

Package: MultimodalExperiment (via r-universe)

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Title Integrative Bulk and Single-Cell Experiment Container

Version 1.12.0

Description MultimodalExperiment is an S4 class that integrates bulk and single-cell experiment data; it is optimally storage-efficient, and its methods are exceptionally fast. It effortlessly represents multimodal data of any nature and features normalized experiment, subject, sample, and cell annotations, which are related to underlying biological experiments through maps. Its coordination methods are opt-in and employ database-like join operations internally to deliver fast and flexible management of multimodal data.

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annotation-methods	<i>MultimodalExperiment Annotation Methods</i>
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Description

joinAnnotations joins all annotations into an unnormalized [DataFrame](#) object.

Usage

```
## S4 method for signature 'MultimodalExperiment'
joinAnnotations(x)
```

Arguments

x a [MultimodalExperiment](#) object

Value

joinAnnotations returns a [DataFrame](#) object.

See Also

`browseVignettes("MultimodalExperiment")`

Examples

```
ME <-
  MultimodalExperiment()

bulkExperiments(ME) <-
  ExperimentList(
    pbRNAseq = pbRNAseq
  )

singleCellExperiments(ME) <-
```

```
ExperimentList(  
  scADTseq = scADTseq,  
  scRNAseq = scRNAseq  
)  
  
subjectMap(ME)[["subject"]] <-  
  "SUBJECT-1"  
  
sampleMap(ME)[["subject"]] <-  
  "SUBJECT-1"  
  
cellMap(ME)[["sample"]] <-  
  "SAMPLE-1"  
  
ME <-  
  propagate(ME)  
  
experimentData(ME)[["published"]] <-  
  c(NA_character_, "2018-11-19", "2018-11-19") |>  
  as.Date()  
  
subjectData(ME)[["condition"]] <-  
  as.character("healthy")  
  
sampleData(ME)[["sampleType"]] <-  
  as.character("peripheral blood mononuclear cells")  
  
cellType <- function(x) {  
  if (x[["CD4"]] > 0L) {  
    return("T Cell")  
  }  
  
  if (x[["CD14"]] > 0L) {  
    return("Monocyte")  
  }  
  
  if (x[["CD19"]] > 0L) {  
    return("B Cell")  
  }  
  
  if (x[["CD56"]] > 0L) {  
    return("NK Cell")  
  }  
  
  NA_character_  
}  
  
cellData(ME)[["cellType"]] <-  
  experiment(ME, "scADTseq") |>  
  apply(2L, cellType)  
  
joinAnnotations(ME)
```

coordination-methods *MultimodalExperiment Coordination Methods*

Description

Propagate or harmonize indices of a [MultimodalExperiment](#) object.

Usage

```
## S4 method for signature 'MultimodalExperiment'  
propagate(x)
```

```
## S4 method for signature 'MultimodalExperiment'  
harmonize(x)
```

Arguments

x a [MultimodalExperiment](#) object

Details

propagate inserts experiment, subject, sample, and cell indices into all relevant tables by taking their union and adding missing indices.

harmonize deletes experiment, subject, sample, and cell indices from all relevant tables by taking their intersection and removing extraneous indices.

Value

propagate returns a [MultimodalExperiment](#) object.

harmonize returns a [MultimodalExperiment](#) object.

