

Package ‘individPath’

March 29, 2015

Type Package

Title Individualized pathway coordination analysis

Version 1.0

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Author Hongwei Wang

Maintainer <biocwhw@126.com>

Description

we present an approach, called individPath, to detect pathways with significantly disrupted intra-pathway relative expression orderings (REOs) for each disease sample compared with the stable, normal intra-pathway REOs pre-determined in previously accumulated normal samples.

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individPath-package	<i>Individualized pathway coordination analysis</i>
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Description

This package is used to individualize the identification of deregulated pathways.

Details

Package:	individPath
Type:	Package
Version:	1.0
Date:	2015-03-05
License:	GPL-2

individPath(tumorFile, refFile, PathwayFile, cutoff)

Author(s)

Hongwei Wang Maintainer: Hongwei Wang <bioccwhw@126.com>

References

Individualized identification of disease-associated pathways with disrupted coordination of gene expression Hongwei Wang et al.,

individPath	<i>Individualized identification of dysregulated pathways</i>
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Description

Taking advantage of relative ordering information of gene expression, a simple approach,individPath, was proposed to identify dysregulated pathways for individual disease samples by comparing different ordering patterns of intra-pathway gene pairs between each disease sample and the accumulated normal samples.

Usage

individPath(tumorFile, refFile, PathwayFile, cutoff)

Arguments

tumorFile	a numeric matrix(or table) with raw representing genes and column representing samples
refFile	a numeric matrix(or table) with raw representing genes and column representing samples
PathwayFile	the name of the pathway file which each row of the table denotes a pathway
cutoff	selection criteria for stable intra-pathway gene pairs. The default setting is 0.99.

Details

The significantly disrupted pathways can be determined by testing whether the frequency of reversal gene pairs observed within each pathway is significantly more than what expected by chance using the hypergeometric distribution model.

Value

Two text files correspond to "individPath_BH_result" and "individPath_pvalue_result", respectively.

References

Individualized identification of disease-associated pathways with disrupted coordination of gene expression Hongwei Wang et al.,

individPathCal	<i>The significance calculation of each pathway dysregulated in individual patients.</i>
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Description

This function is used to determine whether each pathway is significantly dysregulated in individual patients.

Usage

```
individPathCal(CaseData, StableGP, ReversalGP, NumStable, PathGP)
```

Arguments

CaseData	a numeric matrix with one column.
StableGP	all stable intra-pathway gene pairs
ReversalGP	the number of reversal gene pairs for each pathway in individual patients
NumStable	the number of all stable intra-pathway gene pairs
PathGP	the number of stable intra-pathway gene pairs in each pathway

Value

A numeric matrix containing the p-value and adjusted-pvalue of each pathway dysregulated in individual patients.

SRGenePair	<i>Identification of stable and reversal intra-pathway gene pairs.</i>
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Description

This function is used to identify stable and reversal intra-pathway gene pairs.

Usage

```
SRGenePair(ControlData, CaseData, PathData, cutoff)
```

Arguments

ControlData	a numeric matrix(or table) with row representing genes and column representing samples
CaseData	a numeric matrix(or table) with row representing genes and column representing samples
PathData	the name of the pathway file which each row of the table denotes a pathway
cutoff	the selection criteria for stable intra-pathway gene pairs. The default setting is 0.99.

Value

A list with class "SRGgenePair.result" containing the following components:

ReversalStat	the number of reversal gene pairs for each pathway in individual patients
BG.GenePairs	all stable intra-pathway gene pairs in normal samples
PathGP	the number of stable intra-pathway gene pairs in each pathway

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