

Package ‘ADVOCATE’

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Type Package

Title The ADVOCATE algorithm uses a Machine Learning based algorithm to combine weak evidence derived from the expression of individual genes into a model that provides an optimal estimate of the compartment-specific composition of a heterogeneous bulk tissue.

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Description

License file LICENSE

LazyData TRUE

RoxygenNote 6.0.1

NeedsCompilation no

R topics documented:

calCellTypeExpression	1
calCellTypeExpression_3comp	2
calGeneWiseProbability	3
hedgeBeta_deg	4
predict_bulk	4
predict_bulk_3comp	5
Index	6

calCellTypeExpression

Inferring Epithelium, Stromal virtual Expression of give bulk PDA samples Expression

Description

calCellTypeExpression uses LCM compartment specific expression from experiments, output of predict_bulk to infer virtual epithelium/stromal compartment specific gene expression.

Usage

```
calCellTypeExpression(lcmexp, deg, fc, pval, sampleInfo, inputexpmat, fracAll,
  method = "lcm")
```

Arguments

lcmexp	LCM sample expression
deg,	result from hedgeBeta_deg
fc,	output from hedgeBeta_deg
pval,	output from hedgeBeta_deg
sampleInfo,	output from hedgeBeta_deg
inputexpmat	input bulk PDA sample normalized expression (VST and Z transformed)
fracAll	result from predict_bulk
method	method for inference, currently support 'lcm'

Value

a matrix of n_gene * (nsample * 2)

Author(s)

J.HE

calCellTypeExpression_3comp

Inferring Epithelium, Stromal virtual Expression of give bulk PDA samples Expression

Description

calCellTypeExpression uses LCM compartment specific expression from experiments, output of predict_bulk_3comp to infer virtual epithelium/stromal compartment specific gene expression.

Usage

```
calCellTypeExpression_3comp(lcmexp, deg, fc, pval, sampleInfo, inputexpmat,
  fracAll, method = "lcm")
```

Arguments

lcmexp	LCM sample expression
deg,	result from hedgeBeta_deg
fc,	output from hedgeBeta_deg
pval,	output from hedgeBeta_deg
sampleInfo,	output from hedgeBeta_deg
inputexpmat	input bulk PDA sample normalized expression (VST and Z transformed)
fracAll	result from predict_bulk_3comp
method	method for inference, currently support 'lcm'

Value

a matrix of $n_gene * (nsample * 2)$

Author(s)

J.HE

calGeneWiseProbability

Calculate each genes probability of coming from Epithelium and Stromal compartment

Description

calGeneWiseProbability uses LCM gene expression from epithelium and stromal to calculate the bulk sample genes probability of epithelium/stromal compartment

Usage

```
calGeneWiseProbability(trainfile, bulkexp, n_comp = 2, epsilon = 0.01,
  betaFunc = "pval")
```

Arguments

trainfile	train file generated using hedgeBeta_deg function.
bulkexp	input bulk PDA sample normalized expression (VST and Z transformed)
n_comp	number of compartments, default 2
epsilon	accuracy of estimation, default 0.01
betaFunc	weighting metric for learning rate, default p-value

Value

a matrix of $number_gene * (number_sample*2)$

Author(s)

J.HE

hedgeBeta_deg	<i>Calculate DEG and its weighting metric for ADVOCATE training</i>
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Description

hedgeBeta_deg uses raw LCM samples from epi and stroma to calculate DEG and the weight metric for ADVOCATE model training.

Usage

```
hedgeBeta_deg(rawcounts, idxE, idxS, outfile = "input_advocate_train.rda")
```

Arguments

rawcounts	raw counts matrix from LCM RNAseq
idxE	group1 (Epithelium) sample name
idxS	group2 (stromal) sample name
outfile	rda file name to store all metrics needed for training

Author(s)

J.HE

predict_bulk	<i>Predict Epithelium and Stromal fraction of give bulk PDA samples expression</i>
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Description

predict_bulk uses probabilistic model to calculate the fraction of epithelium/stromal compartment using gene expression.

Usage

```
predict_bulk(trainfile, bulkexp, epsilon = 0.01, betaFunc = "pval")
```

Arguments

trainfile	train file generated using hedgeBeta_deg function.
bulkexp	input bulk PDA sample normalized expression (VST and Z transformed)
epsilon	accuracy of estimation, default 0.01
betaFunc	weighting metric for learning rate, default p-value

Value

a matrix of number_inputbulkexp * 7, first 2 columns are the epithelium and stromal fractions

Author(s)

J.HE

predict_bulk_3comp *Predict Epithelium, Stromal and Other compartment fractions of give bulk PDA samples expression*

Description

predict_bulk_3comp uses probabilistic model to calculate the fraction of epithelium/stromal/other compartment using gene expression.

Usage

```
predict_bulk_3comp(trainfile, bulkexp, epsilon = 0.01, betaFunc = "pval",  
  type = "p3l2fast")
```

Arguments

trainfile	train file generated using hedgeBeta_deg function.
bulkexp	input bulk PDA sample normalized expression (VST and Z transformed)
epsilon	accurray of estimation, default 0.01
betaFunc	weighting metric for learning rate, defaul p-value

Value

a matrix of number_inputbulkexp * 7, first 3 columns are the epithelium, stromal and other fractions

Author(s)

J.HE

Index

calCellTypeExpression, [1](#)
calCellTypeExpression_3comp, [2](#)
calGeneWiseProbability, [3](#)

hedgeBeta_deg, [4](#)

predict_bulk, [4](#)
predict_bulk_3comp, [5](#)