**VGAELDA** (Shi *et al*., 2021): VGAELDA is an end-to-end model, which integrates variational graph autoencoders and graph autoencoders for predicting disease-related lncRNAs. The method contains two kinds of graph autoencoders. Variational graph autoencoders infer representations from lncRNA and disease features, respectively, while graph autoencoders propagate labels through known lncRNA-disease associations. These two autoencoders are trained alternately by adopting variational expectation maximization algorithm. Finally, the whole framework is optimized by co-training the loss to obtain the final lncRNA-disease association score matrix as follows,

where is the output score matrix obtained from lncRNA space and is the output score matrix obtained from disease space. is the weight parameter that balances information capturing from lncRNA space and disease space."

**GAERF** (Wu *et al*., 2021): GAERF is a classification method based on machine learning techniques to predict disease-related lncRNAs. First, GAERF constructed a heterogeneous network using the relationship between lncRNA, miRNA, and disease. Secondly, graph autoencoder is used to extract low-dimensional representations vector of nodes from the heterogeneous network. Finally, these feature vectors are leveraged as input to random forest classifier to predict new lncRNA-disease associations.

**CNNDLP** (Xuan *et al*., 2019): CNNDLP is a deep learning method for predicting lncRNA-disease association. The model combined the diverse biological premises to constructed two different embedding layers by integrating the associations, similarities, and interactions of lncRNAs, diseases, and miRNAs. The model has left and right components. The left side of which learns the attentional representation of node through convolutional neural network with an attentional mechanism. The fully connected layer and softmax layer are used to obtains the association score . On the right side of, the model utilized convolutional autoencoder to capture the low-dimensional representation of node, and the association score is acquired by the fully connected layer and the softmax layer. The final scores of the model are integrated as the final association scores by a weighted sum and , as follows,

(1)

where is hyperparameters to adjust the importance of and .

**GCNLDA** (Xuan *et al*., 2019):The method used graph convolutional networks and convolutional neural networks to infer disease-associated lncRNA candidates. GCNLDA is also composed of two parts, left and right. In the left part of the framework, the lncRNA-miRNA-disease heterogeneous network is established by using lncRNA network, disease network, miRNA network. Then, the graph convolutional network module with attention mechanism is developed learns the network representation of lncRNA-disease node pairs. Finally, the node pair vector is served as the input of the fully connected layer to predict the association probability of node pairs. In the right part of the framework, the model constructs the embedding matrix of node pair, and then the convolutional neural network and the fully connected layer are used to predict the association probability of node pairs. The final association probability is integrated by using a weighted sum.

**Ping’s method** (Ping *et al*., 2019):This method relies only on lncRNA-disease association information to identify potential disease-related lncRNAs. First, the method considers the assumption that two nodes are similar if they have common neighbors. The 1-order similarity for lncRNA and the 1-order similarity for disease 1 are obtained based on the lncRNA-disease association. According to the assumption that if two nodes do not have common neighboring nodes but are connected to similar nodes, then they are also considered to be related each other. The 2-order similarity SL2 and SD2 for lncRNA and disease, respectively. The similarity scores the computed above are integrated as follows,

(2)

(3)

Given the lncRNA-disease association matrix , the lncRNA similarity matrix and the disease similarity matrix , the method constructs two recommendation score matrices R1 and R2.

(4)

(5)

Therefore, by integrating the above two recommendation matrices, the model can obtain a new association score between lncRNA and disease as follows,

(6)

where, is a parameter utilized to regulate the relative importance between lncRNA similarity and disease similarity.

**SIMCLDA** (Lu *et al*., 2018): SIMCLDA is an inductive matrix complementation-based method to predict lncRNA-disease associations. The method consists of five main steps. Step 1, the model calculates the Gaussian interaction profile kernel similarity of lncRNAs from known lncRNA-disease associations. Step 2, based on disease-gene and gene-gene ontology associations, the functional similarity of diseases is computing by using Jaccard coefficients. Step 3, SIMCLDA extracts the primary feature vectors from lncRNA similarity and disease similarity by PCA. Step 4, the model calculates the interaction profile for a new lncRNA with the interaction profile of its neighbors. Step 5, SIMCLDA utilizes the primary feature vector and the constructed interaction profile to complete the association matrix with IMC.

**MFLDA** (Fu *et al*., 2017):The method is a matrix factorization-based lncRNA-disease association prediction model. MFLDA integrates multiple data sources, including relationships between six object types, such as lncRNAs, miRNAs, genes, Gene Ontology, disease Ontology and drugs. Firstly, the method encodes directly (or indirectly) relevant data sources related to lncRNA or disease in individual correlation data matrices, and presets weights for these data matrices. Secondly, weight optimization and low-rank matrix tri-factorization are performed simultaneously for each relational data matrix. To obtain consistent and interpretable low-rank matrices, whose product pursues to approximate the respective data matrix, MFLDA regulates the low-rank matrix approximation process using constraints on the respective data sources and shared low-rank matrices across inter-related data sources.

**Reference**

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