Package ‘node2vec’

May 9, 2026

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 <doi:10.48550/arXiv.1607.00653>.

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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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Repository CRAN

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Contents

`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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