

# Package: ondisc (via r-universe)

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**Title** Fast, Universal, and Intuitive Computing on Large-Scale Single-Cell Data

**Version** 1.0.0

**Description** Single-cell datasets are growing in size, posing challenges as well as opportunities for biology researchers. 'ondisc' (short for ``on-disk single cell'') enables users to easily and efficiently analyze large-scale single-cell data. 'ondisc' makes computing on large-scale single-cell data FUN: Fast, Universal, and iNtuitive.

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create\_ondisc\_matrix\_from\_mtx

*Create an ondisc\_matrix from a .mtx file.*

---

## Description

Initializes an ondisc\_matrix from a .mtx file, a features.tsv file, and a barcodes.tsv file. Returns an ondisc\_matrix along with cell-specific and feature-specific covariate matrices.

## Usage

```
create_ondisc_matrix_from_mtx(
  mtx_fp,
  barcodes_fp,
  features_fp,
  n_lines_per_chunk = 3e+08,
  on_disk_dir = NULL,
  file_name = NULL,
  return_metadata_ondisc_matrix = FALSE,
  progress = TRUE
)
```

**Arguments**

|                               |  |
|-------------------------------|--|
| mtx_fp                        | file path to a .mtx file storing the expression data. The .mtx file can represent either an integer matrix or a logical (i.e., binary) matrix. If the .mtx file contains only two columns (after the initial three-column row of metadata), then the .mtx file is assumed to represent a logical matrix. |
| barcodes_fp                   | file path to the .tsv file containing the cell barcodes.   |
| features_fp                   | file path to the features.tsv file. The first column (required) contains the feature IDs (e.g., ENSG00000186092), and the second column (optional) contains the human-readable feature names (e.g., OR4F5). Subsequent columns are discarded.  |
| n_lines_per_chunk             | (optional) number of lines in .mtx file to process per chunk. Defaults to 3e+08.   |
| on_disk_dir                   | (optional) directory in which to store the on-disk portion of the ondisc_matrix. Defaults to the directory in which the .mtx file is located.  |
| file_name                     | (optional) name of the file in which to store the .h5 data on-disk. Defaults to ondisc_matrix_x.h5, where x is a unique integer starting at 1.   |
| return_metadata_ondisc_matrix | (optional) return the output as a metadata_ondisc_matrix (instead of a list)? Defaults to FALSE.   |
| progress                      | (optional; default FALSE) print progress messages?   |

**Details**

The function can compute the following cell-specific and feature-specific covariates:

- cell-specific: (i) total number of features expressed in cell (`n_nonzero_cell`), (ii) total UMI count (`n_umis_cell`), and (iii) percentage of UMIs that map to mitochondrial genes (`p_mito_cell`).
- feature-specific: (i) total number of cells in which feature is expressed (`n_nonzero_feature`), (ii) mean expression of feature across cells (`mean_expression_feature`), (iii) coefficient of variation of feature expression across cells (`coef_of_variation_feature`).

The function decides which covariates to compute given the input; in general, the function computes the maximum set of covariates possible.

**Value**

A list containing (i) an `ondisc_matrix`, (ii) a cell-specific covariate matrix, and (iii) a feature-specific covariate matrix; if the parameter `return_metadata_ondisc_matrix` set to `TRUE`, converts the list to a `metadata_ondisc_matrix` before returning.

**Examples**

```
## Not run:
# First example: initialize a metadata_ondisc_matrix
# using simulated expression data; store output in tempdir()
file_locs <- system.file("extdata", package = "ondisc",
  c("gene_expression.mtx", "genes.tsv", "cell_barcodes.tsv"))
names(file_locs) <- c("expressions", "features", "barcodes")
```

```

expression_data <- create_ondisc_matrix_from_mtx(mtx_fp = file_locs[["expressions"]],
barcodes_fp = file_locs[["barcodes"]],
features_fp = file_locs[["features"]],
on_disk_dir = tempdir(),
file_name = "expressions",
return_metadata_ondisc_matrix = TRUE)
saveRDS(object = expression_data, file = paste0(tempdir(), "/expressions.rds"))

# Second example: initialize a metadata_ondisc_matrix using simulated
# gRNA perturbation data; store in tempdir()
file_locs <- system.file("extdata", package = "ondisc",
c("perturbation.mtx", "guides.tsv", "cell_barcode.tsv"))
names(file_locs) <- c("perturbations", "features", "barcodes")
perturbation_data <- create_ondisc_matrix_from_mtx(mtx_fp = file_locs[["perturbations"]],
barcodes_fp = file_locs[["barcodes"]],
features_fp = file_locs[["features"]],
on_disk_dir = tempdir(),
file_name = "perturbations",
return_metadata_ondisc_matrix = TRUE)
saveRDS(object = perturbation_data, file = paste0(tempdir(), "/perturbations.rds"))

## End(Not run)

