# Package: pathlinkR (via r-universe)

November 9, 2026

**Type** Package

**Title** Analyze and interpret RNA-Seq results

**Version** 1.8.0

**Description** pathlinkR is an R package designed to facilitate analysis of RNA-Seq results. Specifically, our aim with pathlinkR was to provide a number of tools which take a list of DE genes and perform different analyses on them, aiding with the interpretation of results. Functions are included to perform pathway enrichment, with muliplte databases supported, and tools for visualizing these results. Genes can also be used to create and plot protein-protein interaction networks, all from inside of R.

**biocViews** GeneSetEnrichment, Network, Pathways, Reactome, RNASeq, NetworkEnrichment

**BiocType** Software

**BugReports** https://github.com/hancockinformatics/pathlinkR/issues

**License** GPL-3 + file LICENSE

**URL** https://github.com/hancockinformatics/pathlinkR

**Encoding** UTF-8

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# Contents

.eruptionBreaks . . . 3
.plotFoldChangeLegend . . . 3
.runSigora . . . 4
.truncNeatly . . . 5
eruption . . . 5
exampleDESeqResults . . . 8
getPathwayDistances . . . 8
groupedPathwayColours . . . 9
hallmarkDatabase . . . 10
innateDbPPI . . . 10
keggDatabase . . . 11
mappingFile . . . 12
pathnetCreate . . . 12
pathnetFoundation . . . 15
pathnetGGraph . . . 16
pathnetVisNetwork . . . 18
pathwayCategories . . . 20
pathwayEnrichment . . . 21
pathwayPlots . . . 24
plotFoldChange . . . 26
ppiBuildNetwork . . . 29
ppiCleanNetwork . . . 31
ppiEnrichNetwork . . . 32
ppiExtractSubnetwork . . . 34
ppiPlotNetwork . . . 36
ppiRemoveSubnetworks . . . 39
reactomeDatabase . . . 39
sigoraDatabase . . . 40
sigoraExamples . . . 40

**Index** **42**

## .eruptionBreaks *INTERNAL Create manual breaks/labels for volcano plots*

### Description

Internal function which is used to create even breaks for volcano plots produced by `eruption`.

### Usage

```
.eruptionBreaks(x)
```

### Arguments

| | |
|---|---|
| x | Length-two numeric vector to manually specify limits of the x-axis in log2 fold change; defaults to NA which lets ggplot2 determine the best values. |

### Value

ggplot scale object

### See Also

https://github.com/hancockinformatics/pathlinkR

## .plotFoldChangeLegend *INTERNAL Construct heatmap legend*

### Description

Helper function to handle heatmap legends without clutteing up the main function.

### Usage

```
.plotFoldChangeLegend(
  .matFC,
  .log2FoldChange,
  .cellColours,
  .titlegp,
  .labelsgp
)
```

### Arguments

| | |
|---|---|
| `.matFC` | Matrix of fold change values |
| `.log2FoldChange` | Boolean denoting if values will be in log2 |
| `.cellColours` | Colours for fold change values |
| `.titlegp` | Font size for the title of the legend |
| `.labelsgp` | Font size for the labels of the legend |

### Value

A list containing heatmap legend parameters and colour function

### See Also

https://github.com/hancockinformatics/pathlinkR

---

## .runSigora *INTERNAL Wrapper around Sigora's enrichment function*

---

### Description

Internal wrapper function to run Sigora and return the results with desired columns

### Usage

```
.runSigora(enrichGenes, gpsRepo, gpsLevel, pValFilter = NA)
```

### Arguments

| | |
|---|---|
| `enrichGenes` | Vector of genes to enrich |
| `gpsRepo` | GPS object to use for testing pathways |
| `gpsLevel` | Level to use for enrichment testing |
| `pValFilter` | Desired threshold for filtering results |

### Value

A "data.frame" (tibble) of results from Sigora

### References

https://cran.r-project.org/package=sigora

### See Also

https://github.com/hancockinformatics/pathlinkR

## .truncNeatly *INTERNAL Break long strings at spaces*

### Description

Trims a character string to the desired length, without breaking in the middle of a word (i.e. chops at the nearest space). Appends an ellipsis at the end to indicate some text has been removed.

### Usage

```
.truncNeatly(x, l = 60)
```

### Arguments

| | |
|---|---|
| x | Character to be truncated |
| l | Desired maximum length for the output character |

### Value

Character vector

### See Also

https://github.com/hancockinformatics/pathlinkR

## eruption *Create a volcano plot of RNA-Seq results*

### Description

Creates a volcano plot of genes from RNA-Seq results, with various options for tweaking the appearance. Ensembl gene IDs should be the rownames of the input object.

### Usage

```
eruption(
  rnaseqResult,
  columnFC = NA,
  columnP = NA,
  pCutoff = 0.05,
  fcCutoff = 1.5,
  labelCutoffs = FALSE,
  baseColour = "steelblue4",
  nonsigColour = "lightgrey",
  alpha = 0.5,
```

```
  pointSize = 1,
  title = NA,
  nonlog2 = FALSE,
  xaxis = NA,
  yaxis = NA,
  highlightGenes = c(),
  highlightColour = "red",
  highlightName = "Selected",
  label = "auto",
  n = 10,
  manualGenes = c(),
  removeUnannotated = TRUE,
  labelSize = 3.5,
  pad = 1.4
)
```

## Arguments

| | |
|---|---|
| rnaseqResult | Data frame of RNASeq results, with Ensembl gene IDs as rownames. Can be a "DESeqResults" or "TopTags" object, or a simple data frame. See "Details" for more information. |
| columnFC | Character; Column to plot along the x-axis, typically log2 fold change values. Only required when rnaseqResult is a simple data frame. Defaults to NA. |
| columnP | Character; Column to plot along the y-axis, typically nominal or adjusted p values. Only required when rnaseqResult is a simple data frame. Defaults to NA. |
| pCutoff | Adjusted p value cutoff, defaults to < 0.05 |
| fcCutoff | Absolute fold change cutoff, defaults to > 1.5 |
| labelCutoffs | Logical; Should cutoff lines for p value and fold change be labeled? Size of the label is controlled by labelSize. Defaults to FALSE. |
| baseColour | Colour of points for all significant DE genes ("steelblue4") |
| nonsigColour | Colour of non-significant DE genes ("lightgrey") |
| alpha | Transparency of the points (0.5) |
| pointSize | Size of the points (1) |
| title | Title of the plot |
| nonlog2 | Show non-log2 fold changes instead of log2 fold change (FALSE) |
| xaxis | Length-two numeric vector to manually specify limits of the x-axis in log2 fold change; defaults to NA which lets ggplot2 determine the best values. |
| yaxis | Length-two numeric vector to manually specify limits of the y-axis (in -log10). Defaults to NA which lets ggplot2 determine the best values. |
| highlightGenes | Vector of genes to emphasize by colouring differently (e.g. genes of interest). Must be Ensembl IDs. |
| highlightColour | Colour for the genes specified in highlightGenes |

| | |
|---|---|
| highlightName | Optional name to call the highlightGenes (e.g. Unique, Shared, Immune related, etc.) |
| label | When set to "auto" (default), label the top n up- and down-regulated DE genes. When set to "highlight", label top n up- and down-regulated genes provided in highlightGenes. When set to "manual" label a custom selection of genes provided in manualGenes. |
| n | number of top up- and down-regulated genes to label. Applies when label is set to "auto" or "highlight". |
| manualGenes | If label="manual", these are the genes to be specifically label. Can be HGNC symbols or Ensembl gene IDs. |
| removeUnannotated | Boolean (TRUE): Remove genes without annotations (no HGNC symbol). |
| labelSize | Size of font for labels (3.5) |
| pad | Padding of labels; adjust this if the labels overlap |

## Details

The input to eruption() can be of class "DESeqResults" (from DESeq2), "TopTags" (edgeR), or a simple data frame. When providing either of the former, the columns to plot are automatically pulled ("log2FoldChange" and "padj" for DESeqResults, or "logFC" and "FDR" for TopTags). Otherwise, the arguments "columnFC" and "columnP" must be specified. If one wishes to override the default behaviour for "DESeqResults" or "TopTags" (e.g. plot nominal p values on the y-axis), convert those objects to data frames, then supply "columnFC" and "columnP".

