# Package ‘shinyMethylData’

March 23, 2017

**Version** 0.108.0  
**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]  
**NeedsCompilation** no

```r
R topics documented:

<table>
<thead>
<tr>
<th>topic</th>
<th>pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>summary.tcga.norm</td>
<td>1</td>
</tr>
<tr>
<td>summary.tcga.raw</td>
<td>2</td>
</tr>
</tbody>
</table>
```

**Index**

<table>
<thead>
<tr>
<th>topic</th>
<th>pages</th>
</tr>
</thead>
<tbody>
<tr>
<td>summary.tcga.norm</td>
<td>4</td>
</tr>
</tbody>
</table>

---

**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

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.

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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)
Index

*Topic datasets
  summary.tcga.norm, 1
  summary.tcga.raw, 2

runShinyMethyl, 2

shinySummarize, 2
summary.tcga.norm, 1
summary.tcga.raw, 2