```

---

dim

*Get dimension*


---

## Description

Return the dimension of an `ondisc_matrix`, `metadata_ondisc_matrix`, or `multimodal_ondisc_matrix`.

## Usage

```

## S4 method for signature 'ondisc_matrix'
dim(x)

## S4 method for signature 'metadata_ondisc_matrix'
dim(x)

## S4 method for signature 'multimodal_ondisc_matrix'
dim(x)

ncol(x)

nrow(x)

## S4 method for signature 'multimodal_ondisc_matrix'
ncol(x)

## S4 method for signature 'multimodal_ondisc_matrix'
nrow(x)

```

**Arguments**

`x` an `ondisc_matrix`, `metadata_ondisc_matrix`, or `multimodal_ondisc_matrix`.

**Value**

If `x` is an `ondisc_matrix` or `metadata_ondisc_matrix`, length-two integer vector containing the dimension of `x`; if `x` is a `multimodal_ondisc_matrix`, a list of integer vectors containing the dimensions of the constituent modalities of `x`.

**Examples**

```
# NOTE: You must create the RDS files "expressions.rds" and
# "perturbations.rds" to run this example. Navigate to the help file of
# "create_ondisc_matrix_from_mtx" (via ?create_ondisc_matrix_from_mtx),
# and execute both code blocks.

# dimension of an ondisc_matrix
h5_fp <- paste0(tempdir(), "/expressions.h5")
if (file.exists(h5_fp)) {
  odm <- ondisc_matrix(h5_file = h5_fp)
  dim(odm)
}

# dimension of a metadata_ondisc_matrix
expressions_fp <- paste0(tempdir(), "/expressions.rds")
if (file.exists(expressions_fp)) {
  expressions <- readRDS(expressions_fp)
  dim(expressions)
}

# dimension of a multimodal_ondisc_matrix
expression_fp <- paste0(tempdir(), "/expressions.rds")
perturbations_fp <- paste0(tempdir(), "/perturbations.rds")
if (file.exists(expression_fp) && file.exists(perturbations_fp)) {
  crispr_experiment <- multimodal_ondisc_matrix(list(expressions = readRDS(expression_fp),
  perturbations = readRDS(perturbations_fp)))
  dim(crispr_experiment)
}
```

---

 extract-odm

---

*Pull a submatrix into memory using the `[[` operator.*


---

**Description**

Apply the `[[` operator to an `ondisc_matrix` to pull a submatrix into memory. You can pass logical, character, or numeric vectors to `[[`; character vectors are assumed to refer to feature IDs (for rows) and cell barcodes (for columns).

**Usage**

```
## S4 method for signature 'ondisc_matrix,missing,missing'
x[[i, j]]

## S4 method for signature 'ondisc_matrix,ANY,missing'
x[[i, j]]

## S4 method for signature 'ondisc_matrix,missing,ANY'
x[[i, j]]

## S4 method for signature 'ondisc_matrix,ANY,ANY'
x[[i, j]]

## S4 method for signature 'metadata_ondisc_matrix,ANY,ANY'
x[[i, j]]

## S4 method for signature 'multimodal_ondisc_matrix,ANY,ANY'
x[[i, j]]
```

**Arguments**

x                    an `ondisc_matrix` object.

i                    a vector (numeric, logical, or character) indicating features to pull into memory.

j                    a vector (numeric, logical, or character) indicating cells to pull into memory.

**Details**

You can apply `[[` to `ondisc_matrix` objects only. You cannot apply `[[` to `metadata_ondisc_matrix` or `multimodal_ondisc_matrix` objects, because in the latter case the data to be accessed is ambiguous.

