Package ‘InterSIM’

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Type Package

Title Simulation of Inter-Related Genomic Datasets

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Description Generates three inter-related genomic datasets: methylation, gene expression and protein expression.

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Depends R (>= 3.5.0), MASS, NMF, tools

NeedsCompilation no

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InterSIM-package Simulation of inter-related genomic datasets

Description

InterSIM is an R package that generates three inter-related data set with realistic inter- and intra-relationships based on the DNA methylation, mRNA expression and protein expression from the TCGA ovarian cancer study.

Details
Author(s)
Prabhakar Chalise, Rama Raghavan, Brooke Fridley; Maintainer: Prabhakar Chalise

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Description
This function simulates three inter-related genomic datasets: DNA methylation, gene expression and protein expression.

Usage
`InterSIM(n.sample=500, cluster.sample.prop=c(0.30,0.30,0.40), delta.methyl=2.0, delta.expr=2.0, delta.protein=2.0, p.DMP=0.2, p.DEG=NULL, p.DEP=NULL, sigma.methyl=NULL, sigma.expr=NULL, sigma.protein=NULL, cor.methyl.expr=NULL, cor.expr.protein=NULL, do.plot=FALSE, sample.cluster=TRUE, feature.cluster=TRUE)`

Arguments
- `n.sample`: Number of subjects to simulate
- `cluster.sample.prop`: Proportion of samples in the clusters. The number of proportions entered is used to determine the number of clusters in the simulated data. e.g. if (0.3,0.4,0.3) is entered then the number of clusters will be 3.
- `delta.methyl`: Cluster mean shift for methylation data
- `delta.expr`: Cluster mean shift for expression data
- `delta.protein`: Cluster mean shift for protein data
- `p.DMP`: proportion of DE CpGs (DE = Differentially Expressed)
- `p.DEG`: proportion of DE mRNA, if NULL (default) mRNAs mapped by DE CpGs will be selected
- `p.DEP`: proportion of DE protein, if NULL (default) proteins mapped by DE mRNAs will be selected
**InterSIM**

sigma.methyl  Covariance structure methylation data, if NULL (default) precomputed values will be used. "indep" gives covariance structure with diagonal elements only (Independent features)

sigma.expr  Covariance structure mRNA data, if NULL (default) precomputed values will be used. "indep" gives covariance structure with diagonal elements only (Independent features)

sigma.protein  Covariance structure Protein data, if NULL (default) precomputed values will be used. "indep" gives covariance structure with diagonal elements only (Independent features)

do.plot  TRUE to generate heatmap, default is FALSE

sample.cluster  TRUE (default), if clustering should be done on samples for heatmap. This option will be applicable only if do.plot=TRUE.

feature.cluster  TRUE (default), if clustering should be done on genomic features for heatmap. This option will be applicable only if do.plot=TRUE.

cor.methyl.expr  Correlation between methylation and mRNA, if NULL (default) precomputed values will be used

cor.expr.protein  Correlation between mRNA and protein, if NULL (default) precomputed values will be used

**Value**

This function returns three datasets as matrices - DNA methylation, gene expression and protein expression. It also returns a vector that has true cluster assignment for each subject in the generated data.

**Author(s)**

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**Examples**

```r
#
prop <- c(0.20,0.30,0.27,0.23)
effect <- 5
sim.data <- InterSIM(n.sample=500, cluster.sample.prop = prop, delta.methyl=effect, delta.expr=effect, delta.protein=effect, p.DMP=0.2, p.DEG=NULL, p.DEP=NULL, sigma.methyl=NULL, sigma.expr=NULL, sigma.protein=NULL, cor.methyl.expr=NULL, cor.expr.protein=NULL, do.plot=FALSE, sample.cluster=TRUE, feature.cluster=TRUE)
sim.methyl <- sim.data$dat.methyl
sim.expr <- sim.data$dat.expr
sim.protein <- sim.data$dat.protein
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