Package ‘imcExperiment’

October 13, 2022

Title Mass Cytometry S4 Class Structure Pipeline for Images
Version 0.99.0
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Description Containerizes cytometry data and allows for S4 class structure to extend slots related to cell morphology, spatial coordinates, phenotype network information, and unique cellular labeling.
Depends R (>= 4.0), SingleCellExperiment, methods
Imports SummarizedExperiment, S4Vectors, spatstat.geom, stats
Suggests knitr, rmarkdown
License MIT + file LICENSE
biocViews Software, WorkflowStep, MultipleComparison
Encoding UTF-8
RoxygenNote 7.1.1
VignetteBuilder knitr
NeedsCompilation no
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Repository CRAN
Date/Publication 2021-08-19 09:20:02 UTC

R topics documented:

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### .checkSpatialDimension

The rows are the panel names, the columns are the single cells, the column are the single cells to match the SCE designs (scRNA).

**Description**

The rows are the panel names, the columns are the single cells, the column are the single cells to match the SCE designs (scRNA).

**Usage**

```r
.checkSpatialDimension(object)
```

**Arguments**

- `object`: imcExperiment object, class imcExperiment container

**Value**

imcExperiment container that has proper dimensions

### .imcExperimentToPPP

Map to point pattern from imcExperiment class.

**Description**

Map to point pattern from imcExperiment class.

**Usage**

```r
.imcExperimentToPPP(caseExperiment = NULL, phenotypeToUse = 1)
```

**Arguments**

- `caseExperiment`: the subset IMC experiment to cast into a point pattern
- `phenotypeToUse`: the cluster id to annotate the pattern
cellIntensity

Value
imcExperiment container converted to a point pattern set

Description
finds the intensities getter.
sets cell Intensity slot to a new matrix. rows protein, columns are cells.

Usage

```r
cellIntensity(object, ...)  
## S4 method for signature 'imcExperiment'  
cellIntensity(object)  

cellIntensity(object) <- value  
## S4 replacement method for signature 'imcExperiment,matrix'  
cellIntensity(object) <- value
```

Arguments
- **object** IMC container
- **...** additional arguments
- **value** matrix rows protein, columns are cells

Value
imcExperiment container
imcExperiment container
imcExperiment container
imcExperiment container

Examples
```r
data(imcdata)  
dim(cellIntensity(imcdata))  
data(imcdata);dim(cellIntensity(imcdata))  
head(t(cellIntensity(imcdata))))  
data(imcdata)  
x<-asinh(counts(imcdata))  
cellIntensity(imcdata)<-x
```
Description

Data set containing 1,000 cells and 73 features which include panel antibody, neighborhood computations, and phenograph clustering.

Usage

data(data)

Format

A data frame of 1,000 cells and histoCAT features

- **ImageId**: feature from histoCAT
- **CellId**: feature from histoCAT
- **marker1**: feature from histoCAT
- **marker2**: feature from histoCAT
- **marker3**: feature from histoCAT
- **marker4**: feature from histoCAT
- **marker5**: feature from histoCAT
- **marker6**: feature from histoCAT
- **marker7**: feature from histoCAT
- **marker8**: feature from histoCAT
- **marker9**: feature from histoCAT
- **marker10**: feature from histoCAT
- **marker11**: feature from histoCAT
- **marker12**: feature from histoCAT
- **marker13**: feature from histoCAT
- **marker14**: feature from histoCAT
- **marker15**: feature from histoCAT
- **marker16**: feature from histoCAT
- **marker17**: feature from histoCAT
- **marker18**: feature from histoCAT
- **marker19**: feature from histoCAT
- **marker20**: feature from histoCAT
- **marker21**: feature from histoCAT
- **marker22**: feature from histoCAT
marker23 feature from histoCAT
marker24 feature from histoCAT
marker25 feature from histoCAT
marker26 feature from histoCAT
marker27 feature from histoCAT
marker28 feature from histoCAT
marker29 feature from histoCAT
marker30 feature from histoCAT
marker31 feature from histoCAT
marker32 feature from histoCAT
marker33 feature from histoCAT
marker34 feature from histoCAT
Area feature from histoCAT
Eccentricity feature from histoCAT
Solidity feature from histoCAT
Extent feature from histoCAT
EulerNumber feature from histoCAT
Perimeter feature from histoCAT
MajorAxisLength feature from histoCAT
MinorAxisLength feature from histoCAT
Orientation feature from histoCAT
X_position feature from histoCAT
Y_position feature from histoCAT
Percent_Touching feature from histoCAT
Number_Neighbors feature from histoCAT
neighbour_4_CellId1 feature from histoCAT
neighbour_4_CellId2 feature from histoCAT
neighbour_4_CellId3 feature from histoCAT
neighbour_4_CellId4 feature from histoCAT
neighbour_4_CellId5 feature from histoCAT
neighbour_4_CellId6 feature from histoCAT
neighbour_4_CellId7 feature from histoCAT
neighbour_4_CellId8 feature from histoCAT
neighbour_4_CellId9 feature from histoCAT
neighbour_4_CellId10 feature from histoCAT
Phenograph7851534969 feature from histoCAT
tSNE4148542692_1 feature from histoCAT
tSNE4148542692_2 feature from histoCAT
getCoordinates  