You can remember the difference between `[` and `[[` by thinking about R lists: `[` is used to subset a list, and `[[` is used to access elements stored *inside* a list. Similarly, `[` is used to subset an `ondisc_matrix`, and `[[` is used to access a submatrix usable within R.

**Value**

a matrix (as implemented by the Matrix package).

**Examples**

```
# NOTE: You must create the HDF5 file "expressions.h5" to run this example.
# Navigate to the help file of "create_ondisc_matrix_from_mtx"
# (via ?create_ondisc_matrix_from_mtx), and execute the code in the first code block.

h5_fp <- paste0(tempdir(), "/expressions.h5")
if (file.exists(h5_fp)) {
  odm <- ondisc_matrix(h5_file = h5_fp)
  # extract cells 100-110:
  x <- odm[[,100:110]]
```

```
# extract genes ENSG00000188305, ENSG00000257284, ENSG00000251655:
x <- odm[[c("ENSG00000188305", "ENSG00000257284", "ENSG00000251655"),]]
# extract cells CTTAGGACACTGGCGT-1 and AAAGGATTCACATCAG-1:
x <- odm[[,c("CTTAGGACACTGGCGT-1", "AAAGGATTCACATCAG-1")]]
}
```

---

get-names

*Get cell barcodes, feature names, and feature IDs*

---

## Description

Obtain cell barcodes, feature names, and feature IDs of an `ondisc_matrix`, `metadata_ondisc_matrix`, or `multimodal_ondisc_matrix`.

## Usage

```
get_feature_ids(x)
```

```
get_feature_names(x)
```

```
get_cell_barcodes(x)
```

```
## S4 method for signature 'ondisc_matrix'
```

```
get_feature_ids(x)
```

```
## S4 method for signature 'ondisc_matrix'
```

```
get_feature_names(x)
```

```
## S4 method for signature 'ondisc_matrix'
```

```
get_cell_barcodes(x)
```

```
## S4 method for signature 'metadata_ondisc_matrix'
```

```
get_feature_ids(x)
```

```
## S4 method for signature 'metadata_ondisc_matrix'
```

```
get_feature_names(x)
```

```
## S4 method for signature 'metadata_ondisc_matrix'
```

```
get_cell_barcodes(x)
```

```
## S4 method for signature 'multimodal_ondisc_matrix'
```

```
get_feature_ids(x)
```

```
## S4 method for signature 'multimodal_ondisc_matrix'
```

```
get_feature_names(x)
```

```
## S4 method for signature 'multimodal_ondisc_matrix'
```

```
get_cell_barcodes(x)
```

## Arguments

x an object of class `ondisc_matrix`, `covaraite_ondisc_matrix`, or `multimodal_ondisc_matrix`.

## Details

The following functions can be used to obtain feature and cell identifiers:

- `get_cell_barcodes`: return the cell barcodes.
- `get_feature_names`: return the feature names.
- `get_feature_ids`: return the IDs of the features.

In general, these functions return a character vector containing the requested identifiers. When `get_feature_names` or `get_feature_ids` is called on a `multimodal_ondisc_matrix`, the function instead returns a list containing the feature names and feature IDs, respectively, of the modalities contained within the `multimodal_ondisc_matrix`.

## Value

A character vector or list of character vectors containing the requested identifiers.

## Examples

```
# NOTE: You must create the RDS files "expressions.rds" and
# "perturbations.rds" to run this example. Navigate to the help file of
# "create_ondisc_matrix_from_mtx" (via ?create_ondisc_matrix_from_mtx),
# and execute both code blocks.

# ondisc_matrix
h5_fp <- paste0(tempdir(), "/expressions.h5")
if (file.exists(h5_fp)) {
  odm <- ondisc_matrix(h5_file = h5_fp)
  barcodes <- get_cell_barcodes(odm)
  feature_names <- get_feature_names(odm)
  feature_ids <- get_feature_ids(odm)
}

# metadata_ondic_matrix
expressions_fp <- paste0(tempdir(), "/expressions.rds")
if (file.exists(expressions_fp)) {
  expressions <- readRDS(expressions_fp)
  barcodes <- get_cell_barcodes(odm)
  feature_names <- get_feature_names(odm)
  feature_ids <- get_feature_ids(odm)
}

# multimodal_ondisc_matrix
expression_fp <- paste0(tempdir(), "/expressions.rds")
perturbations_fp <- paste0(tempdir(), "/perturbations.rds")
if (file.exists(expression_fp) && file.exists(perturbations_fp)) {
  crispr_experiment <- multimodal_ondisc_matrix(list(expressions = readRDS(expression_fp),
  perturbations = readRDS(perturbations_fp)))
}
```

```

    barcodes <- get_cell_barcodes(crispr_experiment)
    feature_ids <- get_feature_ids(crispr_experiment)
  }

