# 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

**Author** Yang Tian [aut, cre],
Xu Li [aut],
Jing Ren [aut]

**Maintainer** Yang Tian `<tianyang1211@126.com>`

**Repository** CRAN

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## R topics documented:

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`gene_edges` *6 edges information between two genes of human*

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### 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/

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`node2vecR` *Algorithmic Framework for Representational Learning on Graphs*

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### 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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