See Also

```
browseVignettes("MultimodalExperiment")
```

Examples

```
ME <-  
  MultimodalExperiment()  
  
bulkExperiments(ME) <-  
  ExperimentList(  
    pbRNAseq = pbRNAseq  
  )  
  
singleCellExperiments(ME) <-  
  ExperimentList(  
    scADTseq = scADTseq,
```

```
        scRNAseq = scRNAseq
    )

    subjectMap(ME)[["subject"]] <-
        "SUBJECT-1"

    sampleMap(ME)[["subject"]] <-
        "SUBJECT-1"

    cellMap(ME)[["sample"]] <-
        "SAMPLE-1"

    ME <-
        propagate(ME)

    experimentData(ME)[["published"]] <-
        c(NA_character_, "2018-11-19", "2018-11-19") |>
        as.Date()

    subjectData(ME)[["condition"]] <-
        as.character("healthy")

    sampleData(ME)[["sampleType"]] <-
        as.character("peripheral blood mononuclear cells")

    cellType <- function(x) {
        if (x[["CD4"]] > 0L) {
            return("T Cell")
        }

        if (x[["CD14"]] > 0L) {
            return("Monocyte")
        }

        if (x[["CD19"]] > 0L) {
            return("B Cell")
        }

        if (x[["CD56"]] > 0L) {
            return("NK Cell")
        }

        NA_character_
    }

    cellData(ME)[["cellType"]] <-
        experiment(ME, "scADTseq") |>
        apply(2L, cellType)

    isMonocyte <-
        cellData(ME)[["cellType"]] %in% "Monocyte"

    cellData(ME) <-
```

```
cellData(ME)[isMonocyte, , drop = FALSE]  
harmonize(ME)
```

example-data

MultimodalExperiment Example Data

Description

Human peripheral blood mononuclear cells (PBMCs) from a single healthy donor were profiled by cellular indexing of transcriptomes and epitopes by sequencing (CITE-seq) to generate single-cell antibody-derived tag sequencing (scADTseq) and single-cell RNA sequencing (scRNAseq) data simultaneously; the scRNAseq data was summed into pseudo-bulk RNA sequencing (pbRNAseq) data. The dimensions of resulting matrices were reduced to conserve storage because these data are only used to demonstrate the functionality of the [MultimodalExperiment](#) class.

Usage

```
pbRNAseq  
scADTseq  
scRNAseq
```

Format

An object of class `matrix` (inherits from `array`) with 3000 rows and 1 columns.

An object of class `matrix` (inherits from `array`) with 8 rows and 5000 columns.

An object of class `matrix` (inherits from `array`) with 3000 rows and 5000 columns.

Source

PBMCs of a Healthy Donor - 5' Gene Expression with a Panel of TotalSeq™-C Antibodies, Single Cell Immune Profiling Dataset by Cell Ranger 3.0.0, 10x Genomics, (2018, November 19).

Examples

```
pbRNAseq[1:4, 1:1, drop = FALSE]  
scADTseq[1:4, 1:4, drop = FALSE]  
scRNAseq[1:4, 1:4, drop = FALSE]
```

Description

Extract or replace experiments of a [MultimodalExperiment](#) object by index, name, or type.

Usage

```
## S4 method for signature 'MultimodalExperiment'  
experiment(x, i)  
  
## S4 replacement method for signature 'MultimodalExperiment'  
experiment(x, i) <- value  
  
## S4 method for signature 'MultimodalExperiment'  
bulkExperiments(x)  
  
## S4 replacement method for signature 'MultimodalExperiment'  
bulkExperiments(x) <- value  
  
## S4 method for signature 'MultimodalExperiment'  
singleCellExperiments(x)  
  
## S4 replacement method for signature 'MultimodalExperiment'  
singleCellExperiments(x) <- value
```

Arguments

x	a MultimodalExperiment object
i	an integer or character index
value	a replacement value

Details

The term matrix-like objects refers to [matrix](#) objects or Bioconductor S4 objects that contain them ([SummarizedExperiment](#), [SingleCellExperiment](#), etc.) where rows represent features and columns represent observations.

Value

`experiment` returns a matrix-like object.

`bulkExperiments` returns an [ExperimentList](#) of matrix-like objects.

`singleCellExperiments` returns an [ExperimentList](#) of matrix-like objects.