The argument highlightGenes can be used to draw attention to a specific set of genes, e.g. those from a pathway of interest. Setting the argument label="highlight" will also mean those same genes (at least some of them) will be given labels, further emphasizing them in the volcano plot.

Since this function returns a ggplot object, further custom changes could be applied using the standard ggplot2 functions (labs(), theme(), etc.).

## Value

Volcano plot of genes from an RNA-Seq experiment; a "ggplot" object

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("exampleDESeqResults")
eruption(rnaseqResult=exampleDESeqResults[[1]])
```

## exampleDESeqResults *List of example results from DESeq2*

### Description

List of example results from DESeq2

### Usage

```
data(exampleDESeqResults)
```

### Format

A list of two "DESeqResults" objects, each with 5000 rows and 6 columns:

**baseMean** A combined score for the gene

**log2FoldChange** Fold change value for the gene

**lfcSE** Standard error for the fold change value

**stat** The statistic value

**pvalue** The nominal p value for the gene

**padj** The adjusted p value for the gene

### Value

An object of class "list"

### Source

For details on DESeq2 and its data structures/methods, please see https://bioconductor.org/packages/DESeq2/

## getPathwayDistances *Calculate pairwise distances from a table of pathways and genes*

### Description

Given a data frame of pathways and their member genes, calculate the pairwise distances using a constructed identity matrix. Zero means two pathways are identical, while one means two pathways share no genes in common.

### Usage

```
getPathwayDistances(pathwayData = sigoraDatabase, distMethod = "jaccard")
```

### Arguments

| | |
|---|---|
| pathwayData | Three column data frame of pathways and their constituent genes. Defaults to the provided sigoraDatabase object, but can be any set of Reactome pathways. Must contain Ensembl gene IDs in the first column, human Reactome pathway IDs in the second, and pathway descriptions in the third. |
| distMethod | Character; method used to determine pairwise pathway distances. Can be any option supported by vegan::vegdist(). |

### Value

Matrix of the pairwise pathway distances (dissimilarity) based on overlap of their constituent genes; object of class "matrix".

### References

None.

### See Also

https://github.com/hancockinformatics/pathlinkR

### Examples

```
# Here we'll use a subset of all the pathways, to save time
data("sigoraDatabase")

getPathwayDistances(
    pathwayData=dplyr::slice_head(
        dplyr::arrange(sigoraDatabase, pathwayId),
        prop=0.05
    ),
    distMethod="jaccard"
)
```

---

## groupedPathwayColours *Colour assignments for grouped pathways*

---

### Description

Colour assignments for grouped pathways

### Usage

```
data(groupedPathwayColours)
```

### Format

A length 8 named vector of hex colour values

### Value

An object of class "character"

---

`hallmarkDatabase` *Table of Hallmark gene sets and their genes*

---

### Description

Table of Hallmark gene sets and their genes

### Usage

```
data(hallmarkDatabase)
```

### Format

A data frame (tibble) with 7333 rows and 2 columns

**pathwayId** Name of the Hallmark Gene Set

**ensemblGeneId** Ensembl gene IDs

### Value

An object of class "tbl", "tbl.df", "data.frame"

### Source

For more information on the MSigDB Hallmark gene sets, please see https://www.gsea-msigdb.org/gsea/msigdb/collections.jsp

---

`innateDbPPI` *InnateDB PPI data*

---

### Description

A data frame containing human PPI data from InnateDB, from the entry "All Experimentally Validated Interactions (updated weekly)" at https://innatedb.com/redirect.do?go=downloadImported. A few important steps have been taken to filter the data, namely the removal of duplicate interactions, and removing interactions that have the same components but are swapped between A and B.

### Usage

```
data(innateDbPPI)
```

### Format

A data frame (tibble) with 152256 rows and 2 columns:

**ensemblGeneA** Ensembl gene ID for the first gene/protein in the interaction

**ensemblGeneB** Ensembl gene ID for the second gene/protein in the interaction

### Value

An object of class "tbl", "tbl.df", "data.frame"

### Source

For more details on the data sourced from InnateDB, please see their website: https://www.innatedb.com

---

## keggDatabase *Table of KEGG pathways and genes*

---

### Description

Table of KEGG pathways and genes

### Usage

```
data(keggDatabase)
```

### Format

A data frame (tibble) with 32883 rows and 4 columns

**pathwayId** KEGG pathway ID

**pathwayName** Name of the Reactome pathway

**ensemblGeneId** Ensembl gene ID

**hgncSymbol** HGNC gene symbol

### Value

An object of class "tbl", "tbl.df", "data.frame"

### Source

See https://kegg.jp for more information.

## mappingFile *Table of human gene ID mappings*

### Description

A data frame to aid in mapping human gene IDs between different formats, inclusing Ensembl IDs, HGNC symbols, and Entrez IDs. Mapping information was sourced using `biomaRt` and `AnnotationDbi`.

### Usage

```
data(mappingFile)
```

### Format

A data frame (tibble) with 45776 rows and 3 columns

**ensemblGeneId** Ensembl IDs

**hgncSymbol** HGNC symbols

**entrezGeneId** NCBI Entrez IDs

### Value

An object of class "tbl", "tbl.df", "data.frame"

### Source

See https://bioconductor.org/packages/biomaRt/ and https://bioconductor.org/packages/AnnotationDbi/ for information on each of the utilized packages and functions.

## pathnetCreate *Create a pathway network from enrichment results and a pathway interaction foundation*

### Description

Creates a tidygraph network object from the provided pathway information, ready to be visualized with `pathnetGGraph` or `pathnetVisNetwork`.

## Usage