```

---

head,ondisc\_matrix-method

*head*

---

### Description

Print the first few rows and columns of an `ondisc_matrix`.

### Usage

```

## S4 method for signature 'ondisc_matrix'
head(x)

```

### Arguments

`x` an `ondisc_matrix`.

### Value

NULL; called for printing

### Examples

```

# NOTE: You must create the HDF5 file "expressions.h5" to run this example.
# Navigate to the help file of "create_ondisc_matrix_from_mtx"
# (via ?create_ondisc_matrix_from_mtx), and execute the code in the first code block.

```

```

h5_fp <- paste0(tempdir(), "/expressions.h5")
if (file.exists(h5_fp)) {
  odm <- ondisc_matrix(h5_file = h5_fp)
  head(odm)
}

```

---

metadata\_ondisc\_matrix

metadata\_ondisc\_matrix *class*

---

### Description

A `metadata_ondisc_matrix` stores an `ondisc_matrix`, along with cell-specific and feature-specific covariate matrices.

Construct a `metadata_ondisc_matrix` by passing an `ondisc_matrix`, along with its associated `cell_covariates` and `feature_covariates`.

**Usage**

```
metadata_ondisc_matrix(ondisc_matrix, cell_covariates, feature_covariates)
```

```
metadata_ondisc_matrix(ondisc_matrix, cell_covariates, feature_covariates)
```

**Arguments**

`ondisc_matrix` an `ondisc_matrix`.

`cell_covariates`

a data frame storing the cell-specific covariates.

`feature_covariates`

a data frame storing the feature-specific covariates.

**Value**

a `metadata_ondisc_matrix`.

**Slots**

`ondisc_matrix` an `ondisc_matrix`.

`cell_covariates` a data frame of cell covariates.

`feature_covariates` a data frame of feature covariates.

**Examples**

```
# NOTE: You must create the HDF5 file "expressions.h5" and the RDS file
# "expressions.rds" to run this example. Navigate to the help file of
# "create_ondisc_matrix_from_mtx" (via ?create_ondisc_matrix_from_mtx),
# and execute the code in the first code block.
covariates_fp <- paste0(tempdir(), "/expressions.rds")
h5_fp <- paste0(tempdir(), "/expressions.h5")
if (file.exists(covariates_fp) && file.exists(h5_fp)) {
  covariate_odm <- readRDS(covariates_fp)
  cell_covariate_matrix <- covariate_odm@cell_covariates
  feature_covariate_matrix <- covariate_odm@feature_covariates
  covariate_odm_copy <- metadata_ondisc_matrix(
    ondisc_matrix = ondisc_matrix(h5_file = h5_fp),
    cell_covariates = cell_covariate_matrix,
    feature_covariates = feature_covariate_matrix)
}
```

---

```
multimodal_ondisc_matrix
      multimodal_ondisc_matrix class
```

---

### Description

A `multimodal_ondisc_matrix` represents multimodal data.

Construct a `multimodal_ondisc_matrix` from a list of `metadata_ondisc_matrix` objects.

### Usage

```
multimodal_ondisc_matrix(metadata_ondisc_matrix_list)
```

```
multimodal_ondisc_matrix(metadata_ondisc_matrix_list)
```

### Arguments

```
metadata_ondisc_matrix_list
      a named list containing metadata_ondisc_matrices; the names are taken to
      be the names of the modalities.
```

### Value

a `multimodal_ondisc_matrix`

### Slots

`modalities` a list containing `metadata_ondisc_matrix` objects representing different modalities.

