

# secuTrial R package vignette

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This R package provides functions for handling data from the clinical data management system secuTrial. The most important components are related to loading data exports from secuTrial into R. For this vignette and also to test your installation of the R secuTrial package some example export data is delivered with the package. The data (*calcium*) was retrieved from the **lava** package and prepared for the import into a secuTrial eCRF. It was then exported and added to the secuTrial R package.

## Load the secuTrial library

```
library(secuTrial)
```

## Loading data from a rectangular export

```
load.tables(data.dir=system.file("extdata",
                                  "s_export_rt-CSV-xls_DEM00_20181016-151332.zip",
                                  package = "secuTrial"),
             decode.rt.visitlabels = TRUE)

#> --- rectangular data written into variable rtdata ---
```

The above command loads the rectangular export and writes it into the variable *rtdata*. Furthermore, the visitlabels are automatically translated if *decode.rt.visitlabels* is set to TRUE.

## Loading data from a non-rectangular export

```
load.tables(data.dir=system.file("extdata",
                                  "s_export_CSV-xls_DEM00_20180912-125720.zip",
                                  package = "secuTrial"),
             tables=c("bmd.xls", "ctr.xls"))

#> ** Checking for 'Column names' in ExportOptions.html '
#> ** 'Column names' ('Spaltennamen') was found in ExportOptions.html
#> ** Checking for 'Add-ID' in ExportOptions.html
#> ** 'Add-ID' ('Zus-ID', 'Patient-ID') was found in ExportOptions.html
#> ** Loading tables as defined in input tables = ...
#> --- table cn.xls loaded as patient ---
#> --- table bmd.xls loaded as bmd ---
#> --- table ctr.xls loaded as center ---
```

The above command reads export tables into R variables. The central table in this case is *bmd* which contains the form data of the bone mineral density dataset. The *tables* argument has been set to prevent loading of all tables.

## Column moving

```
bmd_subset <- bmd[,c("pat.id", "mnpvispdt", "age", "grouping", "bmd")]
names(bmd_subset)
#> [1] "pat.id"      "mnpvispdt" "age"        "grouping"   "bmd"
# position "grouping" and "bmd" behind "mnpvispdt"
bmd_subset_moved_1 <- move.column.after(df=bmd_subset,
                                         col.name=c("grouping", "bmd"),
                                         "mnpvispdt")
names(bmd_subset_moved_1)
#> [1] "pat.id"      "mnpvispdt" "grouping"   "bmd"        "age"
# position "age" back to position 3 with "move.column.to.pos"
bmd_subset_moved_2 <- move.column.to.pos(df=bmd_subset_moved_1, col.idx=5, new.col.idx=3)
names(bmd_subset_moved_2)
#> [1] "pat.id"      "mnpvispdt" "age"        "grouping"   "bmd"
```

## Translating IDs

```
mnppid2mnpaid(1512)
#> [1] 104
mnpaid2mnppid(104)
#> [1] 1512
```

## Stripping center tags

```
remove.center.tag("Universitätsspital Basel (SWISS-AF)")
#> [1] "Universitätsspital Basel"
remove.center.tag("HUG Genève (SSR)")
#> [1] "HUG Genève"
```

## Retrieve center from mnppid

```
mnppid2center(1509)
#> [1] Hospital
#> Levels: Hospital
mnppid2center(1509, remove.ctag = 0)
#> [1] Hospital (BMD)
#> Levels: Hospital (BMD)
```

## Adding center to tables

```
bmd_with_center_col <- add.center(bmd)
length(names(bmd))
#> [1] 25
length(names(bmd_with_center_col))
#> [1] 26
```