```
pathnetCreate(
  pathwayEnrichmentResult,
  columnId = "pathwayId",
  columnP = "pValueAdjusted",
  foundation,
  trim = TRUE,
  trimOrder = 1
)
```

## Arguments

| | |
|---|---|
| pathwayEnrichmentResult | Data frame of results from `pathwayEnrichment` run with Sigora or ReactomePA (should be based on Reactome data). |
| columnId | Character; column containing the Reactome pathway IDs. Defaults to "pathwayID". |
| columnP | Character; column containing the adjusted p values. Defaults to "pValueAdjusted". |
| foundation | List of pathway pairs to use in constructing a network. Typically this will be the output from `createFoundation`. |
| trim | Remove independent subgraphs which don't contain any enriched pathways (default is `TRUE`). |
| trimOrder | Order to use when removing subgraphs; Higher values will keep more non-enriched pathway nodes. Defaults to `1`. |

## Details

With the "trim" option enabled, nodes (pathways) and subgraphs which are not sufficiently connected to enriched pathways will be removed. How aggressively this is done can be controlled via the `trimOrder` argument, and the optimal value will depend on the number of enriched pathways and the number of interacting pathways (i.e. number of rows in "foundation").

## Value

A pathway network as a "tidygraph" object, with the following columns for nodes:

| | |
|---|---|
| pathwayId | Reactome pathway ID |
| pathwayName | Reactome pathway name |
| comparison | Name of source comparison, if this pathway was enriched |
| direction | Whether an enriched pathway was found in all genes or up- or down-regulated genes |
| pValue | Nominal p-value from the enrichment result |
| pValueAdjusted | Corrected p-value from the enrichment |
| genes | Candidate genes for the given pathway if it was enriched |

| | |
|---|---|
| numCandidateGenes | Number of candidate genes |
| numBgGenes | Number of background genes |
| geneRatio | Ratio of candidate and background genes |
| totalGenes | Total number of DE genes tested, for an enriched pathway |
| topLevelPathway | Highest level Reactome term for a given pathway |
| groupedPathway | Custom pathway category used in visualizations |

For edges, the following information is also included:

| | |
|---|---|
| from | Starting node (row number) for the edge |
| to | Ending node (row number) for the edge |
| similarity | Similarity of two nodes/pathways |
| distance | Inverse of similarity |

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("sigoraDatabase", "sigoraExamples")

pathwayDistancesJaccard <- getPathwayDistances(
    pathwayData=dplyr::slice_head(
        dplyr::arrange(sigoraDatabase, pathwayId),
        prop=0.05
    ),
    distMethod="jaccard"
)

startingPathways <- pathnetFoundation(
    mat=pathwayDistancesJaccard,
    maxDistance=0.8
)

pathnetCreate(
    pathwayEnrichmentResult=sigoraExamples[grepl(
        "Pos",
        sigoraExamples$comparison
    ), ],
    foundation=startingPathways,
    trim=TRUE,
    trimOrder=1
)
```

`pathnetFoundation` *Create the foundation for pathway networks using pathway distances*

## Description

From a "n by n" distance matrix, generate a table of interacting pathways to use in constructing a pathway network. The cutoff can be adjusted to have more or fewer edges in the final network, depending on the number of pathways involved, i.e. the number of enriched pathways you're trying to visualize.

The desired cutoff will also vary based on the distance measure used, so some trial-and-error may be needed to find an appropriate value.

## Usage

```
pathnetFoundation(mat, maxDistance = NA, propToKeep = NA)
```

## Arguments

| | |
|---|---|
| `mat` | Matrix of distances between pathways, i.e. 0 means two pathways are identical. Should match the output from `getPathwayDistances`. |
| `maxDistance` | Numeric distance cutoff (less than or equal) used to determine if two pathways should share an edge. Pathway pairs with a distance of 0 are always removed. One of `maxDistance` or `propToKeep` must be provided. |
| `propToKeep` | Top proportion of pathway pairs to keep as edges, ranked based distance. One of `maxDistance` or `propToKeep` must be provided. |

## Value

A "data.frame" (tibble) of interacting pathway pairs with the following columns:

| | |
|---|---|
| `pathwayName1` | Name of the first pathway in the pair |
| `pathwayName2` | Name of the second pathway in the pair |
| `distance` | Distance measure for the two pathways |
| `pathway1` | Reactome ID for the first pathway in the pair |
| `pathway2` | Reactome ID for the first pathway in the pair |

## References

None.

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("sigoraDatabase")

pathwayDistancesJaccard <- getPathwayDistances(
    pathwayData=dplyr::slice_head(
        dplyr::arrange(sigoraDatabase, pathwayId),
        prop=0.05
    ),
    distMethod="jaccard"
)

startingPathways <- pathnetFoundation(
    mat=pathwayDistancesJaccard,
    maxDistance=0.8
)
```

---

pathnetGGraph *Visualize enriched Reactome pathways as a static network*

---

## Description

Plots the network object generated from `createPathnet`, creating a visual representation of pathway similarity/interactions based on overlapping genes.

## Usage

```
pathnetGGraph(
  network,
  networkLayout = "nicely",
  nodeSizeRange = c(4, 8),
  nodeSizeLegend = 5,
  nodeBorderWidth = 1.5,
  nodeLabelSize = 5,
  nodeLabelColour = "black",
  nodeLabelAlpha = 0.67,
  nodeLabelOverlaps = 6,
  nodeLabelLength = 40,
  nodeLabelWrap = 20,
  labelProp = 0.25,
  segColour = "black",
  edgeColour = "grey30",
  edgeWidthRange = c(0.33, 3),
  edgeAlpha = 1,
  themeBaseSize = 16
)
```

## Arguments

| | |
|---|---|
| network | Tidygraph network object, output from createPathnet. |
| networkLayout | Desired layout for the network visualization. Defaults to "nicely", but supports any method found in ?layout_tbl_graph_igraph |
| nodeSizeRange | Size range for nodes, mapped to significance (Bonferroni p-value). Defaults to c(4, 8). |
| nodeSizeLegend | Shape size in the legend for Pathway Type. Defaults to 5. |
| nodeBorderWidth | Width of borders on nodes, defaults to 1.5 |
| nodeLabelSize | Size of node labels; defaults to 5. |
| nodeLabelColour | Colour of the node labels; defaults to "black". |
| nodeLabelAlpha | Transparency of node labels. Defaults to 0.67. |
| nodeLabelOverlaps | Max overlaps for node labels, from ggrepel. Defaults to 6. |
| nodeLabelLength | Length of the pathway name displayed before truncation. Defaults to 40. |
| nodeLabelWrap | Line length before pathway name is wrapped onto a new line. Defaults to 20. |
| labelProp | Proportion of "interactor" (i.e. non-enriched) pathways that the function will attempt to label. E.g. setting this to 0.5 (the default) means half of the non-enriched pathways will *potentially* be labeled - it won't be exact because the node labeling is done with ggrepel. |
| segColour | Colour of line segments connecting labels to nodes. Defaults to "black". |
| edgeColour | Colour of network edges; defaults to "grey30". |
| edgeWidthRange | Range of edge widths, mapped to log10(similarity). Defaults to c(0.33, 3). |
| edgeAlpha | Alpha value for edges; defaults to 1. |
| themeBaseSize | Base font size for all plot elements. Defaults to 16. |

## Details

A note regarding node labels: The function tries to prioritize labeling enriched pathways (filled nodes), with the labelProp argument determining roughly how many of the remaining interactor pathways might get labels. You'll likely need to tweak this value, and try different seeds, to get the desired effect.

## Value

A pathway network or "pathnet"; a plot object of class "ggplot"

## References

None.

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("sigoraDatabase", "sigoraExamples")

pathwayDistancesJaccard <- getPathwayDistances(
    pathwayData=dplyr::slice_head(
        dplyr::arrange(sigoraDatabase, pathwayId),
        prop=0.05
    ),
    distMethod="jaccard"
)

startingPathways <- pathnetFoundation(
    mat=pathwayDistancesJaccard,
    maxDistance=0.8
)

exPathnet <- pathnetCreate(
    pathwayEnrichmentResult=sigoraExamples[grepl(
        "Pos",
        sigoraExamples$comparison
    ), ],
    foundation=startingPathways,
    trim=TRUE,
    trimOrder=1
)

pathnetGGraph(
    exPathnet,
    labelProp=0.1,
    nodeLabelSize=4,
    nodeLabelOverlaps=8,
    segColour="red"
)
```

---

`pathnetVisNetwork` *Visualize enriched Reactome pathways as an interactive network*

---

## Description

Plots the network object generated from `createPathnet`, creating a visual and interactive representation of similarities/ interactions between pathways using their overlapping genes.

