**GTAN**: GTAN built a prediction model based on convolutional neural networks (CNN) and graph neural networks (GNN). The CNN-based module was used to learn the deep and shallow features of lncRNA-disease node pairs, while the GNN-based module focused on aggregating the information from the neighbor nodes whose node type is same as that of the target node.

**VADLP**: VADLP is constructed based on convolutional autoencoder and variational autoencoder. It integrated the pairwise topology and the distribution of node attributes for predicting lncRNA-disease associations.

**CNNLDA**: CNNLDA is a dual convolutional neural networks-based prediction method which encoded the attribute information of a pair of lncRNA and disease nodes.

**Ping’s Method**: Ping's Method is a method based on information flow propagation on lncRNA-disease network to infer the propensities between lncRNAs and diseases.

**SIMCLDA**: SIMCLDA constructed a lncRNA-disease association prediction model based on inductive matrix completion. Furthermore, it utilized the lncRNA similarities as its constraint.

**MFLDA**: MFLDA integrated the data about lncRNAs and diseases from multiple sources, and its model was established based on matrix tri-factorization decomposition.

**LDAP**: LDAP is a support vector machine (SVM) based prediction model, which integrated multiple kinds of lncRNA similarities and multiple kinds of disease similarities.