

Package: MOObject (via r-universe)

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Title multiOmicDataSet object class for MOSuite

Version 0.5.0.9000

Description MOObject defines the multiOmicDataSet object class which is used in MOSuite for differential RNA-seq and multi-omics analyses. Separating the MOObject class definition from MOSuite allows for lightweight installations in downstream workflows.

See the website for more information:

<<https://ccbr.github.io/MOObject/>>. See the MOSuite website for the most comprehensive documentation:

<<https://ccbr.github.io/MOSuite/>>.

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URL <https://github.com/CCBR/MOObject>, <https://ccbr.github.io/MOObject/>

BugReports <https://github.com/CCBR/MOObject/issues>

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create_multiOmicDataSet_from_dataframes
<i>Construct a multiOmicDataSet object from data frames</i>

Description

Construct a multiOmicDataSet object from data frames

Usage

```
create_multiOmicDataSet_from_dataframes(  
  sample_metadata,  
  counts_dat,  
  sample_id_colname = NULL,  
  feature_id_colname = NULL,  
  count_type = "raw"  
)
```

Arguments

- sample_metadata
sample metadata as a data frame or tibble. The first column is assumed to contain the sample IDs which must correspond to column names in the raw counts.
- counts_dat
data frame of feature counts (e.g. expected feature counts from RSEM).
- sample_id_colname
name of the column in sample_metadata that contains the sample IDs. (Default: NULL - first column in the sample metadata will be used.)
- feature_id_colname
name of the column in counts_dat that contains feature/gene IDs. (Default: NULL - first column in the count data will be used.)
- count_type
type to assign the values of counts_dat to in the counts slot

Value

A [multiOmicDataSet](#) object.

See Also

Other moo: `create_multiOmicDataSet_from_files()`, `extract_counts()`, `multiOmicDataSet()`, `read_multiOmicDataSet()`, `read_multiOmicDataSet_properties()`, `write_multiOmicDataSet()`, `write_multiOmicDataSet_properties()`

Examples

```
sample_meta_dat <- data.frame(sample_id = c("s1", "s2"), group = c("A", "B"))
feature_counts_dat <- data.frame(
  feature_id = c("gene1", "gene2"),
  s1 = c(10, 20),
  s2 = c(15, 25)
)
moo <- create_multiOmicDataSet_from_dataframes(
  sample_metadata = sample_meta_dat,
  counts_dat = feature_counts_dat
)
head(moo@sample_meta)
head(moo@counts[['raw']])
```

`create_multiOmicDataSet_from_files`

Construct a multiOmicDataSet object from text files (e.g. TSV, CSV).

Description

Construct a multiOmicDataSet object from text files (e.g. TSV, CSV).

Usage

```
create_multiOmicDataSet_from_files(
  sample_meta_filepath,
  feature_counts_filepath,
  count_type = "raw",
  sample_id_colname = NULL,
  feature_id_colname = NULL,
  delim = NULL,
  ...
)
```

Arguments

`sample_meta_filepath`

path to text file with sample IDs and metadata for differential analysis.

`feature_counts_filepath`

path to text file of expected feature counts (e.g. gene counts from RSEM).

count_type	type to assign the values of counts_dat to in the counts slot
sample_id_colname	name of the column in sample_metadata that contains the sample IDs. (Default: NULL - first column in the sample metadata will be used.)
feature_id_colname	name of the column in counts_dat that contains feature/gene IDs. (Default: NULL - first column in the count data will be used.)
delim	Delimiter used in the input files. Any delimiter accepted by readr::read_delim() can be used. If the files are in CSV format, set delim = ','; for TSV format, set delim = '\t'.
...	additional arguments forwarded to readr::read_delim().

Value

A [multiOmicDataSet](#) object.

See Also

Other moo: [create_multiOmicDataSet_from_dataframes\(\)](#), [extract_counts\(\)](#), [multiOmicDataSet\(\)](#), [read_multiOmicDataSet\(\)](#), [read_multiOmicDataSet_properties\(\)](#), [write_multiOmicDataSet\(\)](#), [write_multiOmicDataSet_properties\(\)](#)

Examples

```
sample_meta_dat <- data.frame(sample_id = c("s1", "s2"), group = c("A", "B"))
feature_counts_dat <- data.frame(
  feature_id = c("gene1", "gene2"),
  s1 = c(10, 20),
  s2 = c(15, 25)
)
sample_meta_filepath <- tempfile(fileext = ".csv")
feature_counts_filepath <- tempfile(fileext = ".csv")
readr::write_csv(sample_meta_dat, sample_meta_filepath)
readr::write_csv(feature_counts_dat, feature_counts_filepath)

moo <- create_multiOmicDataSet_from_files(
  sample_meta_filepath = sample_meta_filepath,
  feature_counts_filepath = feature_counts_filepath,
  delim = ",",
)
head(moo@sample_meta)
head(moo@counts[['raw']])
```

extract_counts	<i>Extract count data</i>
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Description

Extract count data

Usage

```
extract_counts(moo, count_type, sub_count_type = NULL)

## S7 method for class <MOOobject::multiOmicDataSet>
extract_counts(moo, count_type, sub_count_type = NULL)
```

Arguments

- moo multiOmicDataSet containing count_type & sub_count_type in the counts slot
- count_type the type of counts to use – must be a name in the counts slot (moo@counts[[count_type]])
- sub_count_type if count_type is a list, specify the sub count type within the list (moo@counts[[count_type]][[sub_count_type]] (Default: NULL)

Value

A data frame of counts.

