposed essential protein discovery method GOS is to improve neighborhood-based methods by determining reliable neighbors. The gene expressions and subcellular location information were used to determine whether a neighbor in the PPI network is reliable. Then only the reliable neighbors are taken into account to analyze a protein’s essentiality. Finally, the topological characteristics of a protein based on the reliable neighbors are further combined with its orthology.

#### 2.1 Determining reliable neighbors

A PPI network is usually described as an undirected graph \(G(V,E)\), where \(V = \{v_1, \ldots, v_n\}\) represents the proteins and \(E = \{e(v_i, v_j)\}\) is the set of edges connecting two proteins \(v_i\) and \(v_j\). For a given protein \(v\), its neighbors are all the proteins connected to it and the neighbor is denoted as \(N_v\). As a PPI network is generally constructed by all PPIs collected from different labs with different environments at different times, there may be many false interactions in the PPI network. Hence, for a given protein, there may be some false neighbors. Here, we try to distinguish the reliable neighbors from those unreliable neighbors by integrating gene expressions and subcellular localization information. According to the fact that two proteins can physically interact with each other only if they are active together at least at a time point in the cell cycle and appear together at the same subcellular location, we define reliable neighbor as follows:

**Definition 1 Reliable neighbor:** For a given protein \(v\), only the neighbors which physically interact with it at at least one subcellular localization \(l_i\) and active together with it at at least one time point \(t_j\). The reliable neighbor set of a given protein \(v\) is denoted as \(RN_v\).

For example in Fig. 1, protein A has eight neighbors: B, C, D, E, F, G, H, and I. Out of the eight neighbors, only four proteins (C, D, F, H) occur at the same subcellular location with protein A. Protein A is active at the time points 1, 2, 3, and 9. Proteins B, C, D, E, F, and G are active together with it at least at one same time point. As a result, three proteins C, D, and F are reliable neighbors of protein A as they are active at the time point 2 or 3 and occur at the same subcellular location Nucleus or Mitochondrion.

#### 2.2 Network centrality based on reliable neighbors

It has been proved that ECC is effective to describe the local closeness of two connected proteins in a...
PPI network and works well on the identification of protein complexes\cite{35} and essential proteins\cite{14}. In this study, we also use ECC to evaluate the closeness of a protein and its reliable neighbors. Different from the original definition of ECC, here we define new reliable neighbor-based ECC as follows.

**Definition 2 Reliable neighbor-based ECC (RECC):** For an edge $e \in E$ connecting protein $u$ and protein $v$, its RECC is defined as following:

$$RECC(u, v) = \frac{|RN_u \cap RN_v|}{\min(|RN_u| - 1, |RN_v| - 1)}$$

where $RN_u$ and $RN_v$ are the sets of reliable neighbors of protein $u$ and protein $v$, respectively.

Similar to NC\cite{14}, based on the definition of RECC, we can define the Reliable Neighbor-based network Centrality (RNC) as follows.

**Definition 3 RNC:** For a given protein $v$, its reliable neighbor-based network centrality $RNC(v)$ is defined as the sum of RECC between it and its reliable neighbors.

$$RNC(u, v) = \sum_{u \in RN_v} RECC(u, v)$$

(2)

### 2.3 Essential protein discovery method GOS

Considering that a protein’s conservation is highly related to its essentiality we also performed the orthology analysis as in Ref. \cite{8}. We collected the protein orthologous information from the InParanoid database\cite{50}, which includes 99 eukaryotes and 1 prokaryote constructed by the INPARANIOOD program. The yeast PPIs used in this study was downloaded from the DIP database\cite{51}. The final yeast PPI network contains 5093 proteins and 24,743 edges after filtering self interactions and repeats. Out of the 5093 yeast proteins, 4511 proteins have orthologous proteins in at least one reference species. Out of the 1167 essential proteins in the PPI network, 1118 have orthologous proteins in at least one reference species. The analysis and previous studies all show that a protein’s conservation is highly related to its essentiality. Hence, we further combined a protein’s conservation with its RNC.

A protein’s conservation is evaluated by the number of reference species in which its orthologous proteins exist. Let $R$ be the set of reference organisms which is used to get orthologous information for the proteins in the PPI network $G(V, E)$. For a specific reference species $i$, we use $X_i$ to represent the subset of node $V$ in which its element has orthologs in organism $s$. Let $O(v)$ be the number of times that protein $v \in V$ has orthologs in reference organisms.

$$O(v) = \sum_{i=1}^{K} T_v(i)$$

(3)

$$T_v(i) = \begin{cases} 1, & \text{if } v \in X_i; \\ 0, & \text{otherwise} \end{cases}$$

(4)

where $K$ is the number of reference species.