## Usage

```
pathnetVisNetwork(
  network,
  networkLayout = "layout_nicely",
  nodeSizeRange = c(20, 50),
  nodeBorderWidth = 2.5,
  labelNodes = TRUE,
  nodeLabelSize = 60,
  nodeLabelColour = "black",
  nodeLabelLength = 40,
  edgeColour = "#848484",
  edgeWidthRange = c(5, 20),
  highlighting = TRUE
)
```

## Arguments

| | |
|---|---|
| network | Tidygraph network object as output by `createPathnet` |
| networkLayout | Desired layout for the network visualization. Defaults to "layout_nicely", and should support most igraph layouts. See `?visIgraphLayout` for more details. |
| nodeSizeRange | Node size is mapped to the negative log of the Bonferroni-adjusted p value, and this length-two numeric vector controls the minimum and maximum. Defaults to `c(20, 50)`. |
| nodeBorderWidth | Size of the node border, defaults to 2.5 |
| labelNodes | Boolean determining if nodes should be labeled. Note it will only ever label enriched nodes/pathways. |
| nodeLabelSize | Size of the node labels in pixels; defaults to 60. |
| nodeLabelColour | Colour of the node labels; defaults to "black". |
| nodeLabelLength | Length of the pathway name displayed before truncation. Defaults to `40`. |
| edgeColour | Colour of network edges; defaults to "#848484". |
| edgeWidthRange | Edge width is mapped to the similarity measure (one over distance). This length-two numeric vector controls the minimum and maximum width of edges. Defaults to `c(5, 20)`. |
| highlighting | When clicking on a node, should directly neighbouring nodes be highlighted (other nodes are dimmed)? Defaults to TRUE. |

## Details

This function makes use of the visNetwork library, which allows for various forms of interactivity, such as including text when hovering over nodes, node selection and dragging (including multiple selections), and highlighting nodes belonging to a larger group (e.g. top-level Reactome category).

## Value

An interactive pathway, network or "pathnet"; object of class "visNetwork"

## References

https://datastorm-open.github.io/visNetwork/

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("sigoraDatabase", "sigoraExamples")

pathwayDistancesJaccard <- getPathwayDistances(
    pathwayData=dplyr::slice_head(
        dplyr::arrange(sigoraDatabase, pathwayId),
        prop=0.05
    ),
    distMethod="jaccard"
)

startingPathways <- pathnetFoundation(
    mat=pathwayDistancesJaccard,
    maxDistance=0.8
)

exPathnet <- pathnetCreate(
    pathwayEnrichmentResult=sigoraExamples[grepl(
        "Pos",
        sigoraExamples$comparison
    ), ],
    foundation=startingPathways,
    trim=TRUE,
    trimOrder=1
)

pathnetVisNetwork(exPathnet)
```

---

# pathwayCategories *Top-level pathway categories*

---

## Description

A data frame containing all Reactome, Hallmark, and KEGG pathways/terms, along with a manually-curated top-level category for each entry.

## Usage

```
data(pathwayCategories)
```

## Format

A data frame (tibble) with 3499 rows and 5 columns

**pathwayId** Reactome, Hallmark, or KEGG pathway identifier

**pathwayName** Pathway name

**topLevelPathway** Top hierarchy pathway term, shortened in some cases

**groupedPathway** Top grouped pathway

**topLevelOriginal** Original top pathway name

## Value

An object of class "tbl", "tbl.df", "data.frame"

## Source

See https://reactome.org/, https://www.gsea-msigdb.org/gsea/msigdb/collections.jsp, and https://kegg.jp for information on each of these databases.

---

# pathwayEnrichment *Test significant DE genes for enriched pathways*

---

## Description

This function provides a simple and consistent interface to three different pathway enrichment tools: Sigora and ReactomePA (which both test for Reactome pathways), and MSigDB Hallmark gene set enrichment.

## Usage

```
pathwayEnrichment(
  inputList,
  columnFC = NA,
  columnP = NA,
  filterInput = TRUE,
  pCutoff = 0.05,
  fcCutoff = 1.5,
  split = TRUE,
  analysis = "sigora",
  filterResults = "default",
  gpsRepo = "reaH",
  gpsLevel = "default",
  geneUniverse = NULL,
  verbose = FALSE
)
```

## Arguments

| | |
|---|---|
| inputList | A list, with each element containing RNA-Seq results as a "DESeqResults", "TopTags", or "data.frame" object. Rownames of each table must contain Ensembl Gene IDs. The list names are used as the comparison name for each element (e.g. "COVID vs Healthy"). See Details for more information on supported input types. |
| columnFC | Character; Column to plot along the x-axis, typically log2 fold change values. Only required when rnaseqResult is a simple data frame. Defaults to NA. |
| columnP | Character; Column to plot along the y-axis, typically nominal or adjusted p values. Only required when rnaseqResult is a simple data frame. Defaults to NA. |
| filterInput | When providing list of data frames containing the unfiltered RNA-Seq results (i.e. not all genes are significant), set this to TRUE to remove non-significant genes using the thresholds set by the pCutoff and fcCutoff. When this argument is FALSE its assumed your passing a pre-filtered data in inputList, and no more filtering will be done. |
| pCutoff | Adjusted p value cutoff when filtering. Defaults to < 0.05. |
| fcCutoff | Minimum absolute fold change value when filtering. Defaults to > 1.5 |
| split | Boolean (TRUE); Split into up- and down-regulated DE genes using the fold change column, and do enrichment independently on each. Results are combined at the end, with an added "direction" column. |
| analysis | Method/database to use for enrichment analysis. The default is "sigora", but can also be "reactome"/"reactomepa", "hallmark", "kegg", "fgsea_reactome" or "fgsea_hallmark". |
| filterResults | Should the output be filtered for significance? Use 1 to return the unfiltered results, or any number less than 1 for a custom p-value cutoff. If left as default, the significance cutoff for analysis="sigora" is 0.001, or 0.05 for "reactome", "hallmark", and "kegg". |
| gpsRepo | Only applies to analysis="sigora". Gene Pair Signature (GPS) object for Sigora to use to test for enriched pathways. "reaH" (default) will use the Reactome GPS object from Sigora; "kegH" will use the KEGG GPS. One can also provide their own GPS object; see Sigora's documentation for details. |
| gpsLevel | Only applies to analysis="sigora". If left as default, will be set to 4 for gpsRepo="reaH" or 2 for gpeRepo="kegH". If providing your own GPS object, can be set as desired; see Sigora's documentation for details. |
| geneUniverse | Only applies when analysis is "reactome"/"reactomepa", "hallmark", or "kegg". The set of background genes to use when testing with Reactome, Hallmark, or KEGG gene sets. For Reactome this must be a character vector of Entrez genes. For Hallmark or KEGG, it must be Ensembl IDs. |
| verbose | Logical; If FALSE (the default), don't print info/progress messages. |

## Details

inputList must be a named list of RNA-Seq results, with each element being of class "DESeqResults" from DESeq2, "TopTags" from edgeR, or a simple data frame. For the first two cases, column

names are expected to be the standard defined by each class ("log2FoldChange" and "padj" for "DESeqResults", and "logFC" and "FDR" for "TopTags"). Hence for these two cases the arguments `columnFC` and `columnP` can be left as `NA`.

In the last case (elements are "data.frame"), both `columnFC` and `columnP` must be supplied when `filterInput=TRUE`, and `columnFC` must be given if `split=TRUE`.

Setting `analysis` to any of "reactome", "reactomepa", "hallmark", or "kegg" will execute traditional over-representation analysis, the only difference being the database used ("reactome" and "reactomepa" are treated the same). Setting `analysis="sigora"` will use a gene pair-based approach, which can be performed on either Reactome data when `gpsRepo="reaH"` or KEGG data with `gpsRepo="kegH"`.

## Value

A "data.frame" (tibble) of pathway enrichment results for all input comparisons, with the following columns:

| | |
|---|---|
| `comparison` | Source comparison from the names of `inputList` |
| `direction` | Whether the pathway was enriched in all genes (`split=FALSE`), or up- or down-regulated genes (`split=TRUE`) |
| `pathwayId` | Pathway identifier |
| `pathwayName` | Pathway name |
| `pValue` | Nominal p value for the pathway |
| `pValueAdjusted` | p value, corrected for multiple testing |
| `genes` | Candidate genes, which were DE for the comparison and also in the pathway |
| `numCandidateGenes` | Number of candidate genes |
| `numBgGenes` | Number of background genes for the pathway |
| `geneRatio` | Ratio of candidate and background genes |
| `totalGenes` | Number of DE genes which were tested for enriched pathways |
| `topLevelPathway` | High level Reactome term which serves to group similar pathways |

## References

Sigora: https://cran.r-project.org/package=sigora ReactomePA: https://www.bioconductor.org/packages/ReactomePA/ Reactome: https://reactome.org/ MSigDB/Hallmark: https://www.gsea-msigdb.org/gsea/msigdb/collections.jsp KEGG: https://www.kegg.jp/

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("exampleDESeqResults")

pathwayEnrichment(
    inputList=exampleDESeqResults[1],
    filterInput=TRUE,
    split=TRUE,
    analysis="hallmark",
    filterResults="default"
)
```

