

# Package ‘CellBench’

April 12, 2022

**Type** Package

**Title** Construct Benchmarks for Single Cell Analysis Methods

**Version** 1.10.0

**Description** This package contains infrastructure for benchmarking analysis methods and access to single cell mixture benchmarking data. It provides a framework for organising analysis methods and testing combinations of methods in a pipeline without explicitly laying out each combination. It also provides utilities for sampling and filtering SingleCellExperiment objects, constructing lists of functions with varying parameters, and multithreaded evaluation of analysis methods.

**biocViews** Software, Infrastructure

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|-------------------|--|
| CellBench-package | <i>A framework for benchmarking combinations of methods in multi-stage pipelines</i> |
|-------------------|--|

---

### Description

This package contains a framework for benchmarking combinations of methods in a multi-stage pipeline. It is mainly based around the `apply_methods` function, which takes lists of functions to be applied in stages of a pipeline.

### Author(s)

Shian Su <<https://www.github.com/shians>>

### See Also

The core function in this package is `apply_methods`, see `vignette("Introduction", package = "CellBench")` for basic usage. Run `cellbench_case_study()` to see a case study using CellBench. The data loading functions from `load_all_data` may also be of interest.

---

|                              |   |
|------------------------------|---|
| <code>any_task_errors</code> | <i>Check if any tasks produced errors</i> |
|------------------------------|---|

---

### Description

Check the results column of a benchmark tibble for any `task_error` objects.

### Usage

```
any_task_errors(x, verbose)

## S3 method for class 'benchmark_tbl'
any_task_errors(x, verbose = FALSE)
```

### Arguments

|                      |   |
|----------------------|---|
| <code>x</code>       | the tibble to check                             |
| <code>verbose</code> | TRUE if the rows with errors should be reported |

### Value

TRUE if any entry in the result column is a `task_error` object

### Methods (by class)

- `benchmark_tbl`:

---

`apply_methods`*Apply methods*

---

### Description

`apply_methods()` and its aliases `apply_metrics` and `begin_benchmark` take either lists of datasets or `benchmark_tbl` objects and applies a list of functions. The output is a `benchmark_tbl` where each method has been applied to each dataset or preceding result.

### Usage

```
apply_methods(x, fn_list, name = NULL, suppress.messages = TRUE)

## S3 method for class 'list'
apply_methods(x, fn_list, name = NULL, suppress.messages = TRUE)

## S3 method for class 'benchmark_tbl'
apply_methods(x, fn_list, name = NULL, suppress.messages = TRUE)

## S3 method for class 'tbl_df'
apply_methods(x, fn_list, name = NULL, suppress.messages = TRUE)

apply_metrics(x, fn_list, name = NULL, suppress.messages = TRUE)

begin_benchmark(x, fn_list, name = NULL, suppress.messages = TRUE)
```

### Arguments

|                                |  |
|--------------------------------|--|
| <code>x</code>                 | the list of data or benchmark tibble to apply methods to   |
| <code>fn_list</code>           | the list of methods to be applied                          |
| <code>name</code>              | (optional) the name of the column for methods applied      |
| <code>suppress.messages</code> | TRUE if messages from running methods should be suppressed |

### Value

`benchmark_tbl` object containing results from methods applied, the first column is the name of the dataset as factors, middle columns contain method names as factors and the final column is a list of results of applying the methods.

### See Also

[time\\_methods](#)

**Examples**

```
# list of data
datasets <- list(
  set1 = rnorm(500, mean = 2, sd = 1),
  set2 = rnorm(500, mean = 1, sd = 2)
)

# list of functions
add_noise <- list(
  none = identity,
  add_bias = function(x) { x + 1 }
)

res <- apply_methods(datasets, add_noise)
```

---

arrow\_sep

*Unicode arrow separators*

---

**Description**

Utility function for generating unicode arrow separators.

**Usage**

```
arrow_sep(towards = c("right", "left"), unicode = FALSE)
```

**Arguments**

|         |   |
|---------|---|
| towards | the direction the unicode arrow points towards  |
| unicode | whether unicode arrows should be used. Does not work inside plots within knitted PDF documents. |

**Value**

a string containing an unicode arrow surrounded by two spaces

**Examples**

```
arrow_sep("left") # left arrow
arrow_sep("right") # right arrow
```

---

as\_pipeline\_list      *convert benchmark\_tbl to list*

---

### Description

convert a benchmark\_tbl to a list where the name of the elements represent the pipeline steps separated by "..". This can be useful for using the apply family of functions.