See Also

```
browseVignettes("MultimodalExperiment")
```

Examples

```
ME <-
  MultimodalExperiment()

bulkExperiments(ME) <-
  ExperimentList(
    pbRNAseq = pbRNAseq
  )

singleCellExperiments(ME) <-
  ExperimentList(
    scADTseq = scADTseq,
    scRNAseq = scRNAseq
  )

subjectMap(ME)[["subject"]] <-
  "SUBJECT-1"

sampleMap(ME)[["subject"]] <-
  "SUBJECT-1"

cellMap(ME)[["sample"]] <-
  "SAMPLE-1"

ME <-
  propagate(ME)

experimentData(ME)[["published"]] <-
  c(NA_character_, "2018-11-19", "2018-11-19") |>
  as.Date()

subjectData(ME)[["condition"]] <-
  as.character("healthy")

sampleData(ME)[["sampleType"]] <-
  as.character("peripheral blood mononuclear cells")

cellType <- function(x) {
  if (x[["CD4"]] > 0L) {
    return("T Cell")
  }

  if (x[["CD14"]] > 0L) {
    return("Monocyte")
  }

  if (x[["CD19"]] > 0L) {
    return("B Cell")
  }
}
```

```
    }  
    if (x[["CD56"]] > 0L) {  
      return("NK Cell")  
    }  
  }  
  NA_character_  
}  
  
cellData(ME)[["cellType"]] <-  
  experiment(ME, "scADTseq") |>  
  apply(2L, cellType)  
  
experiment(ME, 2L) <-  
  experiment(ME, 2L)[1:4, 1:4]  
  
experiment(ME, 2L)  
  
experiment(ME, "scRNAseq") <-  
  experiment(ME, "scRNAseq")[1:4, 1:4]  
  
experiment(ME, "scRNAseq")  
  
bulkExperiments(ME) <-  
  bulkExperiments(ME)[1L]  
  
bulkExperiments(ME)  
  
singleCellExperiments(ME) <-  
  singleCellExperiments(ME)[2L]  
  
singleCellExperiments(ME)
```

map-methods

MultimodalExperiment Map Methods

Description

joinMaps joins all maps into an unnormalized [DataFrame](#) object.

Usage

```
## S4 method for signature 'MultimodalExperiment'  
joinMaps(x)
```

Arguments

x a [MultimodalExperiment](#) object

Value

joinMaps returns a [DataFrame](#) object.

See Also

`browseVignettes("MultimodalExperiment")`

Examples

```
ME <-
  MultimodalExperiment()

bulkExperiments(ME) <-
  ExperimentList(
    pbRNAseq = pbRNAseq
  )

singleCellExperiments(ME) <-
  ExperimentList(
    scADTseq = scADTseq,
    scRNAseq = scRNAseq
  )

subjectMap(ME)[["subject"]] <-
  "SUBJECT-1"

sampleMap(ME)[["subject"]] <-
  "SUBJECT-1"

cellMap(ME)[["sample"]] <-
  "SAMPLE-1"

ME <-
  propagate(ME)

experimentData(ME)[["published"]] <-
  c(NA_character_, "2018-11-19", "2018-11-19") |>
  as.Date()

subjectData(ME)[["condition"]] <-
  as.character("healthy")

sampleData(ME)[["sampleType"]] <-
  as.character("peripheral blood mononuclear cells")

cellType <- function(x) {
  if (x[["CD4"]] > 0L) {
    return("T Cell")
  }

  if (x[["CD14"]] > 0L) {
    return("Monocyte")
  }
}
```

```

    }

    if (x[["CD19"]] > 0L) {
      return("B Cell")
    }

    if (x[["CD56"]] > 0L) {
      return("NK Cell")
    }

    NA_character_
  }

  cellData(ME)[["cellType"]] <-
    experiment(ME, "scADTseq") |>
    apply(2L, cellType)

  joinMaps(ME)

```

MultimodalExperiment *MultimodalExperiment Constructor Function*

Description

MultimodalExperiment constructs a [MultimodalExperiment](#) object.

