



Ontology-based disease similarity network for disease gene prediction

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Abstract Finding underlying molecular mechanisms of diseases is one of the important issues in biomedical research. In which, prediction of novel disease-associated genes is mostly focused. Many methods have been proposed based on biological networks and shown effectively for the problem. These network-based methods are usually relied on a “disease module” principle that functionally similar genes are associated with similar phenotypes or diseases. Among them, methods solely based on gene/protein networks only exploit that principle by structural modules in the gene/protein networks. Meanwhile, others based on integration of these networks with a disease similarity network better exploit the principle and consequently result in higher prediction performance. In these studies, the disease similarity network is extracted from a disease similarity matrix which was calculated using text mining techniques on OMIM records. Considering that diseases have been recently well annotated by human phenotype ontology (i.e., a controlled vocabulary database) and semantic similarity measures can be used to calculate similarities among them. Therefore, it would be more accurate to construct disease similarity network based on semantic similarity measures on phenotype ontol-

ogy database. In this study, we constructed such network and integrated them with several kinds of gene/protein networks. Experiment results show that the ontology-based disease similarity network much improves the prediction performance compared to the one based on OMIM records, irrespective of gene/protein networks. In addition, we show ability of our method in predicting novel Alzheimer’s disease-associated genes, in which 19 out of top 100 ranked candidate genes are supported with evidences from literature.

Keywords Disease-associated gene · Human phenotype ontology · Semantic similarity · Random walk with restart algorithm · RWR · Alzheimer’s disease

1 Introduction

Disease gene prediction, the task of identifying the most plausible candidate disease genes, is an important issue in biomedical research and many studies have been done for this [1,2]. Identification of disease-associated genes also leads to more effective researches about therapies for genetic diseases and gradually approaches a future of personalized medicine [3–5]. In past decades, linkage analysis was usually used to identify novel disease genes, in which susceptible loci including hundreds of genes are investigated, and thus it is much costly for doing many experiments in wet lab. Therefore, ranking/prioritization methods for such candidate genes are introduced (i.e., genes are ranked by their relevance to a disease of interest). Highly ranked genes are further investigated to find out associated biomedical evidences. And therefore, the goal of gene ranking/prioritization is to predict novel disease-associated genes.

The prediction of novel disease-associated genes are usually approached by three main directions: (1) functional