---

`pathwayPlots` *Plot pathway enrichment results*

---

## Description

Creates a plot to visualize and compare pathway enrichment results from multiple DE comparisons. Can automatically assign each pathway into an informative top-level category.

## Usage

```
pathwayPlots(
  pathwayEnrichmentResults,
  columns = 1,
  specificTopPathways = "any",
  specificPathways = "any",
  colourValues = c("blue", "red"),
  nameWidth = 35,
  nameRows = 1,
  xAngle = "angled",
  maxPVal = 50,
  intercepts = NA,
  includeGeneRatio = FALSE,
  size = 4,
  legendMultiply = 1,
  showNumGenes = FALSE,
  pathwayPosition = "right",
  newGroupNames = NA,
  fontSize = 12
)
```

## Arguments

`pathwayEnrichmentResults`
: Data frame of results from the function `enrichPathway`

`columns` Number of columns to split the pathways across, particularly relevant if there are many significant pathways. Can specify up to 3 columns, with a default of 1.

`specificTopPathways`
Only plot pathways from a specific vector of "topLevelPathway". Defaults to "any" which includes all pathway results, or see `unique(pathwayEnrichmentResults$topLevelPathwa` (i.e. the input) for possible values.

`specificPathways`
Only plot specific pathways. Defaults to "any".

`colourValues` Length-two character vector of colours to use for the scale. Defaults to `c("blue", "red")`.

`nameWidth` How many characters to show for pathway name before truncating? Defaults to 35.

`nameRows` For pathway names (y axis), how many rows (lines) should names wrap across when they're too long? Defaults to 1.

`xAngle` Angle of x axis labels, set to "angled" (45 degrees), "horizontal" (0 degrees), or "vertical" (90 degrees).

`maxPVal` P values below `10 ^ -maxPVal` will be set to that value.

`intercepts` Add vertical lines to separate different groupings, by providing a vector of intercepts (e.g. `c(1.5, 2.5)`). Defaults to `NA`.

`includeGeneRatio`
Boolean (FALSE). Should the gene ratio be included as an aesthetic mapping?If so, then it is attributed to the size of the triangles.

`size` Size of points if not scaling to gene ratio. Defaults to 4.

`legendMultiply` Size of the legend, e.g. increase if there are a lot of pathways which makes the legend small and unreadable by comparison. Defaults to 1, i.e. no increase in legend size.

`showNumGenes` Boolean, defaults to FALSE. Show the number of genes for each comparison as brackets under the comparison's name.

`pathwayPosition`
Whether to have the y-axis labels (pathway names) on the left or right side. Default is "right".

`newGroupNames` If you want to change the names of the comparisons to different names. Input a vector in the order as they appear.

`fontSize` Base font size for all text elements of the plot. Defaults to 12.

## Value

A plot of enriched pathways; a "ggplot" object

## See Also

`https://github.com/hancockinformatics/pathlinkR` `https://bioconductor.org/packages/fgsea/`

## Examples

```
data("sigoraExamples")
pathwayPlots(sigoraExamples, columns=2)
```

---

`plotFoldChange` *Create a heatmap of fold changes to visualize RNA-Seq results*

---

## Description

Creates a heatmap of fold changes values for results from RNA-Seq results, with various parameters to tweak the appearance.

## Usage

```
plotFoldChange(
  inputList,
  columnFC = NA,
  columnP = NA,
  pathName = NA,
  pathId = NA,
  genesToPlot = NA,
  manualTitle = NA,
  fontSizes = c(13.2, 13.2, 12, 12, 10, 10),
  geneFormat = "ensembl",
  pCutoff = 0.05,
  fcCutoff = 1.5,
  cellColours = c("blue", "white", "red"),
  cellBorder = gpar(col = "grey"),
  plotSignificantOnly = TRUE,
  showStars = TRUE,
  hideNonsigFC = TRUE,
  vjust = 0.75,
  rot = 0,
  invert = FALSE,
  log2FoldChange = FALSE,
  colSplit = NA,
  clusterRows = TRUE,
  clusterColumns = FALSE,
  colAngle = 90,
  colCenter = TRUE,
  rowAngle = 0,
  rowCenter = FALSE,
  returnData = FALSE
)
```

## Arguments

| | |
|---|---|
| inputList | A list, with each element containing RNA-Seq results as a "DESeqResults", "TopTags", or "data.frame" object, with Ensembl gene IDs in the rownames. The list names are used as the comparison name for each dataframe (e.g. "COVID vs Healthy"). See Details for more information on supported input types. |
| columnFC | Character; Column to plot along the x-axis, typically log2 fold change values. Only required when rnaseqResult is a simple data frame. Defaults to NA. |
| columnP | Character; Column to plot along the y-axis, typically nominal or adjusted p values. Only required when rnaseqResult is a simple data frame. Defaults to NA. |
| pathName | The name of a Reactome pathway to pull genes from, also used for the plot title. Alternative to pathID. |
| pathId | ID of a Reactome pathway to pull genes from. Alternative to pathName. |
| genesToPlot | Vector of Ensembl gene IDs you want to plot, instead of pulling the genes from a pathway, i.e. this option and pathName/pathID are mutually exclusive. |
| manualTitle | Provide your own title, and override the use of a pathway name the title. |
| fontSizes | Font sizes for the elements: column title, row title, column names, row names, legend title, legend labels. Defaults to c(13.2, 13.2, 12, 12, 10, 10). |
| geneFormat | Type of genes given in genesToPlot. Default is Ensembl gene IDs ("ensembl"), but can also input a vector of HGNC symbols ("hgnc"). |
| pCutoff | P value cutoff, default is <0.05 |
| fcCutoff | Absolute fold change cutoff, default is >1.5 |
| cellColours | Vector specifying desired colours to use for the cells in the heatmap. Defaults to c("blue", "white", "red"). |
| cellBorder | A call to grid::gpar() to specify borders between cells in the heatmap. The default is gpar(col="grey"). To remove borders set to gpar(col=NA) |
| plotSignificantOnly | Boolean (TRUE). Only plot genes that are differentially expressed (i.e. they pass pCutoff and fcCutoff) in any comparison from the provided list of data frames. |
| showStars | Boolean (TRUE) show significance stars on the heatmap |
| hideNonsigFC | Boolean (TRUE). If a gene is significant in one comparison but not in another, this will set the colour of the non- significant gene as grey to visually emphasize the significant genes. If set to FALSE, it will be set the colour to the fold change, and if the p value passes pCutoff, it will also display the p value (the asterisks will be grey instead of black). |
| vjust | Adjustment of the position of the significance stars. Default is 0.75. May need to adjust if there are many genes. |
| rot | Rotation of the position of the significance stars. Default is 0. |
| invert | Boolean (FALSE). The default setting plots genes as rows and comparisons as columns. Setting this to TRUE will place genes as columns and comparisons as rows. |