Then for a given protein $v$, its orthologous score $OS(v)$ is defined as the normalized value of $O(v)$:

$$OS(v) = \frac{O(v)}{\max(O(u))}, \quad u \in V$$

(5)
Finally, a linear combination model is used to integrate RNC and the orthologous score. For a given protein \( v \), its essentiality is evaluated by \( \text{GOS}(v) \) :

\[
\text{GOS}(v) = \alpha \times \text{RNC}(v) + (1 - \alpha) \times \text{OS}(v)
\]

where \( \alpha \) is a parameter to adjust the contributions of RNC and OS. When \( \alpha = 0 \), only the orthologous information is considered, and when \( \alpha = 1 \), only the topological character RNC is considered. In this study, 0.5 is used as a default value for \( \alpha \).

3 Results and Discussion

To validate the performance of proposed method GOS, we carry out a comparison between GOS and ten existing essential protein discovery methods: DC\cite{[1]}, NC\cite{[14]}, BC\cite{[17, 18]}, CC\cite{[19]}, SC\cite{[21]}, IC\cite{[20]}, EC\cite{[22]}, PeC\cite{[28]}, ION\cite{[8]}, and CSC\cite{[40]}. All these methods were implemented on the yeast PPI network as the essential proteins of yeast were the most complete one and were well studied. The biological data used in this study are described as follows.

PPI network The yeast PPIs were downloaded from the DIP database (http://dip.mbi.ucla.edu/dip/\cite{[51]}). The final yeast PPI network was constructed by using these PPIs after filtering the repeated and self-interactions. There are 5093 proteins and 24 743 interactions in the final PPI network.

Gene expression data The yeast gene expression data were obtained from the GEO database (http://www.ncbi.nlm.nih.gov/geo/), called GSE3431. It contains 6777 gene expression profiles at 36 time points from three consecutive metabolic cycles, each cycle contains 12 time points. The corresponding proteins of 6777 genes cover 95% of the proteins in the PPI network.

Orthologous information The protein orthologous information was collected from the InParanoid database with version 7 (http://inparanoid.sbc.su.se/cgi-bin/index.cgi\cite{[37]}), which contains 100 whole genomes (99 eukaryotes and 1 prokaryote) constructed by the INPARANOID program.

Subcellular localization annotation information The protein subcellular localization annotation information of yeast was obtained from the COMPARTMENTS database (http://compartments.jensenlab.org/Download\cite{[52]}), which integrates the experimental-based subcellular localization annotation information from UniProtKB\cite{[53]}, MGI\cite{[54]}, SGD\cite{[55]}, FlyBase\cite{[56]}, and WormBase database\cite{[57]}. In total, the yeast proteins have 11 subcellular localizations.

Known essential proteins The known essential proteins data were collected from four different databases: MIPS\cite{[58]}, SGD (http://www.yeastgenome.org/)\cite{[55]}, DEG\cite{[59]}, and SGDP’s (http://www-sequence.stanford.edu/group/yeast_deletion_project). In total, we collected 1285 essential proteins from these four databases. After mapping to the PPI network, we got 1167 known essential proteins by removing those unmapped ones.

3.1 Compare GOS with other methods

To validate the effectiveness of our proposed method GOS, we compare it with different types of other approaches. First, we compare it with two other typical neighbor-based methods DC and NC. Similar to previous experimental procedures\cite{[8, 33]}, we rank the proteins in descending order and choose top 100, top 200, top 300, top 400, top 500, and top 600 proteins as essential candidates for each method. Then we calculate how many candidates are true essential proteins based on the collected known essential protein set. The comparison results of DC, NC, and GOS were shown in Fig. 2. From Fig. 2, we can see that GOS outperforms DC and NC obviously when predicting no more than 600 candidates. Taking top 100 predicted essential proteins for example, 89 essential proteins are correctly identified by the GOS while 46 and 56 are correctly predicted by DC and NC, respectively. For predicting no more 600 essential candidates, GOS achieves more than 50% improvements compared with DC, and more than 20% improvements compared with NC.

Then, we also compare GOS with four path-based methods BC, CC, SC, and IC. As shown in Fig. 2, when predicting no more than 600 candidates, GOS outperforms these four methods obviously too. Especially, GOS achieves more than 97% improvements compared to BC when selecting up to 400 candidates. With the increase of the number of the selected essential candidates, less improvement is obtained by GOS. However, even if the top 600 proteins are selected as essential candidates, the number of true essential proteins produced by GOS is 73% higher than that produced by BC.

The iterative refinement centrality EC is also compared with GOS. As shown in Fig. 2, the number
of true essential proteins produced by GOS is much higher than that produced by EC. As GOS integrates biological information, we also compare it with several other network-based methods by integrating biological information. Here, PeC[28] which integrates gene expressions, ION[8] which integrates orthologous information, and CSC[40] which integrates protein complexes were compared respectively. As shown in Fig. 2, GOS still outperforms these methods consistently even not so much improvement is obtained compared with those only network-based methods.

