LDA: a LncRNA-Disease Association predictor.

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1 Datasets

LDA creates a tripartite graph using several data from heterogeneous sources. Three kind of data are used, namely *Long non-coding RNA* (lncRNA), *Micro RNA* (miRNA) and *diseases*. In order to create the tripartite graph, three datasets are used:

- **HMDD version 2 and 3.2**: this dataset contains miRNA-disease associations.
  Version 2 (January 2015) has 495 distinct miRNA, 380 distinct diseases and 5425 distinct associations. *Version 3.2 (March 2019)* contains 1206 miRNA, 894 diseases and 18732 associations. The datasets are available at `http://www.cuilab.cn/hmdd#fragment-4`. Since version 3.2 contains some terms update, it is necessary to map the values to version 2. This procedure is necessary in order to correctly use the dataset of lncRNA-disease associations. The mapping results consists of 1058 miRNAs, 885 diseases and 16904 associations. The mapping is available here `http://www.cuilab.cn/static/hmdd3/data/disease_mapping2019.txt`.

- **starBase 2.0**: this dataset contains 10112 miRNA-lncRNA associations, obtained from 275 miRNAs and 1114 lncRNAs. The dataset is available at `https://static-content.springer.com/esm/art%3A10.1038%2Fsrep13186/MediaObjects/41598_2015_BFsrep13186_MOESM5_ESM.xls`.

- **LncRNADisease**: this dataset contains 183 lncRNA-disease associations, from 35 lncRNA and 75 diseases. This dataset is our **gold standard** and it is available at `https://static-content.springer.com/esm/art%3A10.1038%2Fsrep13186/MediaObjects/41598_2015_BFsrep13186_MOESM6_ESM.xls`. Using dataset HMDD version 3.2, the mapping of diseases to version 2.0 will lower the number of associations from 183 to 179, since 4 diseases cannot be mapped to older versions.

2 Models

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3 Results

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