

# Package ‘VAN’

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**Type** Package

**Title** Differential variability analysis in networks

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**Description** This package enables the identification of hubs whose association with their partners (interactors) changes across biological conditions

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**ZipData** no

**Depends** R (>= 2.15.0), doParallel, marray, xlsx, igraph, annotate, AnnotationDbi, org.Hs.eg.db, VAN-Data, qvalue

**Suggests** MADAM

**License** LGPL (>=2.1)

**LazyLoad** yes

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VAN-package

*Differential variability analysis in networks*


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### Description

This package enables the identification of hubs whose association with their partners (interactors) changes across biological conditions.

### Details

|           |             |
|-----------|-------------|
| Package:  | VAN         |
| Type:     | Package     |
| Version:  | 1.0.0       |
| Date:     | 2012-12-01  |
| License:  | LGPL(>=2.1) |
| LazyLoad: | yes         |

### Author(s)

Vivek Jayaswal, Sarah-Jane Schramm and Yee Hwa (Jean) Yang Maintainer: Vivek Jayaswal <vivek@maths.usyd.edu.au>

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generateMicroRnaMap

*Obtain the miRnome mapping*


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### Description

This function is used to generate an output file corresponding to microRNAs as hubs and their potential targets as interactors.

### Usage

```
generateMicroRnaMap(databaseName, outFileHeader)
```

### Arguments

|               |  |
|---------------|--|
| databaseName  | Name of miRNA-mRNA mapping database. Currently supports "Targetscan" and "Microcosm" |
| outFileHeader | Output file name   |

### Value

Two tab-separated output files. The first file saves the target genes (or interactors) as Entrez IDs and the second saves the interactors as gene symbols. The first file has the suffix "Entrez.txt" and the latter has the suffix "Symb.txt"

**Author(s)**

Vivek Jayaswal

**Examples**

## Refer User Guide

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|                |                               |
|----------------|-------------------------------|
| generatePpiMap | <i>Obtain the PPI mapping</i> |
|----------------|-------------------------------|

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**Description**

This function is used to generate an output file corresponding to protein-protein interaction. The input should be a MINI-Tab file downloaded from Wodak lab website

**Usage**

```
generatePpiMap(mapFile, outFileHeader)
```

**Arguments**

|               |                  |
|---------------|------------------|
| mapFile       | MINI tab file    |
| outFileHeader | Output file name |

**Value**

Two tab-separated output files. The first file saves the target genes (or interactors) as Entrez IDs and the second saves the interactors as gene symbols. The first file has the suffix "Entrez.txt" and the latter has the suffix "Symb.txt"

**Author(s)**

Vivek Jayaswal

**Examples**

## Refer User Guide

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identifySignificantHubs

*Identify the enriched hubs for a given combination of expression and PPI/miRnome datasets*

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## Description

This function estimates the p-value for the hypothesis that the correlation between a hub and its interactors changes across two or more biological conditions

## Usage

```
identifySignificantHubs(exprFile, labelIndex, mapFile, outFile
  , hubSize = 5, randomizeCount = 1000
  , adjustMethod="BH", assocType = "TCC"
  , labelVect = NULL
  , exprDataType="SYMB", ppiDataType="SYMB", outputDataType="SYMB"
  , species="Human", inputCores=4
  , hubVect = NULL, interactomeVect = NULL)
```

## Arguments

|                 |   |
|-----------------|---|
| exprFile        | Vector of file names corresponding to normalized expression data              |
| labelIndex      | Row of the exprFile which contains the sample labels                          |
| mapFile         | File name corresponding to PPI/Mirnome  |
| outFile         | Output file name  |
| hubSize         | Minimum number of interactors in the expression dataset. Default: 5           |
| randomizeCount  | Number of permutations to consider for estimating the p-values. Default: 1000 |
| adjustMethod    | Method for adjusting the p-values. Default:"BH"                               |
| assocType       | Type of correlation to calculate - TCC or PCC or FSTAT. Default:TCC           |
| labelVect       | Vector of conditions to test. Default: NULL                                   |
| exprDataType    | "ENTREZ" or "SYMB". Default:SYMB  |
| ppiDataType     | "ENTREZ" or "SYMB". Default:SYMB  |
| outputDataType  | "ENTREZ" or "SYMB". Default:SYMB  |
| species         | Name of species. At present only "Human" is supported                         |
| inputCores      | Number of threads for executing the code. Default:4                           |
| hubVect         | A vector of hub genes to consider. Default: NULL                              |
| interactomeVect | A vector of interactors to consider. Default: NULL                            |

## Value

Two output files are generated - one containing the p-values for the hubs and another containing the actual correlation coefficients per condition per hub-interactor pair. While the name of the first output file is provided as an input parameter, the name of the second file is obtained by adding the suffix "Cor.txt" to the use-specified input parameter.