3.2 Evaluation using Jackknife curve and precision-recall curve

To further verify the performance of GOS and other ten network-based methods for predicting essential proteins, we use Jackknife method. The experimental results validated by Jackknife method are shown in Fig. 3. In Fig. 3, the horizontal axis represents the top $N$ essential candidates and the vertical axis represents the accumulation quantity of the correct predictions for each method. The Area Under Curve (AUC) corresponding to each method is used to measure their performance. The bigger the area is, the better performance the method has. As shown in Fig. 3, our proposed method GOS performs better than the ten other network-based methods DC, NC, BC, CC, SC, IC, EC, PeC, ION, and CSC consistently in terms of AUC. It demonstrates that GOS is effective to predict yeast essential proteins and superior to the ten existing methods.

In addition, we calculate the precision and recall of GOS and the ten network-based methods DC, NC, BC, CC, SC, IC, EC, PeC, ION, and CSC, respectively. The precision-recall curve for each method is shown in Fig. 4. From Fig. 4 we can see that the precision-recall curve still supports that GOS outperforms the ten network-based methods DC, NC, BC, CC, SC, IC, EC, PeC, ION, and CSC for predicting yeast essential proteins.
proteins.

3.3 Effect of the parameter \( \alpha \) on the results

In the above discussions, the default value \( \alpha = 0.5 \) is used in GOS. To analyze the effect of the parameter \( \alpha \) on the results of GOS, we set \( \alpha \) vary from 0 to 1 and observe the number of true essential proteins identified by GOS. The analysis results are shown in Table 1 with \( \alpha \) varying from 0, 0.1, 0.2, \ldots to 1.0. From Table 1 we can see that GOS performs the worst when \( \alpha = 0 \) or 1. That is to say, both the orthologous information and the topological characteristics RNC contribute to the final results. When \( \alpha \) varies from 0.4 to 0.7, there are not too much changes for GOS while GOS performs slightly better when \( \alpha = 0.7 \) for predicting no more than 100 essential candidates. However, when predicting more essential candidates, GOS with smaller \( \alpha \) will perform better. In addition, we also use the precision-recall curve to show the effect of parameter \( \alpha \), as shown in Fig. 5 where similar results can be observed.

![Fig. 4 Comparison of DC, BC, CC, SC, EC, IC, NC, PeC, ION, CSC, and GOS validated by precision recall curve.](image)

![Fig. 5 Precision-recall curves of GOS with different \( \alpha \).](image)

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4 Conclusion

It is believed that the identification of essential proteins is very useful to disease study and drug design. In this study, we have presented a new neighbor-based essential protein discovery method GOS and tested it on the yeast PPI network. We have compared GOS with two neighbor-based methods DC and NC, four path-based methods BC, CC, SC, and IC, an iterative refinement centrality EC, and three other network-based methods with the integration of different biological data PeC, ION, and CSC. The comparison results have shown GOS outperforms these ten methods for predicting yeast essential proteins. Our experimental results have also shown that the reliable neighbors can effectively reduce the effect of false positives in the PPI networks as both the reliable neighbor-based network centrality and the conservation contribute to predicting essential proteins more accurately.

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**References**


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Yi Pan is a Regents’ Professor of computer science and an Interim Associate Dean and Chair of Biology at Georgia State University, USA. Dr. Pan joined Georgia State University in 2000 and was promoted to full professor in 2004, named a Distinguished University Professor in 2013 and designated a Regents’ Professor (the highest recognition given to a faculty member by the University System of Georgia) in 2015. He served as the Chair of Computer Science Department from 2005-2013. He is also a visiting Changjiang Chair Professor at Central South University, China. Dr. Pan received the BEng and MEng degrees in computer engineering from Tsinghua University, China, in 1982 and 1984, respectively, and the PhD degree in computer science from the University of Pittsburgh, USA, in 1991. His profile has been featured as a distinguished alumnus in both Tsinghua Alumni Newsletter and University of Pittsburgh CS Alumni Newsletter. Dr. Pan’s research interests include parallel and cloud computing, wireless networks, and bioinformatics. Dr. Pan has published more than 330 papers including over 180 SCI journal papers and 60 IEEE/ACM Transactions papers. In addition, he has edited/authored 40 books. His work has been cited more than 6500 times. Dr. Pan has served as an editor-in-chief or editorial board member for 15 journals including 7 IEEE Transactions. He is the recipient of many awards including IEEE Transactions Best Paper Award, 4 other international conference or journal Best Paper Awards, 4 IBM Faculty Awards, 2 JSPS Senior Invitation Fellowships, IEEE BIBE Outstanding Achievement Award, NSF Research Opportunity Award, and AFOSR Summer Faculty Research Fellowship. He has organized many international conferences and delivered keynote speeches at over 50 international conferences around the world.