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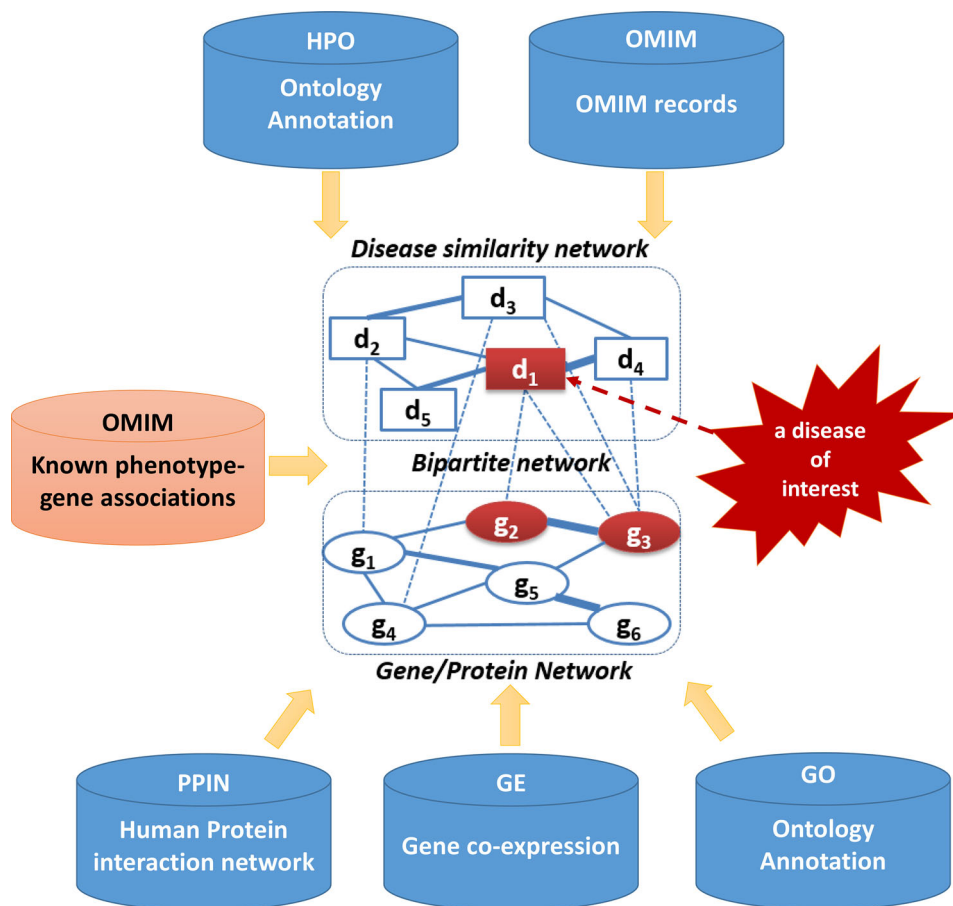
annotation based; (2) machine learning based; and (3) network based. In which, functional annotation-based methods have prioritized candidate genes by measuring the degree of similarity of each candidate genes to a set of known disease genes based on profiles which were built from many functional annotation data sources [6–8]. Therefore, those methods mostly focused on the integration of various biological datasets to obtain more accurate similarity. However, those approaches are limited in that functional annotation data sources have not covered whole human genome yet. For the second approach, many learning techniques have been applied to predict disease-associated genes. In which, the problem is considered as a classification one, where a classifier is learned from training data; then the learned classifier is used to predict whether or not a test/candidate gene is a disease gene. Briefly, at the early, machine learning-based studies usually approached disease gene prediction as a binary classification problem [9], where the learning samples are comprised of positive training samples and negative training samples [9] such as decision trees (DT) [10,11] k -nearest neighbor (kNN) [12], naive Bayesian classifier [13,14], binary support vector machine classifier [15–17], artificial neural network (ANN) techniques [18] and random forest (RF) [9]. In these binary classifier-based methods, positive training samples are constructed from known disease genes, whereas negative training samples are the remaining which are not known to be associated with diseases. This is the limitation of binary classifier-based solutions for the disease gene prediction problem, since the negative training set should be actual non-disease genes. However, construction of this set is nearly impossible in biomedical researches. Therefore, more advanced machine learning techniques, which do not require to define a the negative training set, have been recently introduced for this problem [19]. However, the problem was still formulated as a classification, while it should be a ranking/prioritization one. Therefore, methods for prediction of disease-associated genes have extended to network-based ones [20,21] and shown to outperform functional annotation- and machine learning-based ones [22,23]. These network-based methods are mostly based on biological networks, which are constructed based on various kinds of biomedical data, and therefore they are not limited by the coverage of functional annotation data sources. In addition, these methods can be considered as positive and unlabeled learning techniques where the rankings of candidate genes are estimated based on their relative similarities to known disease ones and others. Moreover, the dominance of network-based methods is also because they are based on a principle of “disease module” (e.g., functionally similar genes are associated with similar phenotypes or diseases). Among methods solely based on gene/protein networks, a method using a random walk with restart (RWR) algorithm [22,24,25] is more dominant compared to other methods such as nearest neighbor,

shortest path and clustering [26]. Because this algorithm calculates a global similarity among candidate and known disease genes on whole network and therefore not only genes directly connected to disease genes are considered, but also indirect ones. This algorithm has been successfully applied to other problems such as prediction of disease-associated miRNAs [27] and protein complexes [28]. However, this method can only exploit the “disease module” in the gene/protein network (i.e., genes/proteins associated with the same or similar diseases usually form functional/physical modules on gene/protein interaction networks [29–31]).