| | |
|---|---|
| log2FoldChange | Boolean (FALSE). Default plots the fold changes in the legend as the true fold change. Set to TRUE if you want log2 fold change. |
| colSplit | A vector, with the same length as inputList, which assigns each data frame in inputList to a group, and splits the heatmap on these larger groupings. The order of groups in the heatmap will be carried over, so one can alter the order of inputList and colSplit to affect the heatmap. This argument will be ignored if clusterColumns is set to TRUE. See Details for more information. |
| clusterRows | Boolean (TRUE). Whether to cluster the rows (genes). May need to change if invert=TRUE. |
| clusterColumns | Boolean (FALSE). Whether to cluster the columns (comparisons). Will override order of colSplit if set to TRUE. May need to change if invert=TRUE. |
| colAngle | Angle of column text. Defaults to 90. |
| colCenter | Whether to center column text. Default is TRUE, but it should be set to FALSE if the column name is angled (e.g. colAngle=45). |
| rowAngle | Angle of row text, defaults to 0. |
| rowCenter | Whether to center column text. The default is FALSE, but it should be set to TRUE if vertical column name (e.g. rowAngle=90). |
| returnData | Boolean (FALSE). Whether to draw the heatmap (default) or return the underlying matrix. |

## Details

All elements of inputList should belong to one of the following classes: "DESeqResults" from DESeq2, "TopTags" from edgeR, or a simple "data.frame". In the first two cases, the proper columns for fold change and p values are detected automatically ("log2FoldChange" and "padj" for "DESeqResults", or "logFC" and "FDR" for "TopTags"). In the third case, the arguments columnFC and columnP must be supplied. Additionally, if one wished to override the default columns for either "DESeqResults" or "TopTags" objects, simply coerce the object to a simple "data.frame" and supply columnFC and columnP as desired.

The cellColours argument is designed to map a range of negative and positive values to the three provided colours, with zero as the middle colour. If the plotted matrix contains only positive (or negative) values, then it will become a two-colour scale, white-to-red (or blue-to-white).

The colSplit argument can be used to define larger groups represented in inputList. For example, consider an experiment comparing two different treatments to an untreated control, in both wild type and mutant cells. This would give the following comparisons: "wildtype_treatment1_vs_untreated", "wildtype_treatment2_vs_untreated", "mutant_treatment1_vs_untreated", and "mutant_treatment2_vs_untreated". One could then specify colSplit as `c("Wild type", "Wild type", "Mutant", "Mutant")` to make the wild type and mutant results more visually distinct.

## Value

A heatmap of fold changes for genes of interest; an "ggplot" class object

## References

https://bioconductor.org/packages/ComplexHeatmap/

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("exampleDESeqResults")

plotFoldChange(
    exampleDESeqResults,
    pathName="Generation of second messenger molecules"
)
```

---

ppiBuildNetwork *Construct a PPI network from input genes and InnateDB's database*

---

## Description

Creates a protein-protein interaction (PPI) network using data from InnateDB, with options for network order, and filtering input.

## Usage

```
ppiBuildNetwork(
  rnaseqResult,
  filterInput = TRUE,
  columnFC = NA,
  columnP = NA,
  pCutoff = 0.05,
  fcCutoff = 1.5,
  order = "zero",
  hubMeasure = "betweenness",
  ppiData = innateDbPPI
)
```

## Arguments

| | |
|---|---|
| rnaseqResult | An object of class "DESeqResults", "TopTags", or a simple data frame. See Details for more information on input types. |
| filterInput | If providing list of data frames containing the unfiltered output from DESeq2::results(), set this to TRUE to filter for DE genes using the thresholds set by the pCutoff and fcCutoff arguments. When FALSE it's assumed your passing the filtered results into inputList and no more filtering will be done. |
| columnFC | Character; optional column containing fold change values, used only when filterInput=TRUE and the input is a data frame. |
| columnP | Character; optional column containing p values, used only when filterInput=TRUE and the input is a data frame. |

| | |
|---|---|
| pCutoff | Adjusted p value cutoff, defaults to <0.05 |
| fcCutoff | Absolute fold change cutoff, defaults to an absolute value of >1.5 |
| order | Desired network order. Possible options are "zero" (default), "first," "minSimple." |
| hubMeasure | Character denoting what measure should be used in determining which nodes to highlight as hubs when plotting the network. Options include "betweenness" (default), "degree", and "hubscore". These represent network statistics calculated by their respective tidygraph::centrality_x, functions. |
| ppiData | Data frame of PPI data; must contain rows of interactions as pairs of Ensembl gene IDs, with columns named "ensemblGeneA" and "ensemblGeneB". Defaults to pre-packaged InnateDB PPI data. |

## Details

The input to ppiBuildNetwork() can be a "DESeqResults" object (from DESeq2), "TopTags" (edgeR), or a simple data frame. When not providing a basic data frame, the columns for filtering are automatically pulled ("log2FoldChange" and "padj" for DESeqResults, or "logFC" and "FDR" for TopTags). Otherwise, the arguments "columnFC" and "columnP" must be specified.

The "hubMeasure" argument determines how ppiBuildNetwork assesses connectedness of nodes in the network, which will be used to highlight nodes when visualizing with ppiPlotNetwork. The options are "degree", "betweenness", or "hubscore". This last option uses the igraph implementation of the Kleinburg hub centrality score - details on this method can be found at ?igraph::hub_score.

## Value

A Protein-Protein Interaction (PPI) network; a "tidygraph" object for plotting or further analysis, with the minimum set of columns for nodes (additional columns from the input will also be included):

| | |
|---|---|
| name | Ensembl gene ID for the node |
| degree | Degree of the node, i.e. the number of interactions |
| betweenness | Betweenness measure for the node |
| seed | TRUE when the node was part of the input list of genes |
| hubScore | Special hubScore for each node. The suffix denotes the measure being used; e.g. "hubScoreBtw" is for betweenness |
| hgncSymbol | HGNC gene name for the node |

Additionally the following columns are provided for edges:

| | |
|---|---|
| from | Starting node for the interaction/edge as a row number |
| to | Ending node for the interaction/edge as a row number |

## References

InnateDB: https://www.innatedb.com/

## See Also

https://github.com/hancockinformatics/pathlinkR/

## Examples

```
data("exampleDESeqResults")

ppiBuildNetwork(
    rnaseqResult=exampleDESeqResults[[1]],
    filterInput=TRUE,
    order="zero"
)
```

---

`ppiCleanNetwork` *Clean GraphML or JSON input*

---

## Description

Takes network file (GraphML or JSON) and process it into a tidygraph object, adding network statistics along the way.

## Usage