**Author(s)**

Vivek Jayaswal

**Examples**

```
## Refer User Guide
```

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|                  |   |
|------------------|---|
| obtainCancerInfo | <i>Identify the hubs that map to known cancer genes</i> |
|------------------|---|

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**Description**

This function enables the identification of genes that act as hubs and have previously been shown to be associated with cancer. The latter information is downloaded as an XL-sheet from the Sanger institute's website.

**Usage**

```
obtainCancerInfo(hubFile, cancerAnnotationFile, outFile)
```

**Arguments**

|                      |  |
|----------------------|--|
| hubFile              | Output file corresponding to an expression-PPI combination |
| cancerAnnotationFile | XL-sheet containing biological annotation                  |
| outFile              | Output file  |

**Value**

A tab-separated file containing the CIC annotation for enriched hubs, i.e. hubs with unadjusted p-value < 0.05

**Author(s)**

Vivek Jayaswal

**Examples**

```
## Refer User Guide
```

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|                  |   |
|------------------|---|
| obtainPairSubset | <i>Obtain a subset of the hub-interactor pairs file</i> |
|------------------|---|

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### Description

This function enables the extraction of only those hub-interactor pairs that correspond to (a) a pre-determined set of hubs or (b) significant hubs, i.e. hubs with p-values below a threshold

### Usage

```
obtainPairSubset(filePrefix, useAdjustedProb, probThresh, hubNames=NULL)
```

### Arguments

|                 |   |
|-----------------|---|
| filePrefix      | File name prefix corresponding to the enriched hubs file and hub-interactor pairs file    |
| useAdjustedProb | Boolean value. TRUE -> Consider adjusted p-values. FALSE -> Consider un-adjusted p-values |
| probThresh      | p-value cut-off   |
| hubNames        | Vector of hub names. Default: NULL  |

### Value

An output file with the name <filePrefix>\_Cor\_Signif.txt.

### Author(s)

Vivek Jayaswal

### Examples

```
## Refer User Guide
```

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|                  |   |
|------------------|---|
| summarizeHubData | <i>Combine the results obtained using multiple expression and/or PPI datasets</i> |
|------------------|---|

---

### Description

This function generates an output file that summarizes the p-values obtained using multiple expression datasets and/or PPI datasets. The p-values are summarized using Fisher's combined test or Rank Prod method.

### Usage

```
summarizeHubData(fileName=NULL, outFile, metaAnalysis=NULL, rankProdItr=NULL)
```

**Arguments**

|              |  |
|--------------|--|
| fileNames    | Vector of file names corresponding to individual expression-PPI datasets results. If NULL, all files with the extension txt are considered. Default: NULL              |
| outFile      | File name that contains the combined information   |
| metaAnalysis | Type of meta-analysis to perform NULL: No meta-analysis to perform. Fisher: Fisher's combined analysis RankProd: Rank-prod analysis Default: NULL                      |
| rankProdItr  | Number of iteration to perform for significance of rank prod values. Default: NULL. The default value should be used only if rank prod analysis is not being performed |

**Value**

Summarized Output file with optional columns corresponding to meta-analysis results

**Author(s)**

Vivek Jayaswal

**Examples**

```
## Refer user guide
```

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|                  |   |
|------------------|---|
| visualizeNetwork | <i>Visualize the hub-interactor pairs</i> |
|------------------|---|

---

**Description**

This function enables the visualization of changes in correlation between a hub and its interactors across two biological conditions.

**Usage**

```
visualizeNetwork(inputFile, inputHub, paletteVector, numThresh=NULL, condVector=NULL)
```

**Arguments**

|               |  |
|---------------|--|
| inputFile     | File containing the hub-interactor pairs and their correlation values in each condition                          |
| inputHub      | Name of the hub  |
| paletteVector | A vector of three colors   |
| numThresh     | Number of interactors to plot. This value is set to NULL if all the interactors should be plotted. Default: NULL |
| condVector    | Vector of the two states to plot. Default is NULL  |

**Value**

A graph with two columns such that each column represent a condition of interest. Within a column, a user-defined color-coding scheme is used to visualize the strength of relationship between a hub and its interactors.

If the inputFile corresponds to an analysis of three or more conditions, then the parameter condVector should be specified as a vector comprising the two states of interest.

**Author(s)**

Vivek Jayaswal

**Examples**

```
## Refer User Guide
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