

# Package ‘MultimodalExperiment’

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**Title** Integrative Bulk and Single-Cell Experiment Container

**Version** 1.7.0

**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>
--------------------	--

---

### 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 <a href="#">MultimodalExperiment</a> 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 <a href="#">MultimodalExperiment</a> 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)
```



---

reexports                      *Objects exported from other packages*

---

### Description

These objects are imported from other packages. Follow the links below to see their documentation.

**MultiAssayExperiment** [ExperimentList](#)

---

show-method                      *MultimodalExperiment Show Method*

---

### Description

Display details about a [MultimodalExperiment](#) object.

### Usage

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

### Arguments

object                      a [MultimodalExperiment](#) object

### Value

show returns NULL invisibly.

### 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)

show(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 <a href="#">MultimodalExperiment</a> 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 <a href="#">MultimodalExperiment</a> object
i	a <a href="#">list</a> , <a href="#">List</a> , <a href="#">LogicalList</a> , <a href="#">IntegerList</a> , or <a href="#">CharacterList</a> of elements to extract or replace
j	a <a href="#">list</a> , <a href="#">List</a> , <a href="#">LogicalList</a> , <a href="#">IntegerList</a> , or <a href="#">CharacterList</a> 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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