

Package ‘RchyOptimyx’

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Type Package

Title Optimized Cellular Hierarchies for Flow Cytometry

Version 2.4.0

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Description Constructs a hierarchy of cells using flow cytometry for maximization of an external variable (e.g., a clinical outcome or a cytokine response).

Imports Rgraphviz, sfsmisc, graphics, methods, graph, grDevices,flowType (>= 2.0.0)

Depends R (>= 2.10)

Suggests flowCore

biocViews FlowCytometry

License Artistic-2.0

LazyLoad yes

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RchyOptimyx-package *Gating Hierarchy Optimization for Flow Cytometry*

Description

RchyOptimyx is a computational tool which determines the minimal sets of markers that can identify a target population within a given purity standard. This can enable panel redesign using smaller subsets of markers, with consequent savings on reagents, potential for adaptation to older instruments, or the addition of other markers of interest to the panel design.

Details

Package: RchyOptimyx
Type: Package
Version: 0.99.1
Date: 2011-10-12
License: Artistic-2.0
LazyLoad: yes

See the RchyOptimyx function.

Author(s)

Nima Aghaeepour <<naghaeep@gmail.com>> and Adrin Jalali <<ajalali@bccrc.ca>>

References

D. Eppstein, Finding the k shortest paths, SIAM J. Comput., 1998 - Citeseer.

See Also

RchyOptimyx

Examples

```
data(HIVData)

res<-RchyOptimyx(PhenoCodes, -log10(LogRankPvals), 2000102001, 5,FALSE)
plot(res,phenotypeCodes=PhenoCodes,phenotypeScores=-log10(LogRankPvals),marker.names=marker.names)
```

HIVData

HIVData

Description

A dataset of two sets of scores (particularly, correlation with protection against HIV and overlap with the Naive T-cell population) assigned to immunophenotypes measured by flow cytometry. 10 markers were measured: KI-67, CD28, CD45RO, CD8, CD4, CD57, CCR5, CD27, CCR7, and CD127.

Usage

```
data(HIVData)
```

Details

This dataset consists of 2 numeric (`LogRankPvals` and `OverlapScores`) and 2 character (`Pheno.Codes` and `marker.names`).

`Pheno.Codes` vector is described in the `RchyOptimyx` function's manual.

`LogRankPvals` is a vector of log-rank test P-values to determine the correlation between HIV's progression and each of the measured immunophenotypes in 466 HIV positive patients (lower values represent a stronger correlation). For more details see the Aghaeepour et.al. manuscript below.

Ganesan et. al. define Naive T-cells as CD28+CD45RO-CD57-CCR5-CD27+ CCR7+ within the CD3+CD14- compartment. The `OverlapScores` vector has the proportion of Naive T-cells (as defined above) to the total number of cells in any given immunophenotype (a higher value represents a larger overlap).

`marker.names` is the name of all markers involved in the analysis.

Author(s)

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References

Nima Aghaeepour, Pratip K. Chattopadhyay, Anuradha Ganesan, Kieran O'Neill, Habil Zare, Adrin Jalali, Holger H. Hoos, Mario Roederer, and Ryan R. Brinkman. Early Immunologic Correlates of HIV Protection can be Identified from Computational Analysis of Complex Multivariate T-cell Flow Cytometry Assays. *Bioinformatics*, 2012.

Anuradha Ganesan, Pratip K Chattopadhyay, Tess M. Brodie, Jing Qin, Wenjuan Gu, John R. Mascola, Nelson L. Michael, Dean A. Follmann, and Mario Roederer. Immunologic and virologic events in early HIV infection predict subsequent rate of progression. *Journal of Infectious Diseases*, 2010.

merge	<i>Merges two OptimizedHierarchy objects.</i>
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Description

Merges two OptimizedHierarchy objects.

Usage

```
## S4 method for signature OptimizedHierarchy,OptimizedHierarchy
merge(x, y)
```

Arguments

x	First OptimizedHierarchy.
y	Second OptimizedHierarchy.

Value

OptH	An OptimizedHierarchy object
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Author(s)

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plot	<i>Plots an optimized cellular hierarchy</i>
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Description

Plots an optimized cellular hierarchy

Usage

```
## S4 method for signature OptimizedHierarchy,ANY
plot(x, phenotypeScores, phenotypeCodes, marker.names,
      partitions.per.marker = NULL,
      uniformColors = FALSE, ylab = NULL, xlab = NULL, colors = c("blue",
"cyan", "yellow", "red"), edgeWeights = TRUE, edgeLabels = TRUE,
      nodeLabels = TRUE, min.score = NA, max.score = NA, cell.proportions =
NULL, min.proportion = NA, max.proportion = NA, proportion.colors =
c("black", "white"), node.lwd = 5, root.name = "All Cells",
      legend.size=1.25, plot.legend=TRUE, textcol=par(fg))
```