Usage

```

MultimodalExperiment(
  experimentData = DataFrame(),
  subjectData = DataFrame(),
  sampleData = DataFrame(),
  cellData = DataFrame(),
  experimentMap = DataFrame(
    type = character(),
    experiment = character()
  ),
  subjectMap = DataFrame(
    experiment = character(),
    subject = character()
  ),
  sampleMap = DataFrame(
    subject = character(),
    sample = character()
  ),
  cellMap = DataFrame(
    sample = character(),

```

```

        cell = character()
    ),
    experiments = ExperimentList(),
    metadata = list()
)

```

Arguments

experimentData a [DataFrame](#) of experiment annotations with experiment indices as rownames
subjectData a [DataFrame](#) of subject annotations with subject indices as rownames
sampleData a [DataFrame](#) of sample annotations with sample indices as rownames
cellData a [DataFrame](#) of cell annotations with cell indices as rownames
experimentMap a [DataFrame](#) of type (bulk or single-cell) to experiment (index) mappings
subjectMap a [DataFrame](#) of experiment (index) to subject (index) mappings
sampleMap a [DataFrame](#) of subject (index) to sample (index) mappings
cellMap a [DataFrame](#) of sample (index) to cell (index) mappings
experiments an [ExperimentList](#) of matrix-like objects
metadata a [list](#) of metadata objects

Details

The term matrix-like objects refers to [matrix](#) objects or Bioconductor S4 objects that contain them ([SummarizedExperiment](#), [SingleCellExperiment](#), etc.) where rows represent features and columns represent observations.

Value

MultimodalExperiment returns a [MultimodalExperiment](#) object.

See Also

`browseVignettes("MultimodalExperiment")`

Examples

```
MultimodalExperiment()
```

MultimodalExperiment-class

MultimodalExperiment Class Definition

Description

MultimodalExperiment is an S4 class that integrates bulk and single-cell experiment data; it is optimally storage-efficient, and its methods are exceptionally fast. It effortlessly represents multimodal data of any nature and features normalized experiment, subject, sample, and cell annotations, which are related to underlying biological experiments through maps. Its coordination methods are opt-in and employ database-like join operations internally to deliver fast and flexible management of multimodal data.

Details

The term matrix-like objects refers to [matrix](#) objects or Bioconductor S4 objects that contain them ([SummarizedExperiment](#), [SingleCellExperiment](#), etc.) where rows represent features and columns represent observations.

Slots

experimentData a [DataFrame](#) of experiment annotations with experiment indices as rownames

subjectData a [DataFrame](#) of subject annotations with subject indices as rownames

sampleData a [DataFrame](#) of sample annotations with sample indices as rownames

cellData a [DataFrame](#) of cell annotations with cell indices as rownames

experimentMap a [DataFrame](#) of type (bulk or single-cell) to experiment (index) mappings

subjectMap a [DataFrame](#) of experiment (index) to subject (index) mappings

sampleMap a [DataFrame](#) of subject (index) to sample (index) mappings

cellMap a [DataFrame](#) of sample (index) to cell (index) mappings

experiments an [ExperimentList](#) of matrix-like objects

metadata a [list](#) of metadata objects

See Also

`browseVignettes("MultimodalExperiment")`

name-methods

MultimodalExperiment Name Methods

Description

Extract or replace names of a [MultimodalExperiment](#) object.

Usage

```
## S4 method for signature 'MultimodalExperiment'  
names(x)  
  
## S4 replacement method for signature 'MultimodalExperiment'  
names(x) <- value  
  
## S4 method for signature 'MultimodalExperiment'  
rownames(x)  
  
## S4 replacement method for signature 'MultimodalExperiment'  
rownames(x) <- value  
  
## S4 method for signature 'MultimodalExperiment'  
colnames(x)  
  
## S4 replacement method for signature 'MultimodalExperiment,ANY'  
colnames(x) <- value  
  
## S4 method for signature 'MultimodalExperiment'  
dimnames(x)  
  
## S4 replacement method for signature 'MultimodalExperiment,ANY'  
dimnames(x) <- value  
  
## S4 method for signature 'MultimodalExperiment'  
experimentNames(x)  
  
## S4 replacement method for signature 'MultimodalExperiment'  
experimentNames(x) <- value
```

Arguments

x	a MultimodalExperiment object
value	a replacement value

Value

names returns a [CharacterList](#) object.

rownames returns a [CharacterList](#) object.
 colnames returns a [CharacterList](#) object.
 dimnames returns a [list](#) object.
 experimentNames returns a [character](#) vector.