`global_cell_covariates` a data frame containing the cell-specific covariates pooled across all modalities.

### Examples

```
# NOTE: You must create the RDS files "expressions.rds" and
# "perturbations.rds" to run this example. Navigate to the help file of
# "create_ondisc_matrix_from_mtx" (via ?create_ondisc_matrix_from_mtx),
# and execute both code blocks.
expression_fp <- paste0(tempdir(), "/expressions.rds")
perturbations_fp <- paste0(tempdir(), "/perturbations.rds")
if (file.exists(expression_fp) && file.exists(perturbations_fp)) {
  expressions <- readRDS(expression_fp)
  perturbations <- readRDS(perturbations_fp)
  crispr_experiment <- multimodal_ondisc_matrix(list(expressions = expressions,
  perturbations = perturbations))
}
```

---

|        |  |
|--------|--|
| ondisc | <i>ondisc: A package for out-of-memory computing on single-cell data</i> |
|--------|--|

---

### Description

Single-cell datasets are large and are growing in size as sequencing costs drop. The `ondisc` package is designed to facilitate large-scale computing on single-cell expression data by providing access to expression matrices out-of-memory. `ondisc` is functional (i.e., all objects are persistent) and efficient (i.e., all algorithms are theoretically optimal in time).

---

|                            |                                  |
|----------------------------|----------------------------------|
| <code>ondisc_matrix</code> | <code>ondisc_matrix</code> class |
|----------------------------|----------------------------------|

---

### Description

An `ondisc_matrix` represents a feature-by-cell expression matrix stored on-disk.  
Construct an `ondisc_matrix` from an initialized `.h5` file.

### Usage

```
ondisc_matrix(h5_file)
```

```
ondisc_matrix(h5_file)
```

### Arguments

`h5_file` a `.h5` file storing the on-disk portion of an initialized `ondisc_matrix` object.

### Details

It is best to avoid interacting with the slots of an `ondisc_matrix` directly. Instead, use the functions and operators provided by the package.

### Value

an initialized `ondisc_matrix` object.

### Slots

`h5_file` path to an initialized `.h5` file stored on-disk.

`logical_mat` logical value indicating whether the matrix is logical.

`cell_subset` integer vector recording the cells currently in use.

`feature_subset` integer vector recording the features currently in use.

`underlying_dimension` the dimension of the (unsubset) expression matrix.

**Examples**

```
# NOTE: You must create the HDF5 file "expressions.h5" to run this example.
# Navigate to the help file of "create_ondisc_matrix_from_mtx"
# (via ?create_ondisc_matrix_from_mtx), and execute the code in the first code block.
h5_fp <- paste0(tempdir(), "/expressions.h5")
if (file.exists(h5_fp)) {
  odm <- ondisc_matrix(h5_file = h5_fp)
}
```

---

show

---

*Print basic information to the console*


---

**Description**

Print basic information to the console

**Usage**

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

## S4 method for signature 'metadata_ondisc_matrix'
show(object)

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

**Arguments**

object            an object of class `ondisc_matrix`, `covaraite_ondisc_matrix`, or `multimodal_ondisc_matrix`

**Value**

NULL; called for printing

**Examples**

```
# NOTE: You must create the HDF5 file "expressions.h5" to run this example.
# Navigate to the help file of "create_ondisc_matrix_from_mtx"
# (via ?create_ondisc_matrix_from_mtx), and execute the code in the first code block.

h5_fp <- paste0(tempdir(), "/expressions.h5")
if (file.exists(h5_fp)) {
  odm <- ondisc_matrix(h5_file = h5_fp)
  show(odm)
}
```

subset-odm

*Subset using the [ operator.***Description**

Apply the [ operator to an `ondisc_matrix`, `metadata_ondisc_matrix`, or `multimodal_ondisc_matrix` to subset the object. You can pass logical, character, or numeric vectors to [; character vectors are assumed to refer to feature IDs (for rows) and cell barcodes (for columns).

