

A)

Data Acquisition

Functions for exploring, downloading and unpacking data for selected snapshot and cohort directly from TCGA data portal.

```
RTCGA::infoTCGA
RTCGA::checkTCGA
RTCGA::readTCGA
```

```
RTCGA::downloadTCGA
RTCGA::instalTCGA
```

In order to simplify access to TCGA data selected snapshots and cohorts are available as R data packages. Names of packages available in Bioconductor are listed on right side. These packages contain data from the 2015-11-01 release.

```
RTCGA.clinical
RTCGA.mutations
RTCGA.CNV
RTCGA.PANCAN12
```

```
RTCGA.methylation
RTCGA.rnaseq
RTCGA.mRNA
RTCGA.miRNAseq
RTCGA.RPPA
```

B)

Data Preprocessing

Functions for merging different patients characteristics, converging TCGA data into objects of the class GRanges or ExpressionSet.

```
RTCGA::convertTCGA
RTCGA::convertPANCAN12
```

```
RTCGA::expressionsTCGA
RTCGA::mutationsTCGA
```

C)

Data Exploration / Visualisation

Functions for exploratory modeling and data visualization produce elegant and highly customizable plots with the ggplot2 package.

```
RTCGA::survivalTCGA
RTCGA::kmTCGA
RTCGA::boxplotTCGA
```

```
RTCGA::heatmapTCGA
RTCGA::pcaTCGA
```