### Usage

```
as_pipeline_list(x)
```

### Arguments

x                      the benchmark\_tbl object to convert

### Value

list containing the results with names set to data and pipeline steps separated by ..

### See Also

[pipeline\\_collapse](#)

### Examples

```
# list of data
datasets <- list(
  set1 = rnorm(500, mean = 2, sd = 1),
  set2 = rnorm(500, mean = 1, sd = 2)
)

# list of functions
add_noise <- list(
  none = identity,
  add_bias = function(x) { x + 1 }
)

res <- apply_methods(datasets, add_noise)
as_pipeline_list(res)
```

---

`cache_method`*Create a cached function for CellBench*

---

## Description

Take a function and return a cached version. The arguments and results of a cached method is saved to disk and if the cached function is called again with the same arguments then the results will be retrieved from the cache rather than be recomputed.

## Usage

```
cache_method(f, cache = getOption("CellBench.cache"))
```

## Arguments

|                    |  |
|--------------------|--|
| <code>f</code>     | the function to be cached                    |
| <code>cache</code> | the cache information (from memoise package) |

## Details

**(CAUTION)** Because cached functions called with the same argument will always return the same output, pseudo-random methods will not return varying results over repeated runs as one might expect.

This function is a thin wrapper around [memoise](#)

## Value

function whose results are cached and is called identically to `f`

## See Also

[set\\_cellbench\\_cache\\_path](#)

## Examples

```
# sets cache path to a temporary directory
set_cellbench_cache_path(file.path(tempdir(), ".CellBenchCache"))
f <- function(x) { x + 1 }
cached_f <- cache_method(f)
```

---

cellbench\_case\_study    *Open vignette containing a case study using CellBench*

---

**Description**

Open vignette containing a case study using CellBench

**Usage**

```
cellbench_case_study()
```

**Examples**

```
## Not run:  
cellbench_case_study()  
  
## End(Not run)
```

---

cellbench\_file            *Get path to CellBench packaged data*

---

**Description**

Search CellBench package for packaged data, leaving argument empty will list the available data.

**Usage**

```
cellbench_file(filename = NULL)
```

**Arguments**

filename            the name of the file to look for

**Value**

string containing the path to the packaged data

**Examples**

```
cellbench_file() # shows available files  
cellbench_file("10x_sce_sample.rds") # returns path to 10x sample data
```



---

clear\_cached\_datasets *Clear cached datasets*

---

**Description**

Delete the datasets cached by the load\_\*\_data set of functions

**Usage**

```
clear_cached_datasets()
```

**Value**

None

**Examples**

```
## Not run:  
clear_cached_datasets()  
  
## End(Not run)
```

---

clear\_cellbench\_cache *Clear CellBench Cache*

---

**Description**

Clears the method cache for CellBench

**Usage**

```
clear_cellbench_cache()
```

**Value**

None

**Examples**

```
## Not run:  
clear_cellbench_cache()  
  
## End(Not run)
```

---

|           |                                    |
|-----------|------------------------------------|
| data_list | <i>Constructor for a data list</i> |
|-----------|------------------------------------|

---

**Description**

Constructor for a list of data, a thin wrapper around list() which checks that all the inputs are of the same type and have names

**Usage**

```
data_list(...)
```

**Arguments**

... objects, must all be named

**Value**

a list of named data

**Examples**

```
data(iris)
flist <- data_list(
  data1 = iris[1:20, ],
  data2 = iris[21:40, ]
)
```

---

|                   |                                    |
|-------------------|------------------------------------|
| filter_zero_genes | <i>Filter out zero count genes</i> |
|-------------------|------------------------------------|

---

**Description**

Remove all genes (rows) where the total count is 0

**Usage**

```
filter_zero_genes(x)
```

**Arguments**

x the SingleCellExperiment or matrix to filter

**Value**

object of same type as input with all zero count genes removed

**Examples**

```
x <- matrix(rep(0:5, times = 5), nrow = 6, ncol = 5)
filter_zero_genes(x)
```

fn\_arg\_seq

*Create a list of functions with arguments varying over a sequence***Description**

Generate a list of functions where specific arguments have been pre-applied from a sequences of arguments, i.e. a function  $f(x, n)$  may have the 'n' argument pre-applied with specific values to obtain functions  $f_1(x, n = 1)$  and  $f_2(x, n = 2)$  stored in a list.

