

# Package ‘ig.degree.betweenness’

May 8, 2026

**Type** Package

**Title** ``Smith-Pittman Community Detection Algorithm for 'igraph' Objects (2024)''

**Version** 0.2.0

**Description** Implements the ``Smith-Pittman'' community detection algorithm for network analysis using 'igraph' objects. This algorithm combines node degree and betweenness centrality measures to identify communities within networks, with a gradient evident in social partitioning. The package provides functions for community detection, visualization, and analysis of the resulting community structure. Methods are based on results from Smith, Pittman and Xu (2024) <[doi:10.48550/arXiv.2411.01394](https://doi.org/10.48550/arXiv.2411.01394)>.

**License** MIT + file LICENSE

**URL** <https://github.com/benyaminsmith/ig.degree.betweenness>

**BugReports** <https://github.com/benyaminsmith/ig.degree.betweenness/issues>

**Encoding** UTF-8

**LazyData** true

**Imports** igraph, igraphdata, rlist, BBmisc, qgraph, dplyr, tibble, tidy, ggplot2

**Depends** R (>= 4.1.0)

**RoxygenNote** 7.3.2

**Suggests** knitr, rmarkdown

**NeedsCompilation** no

**Author** Benjamin Smith [aut, cre] (ORCID: <<https://orcid.org/0009-0007-2206-0177>>), Tyler Pittman [aut] (ORCID: <<https://orcid.org/0000-0002-5013-6980>>), Wei Xu [aut] (ORCID: <<https://orcid.org/0000-0002-0257-8856>>)

**Maintainer** Benjamin Smith <[benyamin.smith@mail.utoronto.ca](mailto:benyamin.smith@mail.utoronto.ca)>

**Repository** CRAN

**Date/Publication** 2025-06-24 21:30:01 UTC

## Contents

cluster_degree_betweenness . . . . .	2
oncology_network . . . . .	3
plot_node_degrees . . . . .	4
plot_simplified_edgeplot . . . . .	5
prep_unlabeled_graph . . . . .	6
<b>Index</b>	<b>8</b>

---

cluster\_degree\_betweenness

*Community structure detection based on node degree centrality and edge betweenness*

---

### Description

Referred to as the "Smith-Pittman" algorithm in Smith et al (2024). This algorithm detects communities by calculating the degree centrality measures of nodes and edge betweenness.

### Usage

```
cluster_degree_betweenness(graph)
```

### Arguments

graph            The graph to analyze

### Details

This can be thought of as an alternative version of `igraph::cluster_edge_betweenness()`.

The function iteratively removes edges based on their betweenness centrality and the degree of their adjacent nodes. At each iteration, it identifies the edge with the highest betweenness centrality among those connected to nodes with the highest degree. It then removes that edge and recalculates the modularity of the resulting graph. The process continues until all edges have been assessed or until no further subgraph can be created with the optimal number of communities being chosen based on maximization of modularity.

### Value

An `igraph` "communities" object with detected communities via the Smith-Pittman algorithm.

### References

Smith et al (2024) "Centrality in Collaboration: A Novel Algorithm for Social Partitioning Gradients in Community Detection for Multiple Oncology Clinical Trial Enrollments", <doi:10.48550/arXiv.2411.01394>

## Examples

```
library(igraphdata)
data("karate")
ndb <- cluster_degree_betweenness(karate)
plot(
  ndb,
  karate,
  main= "Degree-Betweenness Clustering"
)

ndb

# UNLABELED GRAPH EXAMPLE

data("UKfaculty")
# Making graph undirected so it looks nicer when its plotted
uk_faculty <- prep_unlabeled_graph(UKfaculty) |>
  igraph::as.undirected()

ndb <- cluster_degree_betweenness(uk_faculty)

plot(
  ndb,
  uk_faculty,
  main= "Smith-Pittman Clustering for UK Faculty"
)
```

---

oncology\_network

*Oncology Clinical Trial Referral Network*

---

## Description

A simulated oncology clinical trial referral network from a major research hospital. For the purpose of identifying collaboration networks between oncologists, this dataset only includes referrals of patients who were enrolled in more than one clinical trial. This includes 389 patients enrolled in 288 clinical trials.

## Usage

```
oncology_network
```

## Format

A ‘igraph’ object (e.g. representing the oncology clinical trial referral network. The structure includes:

**nodes** Oncologists or clinical trials (depending on network structure).

**edges** Referral links between nodes, based on shared patient enrollment across trials.

**Details**

Clinical trials are categorized by intervention type, including targeted therapies (prefixed with "T:") and immunotherapies (prefixed with "I:"). There are 16 distinct intervention types (nodes) and 470 patient referrals (edges) in the network.

**Source**

Simulated data based on oncology clinical trial enrollment patterns.