Arguments

<code>x</code>	An OptimizedHierarchy object as generated by RchyOptimyx.
<code>phenotypeScores</code>	The score vector used for determining the colors of the nodes.
<code>phenotypeCodes</code>	A vector of strings of length N (the number of markers) for each phenotype measured. For every phenotype, the character corresponding to a given marker can be 0, 1, 2, etc for neutral, negative, positive, bright, etc. See the provided vignette for more details and examples.
<code>marker.names</code>	A vector of characters representing the names of all markers involved in the analysis.
<code>partitions.per.marker</code>	A vector of integers, one per marker, describing the number of partitions per marker. Default is 2 (positive and negative) for all markers.
<code>uniformColors</code>	Boolean variable. If TRUE, the graph will not have any colors.
<code>ylab</code>	y-axis label of the density plot on the right.
<code>xlab</code>	x-axis label of the density plot of the phenotype cell proportion in the bottom.
<code>colors</code>	Color vector indicating colors to be used in the right pallet.
<code>edgeWeights</code>	Boolean value indicating weather edgeWeights should be plotted or not.
<code>edgeLabels</code>	Boolean value indicating weather edgeLabels should be plotted or not.
<code>nodeLabels</code>	Boolean value indicating weather nodeLabels should be plotted or not.
<code>min.score</code>	Double value indicating the minimum value of scores. Default value will use minimum node scores of the given OptimizedHierarchy object.
<code>max.score</code>	Double value indicating the maximum value of scores. Default value will use maximum node scores of the given OptimizedHierarchy object.
<code>cell.proportions</code>	The score vector used to determine the color of node borders to illustrate phenotype cell proportions.
<code>min.proportion</code>	Double value indicating the minimum value of the cell proportions. Default value will use minimum cell proportion of the given OptimizedHierarchy object.
<code>max.proportion</code>	Double value indicating the minimum value of the cell proportions. Default value will use minimum cell proportion of the given OptimizedHierarchy object.
<code>proportion.colors</code>	Color vector indicating colors to be used in the bottom pallet.
<code>node.lwd</code>	Integer value indicating node border width.
<code>root.name</code>	Character value indicating the root node's name.
<code>legend.size</code>	Size of the color legend in inches.
<code>plot.legend</code>	Boolean indicating wether the color legend should be plotted.
<code>textcol</code>	The color of the axis label(s) for the color legend(s).

Author(s)

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See Also

[RchyOptimyx-methods](#)

RchyOptimyx

Gating Hierarchy Optimization for Flow Cytometry

Description

RchyOptimyx is a computational tool which determines the minimal sets of markers that can identify a target population within a given purity standard. This can enable panel redesign using smaller subsets of markers, with consequent savings on reagents, potential for adaptation to older instruments, or the addition of other markers of interest to the panel design.

Usage

```
## S4 method for signature character,numeric,character,numeric,logical
RchyOptimyx(pheno.codes, phenotypeScores, startPhenotype, pathCount=1, trimPaths=FALSE, trim.tolerance)
```

Arguments

pheno.codes	A vector of strings of length N (the number of markers) for each phenotype measured. For every phenotype, the character corresponding to a given marker can be 0, 1, 2, etc for neutral, negative, positive, bright, etc. See the provided vignette (inst/doc/RchyOptimyx.pdf) for more details and examples.
phenotypeScores	A vector of the scores assigned to every phenotype. The optimization algorithm will try to maximize this score. See the provided vignette (inst/doc/RchyOptimyx.pdf) for more details and examples.
startPhenotype	The terminal phenotype which includes every marker that must be considered in the analysis. This variable is a vector of the length of the number of markers. Every element of the vector can be 0, 1, or 2 for negative, neutral, or positive respectively (see details).
pathCount	The number of paths that must be generated.
trimPaths	A boolean indicating whether the paths should be trimmed or not. If set to TRUE, the paths will be terminated as soon as adding <code>trim.tolerance</code> extra number of edges to the path doesn't result in an improvement in the score.
trim.tolerance	An integer indicating the number of levels before the path is trimmed if the score is decreasing by adding extra edges.
trim.level	An integer indicating from which level the tree is going to be trimmed. This parameter has no effect if set to zero.

Details

Every marker can be positive, negative, or neutral. Neutral markers are not included in the measurement of the respective phenotype.

A path is trimmed in one of the following conditions: 1. If the `trimPaths` parameter is `TRUE`, the path is trimmed as soon as it decreases for equal or more levels that `trim.tolerance` parameter. If the path is decreasing while reaching the `trim.level`, the path is trimmed from the point that it started to decrease. 2. If the path reaches the `trim.level`.

Value

`OptH` An `OptimizedHierarchy` object

Author(s)

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References

D. Eppstein, Finding the k shortest paths, SIAM J. Comput., 1998 - Citeseer.

Nima Aghaeepour, Pratip K. Chattopadhyay, Anuradha Ganesan, Kieran O'Neill, Habil Zare, Holger H. Hoos, Mario Roederer, and Ryan R. Brinkman. Early Immunologic Correlates of HIV Protection can be Identified from Computational Analysis of Complex Multivariate T-cell Flow Cytometry Assays. Bioinformatics, Feb. 2012.

Examples

```
data(HIVData)

res<-RchyOptimyx(PhenoCodes, -log10(LogRankPvals), 2000102001, 5,FALSE)
plot(res,phenotypeCodes=PhenoCodes,phenotypeScores=-log10(LogRankPvals),marker.names=marker.names)
```

summary-methods

~~ *Methods for Function summary* ~~

Description

~~ Methods for function summary ~~

Methods

`signature(object = "OptimizedHierarchy")` Prints basic characteristics of an `OptimizedHierarchy` object.

Author(s)

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See Also

[RchOptimyx-methods](#)

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