**Usage**

```
fn_arg_seq(func, ..., .strict = FALSE)
```

**Arguments**

|         |   |
|---------|---|
| func    | function to generate list from  |
| ...     | vectors of values to use as arguments   |
| .strict | TRUE if argument names are checked, giving an error if specified argument does not appear in function signature. Note that functions with multiple methods generally have only $f(x, \dots)$ as their signature, so the check would fail even if the arguments are passed on. |

**Details**

If multiple argument vectors are provided then the combinations of arguments in the sequences will be generated.

**Value**

list of functions with the specified arguments pre-applied. Names of the list indicate the values that have been pre-applied.

**Examples**

```
f <- function(x) {
  cat("x:", x)
}

f_list <- fn_arg_seq(f, x = c(1, 2))
f_list
f_list[[1]]() # x: 1
f_list[[2]]() # x: 2

g <- function(x, y) {
```

```

      cat("x:", x, "y:", y)
    }

    g_list <- fn_arg_seq(g, x = c(1, 2), y = c(3, 4))
    g_list
    g_list[[1]]() # x: 1 y: 3
    g_list[[2]]() # x: 1 y: 4
    g_list[[3]]() # x: 2 y: 3
    g_list[[4]]() # x: 2 y: 4

```

---

|         |  |
|---------|--|
| fn_list | <i>Constructor for a function list</i> |
|---------|--|

---

### Description

Constructor for a list of functions, a thin wrapper around list() which checks that all the inputs are functions and have names

### Usage

```
fn_list(...)
```

### Arguments

... objects, must all be named

### Value

a list of named functions

### Examples

```

flist <- fn_list(
  mean = mean,
  median = median
)

```

---

|               |                              |
|---------------|------------------------------|
| is.task_error | <i>Check for task errors</i> |
|---------------|------------------------------|

---

### Description

This is a helper function for checking the result column of a benchmark\_tbl for task\_error objects. This is useful for filtering out rows where the result is a task error.

### Usage

```
is.task_error(x)
```

**Arguments**

x                    the object to be tested

**Value**

vector of logicals denoting if elements of the list are task\_error objects

---

*keep\_high\_count\_cells* *Filter down to the highest count cells*

---

**Description**

Filter a SingleCellExperiment or matrix down to the cells (columns) with the highest counts

**Usage**

```
keep_high_count_cells(x, n)
```

**Arguments**

x                    the SingleCellExperiment or matrix  
n                    the number of highest count cells to keep

**Value**

object of same type as input containing the highest count cells

**Examples**

```
data(sample_sce_data)  
keep_high_count_cells(sample_sce_data, 10)
```

---

*keep\_high\_count\_genes* *Filter down to the highest count genes*

---

**Description**

Filter a SingleCellExperiment or matrix down to the genes (rows) with the highest counts

**Usage**

```
keep_high_count_genes(x, n)
```

**Arguments**

x                    the SingleCellExperiment or matrix  
n                    the number of highest count genes to keep

**Value**

object of same type as input containing the highest count genes

**Examples**

```
data(sample_sce_data)
keep_high_count_genes(sample_sce_data, 300)
```

---

`keep_high_var_genes`    *Filter down to the most variable genes*

---

**Description**

Filter a SingleCellExperiment or matrix down to the most variable genes (rows), variability is determined by `var()` scaled by the total counts for the gene.

**Usage**

```
keep_high_var_genes(x, n)
```

**Arguments**

x                    the SingleCellExperiment or matrix  
n                    the number of most variable genes to keep

**Value**

object of same type as input containing the most variable genes

**Examples**

```
data(sample_sce_data)
keep_high_var_genes(sample_sce_data, 50)
```

---

|              |                            |
|--------------|----------------------------|
| load_sc_data | <i>Load CellBench Data</i> |
|--------------|----------------------------|

---

**Description**

Load in all CellBench data described at <[https://github.com/LuyiTian/CellBench\\_data/blob/master/README.md](https://github.com/LuyiTian/CellBench_data/blob/master/README.md)>.

