

# Package ‘STROMA4’

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**Title** Assign Properties to TNBC Patients

**Description** This package estimates four stromal properties identified in TNBC patients in each patient of a gene expression datasets. These stromal property assignments can be combined to subtype patients. These four stromal properties were identified in Triple negative breast cancer (TNBC) patients and represent the presence of different cells in the stroma: T-cells (T), B-cells (B), stromal infiltrating epithelial cells (E), and desmoplasia (D). Additionally this package can also be used to estimate generative properties for the Lehmann subtypes, an alternative TNBC subtyping scheme (PMID: 21633166).

**Depends** R (>= 3.4), Biobase, BiocParallel, cluster, matrixStats, stats, graphics, utils

**License** GPL-3

**LazyData** true

**RoxygenNote** 5.0.1

**Suggests** breastCancerMAINZ

**biocViews** ImmunoOncology, GeneExpression, BiomedicalInformatics, Classification, Microarray, RNASeq, Software

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**Author** Sadiq Saleh [aut, cre],  
Michael Hallett [aut]

**Maintainer** Sadiq Saleh <sadiq.mehdiismailsaleh@mail.mcgill.ca>

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|                   |  |
|-------------------|--|
| assign.properties | <i>Function to assign properties to an expression matrix</i> |
|-------------------|--|

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### Description

assign.properties is a function to assign stromal property and Lehmann generative property levels to a TNBC dataset. Given an expressionset with a gene expression matrix, and a list of HGNC IDs, this function will estimate the status of samples for either the Lehmann generative properties, the stromal properties, or both at the same time. (Saleh et al. , under review at Cancer Research)

### Usage

```
assign.properties(ESet, geneID.column = 1, genelists = c("Stroma4",
  "TNBCType"), n = 1000, seed = 123456, mc.cores = snowWorkers(),
  var.method = function(x) rowIQRs(x, na.rm = TRUE))
```

### Arguments

|               |  |
|---------------|--|
| ESet          | An ExpressionSet object. Rows correspond to genes, columns to samples. If there are genes with multiple probes, they will be collapsed to a single row using the function defined in var.method. |
| geneID.column | Integer or column name corresponding to column in featureData table corresponding to HGNC ID.  |
| genelists     | A vector with either Stroma4, TNBCType, or both to specify which genelists to use.   |
| n             | An integer value specifying the number of random samples to generate.  |
| seed          | An integer value specifying a seed for the random ranks function. Default value is 123456.   |
| mc.cores      | An integer specifying how many cores to use. Defaults to use the function snowWorkers().   |
| var.method    | Function for assessing variance to collapse probes. Default is IQR   |

## Details

We defined a method for estimating stromal and Lehmann generative properties in a gene expression dataset (either LCM stroma or whole tumor breast cancer data). The `assign.properties` function extracts the expression data from the expression set using the `exprs()` function. The HGNC ID annotations for the dataset are required as this is what the function uses to identify genes to estimate property levels. The HGNC IDs should be in the `featureData` of the `expressionset`, and the corresponding column ID should be passed to the `geneID.column` argument. The function can be used to estimate the stromal properties, the Lehmann generative properties or both simultaneously depending on whether `'STROMA4'` (stromal properties), `'TNBCTYPE'` (Lehmann generative properties), or both are passed to the `genelists` argument. This function will then return property assignments.

## Value

The function returns a the `ExpressionSet` with the properties added to the `pData` table.

## Examples

```
library(breastCancerMAINZ)
data(mainz, package='breastCancerMAINZ')
all.properties <- assign.properties(ESet=mainz, geneID.column='Gene.symbol',
genelists=c('Stroma4', 'TNBCTYPE'), n=10)
```

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|                   |                                       |
|-------------------|---------------------------------------|
| B.stroma.property | <i>Genelist for B.stroma.property</i> |
|-------------------|---------------------------------------|

---

## Description

This genelist is used to assign the related property using the `assign.property` function

## Usage

```
data('B.stroma.property')
```

## Format

An object of class `data.frame` with 567 rows and 2 columns.

- `Gene.Symbol`: ID of transcript (HGNC where available)
- `Direction`: Direction of expression (up/down)

## Value

An object of class `data.frame` with 567 rows and 2 columns.

## Source

Identified in related publication

**Examples**

```
data('B.stroma.property')
```

---

|              |                                  |
|--------------|----------------------------------|
| BL1.property | <i>Genelist for BL1.property</i> |
|--------------|----------------------------------|

---

**Description**

This genelist is used to assign the related property using the assign.property function

**Usage**

```
data('BL1.property')
```

**Format**

An object of class data.frame with 473 rows and 2 columns.