Recently, a variant of RWR algorithm, namely RWRH, was proposed for a heterogeneous network. This algorithm was then applied to predict disease-associated genes on a heterogeneous network of proteins and disease phenotypes [32]. This network was constructed by integrating a disease similarity network based on text mining algorithms on OMIM records [33] and a protein interaction network. As a result, it was reported that RWRH better exploit “disease module” principle than RWR [22] since then OMIM-based disease similarity network was additionally integrated [32]. More importantly, the RWRH algorithm can be extended to use any network of genes/proteins as well as disease similarity one. Indeed, a recent RWRH-based method has used a semantic similarity network of genes instead of the protein interaction network [34] and shown to outperform the original one [32]. We also note that a disease similarity network can be constructed based on shared disease gene [30], shared pathways [35], shared miRNA [36], shared protein complex [37], shared disease ontology [38] and disease comorbidity [39]. Similarly to RWR, RWRH algorithm has been successfully applied to other problems such as prediction of novel drug–target interactions [40] as well as novel disease-associated miRNAs [41] and long non-coding RNAs [42].

In this study, we extended the use of RWRH algorithm to the prediction of disease-associated gene by integrating semantic similarities among diseases and a gene/protein network. More specifically, considering that disease phenotypes have been recently annotated by human phenotype ontology (shortly called HPO) [43] (i.e., controlled vocabulary database) and a number of semantic similarity measures have been proposed to calculate the similarity between annotated biomedical objects [44], it would be more accurate to calculate the similarity among diseases based on such the measures. Therefore, we constructed a disease similarity network using a semantic similarity measure on HPO. Then, this network was integrated with a gene/protein network by known disease phenotype–gene associations. We compared our method with the one relied on the OMIM-based disease similarity network as in [32,34]. In which, the gene/protein network can be the protein interaction network as in [32], the gene semantic similarity network as in [34] as well as one constructed based on expression profiles of

Fig. 1 Construction of heterogeneous networks of genes/proteins and diseases. Disease similarity network and gene/protein network are connected by a bipartite network of known disease–gene associations



genes. Experimental results show that the performance of our method is better than that based on the OMIM-based disease similarity network irrespective of the gene/protein networks. This indicates that HPO-based similarity calculation of diseases improves the performance of RWRH algorithm for the prediction of disease-associated genes. In addition, we used our method to find novel genes associated with Alzheimer’s disease. The evidence search from literature about the associations between 100 highly ranked candidate genes and Alzheimer’s disease confirmed 19 of them, which are not yet recorded in public disease–gene association database.

2 Methods

2.1 Construction of heterogeneous networks of diseases and genes

To build heterogeneous networks of diseases and genes, we constructed two kinds of networks: (1) gene/protein network, which connects genes/proteins by functional interactions; (2) disease similarity network, where a link between two diseases is specified by their similarity. Then, we connected these two networks by a bipartite network consisting of

known disease–gene associations. Figure 1 shows construction of such heterogeneous networks of genes/proteins and diseases.

Gene/protein networks

Protein–protein interaction network

First, we collected a human protein interaction network (shortly called PPINet) containing 10,486 genes and 50,791 interactions from NCBI FTP repository.¹ Proteins in this network are connected by physical interactions. Therefore, we considered PPINet as an unweighted network.

Gene expression-based similarity network

Second, we constructed a weighted gene network based on gene expression data (shortly called GENet). More specifically, a gene co-expression database comprising 19,777 human genes was downloaded from COXPRESSdb [45]. To measure the similarity between a pair of genes, we employed the mutual rank method, which evaluates the strength of co-expression [46]. The mutual rank ranges from 0 to 19,776 and the normalized value $w_{ij} = \frac{(19,776 - MR(v_i, v_j))}{19,776}$, where $MR(v_i, v_j)$ denotes the mutual rank between gene v_i and v_j . The GENet was constructed by replacing the original weight of each link in the PPINet network with the normal-

¹ [ftp://ftp.ncbi.nlm.nih.gov/gene/GeneRIF/interactions.gz](http://ftp.ncbi.nlm.nih.gov/gene/GeneRIF/interactions.gz).

