

Package ‘ISAT’

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Title Extract Cell Density and Nearest Distance Based on 'PerkinElmer InForm' Software Output

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Description Reads the output of the 'PerkinElmer InForm' software <<http://www.perkinelmer.com/product/inform-cell-analysis-one-seat-cls135781>>. In addition to cell-density count, it can derive statistics of intercellular spatial distance for each cell-type.

Depends R (>= 3.4)

Suggests knitr, rmarkdown, dplyr

VignetteBuilder knitr

Imports gtools, stats, stringr, utils

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

NeedsCompilation no

Repository CRAN

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Contents

findNN	2
findNNs	2
getFileCount	3
procDist	3
Index	5

findNN	<i>Find the nearest neighbour (NN) given a cell and a group of cells;</i>
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Description

Find the nearest neighbour (NN) given a cell and a group of cells;

Usage

```
findNN(cell, cellList, XY_LABELS = c("Cell.X.Position",
  "Cell.Y.Position"))
```

Arguments

cell	An object cell
cellList	A list of cell types to be calculated for
XY_LABELS	x and y positions of the cell

Value

The Nearest Neighbour Cell distance and calculate the distance

Examples

```
Cell.X.Position=sample (1:100,1)
Cell.Y.Position=sample (1:100,1)
Tcell=data.frame(Cell.X.Position,Cell.Y.Position)
Cell.X.Position=sample(1:500,5,replace=TRUE)
Cell.Y.Position=sample(1:500,5,replace=TRUE)
Tumor.cells=data.frame(Cell.X.Position,Cell.Y.Position)
findNN(Tcell,Tumor.cells,XY_LABELS=c('Cell.X.Position', 'Cell.Y.Position'))
```

findNNs	<i>Read a file and compute the NN through permutations;</i>
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Description

Read a file and compute the NN through permutations;

Usage

```
findNNs(filename, cell_names = NULL)
```

Arguments

filename	the file to be processed
cell_names	A list of cell types

Value

The Nearest Neighbour Cell distance in the file

getFileCount	<i>Get the count number of each phenotype for each tissue category</i>
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Description

Get the count number of each phenotype for each tissue category

Usage

```
getFileCount(dataFile)
```

Arguments

dataFile	File path to the data file
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Value

a data frame summary of count

procDist	<i>Extract the statistics from the result given by findNNs</i>
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Description

Extract the statistics from the result given by findNNs

Usage

```
procDist(distResult, thred = 30)
```

Arguments

distResult	A distance result file from findNNs
thred	a threshold distance as cut-off

Value

The statistics extracted from the distace result file

Examples

```
Cell.X.Position=sample(1:1000, 20, replace=TRUE)
Cell.Y.Position=sample(1:1000, 20, replace=TRUE)
distance = runif(20,min=0,max=100)
distResult = data.frame (Cell.X.Position,Cell.Y.Position,distance)
thred=30
procDist(distResult,thred)
```

Index

findNN, [2](#)

findNNs, [2](#)

getFileCount, [3](#)

procDist, [3](#)