See Also

Other moo: [create_multiOmicDataSet_from_dataframes\(\)](#), [create_multiOmicDataSet_from_files\(\)](#), [multiOmicDataSet\(\)](#), [read_multiOmicDataSet\(\)](#), [read_multiOmicDataSet_properties\(\)](#), [write_multiOmicDataSet\(\)](#), [write_multiOmicDataSet_properties\(\)](#)

Examples

```
sample_metadata <- data.frame(sample_id = c("s1", "s2"), group = c("A", "B"))
counts_dat <- data.frame(
  feature_id = c("gene1", "gene2"),
  s1 = c(10, 20),
  s2 = c(15, 25)
)
moo <- create_multiOmicDataSet_from_dataframes(sample_metadata, counts_dat)
extract_counts(moo, "raw")
```

multiOmicDataSet	<i>multiOmicDataSet</i> class
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Description

multiOmicDataSet class

Usage

```
multiOmicDataSet(sample_metadata, anno_dat, counts_lst, analyses_lst = list())
```

Arguments

sample_metadata	sample metadata as a data frame or tibble. The first column is assumed to contain the sample IDs which must correspond to column names in the raw counts.
anno_dat	data frame of feature annotations, such as gene symbols or any other information about the features in counts_lst.
counts_lst	named list of data frames containing counts, e.g. expected feature counts from RSEM. Each data frame is expected to contain a feature_id column as the first column, and all remaining columns are sample IDs in the sample_meta.
analyses_lst	named list of analysis results, e.g. DESeq results object

Value

A [multiOmicDataSet](#) S7 object.

Additional properties

@sample_meta sample metadata as a data frame or tibble. The first column is assumed to contain the sample IDs which must correspond to column names in the raw counts.

@counts named list of counts data frames (e.g. raw, clean, cpm, filt, norm, batch). Each data frame is expected to contain a feature ID column as the first column, and all remaining columns are sample IDs.

@annotation data frame of feature annotations, such as gene symbols or any other information about the features in the counts list.

@analyses named list of analysis results (e.g. DESeq2 results, colors).

See Also

Other moo: [create_multiOmicDataSet_from_dataframes\(\)](#), [create_multiOmicDataSet_from_files\(\)](#), [extract_counts\(\)](#), [read_multiOmicDataSet\(\)](#), [read_multiOmicDataSet_properties\(\)](#), [write_multiOmicDataSet\(\)](#), [write_multiOmicDataSet_properties\(\)](#)

Examples

```

# sample metadata (sample names, labels, groups, batches, etc.)
sample_metadata <- data.frame(sample_id = c("s1", "s2"), group = c("A", "B"))
# counts data such as from bulk RNA-seq
counts_dat <- data.frame(
  feature_id = c("gene1", "gene2"),
  s1 = c(10, 20),
  s2 = c(15, 25)
)
# annotations for the counts data such as alternative gene names, gene IDs, etc.
anno_dat <- data.frame(feature_id = c("gene1", "gene2"), ensembl_id = c('ENSG000001', 'ENSG000002'))

# construct a multiOmicDataSet object
moo <- multiOmicDataSet(
  sample_metadata = sample_metadata,
  counts_lst = list(raw = counts_dat),
  anno_dat = anno_dat
)
moo
S7::S7_class(moo)

# validate the object
S7::validate(moo)

# Retrieve properties from the object
head(moo@sample_meta)
# Set properties in the object
moo@sample_meta$batch <- c("C", "D")

```

read_multiOmicDataSet *Read a multiOmicDataSet from RDS*

Description

Read a multiOmicDataSet from RDS

Usage

```
read_multiOmicDataSet(filepath)
```

Arguments

filepath Path to an RDS file produced by [write_multiOmicDataSet\(\)](#)

Value

A [multiOmicDataSet](#) object.