Table 1 Size of gene/protein networks and number of testing disease phenotypes for corresponding heterogeneous networks

#	Gene/protein network	Size (number of genes/proteins, number of interactions)	Number of testing disease phenotypes
1	PPINet	(10,486, 50,791)	2639
2	GENet	(9852, 49,404)	2533
3	GONet	(7897, 41,466)	2345

ized mutual rank value of gene pairs that participate in the network.

Gene ontology-based similarity network

Third, we constructed another weighted gene network based on gene ontology data (shortly called GONet). To construct this network, we used the UniProtKB [47] corpus in the GO annotation database [48]. There were 18,245 *Homo sapiens* proteins in total. Among them, there were 15,576 proteins annotated with molecular function terms, 14,911 proteins annotated with biological process terms, and 16,983 proteins annotated with cellular component terms. Then, to construct the network, we first needed to introduce the information content (IC). The IC of a term e in the corpus is defined as follows:

$$IC(e) = -\log(p(e)),$$

where $p(e)$ is the probability of e occurring in the corpus, i.e., $p(e) = \frac{f(e)}{f(\text{root})}$ such that $f(e) = \text{Annot}(e) + \sum_{c \in \text{Children}(e)} f(c)$. In this formula, $\text{Annot}(e)$ means the number of proteins annotated with e in the corpus, $\text{Children}(e)$ represents the set of children terms of e in the GO graph and root is root term of the GO graph. Then, the semantic similarity between the two GO terms, e_i and e_j , based on the most informative common ancestor approach [49], is calculated as follows:

$$\text{simTerm}(e_i, e_j) = \max_{c \in P(e_i, e_j)} (IC(c)),$$

where $P(e_i, e_j)$ is the set of shared ancestors of e_i and e_j . The functional similarity between a pair of genes v_i and v_j is calculated as the maximum of simTerm values between all possible pairs of terms as follows:

$$\text{simGene}(v_i, v_j) = \max_{e_i \in T(v_i), e_j \in T(v_j)} (\text{simTerm}(e_i, e_j)),$$

where $T(v)$ represents the set of terms annotating v . This value is normalized in range [0, 1] to account for an unequal number of GO terms for both genes as follows:

$$w_{ij} = \frac{2 \times \text{simGene}(v_i, v_j)}{\text{simGene}(v_i, v_i) + \text{simGene}(v_j, v_j)}.$$

By employing the sub-ontology databases of biological process, cellular component and molecular function individ-

ually (i.e., root terms for these gene sub-ontology graphs are biological process, cellular component and molecular function, respectively), three GO-based weighted networks were constructed, in which the original weight of each link in the PPINet network was replaced by the normalized similarity value w_{ij} of two genes participating in each link. We referred to these as the BpNet, CCNet and MFNet networks, respectively. Finally, we integrated them using “per-edge average” method to construct GONet network as follows:

$$\bar{w}_{ij} = \frac{1}{M} \sum_{k=1}^M (w_{ij})_k$$

where M is number of networks containing interaction between gene v_i and v_j . $(w_{ij})_k$ is the weight of interaction between v_i and v_j in network k .

After selecting most connected component, we finally obtained PPINet, GENet and GONet networks with size as shown in Table 1.

2.2 Disease similarity networks

OMIM-based disease similarity network

First, following the same procedure as in [32,34], we collected a phenotypic disease similarity matrix from [50], where an element of the matrix represents degree of similarity between two phenotypes. The similarities in this matrix were calculated based on various text mining algorithms on OMIM records, which describe diseases using natural language [33]. By selecting only five neighbors which have largest similarities for each node, we constructed a phenotypic disease similarity network (shortly called OMIMNet) consisting of 19,791 interactions among 5080 phenotypes.