- Gene.Symbol: ID of transcript (HGNC where available)
- Direction: Direction of expression (up/down)

**Value**

An object of class data.frame with 473 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('BL1.property')
```

---

|              |                                  |
|--------------|----------------------------------|
| BL2.property | <i>Genelist for BL2.property</i> |
|--------------|----------------------------------|

---

**Description**

This genelist is used to assign the related property using the assign.property function

**Usage**

```
data('BL2.property')
```

**Format**

An object of class `data.frame` with 291 rows and 2 columns.

- Gene.Symbol: ID of transcript (HGNC where available)
- Direction: Direction of expression (up/down)

**Value**

An object of class `data.frame` with 291 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('BL2.property')
```

---

|                                |                                       |
|--------------------------------|---------------------------------------|
| <code>D.stroma.property</code> | <i>Genelist for D.stroma.property</i> |
|--------------------------------|---------------------------------------|

---

**Description**

This genelist is used to assign the related property using the `assign.property` function

**Usage**

```
data('D.stroma.property')
```

**Format**

An object of class `data.frame` with 297 rows and 2 columns.

- Gene.Symbol: ID of transcript (HGNC where available)
- Direction: Direction of expression (up/down)

**Value**

An object of class `data.frame` with 297 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('D.stroma.property')
```

---

|                   |                                       |
|-------------------|---------------------------------------|
| E.stroma.property | <i>Genelist for E.stroma.property</i> |
|-------------------|---------------------------------------|

---

**Description**

This genelist is used to assign the related property using the assign.property function

**Usage**

```
data('E.stroma.property')
```

**Format**

An object of class data.frame with 27 rows and 2 columns.

- Gene.Symbol: ID of transcript (HGNC where available)
- Direction: Direction of expression (up/down)

**Value**

An object of class data.frame with 27 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('E.stroma.property')
```

---

|             |                                 |
|-------------|---------------------------------|
| IM.property | <i>Genelist for IM.property</i> |
|-------------|---------------------------------|

---

**Description**

This genelist is used to assign the related property using the assign.property function

**Usage**

```
data('IM.property')
```

**Format**

An object of class data.frame with 705 rows and 2 columns.

- Gene.Symbol: ID of transcript (HGNC where available)
- Direction: Direction of expression (up/down)

**Value**

An object of class `data.frame` with 705 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('IM.property')
```

---

LAR.property

*Genelist for LAR.property*

---

**Description**

This genelist is used to assign the related property using the `assign.property` function

**Usage**

```
data('LAR.property')
```

**Format**

An object of class `data.frame` with 1205 rows and 2 columns.

- Gene.Symbol: ID of transcript (HGNC where available)
- Direction: Direction of expression (up/down)

**Value**

An object of class `data.frame` with 1205 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('LAR.property')
```

M.property

*Genelist for M.property*

---

**Description**

This genelist is used to assign the related property using the assign.property function

**Usage**

```
data('M.property')
```

**Format**

An object of class data.frame with 710 rows and 2 columns.

- Gene.Symbol: ID of transcript (HGNC where available)
- Direction: Direction of expression (up/down)

**Value**

An object of class data.frame with 710 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('M.property')
```

---

MSL.property

*Genelist for MSL.property*

---

**Description**

This genelist is used to assign the related property using the assign.property function

**Usage**

```
data('MSL.property')
```

**Format**

An object of class data.frame with 1105 rows and 2 columns.

- Gene.Symbol: ID of transcript (HGNC where available)
- Direction: Direction of expression (up/down)



**Value**

An object of class `data.frame` with 1105 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('MSL.property')
```

---

|                                |                                       |
|--------------------------------|---------------------------------------|
| <code>T.stroma.property</code> | <i>Genelist for T.stroma.property</i> |
|--------------------------------|---------------------------------------|

---

**Description**

This genelist is used to assign the related property using the `assign.property` function

**Usage**

```
data('T.stroma.property')
```

**Format**

An object of class `data.frame` with 458 rows and 2 columns.

- `Gene.Symbol`: ID of transcript (HGNC where available)
- `Direction`: Direction of expression (up/down)

**Value**

An object of class `data.frame` with 458 rows and 2 columns.

**Source**

Identified in related publication

**Examples**

```
data('T.stroma.property')
```

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