Package: PAIRADISE (via r-universe)

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Title PAIRADISE: Paired analysis of differential isoform expression

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Description This package implements the PAIRADISE procedure for detecting differential isoform expression between matched replicates in paired RNA-Seq data.

Depends R (>= 3.6), nloptr

Imports SummarizedExperiment, S4Vectors, stats, methods, abind, BiocParallel

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`counts` *PDseDataSet counts*

Description

PDseDataSet counts

Usage

```
counts(object)
```

Arguments

`object`	A PDseDataSet object

Value

A counts matrix

`pairadise` *pairadise*

Description

Primary function of the PAIRADISE package. Analyzes matched pairs for differences in isoform expression. Uses parallel processing to speed up computation.

Usage

```
pairadise(
  pdat,
  nIter = 100,
  tol = 10^(-2),
  pseudocount = 0,
  seed = 12321,
  equal.variance = FALSE,
  numCluster = 2,
  BPPARAM = MulticoreParam(numCluster)
)
```

Arguments

pdat	A PDseDataSet object
nIter	Positive integer. Specifies the maximum number of iterations of the optimization algorithm allowed. Default is nIter = 100
tol	Positive number. Specifies the tolerance level for terminating the optimization algorithm, defined as the difference in log-likelihood ratios between iterations. Default is tol = 10^(-2)
pseudocount	Positive number. Specifies a value for a pseudocount added to each count at the beginning of the analysis. Default is pseudocount = 0
seed	An integer to set seed.
equal.variance	Are the group variances assumed equal? Default value is FALSE.
numCluster	Number of clusters to use for parallel computing.
BPPARAM	parallel parameters from package BiocParallel.

Details

This is the primary function of the PAIRADISE package that implements the PAIRADISE algorithm.

Value

A PDseDataSet object contains outputs from PAIRADISE algorithm.

Examples

```
############################
## Example: Simulated data ##
############################

set.seed(12345)
data("sample_dataset")
pdat <- PDseDataSetFromMat(sample_dataset)
pdat <- pairadise(pdat, numCluster =4)
results(pdat)
```

PAIRADISE *PAIRADISE Detecting allele-specific alternative splicing from population-scale RNA-seq data*

Description

We introduce PAIRADISE (PAIred Replicate analysis of Allelic DIfferential Splicing Events), a method for detecting allele-specific alternative splicing (ASAS) from RNA-seq data. PAIRADISE uses a statistical model that aggregates ASAS signals across multiple individuals in a population. It formulates ASAS detection as a statistical problem for identifying differential alternative splicing from RNA-seq data with paired replicates. The PAIRADISE statistical model is applicable to many forms of allele-specific isoform variation (e.g. RNA editing), and can be used as a generic statistical model for RNA-seq studies involving paired replicates.

See Also

pairadise

PDseDataSet-class *PDseDataSet object and constuctor*

Description

'PDseDataSet' is a subclass of 'SummarizedExperiment'. It can used to store inclusion and skipping splicing counts for pair designed samples.

Usage

```
PDseDataSet(counts, design, lengths)
```

Arguments

counts	The counts of splicing events, including inclusion and skipping counts in 3 dimensions for each sample.
design	The paired design data.frame, including sample column for sample ids and group column for design factors.
lengths	Two columns iLen and sLen for the effective lengths of inclusion and skipping isoforms.

Value

A PDseDataSet object

Examples

```
icount <- matrix(1:4, 1)
scount <- matrix(5:8, 1)
acount <- abind::abind(icount, scount, along = 3)
design <- data.frame(sample = rep(c("s1", "s2"), 2),
group = rep(c("T", "N"), each = 2))
lens <- data.frame(sLen=1L, iLen=2L)
PDseDataSet(acount, design, lens)
```

PDseDataSetFromMat *PDseDataSet from rMATs/PAIRADISE Mat format*

Description

The Mat format should have 7 columns, arranged as follows: Column 1 contains the ID of the alternative splicing events. Column 2 contains counts of isoform 1 corresponding to the first group. Column 3 contains counts of isoform 2 corresponding to the first group. Column 4 contains counts of isoform 1 corresponding to the second group. Column 5 contains counts of isoform 2 corresponding to the second group. Column 6 contains the effective length of isoform 1. Column 7 contains the effective length of isoform 2. Replicates in columns 2-5 should be separated by commas, e.g. "1623,432,6" for three replicates and the replicate order should be consistent for each column to ensure pairs are matched correctly.

Usage

```
PDseDataSetFromMat(dat)
```

Arguments

dat	The Mat format dataframe.

Value

A PDseDataSet object

Examples

```
data("sample_dataset")
pdat <- PDseDataSetFromMat(sample_dataset)
```

results *Extract results for pairadise analysis*

Description

Extract results for pairadise analysis

Usage

```
results(pdat, p.adj = "BH", sig.level = 0.01, details = FALSE)
```

Arguments

pdat	A PDseDataSet object from pairadise analysis
p.adj	The p ajustment method.
sig.level	The cutoff of significant results
details	Whether to list detailed results.

Value

The function return a results DataFrame.

testStats	Vector of test statistics for paired analysis.
p.value	Vector of pvalues for each exon/event.
p.adj	The adjusted p values

If details is TRUE, more detailed parameter estimates for constrained and unconstrained model will return.

Examples

```
data("sample_dataset")
pdat <- PDseDataSetFromMat(sample_dataset)
pdat <- pairadise(pdat)
results(pdat)
```

---

sample_dataset *sample_dataset*

Description

The CEU dataset was generated by analyzing the allele-specific alternative splicing events in the GEUVADIS CEU data. Allele-specific reads were mapped onto alternative splicing events using rPGA (version 2.0.0). Then the allele-specific bam files mapped onto the two haplotypes are merged together to detect alternative splicing events using rMATS (version 3.2.5)16.

The LUSC dataset was generated by analyzing the tumor versus adjacent control samples from TCGA LUSC RNA-seq data.

Usage

```
data(sample_dataset)

data(sample_dataset_CEU)

data(sample_dataset_LUSC)
```

Format

The dataset has 7 columns, arranged as follows:

ExonID Column 1 contains the ID of the alternative splicing events.

I1 Column 2 contains counts of isoform 1 corresponding to the first group.

S1 Column 3 contains counts of isoform 2 corresponding to the first group.

I2 Column 4 contains counts of isoform 1 corresponding to the second group.

S2 Column 5 contains counts of isoform 2 corresponding to the second group.

I_len Column 6 contains the effective length of isoform 1.

S_len Column 7 contains the effective length of isoform 2.

The dataset has 7 columns, arranged as follows:

ExonID Column 1 contains the ID of the alternative splicing events.

I1 Column 2 contains counts of isoform 1 corresponding to the first group.

S1 Column 3 contains counts of isoform 2 corresponding to the first group.

I2 Column 4 contains counts of isoform 1 corresponding to the second group.

S2 Column 5 contains counts of isoform 2 corresponding to the second group.

I_len Column 6 contains the effective length of isoform 1.

S_len Column 7 contains the effective length of isoform 2.

The dataset has 7 columns, arranged as follows:

ExonID Column 1 contains the ID of the alternative splicing events.

I1 Column 2 contains counts of isoform 1 corresponding to the first group.

S1 Column 3 contains counts of isoform 2 corresponding to the first group.

I2 Column 4 contains counts of isoform 1 corresponding to the second group.

S2 Column 5 contains counts of isoform 2 corresponding to the second group.

I_len Column 6 contains the effective length of isoform 1.

S_len Column 7 contains the effective length of isoform 2.

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