HPO-based disease similarity network

Second, to construct another disease similarity network, we calculated similarity among disease phenotypes based on human phenotype ontology (HPO, a controlled vocabulary database) [43] (i.e., root term for this ontology graph is All). More specifically, we collected HPO terms and corresponding annotation data at Human Phenotype Ontology database² [43]. Then, we followed the same procedure as for

² <http://www.human-phenotype-ontology.org/>.

gene ontology-based similarity networks to calculate similarity between every pair of disease phenotypes. Similarly, by selecting only five neighbors which have largest similarities for each node, we constructed a HPO-based disease similarity network (shortly called HPONet) consisting of 34,476 interactions among 6521 phenotypes.

2.3 A bipartite network

The bipartite network are known disease–gene associations collected from NCBI FTP repository.³ This connects a total of 3284 diseases and 2761 genes.

2.4 RWRH-based method

Given a connected weighted graph $G(V, E)$ with a set of nodes $V = \{v_1, v_2, \dots, v_N\}$ and a set of links $E = \{(v_i, v_j) | v_i, v_j \in V\}$, a set of source/seed nodes $S \subseteq V$ and a $N \times N$ adjacency matrix W of link weights. Here, we are going to introduce algorithms for measuring relative importance of node v_i to S . By modeling a heterogeneous network of genes and diseases as a graph, ranking/prioritization of candidate genes/diseases is to predict novel genes/diseases associated with a disease of interest (d). The rankings of candidate genes/diseases are based on their relative importance to a set of known d -associated genes and d . This value also measures how much a candidate gene/disease is associated with d .

2.5 Random walk with restart (RWR) algorithm

Random walk with restart (RWR) is a variant of the random walk and it mimics a walker that moves from a current node to a randomly selected adjacent node or goes back to source nodes with a back-probability $\gamma \in (0, 1)$. RWR can be formally described as follows:

$$P^{t+1} = (1 - \gamma)W'P^t + \gamma P^0,$$

where P^t is a $N \times 1$ probability vector of $|V|$ nodes at a time step t of which the i th element represents the probability of the walker being at node $v_i \in V$, and P^0 is the $N \times 1$ initial probability vector. W' is the transition matrix of the graph, the (i, j) element in W' , denotes a probability with which a walker at v_i moves to v_j among $V \setminus \{v_i\}$. All nodes in the network are eventually ranked according to the steady-state probability vector P^∞ . The steady state of each node represents its relative importance to the set of source nodes S .

This algorithm was used for disease gene prediction based on a homogeneous network of genes/proteins [22, 24]. In which, the transition matrix W' is defined as follows:

³ http://ftp.ncbi.nlm.nih.gov/gene/DATA/mim2gene_medgen.

$$(W')_{ij} = \frac{(W_G)_{ij}}{\sum_j (W_G)_{ij}},$$

where W_G is adjacency matrix of the network of genes/proteins.

In addition, the set of source nodes (S) was specified by genes known to be associated with d . Therefore, the initial probability vector was defined as follows:

$$P^0 = \begin{cases} \frac{1}{|S|} & \text{if } v_i \in S \\ 0 & \text{otherwise.} \end{cases}$$

