

# Package ‘orca’

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**Version** 1.1-2

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**Title** Computation of Graphlet Orbit Counts in Sparse Graphs

**Description** Implements orbit counting using a fast combinatorial approach.  
Counts orbits of nodes and edges from edge matrix or data frame, or a graph object from the graph package.

**License** LGPL-3

**Depends** R (>= 3.1)

**Enhances** graph

**NeedsCompilation** yes

**Collate** orca.R

**LazyLoad** yes

**LazyData** yes

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**Repository** CRAN

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karate

*Karate Club network*


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### Description

The network representing the friendships between members of a university-based karate club, which was originally used to model the fission process with a mathematical model. The network consists of 34 nodes (club members) and 77 edges (friendships).

### Usage

```
karate
```

### Format

A data frame with 77 observations and 2 columns.

### Source

<https://networkdata.ics.uci.edu/data.php?id=105>

### References

W. W. Zachary (1977) An information flow model for conflict and fission in small groups, *Journal of Anthropological Research* 33(4), 452-473.

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orca

*Orbit counting*


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### Description

Count the node or edge orbits in 4- or 5- node graphlets for all nodes (edges) in the given graph.

### Usage

```
count4(graph)
count5(graph)
ecount4(graph)
ecount5(graph)
```

### Arguments

graph A graph given as a nx2 edge matrix, a data frame with edges or a graph object from the package 'graph'. The nodes in the matrix or data frame are given by integer indices that start with 1.

**Value**

A numeric matrix or orbit counts. Rows correspond to graph nodes or edges in the same order as on the input, and the columns corresponding to orbits.

**Author(s)**

Tomaz Hocevar and Janez Demsar

**References**

Tomaz Hocevar, Janez Demsar (2016): Computation of Graphlet Orbits for Nodes and Edges in Sparse Graphs. *Journal of Statistical Software*, 71(10), pp. 1-24.

**Examples**

```
library(orca)

# Load and show the orbit counts for the Karate graph
data("karate")
count4(karate)

## Not run:
# Simple analysis of School Wikipedia network: find the most similar
# nodes with respect to the local network topology
# Requires data from http://www.biolab.si/supp/Rorca/_downloads/schools-wiki.zip

library("FNN")

nodes <- scan("schools-wiki-nodes.txt", what="", sep="\n")
edges <- read.table("schools-wiki-edges.txt")

orbits <- count4(edges)
nn <- get.knn(orbits, k=10)
neighbours <- nn$nn.index
distances <- nn$nn.dist

check <- c("Canada", "Germany", "Isaac Newton", "Albert Einstein",
           "Mahatma Gandhi", "Mahabharata")
node_indices <- match(check, nodes)
for (i in 1:length(check)) {
  cat("\n\n", check[i], ": ", sep="")
  cat(nodes[neighbours[node_indices[i], ]], sep=" ")
  cat("\n")
  cat(round(distances[node_indices[i], ]), sep=" ")
}

## End(Not run)
```

petersen

*Petersen graph*

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**Description**

The Petersen graph is a graph with 10 vertices and 15 edges, usually drawn as a pentagram within a pentagon.

**Usage**

petersen

**Format**

A data frame with 15 observations and 2 columns.

**References**

J. Petersen Sur la théorème de Tait. *L'Intermédiaire des Math.* 5, 225-227.

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usastates

*Contiguous USA Graph*

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**Description**

The nodes of Contiguous USA Graph represent the 49 contiguous states of the USA. Two nodes are connected if there exists at least one driveable road between the corresponding states.

**Usage**

usastates

**Format**

A data frame with 107 observations and 2 columns.

**Source**

<http://www-cs-staff.stanford.edu/~uno/contiguous-usa.dat>

**References**

D. E. Knuth (2008) *The Art of Computer Programming, Volume 4, Fascicle 0: Introduction to Combinatorial Functions and Boolean Functions*, p. 15. Upper Saddle River, NJ: Addison-Wesley.

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yeast

*Yeast protein-protein interaction network*

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**Description**

The network representing interactions between 2361 proteins.

**Usage**

yeast

**Format**

A data frame with 6646 observations and 2 columns.

**Source**

<http://vlado.fmf.uni-lj.si/pub/networks/data/bio/Yeast/Yeast.htm>

**References**

S. Sun, L. Ling, N. Zhang, G. Li and R. Chen (2003) Topological structure analysis of the protein-protein interaction network in budding yeast, *Nucleic Acids Research*, 31(9), 2443-2450.

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