*finds the spatial coords, getter.*

---

**Description**

finds the spatial coords, getter.

**Usage**

```
getCoordinates(object)
```

```r
## S4 method for signature 'imcExperiment'
getCoordinates(object)

## S4 replacement method for signature 'imcExperiment,matrix'
getCoordinates(object) <- value
```

**Arguments**

- `object` is IMC container
- `value` matrix rows cells, columns are x,y

**Value**

- imcExperiment container
- imcExperiment container
- imcExperiment container

**Examples**

```
data(imcdata)
getCoordinates(imcdata)
data(imcdata)
getCoordinates(imcdata)
data(imcdata)
x<-getCoordinates(imcdata)
getCoordinates(imcdata)<-as.matrix(x)
```
getCoordinates<-  

Sets the coordinate positions of each cell (matrix), columns are X,Y positions.

Description
Sets the coordinate positions of each cell (matrix), columns are X,Y positions.

Usage
getCoordinates(object) <- value

Arguments
object is IMC container
value matrix rows cells, columns are x,y

Value
imcExperiment container

Examples

data(imcdata)
x<-getCoordinates(imcdata)
getCoordinates(imcdata)<-as.matrix(x)

gDistance<-

re-assigns the distance matrix (rows are cells)

Description
re-assigns the distance matrix (rows are cells)

Usage
gDistance(object) <- value

Arguments
object is IMC container
value matrix rows cells, columns are distance measurements

Value
imcExperiment container
getNeighborhood

Examples

data(imcdata)
newD<-matrix(1,nrow=ncol(imcdata),ncol=1)
getDistance(imcdata)<-newD

getMorphology<- re-assigns morphological features can be stored (matrix) rows are cells and columns are Area, etc.

Description

re-assigns morphological features can be stored (matrix) rows are cells and columns are Area, etc.

Usage

getMorphology(object) <- value

Arguments

object is IMC container
value matrix rows cells, columns are Area, Eccentricity, etc.

Value

imcExperiment container

Examples

data(imcdata)
x<-matrix(1,nrow=ncol(imcdata),ncol=4)
getMorphology(imcdata)<-x

getNeighborhood finds the neighborhood information.

Description

finds the neighborhood information.

slow assignment for the histoCAT neighborhood data (matrix) columns are the neighbors
Usage

getNeighborhood(object, ...)

## S4 method for signature 'imcExperiment'
getNeighborhood(object)

getNeighborhood(object) <- value

## S4 replacement method for signature 'imcExperiment,matrix'
getNeighborhood(object) <- value

Arguments

object is IMC container
...
value matrix rows, cells, columns are neighborhood histoCAT output

Value

imcExperiment container
imcExperiment container data(imcdata) getNeighborhood(imcdata)
imcExperiment container
imcExperiment container

Examples

data(imcdata)
getNeighborhood(imcdata)
data(imcdata)
x<-matrix(1,nrow=ncol(imcdata),ncol=2)
getNeighborhood(imcdata)<-x
data(imcdata)
x<-matrix(1,nrow=ncol(imcdata),ncol=2)
getNeighborhood(imcdata)<-x

getNetwork<- re-assigns the network assignment (matrix)

Description

re-assigns the network assignment (matrix)

Usage

getNetwork(object) <- value
Arguments

object is IMC container
value data.frame rows cells, columns are phenograph network ID

Value

imcExperiment container

Examples

data(imcdata)
x<-data.frame(ID=seq_len(ncol(imcdata)))
getNetwork(imcdata)<-x

Description

histoCAT output containerized as IMC container. IMC S4 data set containing 2,452 cells and 44 antibody features which include panel antibody.