**Usage**

```
load_sc_data()
```

```
load_cell_mix_data()
```

```
load_mrna_mix_data()
```

```
load_all_data()
```

**Value**

list of SingleCellExperiment

**Functions**

- load\_sc\_data: Load single cell data
- load\_cell\_mix\_data: Load cell mixture data
- load\_mrna\_mix\_data: Load mrna mixture data

**Examples**

```
## Not run:  
cellbench_file <- load_all_data()  
  
## End(Not run)
```

---

|       |   |
|-------|---|
| mhead | <i>Get head of 2 dimensional object as a square block</i> |
|-------|---|

---

**Description**

head prints all columns which may flood the console, mhead takes a square block which can look nicer and still provide a good inspection of the contents

**Usage**

```
mhead(x, n = 6)
```

**Arguments**

x                    the object with 2 dimensions  
 n                    the size of the n-by-n block to extract

**Value**

an n-by-n sized subset of x

**Examples**

```
x <- matrix(runif(100), nrow = 10, ncol = 10)

mhead(x)
mhead(x, n = 3)
```

---

pipeline\_collapse      *Collapse benchmark\_tbl into a two column summary*

---

**Description**

Collapse benchmark\_tbl into two columns: "pipeline" and "result". The "pipeline" column will be the concatenated values from the data and methods columns while the "result" column remains unchanged from the benchmark\_tbl. This is useful for having a string summary of the pipeline for annotating.

**Usage**

```
pipeline_collapse(
  x,
  sep = arrow_sep("right"),
  drop.steps = TRUE,
  data.name = TRUE
)
```

**Arguments**

x                    the benchmark\_tbl to collapse  
 sep                  the separator to use for concatenating the pipeline steps  
 drop.steps          if the data name and methods steps should be dropped from the output. TRUE by default.  
 data.name           if the dataset name should be included in the pipeline string. Useful if only a single dataset is used.

**Value**

benchmark\_tbl with pipeline and result columns (and all other columns if drop.steps is FALSE)



**See Also**[as\\_pipeline\\_list](#)**Examples**

```
# list of data
datasets <- list(
  set1 = rnorm(500, mean = 2, sd = 1),
  set2 = rnorm(500, mean = 1, sd = 2)
)

# list of functions
add_noise <- list(
  none = identity,
  add_bias = function(x) { x + 1 }
)

res <- apply_methods(datasets, add_noise)
pipeline_collapse(res)
```

---

`sample_cells`*Sample cells from a SingleCellExperiment*

---

**Description**

Sample  $n$  cells from a `SingleCellExperiment` object with no replacement.

**Usage**

```
sample_cells(x, n)
```

**Arguments**

|                |  |
|----------------|--|
| <code>x</code> | the <code>SingleCellExperiment</code> object |
| <code>n</code> | the number of cells to sample                |

**Value**

`SingleCellExperiment` object

**Examples**

```
sample_sce_data <- readRDS(cellbench_file("celseq_sce_sample.rds"))
dim(sample_sce_data)
x <- sample_cells(sample_sce_data, 10)
dim(x)
```

---

|              |   |
|--------------|---|
| sample_genes | <i>Sample genes from a SingleCellExperiment</i> |
|--------------|---|

---

**Description**

Sample n genes from a SingleCellExperiment object with no replacement

**Usage**

```
sample_genes(x, n)
```

**Arguments**

|   |                                 |
|---|---------------------------------|
| x | the SingleCellExperiment object |
| n | the number of genes to sample   |

**Value**

SingleCellExperiment object

**Examples**

```
sample_sce_data <- readRDS(cellbench_file("10x_sce_sample.rds"))
dim(sample_sce_data)
x <- sample_genes(sample_sce_data, 50)
dim(x)
```

---

|                 |   |
|-----------------|---|
| sample_sce_data | <i>This is data for testing functions in CellBench.</i> |
|-----------------|---|

---

**Description**

A dataset containing 200 genes and 50 cells randomly sampled from the CelSeq mRNA mixture dataset, each sample is a mixture of mRNA material from 3 different human adenocarcinoma cell lines. Useful for quick prototyping of method wrappers.