2.6 Random walk with restart on heterogeneous network (RWRH) algorithm

This algorithm can be considered a variant of the RWR algorithm, since it was defined in the same formula as for RWR. The difference is construction of transition matrix W' . More specifically, W' was defined as follows:

$$W' = \begin{bmatrix} W'_G & W'_{GD} \\ W'_{DG} & W'_D \end{bmatrix},$$

where W'_G and W'_D are intra-subnetwork transition matrices of a network of genes/proteins and a disease similarity network, respectively. W'_{GD} , W'_{DG} are inter-subnetwork transition matrices. Let λ be the jumping probability the random walker jumps from the network of genes/proteins to the disease similarity network or vice versa. Then, these matrices were defined as follows:

$$(W'_{GD})_{i,j} = p(d_j | g_i) = \begin{cases} \frac{(\lambda W_{GD})_{ij}}{\sum_j (W_{GD})_{ij}} & \text{if } \sum_j (W_{GD})_{ij} \neq 0 \\ 0 & \text{otherwise,} \end{cases}$$

$$(W'_{DG})_{i,j} = p(g_j | d_i) = \begin{cases} \frac{(\lambda W_{GD})_{ji}}{\sum_j (W_{GD})_{ji}} & \text{if } \sum_j (W_{GD})_{ji} \neq 0 \\ 0 & \text{otherwise,} \end{cases}$$

$$(W'_G)_{i,j} = \begin{cases} \frac{(W_G)_{ij}}{\sum_j (W_G)_{ij}} & \text{if } \sum_j (W_{GD})_{ij} = 0 \\ \frac{(1-\lambda)(W_G)_{ij}}{\sum_j (W_G)_{ij}} & \text{otherwise,} \end{cases}$$

$$(W'_D)_{i,j} = \begin{cases} \frac{(W_D)_{ij}}{\sum_j (W_D)_{ij}} & \text{if } \sum_j (W_{GD})_{ji} = 0 \\ \frac{(1-\lambda)(W_D)_{ij}}{\sum_j (W_D)_{ij}} & \text{otherwise,} \end{cases}$$

where W_D and W_{GD} are adjacency matrices of the disease similarity and the bipartite networks.

By letting η be the parameter to weight the importance of each network, the initial probability vector was defined as follows:

$$P^0 = \begin{cases} (1 - \eta) \frac{1}{|S|} & \text{if } v_i \in S \\ \eta & \text{if } v_i \equiv d \\ 0 & \text{otherwise.} \end{cases}$$

In case we are interested in a disease class/group, which contains set of diseases (D), P^0 was defined as follows:

$$P^0 = \begin{cases} (1 - \eta) \frac{1}{|S|} & \text{if } v_i \in S \\ \eta \frac{1}{|D|} & \text{if } v_i \in D \\ 0 & \text{otherwise.} \end{cases}$$

For these two algorithms, all remaining genes in the networks, which are not known to be associated with d or D , were selected as candidates for ranking.

3 Results and discussion

3.1 Performance comparison

Note that, our method was based on the construction of heterogeneous networks by integrating HPONet network with a gene/protein network. Therefore, three heterogeneous networks were constructed for our method, i.e., HPONet-PPINet, HPONet-GENet and HPONet-GONet. Meanwhile, heterogeneous networks in [32, 34] were OMIMNet-GONet and OMIMNet-PPINet, respectively. In addition to these five heterogeneous networks, we constructed OMIMNet-GENet for the comparison. To compare the performance of our method with that of others, we used leave-one-out cross-validation (LOOCV) method for each disease phenotype in a set of disease phenotypes which associates with at least one gene in the gene/protein networks. Due to the differences in size of gene/protein networks, the number of testing disease phenotypes was little different for different heterogeneous networks as shown in Table 1. Based on results of RWRH algorithm for prediction of disease-associated genes [32, 34] and prediction of disease-associated miRNAs [41], we set back-probability (i.e., γ), jumping probability (i.e., λ) and subnetwork importance weight (i.e., η) to 0.5, 0.6 and 0.7, respectively. For each disease phenotype (d), in each round of LOOCV, we held out one known d -associated gene. The rest of known d -associated genes and d were used as seed nodes. The held-out gene and remaining genes in the homogeneous network, which were not known to be associated with d , were ranked by the methods. Then, we plotted the receiver operating characteristic (ROC) curve and calculated the area under the curve (AUC) to compare the performance of the methods. This curve represents the relationship between sensitivity and (1–specificity), where sensitivity refers to the percentage of known d -associated genes that were ranked above a particular threshold and specificity refers to the percentage of genes which were not known