See Also

`browseVignettes("MultimodalExperiment")`

Examples

```
ME <-
  MultimodalExperiment()

bulkExperiments(ME) <-
  ExperimentList(
    pbRNAseq = pbRNAseq
  )

singleCellExperiments(ME) <-
  ExperimentList(
    scADTseq = scADTseq,
    scRNAseq = scRNAseq
  )

subjectMap(ME)[["subject"]] <-
  "SUBJECT-1"

sampleMap(ME)[["subject"]] <-
  "SUBJECT-1"

cellMap(ME)[["sample"]] <-
  "SAMPLE-1"

ME <-
  propagate(ME)

experimentData(ME)[["published"]] <-
  c(NA_character_, "2018-11-19", "2018-11-19") |>
  as.Date()

subjectData(ME)[["condition"]] <-
  as.character("healthy")

sampleData(ME)[["sampleType"]] <-
  as.character("peripheral blood mononuclear cells")

cellType <- function(x) {
  if (x[["CD4"]] > 0L) {
    return("T Cell")
  }
}
```

```
    if (x[["CD14"]] > 0L) {
      return("Monocyte")
    }

    if (x[["CD19"]] > 0L) {
      return("B Cell")
    }

    if (x[["CD56"]] > 0L) {
      return("NK Cell")
    }

    NA_character_
  }

cellData(ME)[["cellType"]] <-
  experiment(ME, "scADTseq") |>
  apply(2L, cellType)

names(ME) <-
  names(ME) |>
  tolower()

names(ME)

rownames(ME) <-
  rownames(ME) |>
  toupper()

rownames(ME)

colnames(ME) <-
  colnames(ME) |>
  tolower()

colnames(ME)

dimnames(ME)[[2L]] <-
  dimnames(ME)[[2L]] |>
  toupper()

dimnames(ME)[[2L]]

experimentNames(ME) <-
  experimentNames(ME) |>
  gsub(pattern = "seq", replacement = "-seq")

experimentNames(ME)
```

slot-methods	<i>MultimodalExperiment Slot Methods</i>
--------------	--

Description

Extract or replace slots of a [MultimodalExperiment](#) object.

Usage

```
## S4 method for signature 'MultimodalExperiment'
experimentData(object)

## S4 replacement method for signature 'MultimodalExperiment'
experimentData(object) <- value

## S4 method for signature 'MultimodalExperiment'
subjectData(object)

## S4 replacement method for signature 'MultimodalExperiment'
subjectData(object) <- value

## S4 method for signature 'MultimodalExperiment'
sampleData(object)

## S4 replacement method for signature 'MultimodalExperiment'
sampleData(object) <- value

## S4 method for signature 'MultimodalExperiment'
cellData(object)

## S4 replacement method for signature 'MultimodalExperiment'
cellData(object) <- value

## S4 method for signature 'MultimodalExperiment'
experimentMap(object)

## S4 replacement method for signature 'MultimodalExperiment'
experimentMap(object) <- value

## S4 method for signature 'MultimodalExperiment'
subjectMap(object)

## S4 replacement method for signature 'MultimodalExperiment'
subjectMap(object) <- value

## S4 method for signature 'MultimodalExperiment'
sampleMap(object)
```

```
## S4 replacement method for signature 'MultimodalExperiment'  
sampleMap(object) <- value  
  
## S4 method for signature 'MultimodalExperiment'  
cellMap(object)  
  
## S4 replacement method for signature 'MultimodalExperiment'  
cellMap(object) <- value  
  
## S4 method for signature 'MultimodalExperiment'  
experiments(object)  
  
## S4 replacement method for signature 'MultimodalExperiment'  
experiments(object) <- value
```

Arguments

object	a MultimodalExperiment object
value	a replacement value

Value

Extract methods return the value of the slot.

