**Supplementary Data**

**Table 1** Study of different models on CircR2Disease dataset

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| **Sl no.** | **Paper** | **Methodology** | **AUC** | **General Dataset** | **Observations** |
| 1. 1. | Integrating random walk with restart and k-Nearest Neighbour to identify novel circRNA-disease association16 | Random walk with restart  K-Nearest Neighbour | 0.9297 | CircR2Disease | * Disease semantic similarity, circRNA function similarity and GIP kernel similarity * Simple to implement. * It is not applicable to new circRNAs or diseases without any known association |
| 1. 3. | GCNCDA: A new method for predicting circRNA-disease associations based on Graph Convolutional Network Algorithm18 | Graph Convolutional Network | 0.9090 | CircR2Disease | * GIP kernel similarity and disease semantic similarity * It effectively integrates network characteristics * GIP kernel similarity relies heavily on known circRNA-disease associations, thus causing inevitable bias. |
| 1. 4. | Inferring Potential CircRNA–Disease Associations via Deep Autoencoder‑Based Classification20 | Deep Auto encoder,  Random forest | 0.9486 | CircR2Disease | * Integrated circRNA, disease similarities, and experimentally verified circRNA–disease associations and extracted the hidden characteristics from them with the deep autoencoder. * Powerful computational tool for identifying novel circRNA–disease associations * The real negative samples were hard or even impossible to acquire. * Experimentally confirmed circRNA–disease relationships used in this study are far from enough. |
| 1. 5. | SGANRDA: semi-supervised generative adversarial networks for predicting circRNA–disease associations21 | semi-supervised generative adversarial networks | 0.9411 | CircR2Disease | * Integrates a variety of biological information. * Can identify new disease-associated circRNAs effectively. * Features extracted by natural language processing may not be obvious * Not easy to interpret the initialization and optimization process of hyperparameters in GAN network. * the randomly selected samples will bring some errors to the prediction results. |
| 1. 6. | GATCL2CD: Predicting CircRNA-Disease Associations via Feature Convolution Learning With Heterogeneous Graph Attention Network24 | Feature Convolution Learning and  Heterogeneous Graph Attention Network | 0.9355 | CircR2Disease | * Integrates circRNA functional similarity, disease semantic similarity, and GIP similarities. * Uses different feature-aggregated representations of nodes. * A single-layer convolutional network is used with filter kernels of different sizes for feature representations. |
| 1. 7 | AMPCDA: Prediction of circRNA–disease associations by utilizing attention  mechanisms on metapaths | Metapath encoders and Graph attention networks |  | 0.9623 | * Seven metapath patterns to derive the node information. * An encoder to combine meta path contributions. * Graph attention networks for feature extraction. |
| 1. 8 | circRNA-disease association prediction with an improved unbalanced  Bi-Random walk | Linear neighborhood similarity and Unbalanced Bi-Random walk method |  | 0.8910 | * linear neighbor similarity to find the Transition matrices * Unbalanced Bi-Random walk method to predict association. * Use of the limited dataset |