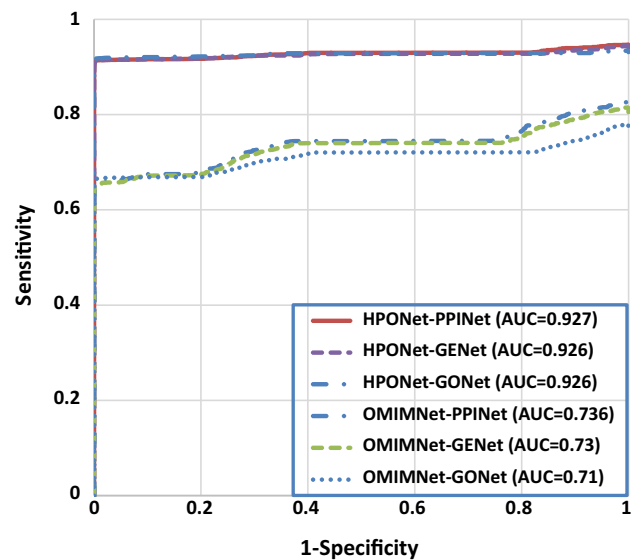


Fig. 2 Performance comparison. Our method is represented by HPONet-PPINet, HPONet-GENet and HPONet-GONet; and others by OMIMNet-PPINet, OMIMNet-GENet and OMIMNet-GONet

to be associated top ranked below this threshold. Figure 2 shows that the performance of our method (i.e., HPONet-PPINet, HPONet-GENet and HPONet-GONet) was better than that of study [34] (i.e., OMIMNet-GONet), study [32] (i.e., OMIMNet-PPINet) and OMIMNet-GENet. In addition, the performance of heterogeneous networks, which were based on HPO, were comparable (i.e., AUC values for HPONet-PPINet, HPONet-GENet and HPONet-GONet were 0.927, 0.926 and 0.926, respectively). Similarly, the performance of heterogeneous networks, which were based on OMIM, were comparable (i.e., AUC values for OMIMNet-PPINet, OMIMNet-GENet and OMIMNet-GONet were 0.736, 0.73 and 0.71, respectively). These results indicate that HPO-based calculation of the disease similarity network (i.e., HPONet) better reflects functional relations among diseases than that based on text mining algorithms on OMIM records for the prediction of disease-associated genes.

3.2 Case study: Alzheimer's disease

In this experiment, we tried to predict novel genes associated with Alzheimer's disease (Shortly called AD) (MIM ID is 104300). AD is a multi-factorial and fatal neurodegenerative disorder for which the mechanisms leading to profound neuronal loss are incompletely recognized. There are 16 genes are known to be associated with AD [33]; however only eleven of them are available in the gene/protein networks. To predict novel genes associated with this disease, we selected the heterogeneous network comprising HPONet and GENet. Then we used these eleven genes and the MIM ID of AD

Table 2 Nineteen evidenced Alzheimer's disease-associated genes in top 100 ranked candidate genes