**Usage**

```
data(sample_sce_data)
```

**Format**

A SingleCellExperiment object with sample annotations in colData(sample\_sce\_data). The annotation contains various QC metrics as well as the cell line mixture proportions

**H2228\_prop** proportion of mRNA from H2228 cell line

**H1975\_prop** proportion of mRNA from H1975 cell line

**HCC827\_prop** proportion of mRNA from HCC827 cell line

**See Also**[load\\_mrna\\_mix\\_data](#)

---

`set_cellbench_bpparam` *Set BiocParallel parameter used CellBench*

---

**Description**

This is a more advanced interface for changing CellBench's parallelism settings. Internally CellBench uses BiocParallel for parallelism, consult the documentation of BiocParallel to see what settings are available.

**Usage**

```
set_cellbench_bpparam(param)
```

**Arguments**

`param`            the BiocParallel parameter object

**Value**

None

**See Also**

[set\\_cellbench\\_threads](#) for more basic interface

**Examples**

```
set_cellbench_threads(1) # CellBench runs on a single thread
```

---

`set_cellbench_cache_path`  
*Set CellBench cache path*

---

**Description**

Set CellBench cache path

**Usage**

```
set_cellbench_cache_path(path = "./CellBenchCache")
```

**Arguments**

path                    the path to where method caches should be stored

**Value**

None

**See Also**

[cache\\_method](#) for constructing cached methods.

**Examples**

```
## Not run:  
# hidden folder in local path  
set_cellbench_cache_path(".CellBenchCache")  
  
## End(Not run)  
# store in temp directory valid for this session  
set_cellbench_cache_path(file.path(tempdir(), ".CellBenchCache"))
```

---

set\_cellbench\_threads *Set number of threads used by CellBench*

---

**Description**

Sets global parameter for CellBench to use multiple threads for applying methods. If any methods applied are multi-threaded then it's recommended to set CellBench threads to 1. It only recommended to use CellBench with multiple threads if methods applied can be set to run on single threads.

**Usage**

```
set_cellbench_threads(nthreads = 1)
```

**Arguments**

nthreads                the number of threads used by CellBench

**Value**

None

**See Also**

[set\\_cellbench\\_bpparam](#) for more advanced interface

**Examples**

```
set_cellbench_threads(1) # CellBench runs on a single thread
```

---

|              |                     |
|--------------|---------------------|
| time_methods | <i>Time methods</i> |
|--------------|---------------------|

---

**Description**

`time_methods()` take either lists of datasets or `benchmark_timing_tbl` objects and applies a list of functions. The output is a `benchmark_timing_tbl` where each method has been applied to each dataset or preceding result. Unlike `apply_methods()`, `time_methods()` is always single threaded as to produce fair and more consistent timings.

**Usage**

```
time_methods(x, fn_list, name = NULL, suppress.messages = TRUE)

## S3 method for class 'list'
time_methods(x, fn_list, name = NULL, suppress.messages = TRUE)

## S3 method for class 'benchmark_timing_tbl'
time_methods(x, fn_list, name = NULL, suppress.messages = TRUE)
```

**Arguments**

|                                |   |
|--------------------------------|---|
| <code>x</code>                 | the list of data or benchmark timing tibble to apply methods to |
| <code>fn_list</code>           | the list of methods to be applied                               |
| <code>name</code>              | (optional) the name of the column for methods applied           |
| <code>suppress.messages</code> | TRUE if messages from running methods should be suppressed      |

**Value**

`benchmark_timing_tbl` object containing results from methods applied, the first column is the name of the dataset as factors, middle columns contain method names as factors and the final column is a list of lists containing the results of applying the methods and timings from calling `system.time()`.

**See Also**

[apply\\_methods](#)

**Examples**

```
datasets <- list(  
  set1 = 1:1e7  
)  
  
transform <- list(  
  sqrt = sqrt,  
  log = log  
)  
  
time_methods(datasets, transform) %>%  
  unpack_timing() # extract timings out of list
```

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