**Usage**

```
## S4 method for signature 'ondisc_matrix,missing,missing,missing'
x[i, j, drop]

## S4 method for signature 'ondisc_matrix,ANY,missing,missing'
x[i, j]

## S4 method for signature 'ondisc_matrix,missing,ANY,missing'
x[i, j]

## S4 method for signature 'ondisc_matrix,ANY,ANY,missing'
x[i, j]

## S4 method for signature 'metadata_ondisc_matrix,ANY,ANY,missing'
x[i, j, drop]

## S4 method for signature 'metadata_ondisc_matrix,ANY,missing,missing'
x[i, j, drop]

## S4 method for signature 'metadata_ondisc_matrix,missing,ANY,missing'
x[i, j, drop]

## S4 method for signature 'metadata_ondisc_matrix,missing,missing,missing'
x[i, j, drop]

## S4 method for signature 'multimodal_ondisc_matrix,missing,missing,missing'
x[i, j, drop]

## S4 method for signature 'multimodal_ondisc_matrix,missing,ANY,missing'
x[i, j, drop]

## S4 method for signature 'multimodal_ondisc_matrix,ANY,ANY,ANY'
x[i, j, drop]
```

**Arguments**

`x` an `ondisc_matrix`, `metadata_ondisc_matrix`, or `multimodal_ondisc_matrix` object.

|      |  |
|------|--|
| i    | a vector (numeric, logical, or character) indicating features to keep. |
| j    | a vector (numeric, logical, or character) indicating cells to keep.    |
| drop | not used   |

### Details

You can subset an `ondisc_matrix` and a `metadata_ondisc_matrix` by cell and/or feature. You can subset a `multimodal_ondisc_matrix` by cell only (because the features differ across modalities).

### Value

An appropriately subset object of the same class as `x`.

### Examples

```
# NOTE: You must create the RDS files "expressions.rds" and
# "perturbations.rds" to run this example. Navigate to the help file of
# "create_ondisc_matrix_from_mtx" (via ?create_ondisc_matrix_from_mtx),
# and execute both code blocks.

# subset an ondisc_matrix
h5_fp <- paste0(tempdir(), "/expressions.h5")
if (file.exists(h5_fp)) {
  odm <- ondisc_matrix(h5_file = h5_fp)
  # keep cells 100-110
  x <- odm[,100:110]
  # keep all cells except 50, 100, 150
  x <- odm[,-c(50, 100, 150)]
  # keep genes ENSG00000188305, ENSG00000257284, and ENSG00000251655:
  x <- odm[c("ENSG00000188305", "ENSG00000257284", "ENSG00000251655"),]
  # keep the cells CTTAGGACACTGGCGT-1 and AAAGGATTCACATCAG-1:
  x <- odm[,c("CTTAGGACACTGGCGT-1", "AAAGGATTCACATCAG-1")]
  # keep all genes except ENSG00000188305 and ENSG00000257284
  x <- odm[!(get_feature_ids(odm) %in% c("ENSG00000188305", "ENSG00000257284")),]
}

# subset a metadata_ondisc_matrix
expressions_fp <- paste0(tempdir(), "/expressions.rds")
if (file.exists(expressions_fp)) {
  expressions <- readRDS(expressions_fp)
  # keep cells 100-110
  x <- expressions[,100:110]
  # keep genes ENSG00000188305, ENSG00000257284, and ENSG00000251655
  x <- expressions[c("ENSG00000188305", "ENSG00000257284", "ENSG00000251655"),]
}

# subset a multimodal ondisc_matrix
expression_fp <- paste0(tempdir(), "/expressions.rds")
perturbations_fp <- paste0(tempdir(), "/perturbations.rds")
if (file.exists(expression_fp) && file.exists(perturbations_fp)) {
  expressions <- readRDS(expression_fp)
  perturbations <- readRDS(perturbations_fp)
}
```

```
crispr_experiment <- multimodal_ondisc_matrix(list(expressions = expressions,  
perturbations = perturbations))  
# Keep all cells except 10,100, and 105.  
x <- crispr_experiment[,-c(10,100,105)]  
# Keep the first 5 cells  
x <- crispr_experiment[,1:5]  
}
```



`ondisc`, [12](#)

`ondisc_matrix`, [12](#)

`show`, [13](#)

`show,metadata_ondisc_matrix-method`  
    `(show)`, [13](#)

`show,multimodal_ondisc_matrix-method`  
    `(show)`, [13](#)

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