```
ppiCleanNetwork(network)
```

## Arguments

| | |
|---|---|
| `network` | `tidygraph` object from a GraphML or JSON file |

## Details

This function was designed so that networks created by other packages or websites (e.g. https://networkanalyst.ca) could be imported and visualized with `ppiPlotNetwork`.

## Value

A Protein-Protein Interaction (PPI) network; a "tidygraph" object, with the minimal set of columns (other from the input are also included):

| | |
|---|---|
| `name` | Identifier for the node |
| `degree` | Degree of the node, i.e. the number of interactions |
| `betweenness` | Betweenness measure for the node |
| `seed` | TRUE when the node was part of the input list of genes |
| `hubScore` | Special hubScore for each node. The suffix denotes the measure being used; e.g. "hubScoreBtw" is for betweenness |
| `hgncSymbol` | HGNC gene name for the node |

Additionally the following columns are provided for edges:

| | |
|---|---|
| from | Starting node for the interaction/edge as a row number |
| to | Ending node for the interaction/edge as a row number |

## See Also

https://github.com/hancockinformatics/pathlinkR/

## Examples

```
tj1 <- jsonlite::read_json(
    system.file("extdata/networkAnalystExample.json", package="pathlinkR"),
    simplifyVector=TRUE
)

tj2 <- igraph::graph_from_data_frame(
    d=dplyr::select(tj1$edges, source, target),
    directed=FALSE,
    vertices=dplyr::select(
        tj1$nodes,
        id,
        label,
        x,
        y,
        "types"=molType,
        expr
    )
)

tj3 <- ppiCleanNetwork(tidygraph::as_tbl_graph(tj2))
```

---

# ppiEnrichNetwork *Test a PPI network for enriched pathways*

---

## Description

Test a PPI network for enriched pathways

## Usage

```
ppiEnrichNetwork(
  network,
  analysis = "sigora",
  filterResults = "default",
  gpsRepo = "default",
  geneUniverse = NULL
)
```

## Arguments

| | |
|---|---|
| network | A "tidygraph" network object, with Ensembl IDs in the first column of the node table |
| analysis | Default is "sigora", but can also be "reactomepa" or "hallmark" |
| filterResults | Should the output be filtered for significance? Use 1 to return the unfiltered results, or any number less than 1 for a custom p-value cutoff. If left as default, the significance cutoff for Sigora is 0.001, or 0.05 for ReactomePA and Hallmark. |
| gpsRepo | Only applies to analysis="sigora". Gene Pair Signature object for Sigora to use to test for enriched pathways. Leaving this set as "default" will use the "reaH" GPS object from Sigora, or you can provide your own custom GPS repository. |
| geneUniverse | Only applies when analysis is "reactomepa" or "hallmark". The set of background genes to use when testing with ReactomePA or Hallmark gene sets. For ReactomePA this must be a character vector of Entrez genes. For Hallmark, it must be Ensembl IDs. |

## Value

A "data.frame" (tibble) of enriched pathways, with the following columns:

| | |
|---|---|
| pathwayId | Pathway identifier |
| pathwayName | Pathway name |
| pValue | Nominal p value for the pathway |
| pValueAdjusted | p value corrected for multiple testing |
| genes | Candidate genes, which were DE for the comparison and also in the pathway |
| numCandidateGenes | Number of candidate genes |
| numBgGenes | Number of background genes for the pathway |
| geneRatio | Ratio of candidate and background genes |
| totalGenes | Number of DE genes which were tested for enriched pathways |
| topLevelPathway | High level Reactome term which serves to group similar pathways |

## References

Sigora: https://cran.r-project.org/package=sigora ReactomePA: https://www.bioconductor.org/packages/ReactomePA/ MSigDB/Hallmark: https://www.gsea-msigdb.org/gsea/msigdb/collections.jsp

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("exampleDESeqResults")

exNetwork <- ppiBuildNetwork(
    rnaseqResult=exampleDESeqResults[[1]],
    filterInput=TRUE,
    order="zero"
)

ppiEnrichNetwork(
    network=exNetwork,
    analysis="hallmark"
)
```

---

# ppiExtractSubnetwork *Extract a subnetwork based on pathway genes*

---

## Description

Extract a subnetwork based on pathway genes

## Usage

```
ppiExtractSubnetwork(
  network,
  genes = NULL,
  pathwayEnrichmentResult = NULL,
  pathwayToExtract
)
```

## Arguments

| | |
|---|---|
| network | Input network object; output from ppiBuildNetwork() |
| genes | Character vector of Ensembl gene IDs to use as the starting point to extract a subnetwork from the initial network. You must provide either the genes or pathwayEnrichmentResult argument. |
| pathwayEnrichmentResult | Pathway enrichment result, output from ppiEnrichNetwork. You must provide either genes or pathwayEnrichmentResult argument. |
| pathwayToExtract | Name of the pathway determining what genes (nodes) are pulled from the input network. Must be present in the "pathwayName" column of pathwayEnrichmentResults. |

## Details

Uses functions from the igraph package to extract a minimally connected subnetwork from the starting network, using either a list of Ensembl genes or genes from an enriched pathway as the basis. To see what genes were pulled out for the pathway, see the "starters" attribute of the output network.

## Value

A Protein-Protein Interaction (PPI) network; a "tidygraph" object for plotting or further analysis, with the minimum set of columns for nodes (additional columns from the input will also be included):

| | |
|---|---|
| `name` | Ensembl gene ID for the node |
| `degree` | Degree of the node, i.e. the number of interactions |
| `betweenness` | Betweenness measure for the node |
| `seed` | TRUE when the node was part of the input list of genes |
| `hubScore` | Special hubScore for each node. The suffix denotes the measure being used; e.g. "hubScoreBtw" is for betweenness |
| `hgncSymbol` | HGNC gene name for the node |

Additionally the following columns are provided for edges:

| | |
|---|---|
| `from` | Starting node for the interaction/edge as a row number |
| `to` | Ending node for the interaction/edge as a row number |

## References

Code for network module (subnetwork) extraction was based off of that used in "jboktor/NetworkAnalystR" on Github.

## See Also

https://github.com/hancockinformatics/pathlinkR

## Examples

```
data("exampleDESeqResults")

exNetwork <- ppiBuildNetwork(
    rnaseqResult=exampleDESeqResults[[1]],
    filterInput=TRUE,
    order="zero"
)

exPathways <- ppiEnrichNetwork(
    network=exNetwork,
    analysis="hallmark"
)
```

```
ppiExtractSubnetwork(
    network=exNetwork,
    pathwayEnrichmentResult=exPathways,
    pathwayToExtract="INTERFERON ALPHA RESPONSE"
)
```

---

ppiPlotNetwork *Plot an undirected PPI network using ggraph*

---

## Description

Visualize a protein-protein interaction (PPI) network using ggraph functions, output from ppiBuildNetwork.

