

# Package: ISAT (via r-universe)

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

**Version** 1.0.5

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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

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**Repository** <https://wangminyu.r-universe.dev>

**RemoteUrl** <https://github.com/cran/ISAT>

**RemoteRef** HEAD

**RemoteSha** 89ff07bbfbcfe4d840364fcf96f4174d8dbeb616

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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'))
```

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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

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getFileCount            *Get the count number of each phenotype for each tissue category*

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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

**Value**

a data frame summary of count

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procDist                *Extract the statistics from the result given by findNNs*

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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)
```

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