Rank	Gene Entrez ID	Gene symbol	PubMed ID
1	6622	SNCA	19022350, 21056999, 22836259, 23820587
2	348	APOE	11803456, 12000192, 12232782, 12498968, 12876259, 12960780, 14741429, 15165699, 15181247, 15184600, 15184629, 15455263, 16165272, 16796589, 17050040, 17089130, 17101827, 17374951, 17474819, 17524782, 17613540, 17659844, 17854398, 18058831, 18083276, 18205760, 18416843, 18505684, 18525129, 19116453, 19199875, 19339712, 19398704, 20198498, 20473139, 20479234, 20535486, 20538374, 21143177, 21283692, 21297273, 21297948, 21409287, 21556001, 21803501, 22016362, 22179327, 22269984, 22383234, 22502727, 22596266, 22712640, 22815080, 22899317, 23050006, 23183136, 23293020, 23571587, 23581910, 23627755, 23663404, 23668794, 23771217, 23948883, 24312462, 24388797, 24446209, 24473795, 24599963, 24603451
3	5621	PRNP	18349519, 19556894
9	1312	COMT	15488308, 22483294, 23034259, 24477323
21	4137	MAPT	15848182, 16165272, 16182262, 17920160, 18431250, 18431254, 18586097, 18806919, 19153649, 19523877, 19524111, 19560101, 20473135, 20678074, 21342022, 21348938, 21442128, 21489990, 23554879, 23597931, 25378699
24	7329	UBE2I	19765634
28	1508	CTSB	23024364
29	5663	PSEN1	12668610, 15159497, 15622541, 17229472, 17594345, 18028191, 18479822, 18525293, 19667325, 19796846, 22133015, 23850332
34	627	BDNF	12192623, 15838855, 15935057, 16054753, 19088493, 19522715, 22212405, 22364688, 24334212
37	5054	SERPINE1	19604604
38	5327	PLAT	22027013
41	4035	LRP1	15048651, 18706476, 22027013
42	5329	PLAUR	11814408
50	1815	DRD4	23034259
53	7345	UCHL1	16626667, 22660851, 22726800
73	5071	PARK2	19716418
83	6667	SP1	16378688, 23435408
94	5340	PLG	22027013
95	3952	LEP	21633502

as source nodes, and other genes in the homogeneous network as candidates. After all candidate genes were ranked, we selected 100 highly ranked candidates for evidence search about the association between them and AD from literature on PubMed using Entrez Programming Utilities [51]. Table 2 shows 19 evidenced candidate genes. For instance, study [52] (PubMed ID: 16378688) showed that SP1 deposition in hyper-phosphorylated tau deposits may have functional consequences in the pathology of AD. In addition, it was suggested that UBE2I polymorphisms might be associated with a risk of AD [53] (PubMed ID: 19765634). Also, low protein levels of UCHL1 are associated with high protein levels of BACE1 in sporadic AD brains [54] (PubMed ID: 22726800). Finally, enhancing CTSB activity could lower Abeta, especially Abeta42, in AD patients with or without familial mutations [55] (PubMed ID: 23024364). Other not yet evidenced genes in the top 100 genes can be good candidates for biologists for further investigation (see Online Resource 1).

4 Conclusions

It was reported in previous studies that disease similarity improves the performance of prediction of novel disease-associated genes, since it better exploits the “disease module” principle. Based on this, methods on a heterogeneous networks comprising a disease similarity network and a gene/protein network are superior to those which are solely based on the gene/protein network. However, construction of the disease similarity network in previous studies are limited since they mostly based on an out-of-date disease similarity matrix, which was constructed using text mining algorithms on OMIM records. Considering that human phenotype ontology is now available and it well annotates to disease phenotypes, disease similarity can be semantically calculated based on such the controlled vocabulary using semantic-based similarity measures. Therefore, in this study, instead of using the OMIM-based disease similarity network, we construct a HPO-based one using a semantic similarity measure. Using the random walk with restart algorithm on

a heterogeneous network, we compared the performance of the heterogeneous network built based on our method with that based on the OMIM-based disease similarity network. Simulation results show that our method is better irrespective of gene/protein networks. This indicates that the HPO-based disease similarity network better exposed functional similarities among diseases than that of OMIM-based one. A case study on Alzheimer's disease has been done to show the ability of our method in predicting novel disease-associated genes. We also note that, many other semantic similarity measures proposed to calculate similarity between annotated biomedical entities can be used to construct disease similarity networks. In addition, these networks can be constructed based on shared pathways [35], shared miRNA [36], shared protein complex [37], shared disease ontology [38] and disease comorbidity [39]. Therefore, it would be interesting for future studies to test which one is best for the prediction of novel disease-associated genes.

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