Package: imcExperiment (via r-universe)

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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

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biocViews Software, WorkflowStep, MultipleComparison

Encoding UTF-8

RoxygenNote 7.1.1

VignetteBuilder knitr

Config/pak/sysreqs libssl-dev

Repository https://arcolombo.r-universe.dev

RemoteUrl https://github.com/arcolombo/imcexperiment

RemoteRef HEAD

RemoteSha 02333b68447ffa7b045e139104f64934b5b77c56

Contents

`.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

```
.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

```
.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

Value

imcExperiment container converted to a point pattern set

`cellIntensity` *finds the intensities getter.*

Description

finds the intensities getter.

sets cell Intensity slot to a new matrix. rows protein, columns are cells.

Usage

```
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

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

`data` *data*

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)

## 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)
```

`getDistance<-` *re-assigns the distance matrix (rows are cells)*

Description

re-assigns the distance matrix (rows are cells)

Usage

```
getDistance(object) <- value
```

Arguments

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

Value

imcExperiment container

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
`...`	additional arguments
`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
```

`imcdata` *imcdata*

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

---

`imcExperiment` *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.*

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

```
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

```
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

```
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'
getLabel(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

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

```
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)
```

Arguments

`object`	IMC container
`value`	this is ROIID vector
`...`	additional parameters

Value

imcExperiment container of selected cases

imcExperiment container of selected cases

Examples

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

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

Description

subsets the imcExperiment to a case along with all slots for a single ROI, using for distance analysis method to subset the slots, requires colData with column "ROIID"

Usage

```
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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