## Usage

```
ppiPlotNetwork(
  network,
  networkLayout = "nicely",
  title = NA,
  nodeSize = c(2, 6),
  fillColumn,
  fillType,
  catFillColours = "Set1",
  foldChangeColours = c("firebrick3", "#188119"),
  intColour = "grey70",
  nodeBorder = "grey30",
  hubColour = "blue2",
  subnetwork = TRUE,
  legend = FALSE,
  legendTitle = NULL,
  edgeColour = "grey40",
  edgeAlpha = 0.5,
  edgeWidth = 0.5,
  label = FALSE,
  labelColumn,
  labelFilter = 5,
  labelSize = 4,
  labelColour = "black",
  labelFace = "bold",
  labelPadding = 0.25,
  minSegLength = 0.25
)
```

## Arguments

| | |
|---|---|
| network | A tidygraph object, output from ppiBuildNetwork |

networkLayout Layout of nodes in the network. Supports all layouts from ggraph/igraph, or a data frame of x and y coordinates for each node (order matters!).

title Optional title for the plot (NA)

nodeSize Length-two numeric vector, specifying size range of node sizes (maps to node degree). Default is c(2, 6).

fillColumn Tidy-select column for mapping node colour. Designed to handle continuous numeric mappings (either positive/negative only, or both), and categorical mappings, plus a special case for displaying fold changes from, for example, RNA-Seq data. See fillType for more details on how to set this up.

fillType String denoting type of fill mapping to perform for nodes. Options are: "foldChange", "twoSided", "oneSided", or "categorical".

catFillColours Colour palette to be used when fillType is set to "categorical." Defaults to "Set1" from RColorBrewer. Will otherwise be passed as the "values" argument in scale_fill_manual().

foldChangeColours
A two-length character vector containing colours for up and down regulated genes. Defaults to c("firebrick3", "#188119").

intColour Fill colour for non-seed nodes, i.e. interactors. Defaults to "grey70".

nodeBorder Colour (stroke or outline) of all nodes in the network. Defaults to "grey30".

hubColour Colour of node labels for hubs. The top 2% of nodes (based on calculated hub score) are highlighted with this colour, if label=TRUE.

subnetwork Logical determining if networks from ppiExtractSubnetwork() should be treated as such. Defaults to TRUE.

legend Should a legend be included? Defaults to FALSE.

legendTitle Optional title for the legend, defaults to NULL.

edgeColour Edge colour, defaults to "grey40"

edgeAlpha Transparency of edges, defaults to 0.5

edgeWidth Thickness of edges connecting nodes. Defaults to 0.5

label Boolean, whether labels should be added to nodes. Defaults to FALSE.

labelColumn Tidy-select column of the network/data to be used in labeling nodes. Recommend setting to hgncSymbol, which contains HGNC symbols mapped from the input Ensembl IDs via biomaRt.

labelFilter Degree filter used to determine which nodes should be labeled. Defaults to 5. This value can be increased to reduce the number of node labels, to prevent the network from being too crowded.

labelSize Size of node labels, defaults to 5.

labelColour Colour of node labels, defaults to "black"

labelFace Font face for node labels, defaults to "bold"

labelPadding Padding around the label, defaults to 0.25 lines.

minSegLength Minimum length of lines to be drawn from labels to points. The default specified here is 0.25, half of the normal default value.

## Details

Any layout supported by ggraph can be specified here - see `?layout_tbl_graph_igraph` for a list of options. Or you can supply a data frame containing coordinates for each node. The first and second columns will be used for x and y, respectively. Note that having columns named "x" and "y" in the input network will generate a warning message when supplying custom coordinates.

Since this function returns a standard ggplot object, you can tweak the final appearance using the normal array of ggplot2 function, e.g. `labs()` and `theme()` to further customize the final appearance.

The `fillType` argument will determine how the node colour is mapped to the desired column. "foldChange" represents a special case, where the fill column is numeric and whose values should be mapped to up (> 0) or down (< 0). "twoSided" and "oneSided" are designed for numeric data that contains either positive and negative values, or only positive/negative values, respectively. "categorical" handles any other non-numeric colour mapping, and uses "Set1" from RColorBrewer.

Node statistics (degree, betweenness, and hub score) are calculated using the respective functions from the `tidygraph` package.

## Value

A Protein-Protein Interaction (PPI) network plot; an object of class "ggplot"

## See Also

https://github.com/hancockinformatics/pathlinkR/

## Examples

```
data("exampleDESeqResults")

exNetwork <- ppiBuildNetwork(
    rnaseqResult=exampleDESeqResults[[1]],
    filterInput=TRUE,
    order="zero"
)

ppiPlotNetwork(
    network=exNetwork,
    title="COVID positive over time",
    fillColumn=LogFoldChange,
    fillType="foldChange",
    legend=TRUE,
    label=FALSE
)
```

## ppiRemoveSubnetworks *INTERNAL Find and return the largest subnetwork*

### Description

INTERNAL Find and return the largest subnetwork

### Usage

```
ppiRemoveSubnetworks(network)
```

### Arguments

| | |
|---|---|
| network | Graph object |

### Value

Largest subnetwork from the input network list as an "igraph" object

### See Also

https://github.com/hancockinformatics/pathlinkR/

## reactomeDatabase *Table of all Reactome pathways and genes*

### Description

Table of all Reactome pathways and genes

### Usage

```
data(reactomeDatabase)
```

### Format

A data frame (tibble) with 129002 rows and 3 columns

**pathwayId** Reactome pathway ID

**entrezGeneId** Entrez gene ID

**pathwayName** Name of the Reactome pathway

### Value

An object of class "tbl", "tbl.df", "data.frame"

### Source

See https://reactome.org/ for more information.

---

## sigoraDatabase *Table of all Sigora pathways and their constituent genes*

---

### Description

Table of all Sigora pathways and their constituent genes

### Usage

```
data(sigoraDatabase)
```

### Format

A data frame (tibble) with 60775 rows and 4 columns

**pathwayId** Reactome pathway identifier

**pathwayName** Reactome pathway description

**ensemblGeneId** Ensembl gene identifier

**hgncSymbol** HGNC gene symbol

### Value

An object of class "tbl", "tbl.df", "data.frame"

### Source

Please refer to the Sigora package for more details: https://cran.r-project.org/package=sigora

---

## sigoraExamples *Sigora enrichment example*

---

### Description

Example Sigora output from running `pathwayEnrichment()` on "exampleDESeqResults"

### Usage

```
data(sigoraExamples)
```

## Format

A data frame (tibble) with 66 rows and 12 columns

**comparison** Comparison from which results are derived; names of the input list

**direction** Was the pathway enriched in up or down regulated genes

**pathwayId** Reactome pathway identifier

**pathwayName** Description of the pathway

**pValue** Nominal p value for the enrichment

**pValueAdjusted** p value adjusted for multiple testing

**genes** Genes in the pathway/input

**numCandidateGenes** Analyzed genes found in the pathway of interest

**numBgGenes** All genes from the pathway database

**geneRatio** Quotient of the number of candidate and background genes

**totalGenes** Total number of input genes

**topLevelPathway** Pathway category

## Value

An object of class "tbl", "tbl.df", "data.frame"

## Source

Please refer to the Sigora package for more details on that method: https://cran.r-project.org/package=sigora

# Index


∗ **datasets**
    exampleDESeqResults, 8
    groupedPathwayColours, 9
    hallmarkDatabase, 10
    innateDbPPI, 10
    keggDatabase, 11
    mappingFile, 12
    pathwayCategories, 20
    reactomeDatabase, 39
    sigoraDatabase, 40
    sigoraExamples, 40
.eruptionBreaks, 3
.plotFoldChangeLegend, 3
.runSigora, 4
.truncNeatly, 5

eruption, 5
exampleDESeqResults, 8

getPathwayDistances, 8
groupedPathwayColours, 9

hallmarkDatabase, 10

innateDbPPI, 10

keggDatabase, 11

mappingFile, 12

pathnetCreate, 12
pathnetFoundation, 15
pathnetGGraph, 16
pathnetVisNetwork, 18
pathwayCategories, 20
pathwayEnrichment, 21
pathwayPlots, 24
plotFoldChange, 26
ppiBuildNetwork, 29
ppiCleanNetwork, 31
ppiEnrichNetwork, 32
ppiExtractSubnetwork, 34
ppiPlotNetwork, 36
ppiRemoveSubnetworks, 39

reactomeDatabase, 39

sigoraDatabase, 40
sigoraExamples, 40