

# Package ‘shinyMethylData’

January 2, 2025

**Version** 1.27.0

**Title** Example dataset of input data for shinyMethyl

**Description** Extracted data from 369 TCGA Head and Neck Cancer DNA methylation samples. The extracted data serve as an example dataset for the package shinyMethyl. Original samples are from 450k methylation arrays, and were obtained from The Cancer Genome Atlas (TCGA). 310 samples are from tumor, 50 are matched normals and 9 are technical replicates of a control cell line.

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**License** Artistic-2.0

**Depends** R (>= 3.0.0)

**LazyData** yes

**biocViews** Genome, CancerData

**Url** <https://github.com/Jfortin1/shinyMethylData>

**Author** Jean-Philippe Fortin [cre, aut], Kasper Daniel Hansen [aut]

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summary.tcga.norm      *Example dataset of input data for shinyMethyl*

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### Description

Extracted data from 369 TCGA Head and Neck Cancer DNA methylation samples. The extracted data serve as an example dataset for the package shinyMethyl. Original samples are from 450k methylation arrays, and were obtained from The Cancer Genome Atlas (TCGA). 310 samples are from tumor, 50 are matched normals and 9 are technical replicates of a control cell line.

### Usage

```
data(summary.tcga.norm)
```

### Format

A list containing the necessary information to launch a shinyMethyl session. See the links below for more details on the data.

### References

The Cancer Genome Atlas (TCGA) Head and Neck Cancer dataset: <http://cancergenome.nih.gov/cancersselected/headandne>

### See Also

These data objects were created by See [shinySummarize](#) for details on how to perform the data extraction. See [runShinyMethyl](#) for how to launch a shinyMethyl session.

### Examples

```
data(summary.tcga.norm)
## Not run:
runShinyMethyl(summary.tcga.norm)

## End(Not run)
```

---

summary.tcga.raw      *Example dataset of input data for shinyMethyl*

---

### Description

Extracted data from 369 TCGA Head and Neck Cancer DNA methylation samples. The extracted data serve as an example dataset for the package shinyMethyl. Original samples are from 450k methylation arrays, and were obtained from The Cancer Genome Atlas (TCGA). 310 samples are from tumor, 50 are matched normals and 9 are technical replicates of a control cell line.

## Usage

```
data(summary.tcga.raw)
```

## Format

A list containing the necessary information to launch a shinyMethyl session. See the links below for more details on the data.

## References

The Cancer Genome Atlas (TCGA) Head and Neck Cancer dataset: <http://cancergenome.nih.gov/cancersselected/headandne>

## See Also

See [shinySummarize](#) for details on how to perform the data extraction. See [runShinyMethyl](#) for how to launch a shinyMethyl session.

## Examples

```
data(summary.tcga.raw)
## Not run:
runShinyMethyl(summary.tcga.raw)

## End(Not run)
```

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