

# Package: methcon5 (via r-universe)

September 23, 2024

**Title** Identify and Rank CpG DNA Methylation Conservation Along the Human Genome

**Version** 0.1.0.9000

**Description** Identify and rank CpG DNA methylation conservation along the human genome. Specifically it includes bootstrapping methods to provide ranking which should adjust for the differences in length as without it short regions tend to get higher conservation scores.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.2

**Depends** R (>= 2.10)

**Imports** magrittr, dplyr, purrr, rlang

**Suggests** ggplot2, testthat (>= 2.1.0), covr

**URL** <https://github.com/EmilHvitfeldt/methcon5>

**BugReports** <https://github.com/EmilHvitfeldt/methcon5/issues>

**Repository** <https://uscbiostats.r-universe.dev>

**RemoteUrl** <https://github.com/uscbiostats/methcon5>

**RemoteRef** HEAD

**RemoteSha** 71aae030b648ebca0dbaa2d45385a14ea0ba7a29

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fake_methylation	<i>Simple simulated methylation dataset</i>
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**Description**

Simple simulated methylation dataset

**Usage**

```
fake_methylation
```

**Format**

A data frame with 2771 rows and 3 variables: gene, cons\_level and meth.

**Details**

This dataset is for example use only. It contains 500 genes identified by gene each with one of 3 types of conservation levels "low", "medium" and "high". The methylation values are independent randomly distributed within each gene. Thus no spacial correlation is assumed.

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meth_aggregate	<i>Calculate region wise summary statistics</i>
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**Description**

Will take a data.frame and apply a function ('fun') to 'value' within the groups defined by the 'id' column.

**Usage**

```
meth_aggregate(data, id, value, fun = mean, ...)
```

**Arguments**

data	a data.frame.
id	variable name, to be aggregated around.
value	variable name, contains the value to take mean over. Must be a single column.
fun	function, summary statistic function to be calculated. Defaults to 'mean'.
...	Additional arguments for the function given to the argument fun.

**Details**

Please note the ordering of the data will matter depending on the choice of aggregation function.

**Value**

A methcon object. Contains the aggregated data along with original data.frame and variable selections.

**Examples**

```
meth_aggregate(fake_methylation, id = gene, value = meth, fun = mean)

meth_aggregate(fake_methylation, id = gene, value = meth, fun = var)

# custom functions can be used as well
mean_diff <- function(x) {
  mean(diff(x))
}

meth_aggregate(fake_methylation, id = gene, value = meth, fun = mean_diff)
```

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meth_bootstrap	<i>Bootstrapped randomly samples values</i>
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**Description**

"perm\_v1" (the default method) will sample the variables the rows independently. "perm\_v2" will sample regions of same size while allowing overlap between different regions. "perm\_v3" will sample regions under the constraint that all sampled regions are contained in the region they are sampled in.

**Usage**

```
meth_bootstrap(data, reps, method = c("perm_v1", "perm_v2", "perm_v3"))
```

**Arguments**

data	a methcon data.frame output from 'meth_bootstrap'.
reps	Number of reps, defaults to 1000.
method	Character, determining which method to use. See details for information about methods. Defaults to "perm_v1".

**Details**

Note that you can apply 'meth\_bootstrap' multiple times to get values for different methods.

**Value**

A methcon object. Contains the aggregated data along with original data.frame and variable selections and bootstrapped values.

**Examples**

```
# Note that you likely want to do more than 10 repetitions.
# rep = 10 was chosen to have the examples run fast.

fake_methylation %>%
  meth_aggregate(id = gene, value = meth, fun = mean) %>%
  meth_bootstrap(10)

fake_methylation %>%
  meth_aggregate(id = gene, value = meth, fun = mean) %>%
  meth_bootstrap(10, method = "perm_v2")

# Get multiple bootstraps
fake_methylation %>%
  meth_aggregate(id = gene, value = meth, fun = mean) %>%
  meth_bootstrap(10, method = "perm_v1") %>%
  meth_bootstrap(10, method = "perm_v2") %>%
  meth_bootstrap(10, method = "perm_v3")
```

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