Package ‘node2vec’

October 13, 2022

Title  Algorithmic Framework for Representational Learning on Graphs
Version  0.1.0
Description  Given any graph, the 'node2vec' algorithm can learn continuous feature representations for the nodes, which can then be used for various downstream machine learning tasks. The techniques are detailed in the paper "node2vec: Scalable Feature Learning for Networks" by Aditya Grover, Jure Leskovec (2016), available at <arXiv:1607.00653>.
License  GPL (>= 3)
Encoding  UTF-8
LazyData  true
RoxygenNote  7.1.0
Imports  data.table, igraph, word2vec, rlist, dplyr, vctrs, vegan
Depends  R (>= 2.10)
NeedsCompilation  no
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gene_edges  6 edges information between two genes of human

Description
A dataset containing the 6 interactions of genes

Usage
gene_edges

Format
A data frame with 6 rows and 2 variables:

- gene1  human genes
- gene2  human genes

Source
https://thebiogrid.org/

node2vecR  Algorithmic Framework for Representational Learning on Graphs

Description
Algorithmic Framework for Representational Learning on Graphs

Usage
node2vecR(
    data, 
    p = NULL, 
    q = NULL, 
    directed = NULL, 
    num_walks = NULL, 
    walk_length = NULL, 
    dim = NULL
)
Arguments

data (input data for edges consisting of at least two columns of data and if there are weights, it must be in the third column.)
p (return parameter. Default to 1.)
q (in-out parameter. Default to 1.)
directed (the network is directed or undirected. Default to undirected.)
num_walks (number of walks per node. Default to 10.)
walk_length (number of nodes in each walk. Default to 80.)
dim (embedding dimensions. Default to 128.)

Value

eMBEDDING results for each node

Examples

# Parameters can be customized as needed
data(gene_edges)
use_data<-gene_edges
emb<-node2vecR(use_data,p=2,q=1,num_walks=5,walk_length=5,dim=10)
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