---

plot\_node\_degrees      *Visualize Node Degree Distribution in a Network Graph*

---

**Description**

Generates a horizontal bar-style plot of node degrees for an igraph network. For undirected graphs, it shows each node's total degree. For directed graphs, it displays in-degrees (as negative bars) alongside out-degrees.

**Usage**

```
plot_node_degrees(graph)
```

**Arguments**

graph      An igraph object. Can be either directed or undirected.

**Details**

This function computes:

**Total degree** Number of edges incident on each node (for undirected graphs).

**In-degree** Number of incoming edges per node (for directed graphs).

**Out-degree** Number of outgoing edges per node (for directed graphs).

For directed graphs, in-degrees are negated so that bars extend leftward, providing an immediate visual comparison to out-degrees.

Internally, it uses:

- `igraph::degree()` to compute degrees,
- `dplyr` and `tidyr` for reshaping the data,
- `ggplot2` for plotting.

**Value**

A `ggplot` object:

- **Undirected graphs:** A bar for each node showing its total degree.
- **Directed graphs:** Split bars per node with negative values for in-degree (pointing left) and positive values for out-degree (pointing right).

### Customization

You can modify the returned ggplot with additional layers, themes, or labels. For example, to add a title or change colors:

```
plot_node_degrees(g) +  
  ggtitle("Degree Distribution") +  
  scale_fill_manual(values = c("in_degree" = "steelblue", "out_degree" = "salmon"))
```

### Examples

```
library(ig.degree.betweenness)  
library(igraphdata)  
data("karate")  
data("oncology_network")  
plot_node_degrees(oncology_network)  
plot_node_degrees(karate)
```

---

```
plot_simplified_edgeplot  
Plot Simplified Edgeplot
```

---

### Description

This function generates a simplified edge plot of an igraph object, optionally highlighting communities if provided.

### Usage

```
plot_simplified_edgeplot(graph, communities = NULL, edge.arrow.size = 0.2, ...)
```

### Arguments

graph	igraph object
communities	optional; A communities object
edge.arrow.size	edge.arrow size arg. See ?igraph::plot.igraph for more details
...	other arguments to be passed to the plot() function

### Details

This function is ideally for networks with a low number of nodes having varying numbers of connection and self loops. See the example for a better visual understanding.

### Value

No return value, called for side effects.

**Examples**

```

# Load the igraph package
library(igraph)
library(ig.degree.betweenness)
# Set parameters
num_nodes <- 15 # Number of nodes (adjust as needed)
initial_edges <- 1 # Starting edges for preferential attachment

# Create a directed, scale-free network using the Barabási-Albert model
g <- sample_pa(n = num_nodes, m = initial_edges, directed = TRUE)

# Introduce additional edges to high-degree nodes to accentuate popularity differences
num_extra_edges <- 350 # Additional edges to create more popular nodes
set.seed(123) # For reproducibility

for (i in 1:num_extra_edges) {
  # Sample nodes with probability proportional to their degree (to reinforce popularity)
  from <- sample(V(g), 1, prob = degree(g, mode = "in") + 1) # +1 to avoid zero probabilities
  to <- sample(V(g), 1)

  # Ensure we don't add the same edge repeatedly unless intended, allowing self-loops
  g <- add_edges(g, c(from, to))
}

# Add self-loops to a subset of nodes
num_self_loops <- 5
for (i in 1:num_self_loops) {
  node <- sample(V(g), 1)
  g <- add_edges(g, c(node, node))
}

g_ <- ig.degree.betweenness::prep_unlabeled_graph(g)

ig.degree.betweenness::plot_simplified_edgeplot(g_, main="Simulated Data")

```

---

```

prep_unlabeled_graph Prepared Unlabeled Graph to work with Degree-Betweenness Algorithm

```

---

**Description**

Presently, `cluster_degree_betweenness()` function only works with labeled graphs. `prep_unlabeled_graph()` is a utility function that gives an unlabeled graph labels which are string values of their vertices.

**Usage**

```
prep_unlabeled_graph(graph)
```

**Arguments**

graph            an unlabeled graph.

**Value**

An "igraph" object with named vertices.

**See Also**

[cluster\_degree\_betweenness()] which this function aids.

**Examples**

```
library(igraph)
library(igraphdata)
library(ig.degree.betweenness)
data("UKfaculty")
# Making graph undirected so it looks nicer when its plotted
uk_faculty <- prep_unlabeled_graph(UKfaculty) |>
  as.undirected()

ndb <- cluster_degree_betweenness(uk_faculty)

plot(
  ndb,
  uk_faculty,
  main= "Node Degree Clustering"
)

ndb
```

# Index

`cluster_degree_betweenness`, [2](#)

`oncology_network`, [3](#)

`plot_node_degrees`, [4](#)

`plot_simplified_edgeplot`, [5](#)

`prep_unlabeled_graph`, [6](#)