See Also

`browseVignettes("MultimodalExperiment")`

Examples

```
ME <-  
  MultimodalExperiment()  
  
bulkExperiments(ME) <-  
  ExperimentList(  
    pbRNAseq = pbRNAseq  
  )  
  
singleCellExperiments(ME) <-  
  ExperimentList(  
    scADTseq = scADTseq,  
    scRNAseq = scRNAseq  
  )  
  
subjectMap(ME)[["subject"]] <-  
  "SUBJECT-1"  
  
sampleMap(ME)[["subject"]] <-  
  "SUBJECT-1"
```

```
cellMap(ME)[["sample"]] <-  
  "SAMPLE-1"  
  
ME <-  
  propagate(ME)  
  
experimentData(ME)[["published"]] <-  
  c(NA_character_, "2018-11-19", "2018-11-19") |>  
  as.Date()  
  
subjectData(ME)[["condition"]] <-  
  as.character("healthy")  
  
sampleData(ME)[["sampleType"]] <-  
  as.character("peripheral blood mononuclear cells")  
  
cellType <- function(x) {  
  if (x[["CD4"]] > 0L) {  
    return("T Cell")  
  }  
  
  if (x[["CD14"]] > 0L) {  
    return("Monocyte")  
  }  
  
  if (x[["CD19"]] > 0L) {  
    return("B Cell")  
  }  
  
  if (x[["CD56"]] > 0L) {  
    return("NK Cell")  
  }  
  
  NA_character_  
}  
  
cellData(ME)[["cellType"]] <-  
  experiment(ME, "scADTseq") |>  
  apply(2L, cellType)  
  
experimentData(ME)  
  
subjectData(ME)  
  
sampleData(ME)  
  
cellData(ME)  
  
experimentMap(ME)  
  
subjectMap(ME)  
  
sampleMap(ME)
```

```
cellMap(ME)
experiments(ME)
```

subset-methods *MultimodalExperiment Subset Methods*

Description

Extract or replace parts of a [MultimodalExperiment](#) object.

Usage

```
## S4 method for signature 'MultimodalExperiment,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 replacement method for signature 'MultimodalExperiment,ANY,ANY,ANY'
x[i, j] <- value
```

Arguments

x	a MultimodalExperiment object
i	a list , List , LogicalList , IntegerList , or CharacterList of elements to extract or replace
j	a list , List , LogicalList , IntegerList , or CharacterList of elements to extract or replace
...	ignored, required by generic
drop	ignored, required by generic
value	a replacement value

Value

[returns a [MultimodalExperiment](#) object.

See Also

```
browseVignettes("MultimodalExperiment")
```

Examples

```
ME <-
  MultimodalExperiment()

bulkExperiments(ME) <-
  ExperimentList(
    pbRNAseq = pbRNAseq
  )

singleCellExperiments(ME) <-
  ExperimentList(
    scADTseq = scADTseq,
    scRNAseq = scRNAseq
  )

subjectMap(ME)[["subject"]] <-
  "SUBJECT-1"

sampleMap(ME)[["subject"]] <-
  "SUBJECT-1"

cellMap(ME)[["sample"]] <-
  "SAMPLE-1"

ME <-
  propagate(ME)

experimentData(ME)[["published"]] <-
  c(NA_character_, "2018-11-19", "2018-11-19") |>
  as.Date()

subjectData(ME)[["condition"]] <-
  as.character("healthy")

sampleData(ME)[["sampleType"]] <-
  as.character("peripheral blood mononuclear cells")

cellType <- function(x) {
  if (x[["CD4"]] > 0L) {
    return("T Cell")
  }

  if (x[["CD14"]] > 0L) {
    return("Monocyte")
  }

  if (x[["CD19"]] > 0L) {
    return("B Cell")
  }

  if (x[["CD56"]] > 0L) {
    return("NK Cell")
  }
}
```

```
    }  
    NA_character_  
  }  
  
  cellData(ME)[["cellType"]] <-  
    experiment(ME, "scADTseq") |>  
    apply(2L, cellType)  
  
  i <-  
    rownames(ME) |>  
    endoapply(sample, 4L)  
  
  j <-  
    colnames(ME) |>  
    endoapply(sample, 1L)  
  
  ME[i, j] <-  
    0L  
  
  experiment(ME[i, j], "pbRNAseq")  
  
  experiment(ME[i, j], "scADTseq")  
  
  experiment(ME[i, j], "scRNAseq")
```

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