Usage

data(imcdata)

Format

A data frame of 2,452 cells and histoCAT features which are containerized into the imcExperiment

Description

Initializes a imcExperiment and performs some rudimentary checks. Many of the arguments CAN be NULL; determination of which is required is done at run-time. A imcExperiment must contain at least the expressions and spatial/coordinate assays.
Usage

```r
imcExperiment(
  coordinates = matrix(1, 3, 3),
  cellIntensity = matrix(1, 3, 3),
  neighborHood = matrix(1, 3, 3),
  network = data.frame(matrix(1, 3, 3)),
  distance = matrix(1, 3, 3),
  morphology = matrix(1, 3, 3),
  uniqueLabel = rep("A", 3),
  panel = as.character(seq_len(3)),
  ROIID = data.frame(ROIID = rep("A", 3)),
  ...
)
```

Arguments

- **coordinates**: matrix of spatial coordinates (x,y)
- **cellIntensity**: matrix of counts
- **neighborHood**: neighborhood results
- **network**: network assignments for each cell
- **distance**: distances for each cell, can be square
- **morphology**: morphology features for each cell, can be square
- **uniqueLabel**: character class each cell is assigned a uniqueLabel
- **panel**: antibody panel rownames set to rowData
- **ROIID**: character for ROI
- **...**: additional arguments

Value

imcExperiment container

Examples

```r
x<-imcExperiment(cellIntensity=matrix(1,nrow=10,ncol=10),
  coordinates=matrix(1,nrow=10,ncol=2),
  neighborHood=matrix(1,nrow=10,ncol=10),
  network=data.frame(matrix(1,nrow=10,ncol=10)),
  distance=matrix(1,nrow=10,ncol=10),
  morphology=matrix(1,nrow=10,ncol=10),
  uniqueLabel=paste0("A",seq_len(10)),
  panel=letters[1:10],
  ROIID=data.frame(ROIID=rep("A",10)))
```
imcExperiment-class  

*a summarized experiment of IMC runs, dimensions of the spatial and intensity data are regulated.*

**Description**

- a summarized experiment of IMC runs, dimensions of the spatial and intensity data are regulated.
- finds the network information.
- assigns cell cluster assignment to the container. rows are cells and column is the cluster ID
- finds the distance information.
- distance matrix can be stored in the distance slot for pairwise distance
- finds the morphology information.
- morphological features can be stored (matrix) rows are cells and columns are Area, etc.
- finds the label information.
- unique cell labels can be assigned (vector)

**Usage**

```r
getNetwork(object)
## S4 method for signature 'imcExperiment'
getNetwork(object)
## S4 replacement method for signature 'imcExperiment,data.frame'
getNetwork(object) <- value

getDistance(object)
## S4 method for signature 'imcExperiment'
getDistance(object)
## S4 replacement method for signature 'imcExperiment,matrix'
getDistance(object) <- value

getMorphology(object)
## S4 method for signature 'imcExperiment'
getMorphology(object)
## S4 replacement method for signature 'imcExperiment,matrix'
getMorphology(object) <- value

getLabel(object)
```
### S4 method for signature 'imcExperiment'

得到Label(object)

**Arguments**

- **object**: imcExperiment
- **value**: matrix rows cells, columns are Area, etc.

