

# Package ‘CellBench’

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**Type** Package

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

**Version** 1.22.0

**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, SingleCell

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**BugReports** <https://github.com/Shians/CellBench/issues>

**License** GPL-3

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CellBench-package	<i>A framework for benchmarking combinations of methods in multi-stage pipelines</i>
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### 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>all_unique</code>	<i>Check if all values in a vector are unique</i>
-------------------------	---

---

### Description

Check if all values in a vector are unique

### Usage

```
all_unique(x)
```

### Arguments

`x` the vector to check

### Value

TRUE if all values in the vector are unique

### Examples

```
all_unique(c(1, 2, 3)) # TRUE
all_unique(c(1, 2, 2)) # FALSE
```

---

any_task_errors	<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**

x	the tibble to check
verbose	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)**

- any\_task\_errors(benchmark\_tbl):

---

apply_methods	<i>Apply methods</i>
---------------	----------------------

---

**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**

x the list of data or benchmark tibble to apply methods to  
 fn\_list the list of methods to be applied  
 name (optional) the name of the column for methods applied  
 suppress.messages 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	<i>convert benchmark_tbl to list</i>
------------------	--------------------------------------

---

**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**

[collapse\\_pipeline](#)

**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	<i>Create a cached function for CellBench</i>
--------------	---

---

## 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

f	the function to be cached
cache	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()
```

**Value**

opens a vignette containing a 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
```



---

check_class	<i>Check class of object</i>
-------------	------------------------------

---

**Description**

Check an object against a vector of class names. Testing if they match any or all of the classes. For `is_all_of`, the object needs to be at least every class specified, but it can have addition classes and still pass the check.

**Usage**

```
is_one_of(x, classes)
```

```
is_any_of(x, classes)
```

```
is_all_of(x, classes)
```

**Arguments**

x	the object to check
classes	the vector of strings of class names

**Value**

boolean value for the result of the check

**Examples**

```
is_one_of(1, c("numeric", "logical")) # TRUE
is_one_of(1, c("character", "logical")) # FALSE

is_all_of(1, c("numeric", "logical")) # FALSE
is_all_of(tibble::tibble(), c("tbl", "data.frame")) # TRUE
```

---

clear_cached_datasets	<i>Clear cached datasets</i>
-----------------------	------------------------------

---

**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)
```

---

collapse\_pipeline *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**

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

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)
collapse_pipeline(res)

```

---

data\_list

*Constructor for a data list*

---

### 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      *Filter out zero count genes*

---

**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             *Load CellBench Data*

---

### 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

*Get head of 2 dimensional object as a square block*

---

**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)
```

---

print.fn\_arg\_seq      *Print method for fn\_arg\_seq output*

---

**Description**

Print method for fn\_arg\_seq output

**Usage**

```
## S3 method for class 'fn_arg_seq'  
print(x, ...)
```

**Arguments**

x                    fn\_arg\_seq object  
...                  addition arguments for print

**Value**

None

**Examples**

```
fn_seq <- fn_arg_seq(kmeans, centers = 1:3)  
fn_seq
```

---

print.task\_error      *Print method for task\_error object*

---

**Description**

task\_error are objects that result from failed methods

**Usage**

```
## S3 method for class 'task_error'  
print(x, ...)
```

**Arguments**

x                    a task\_error object  
...                  not used

**Value**

None

---

sample_cells	<i>Sample cells from a SingleCellExperiment</i>
--------------	---

---

**Description**

Sample n cells from a SingleCellExperiment object with no replacement.

**Usage**

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

**Arguments**

x	the SingleCellExperiment object
n	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	<i>Set BiocParallel parameter used CellBench</i>
-----------------------	--

---

### 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
```

---

split_step	<i>Split combined pipeline step</i>
------------	-------------------------------------

---

**Description**

Some methods perform multiple steps of a pipeline. This function assists with splitting the combined pipeline step into multiple steps with duplicated method names.

**Usage**

```
split_step(x, step, into)
```

**Arguments**

x                    a results data.frame from 'apply\_methods()'.  
step                 the name of the column to split.  
into                 the name of the columns to split into.

**Value**

a results data.frame where the 'step' column has been split into the 'into' columns with duplicated values.

**Examples**

```
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)

res %>%
  split_step("add_noise", c("split1", "split2"))
```

---

strip\_timing

*Strip timing information*

---

**Description**

Takes the result of a `time_methods()` call and remove timing information from the ‘`timed_result`’ column, replacing it with a ‘`result`’ column and converting it to a `benchmark_tbl`.

**Usage**

```
strip_timing(x)

## S3 method for class 'benchmark_timing_tbl'
strip_timing(x)
```

**Arguments**

`x` the `benchmark_timing_tbl` object

**Value**

`benchmark_tbl`

**See Also**

[unpack\\_timing](#)

**Examples**

```
## Not run:
datasets <- list(
  data1 = 1:1e8,
)

transforms <- list(
  log = log,
```

```
    sqrt = sqrt
  )

  datasets %>%
    time_methods(transforms) %>%
    strip_timing()

## End(Not run)
```

---

summary.benchmark\_tbl *Summary of benchmark\_tbl*

---

## Description

Summary of benchmark\_tbl

## Usage

```
## S3 method for class 'benchmark_tbl'
summary(object, ...)
```

## Arguments

object	the benchmark_tbl to be summarised
...	additional arguments affecting the summary produced.

## Value

None

## 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)
summary(res)
```



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time_methods	<i>Time methods</i>
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### 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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unpack_timing	<i>Unpack timing information</i>
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### Description

Takes the result of a `time_methods()` call and remove the 'timed\_result' column, replacing it with three columns of durations representing the 'system', 'user' and 'elapsed' times from a `system.time()` call.

### Usage

```
unpack_timing(x)

## S3 method for class 'benchmark_timing_tbl'
unpack_timing(x)
```

### Arguments

x                    the `benchmark_timing_tbl` object

### Value

a tibble containing pipeline steps and timing information

### See Also

[strip\\_timing](#)

### Examples

```
## Not run:
datasets <- list(
  data1 = c(1, 2, 3)
)

transforms <- list(
  log = function(x) { Sys.sleep(0.1); log(x) },
  sqrt = function(x) { Sys.sleep(0.1); sqrt(x) }
)

datasets %>%
  time_methods(transforms) %>%
  unpack_timing()

## End(Not run)
```

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