See Also

Other moo: [create_multiOmicDataSet_from_dataframes\(\)](#), [create_multiOmicDataSet_from_files\(\)](#), [extract_counts\(\)](#), [multiOmicDataSet\(\)](#), [read_multiOmicDataSet_properties\(\)](#), [write_multiOmicDataSet\(\)](#), [write_multiOmicDataSet_properties\(\)](#)

Examples

```
sample_metadata <- data.frame(sample_id = c("s1", "s2"), group = c("A", "B"))
counts_dat <- data.frame(
  feature_id = c("gene1", "gene2"),
  s1 = c(10, 20),
  s2 = c(15, 25)
)
moo <- create_multiOmicDataSet_from_dataframes(sample_metadata, counts_dat)
filepath <- tempfile(fileext = ".rds")
write_multiOmicDataSet(moo, filepath)
moo2 <- read_multiOmicDataSet(filepath)
```

`read_multiOmicDataSet_properties`

Read multiOmicDataSet properties from individual files.

Description

Reads a directory created by [write_multiOmicDataSet_properties\(\)](#) and reconstructs the [multiOmicDataSet](#) object. The sample_meta and annotation properties are read from CSV files, the counts property is read from the counts/ subdirectory, and the analyses property is read from the analyses/ subdirectory.

Usage

```
read_multiOmicDataSet_properties(input_dir)
```

Arguments

`input_dir` Directory previously created by [write_multiOmicDataSet_properties\(\)](#).

Value

A [multiOmicDataSet](#) object.

See Also

Other moo: [create_multiOmicDataSet_from_dataframes\(\)](#), [create_multiOmicDataSet_from_files\(\)](#), [extract_counts\(\)](#), [multiOmicDataSet\(\)](#), [read_multiOmicDataSet\(\)](#), [write_multiOmicDataSet\(\)](#), [write_multiOmicDataSet_properties\(\)](#)

Examples

```
sample_metadata <- data.frame(sample_id = c("s1", "s2"), group = c("A", "B"))
counts_dat <- data.frame(
  feature_id = c("gene1", "gene2"),
  s1 = c(10, 20),
  s2 = c(15, 25)
)
moo <- create_multiOmicDataSet_from_dataframes(sample_metadata, counts_dat)
output_dir <- tempfile()
write_multiOmicDataSet_properties(moo, output_dir)
moo2 <- read_multiOmicDataSet_properties(output_dir)
```

write_multiOmicDataSet

Write a multiOmicDataSet to RDS

Description

Write a multiOmicDataSet to RDS

Usage

```
write_multiOmicDataSet(moo, filepath = "moo.rds")
```

Arguments

moo	multiOmicDataSet object to serialize
filepath	Path to the RDS file to write (default: "moo.rds")

Value

Invisibly returns filepath.

See Also

Other moo: [create_multiOmicDataSet_from_dataframes\(\)](#), [create_multiOmicDataSet_from_files\(\)](#), [extract_counts\(\)](#), [multiOmicDataSet\(\)](#), [read_multiOmicDataSet\(\)](#), [read_multiOmicDataSet_properties\(\)](#), [write_multiOmicDataSet_properties\(\)](#)

Examples

```
sample_metadata <- data.frame(sample_id = c("s1", "s2"), group = c("A", "B"))
counts_dat <- data.frame(
  feature_id = c("gene1", "gene2"),
  s1 = c(10, 20),
  s2 = c(15, 25)
)
moo <- create_multiOmicDataSet_from_dataframes(sample_metadata, counts_dat)
filepath <- tempfile(fileext = ".rds")
write_multiOmicDataSet(moo, filepath)
```

```
write_multiOmicDataSet_properties
```

Write multiOmicDataSet properties to individual files.

Description

The sample_meta and annotation properties are written to CSV files, the counts property is written to a subdirectory of CSV files, and the analyses property is written to a subdirectory of CSV or RDS files depending on the type of each analysis result.

Usage

```
write_multiOmicDataSet_properties(moo, output_dir = "moo")

## S7 method for class <MOOobject::multiOmicDataSet>
write_multiOmicDataSet_properties(moo, output_dir = "moo")
```

Arguments

moo [multiOmicDataSet](#) object to write properties from
 output_dir Directory where the properties will be saved (default: "moo")

Value

Invisibly returns output_dir.

See Also

Other moo: [create_multiOmicDataSet_from_dataframes\(\)](#), [create_multiOmicDataSet_from_files\(\)](#), [extract_counts\(\)](#), [multiOmicDataSet\(\)](#), [read_multiOmicDataSet\(\)](#), [read_multiOmicDataSet_properties\(\)](#), [write_multiOmicDataSet\(\)](#)

Examples

```
sample_metadata <- data.frame(sample_id = c("s1", "s2"), group = c("A", "B"))
counts_dat <- data.frame(
  feature_id = c("gene1", "gene2"),
  s1 = c(10, 20),
  s2 = c(15, 25)
)
moo <- create_multiOmicDataSet_from_dataframes(sample_metadata, counts_dat)
output_dir <- tempfile()
write_multiOmicDataSet_properties(moo, output_dir)
```

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