**Value**

- imcExperiment container
- imcExperiment container
- imcExperiment container
- imcExperiment container
- imcExperiment container
- imcExperiment container
- imcExperiment container
- imcExperiment container
- imcExperiment container
- imcExperiment container

**Slots**

- **coordinates**: matrix class containing x,y coordinates
- **cellIntensity**: matrix class containing intensity
- **neighborHood**: matrix class containing x,y neighbor
- **network**: data frame class containing network
- **distance**: matrix class containing x,y distances
- **morphology**: matrix class containing morphology
- **uniqueLabel**: labels

**Examples**

```r
x <- imcExperiment(cellIntensity = matrix(1, nrow = 10, ncol = 10),
                    coordinates = matrix(1, nrow = 10, ncol = 2),
                    neighborHood = matrix(1, nrow = 10, ncol = 10),
                    network = data.frame(matrix(1, nrow = 10, ncol = 10)),
                    distance = matrix(1, nrow = 10, ncol = 10),
                    morphology = matrix(1, nrow = 10, ncol = 10),
                    uniqueLabel = paste0("A", seq_len(10)),
                    panel = letters[1:10],
                    ROIID = data.frame(ROIID = rep("A", 10)))
data(imcdata)
getNetwork(imcdata)
```
data(imcdata)
getNetwork(imcdata)
data(imcdata)
x<-data.frame(ID=seq_len(ncol(imcdata)))
getNetwork(imcdata)<-x
data(imcdata)
getDistance(imcdata)
data(imcdata)
getDistance(imcdata)
data(imcdata)
newD<-matrix(1,nrow=ncol(imcdata),ncol=1)
getDistance(imcdata)<-newD
data(imcdata)
getMorphology(imcdata)
data(imcdata)
getMorphology(imcdata)
data(imcdata)
x<-matrix(1,nrow=ncol(imcdata),ncol=4)
getMorphology(imcdata)<-x
data(imcdata)
getLabel(imcdata)
data(imcdata)
getLabel(imcdata)

imcExperimentToHyperFrame

map to point pattern from imcExperiment class.

Description
map to point pattern from imcExperiment class.

Usage
imcExperimentToHyperFrame(imcExperiment = NULL, phenotypeToUse = 1)

Arguments
imcExperiment  imcExperiment class
phenotypeToUse  the network slot can often have many columns, this is the ID for the column
number to use in the network slot.

Value
a hyperframe of point patterns

Examples
data(imcdata)
H<-imcExperimentToHyperFrame(imcExperiment=imcdata,phenotypeToUse = 1)
percentilenormalize  given a matrix of intensity counts, perform min/max norm.

Description

given a matrix of intensity counts, perform min/max norm.

Usage

percentilenormalize(data = NULL, percentile = NULL)

Arguments

data          matrix of numeric data only
percentile    numeric value 0.99 default.

Value

normalized data, each column on [0,1] scale.

Examples

data(data)
dim(data)
expr<-data[,3:36]
normExp<-percentilenormalize(data=expr,percentile=0.99)
normExp<-as.matrix(normExp)

selectCases  subsets the imcExperiment to a case along with all slots for a selected multiple ROIs.

Description

subsets the imcExperiment to a case along with all slots for a selected multiple ROIs.
method to subset the slots, requires colData with column "ROIID"

Usage

selectCases(object, value, ...)

## S4 method for signature 'imcExperiment'
selectCases(object, value)
subsetCase

Arguments

- **object**
  - IMC container
- **value**
  - this is ROIID vector
- ... additional parameters

Value

- imcExperiment container of selected cases
- imcExperiment container of selected cases

Examples

```r
data(imcdata)
myCases<-selectCases(imcdata,c("30-BM16-202_7Pre_s1_p1_r4_a4_ac","B17_350_14post_s1_p1_r5_a5_ac"))
myCases
table(colData(myCases)$ROIID)
```

Description

subsets the imcExperiment to a case along with all slots for a single ROI, using for distance analysis

Usage

```r
subsetCase(object, value, ...)
```

## S4 method for signature 'imcExperiment'
subsetCase(object, value)

Arguments

- **object**
  - IMC container
- **value**
  - this is ROIID a single character ID
- ... additional parameters

Value

- returns IMC object of a single case
- roi imcExperiment
Examples

data(imcdata)
myCase<-subsetCase(imcdata,"30-BM16-202_7Pre_s1_p1_r4_a4_ac")
myCase

data(imcdata)
myCase<-subsetCase(imcdata,"30-BM16-202_7Pre_s1_p1_r4_a4_ac")
myCase
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