secuTrialR - a walkthrough

Patrick R. Wright, Milica Markovic, Alan Haynes

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Introduction

> "If I had just five minutes to chop down a tree I would spend the first two and a half minutes sharpening my axe."
>
> — An anonymous woodsman

This R package provides functions for handling data from the clinical data management system (CDMS) secuTrial. The most important components are related to reading data exports from secuTrial into R. In brief, the package aims to enable swift execution of repetitive tasks in order to allow spending more time on the unique aspects of a dataset. It is developed and maintained by the Swiss Clinical Trial Organisation (SCTO).

This vignette will teach you how to use the `secuTrialR` package and you will likely learn quite a bit about secuTrial exports in general along the way.

Installing

Let's get started by installing the package straight from GitHub and then loading it. For this you will need to have `devtools` installed. We are planning to add `secuTrialR` to CRAN but we are not there yet.

```
# install
devtools::install_github("SwissClinicalTrialOrganisation/secuTrialR")
```

```
# load silently
suppressMessages(library(secuTrialR))
# show secuTrialR version
installed.packages()["secuTrialR", "Version"]
#> [1] "0.8.3"
```

The CTU05 dataset

Before we continue with the functionalities let's briefly talk about the test data which is delivered as a part of the package. We refer to it as the `CTU05` (clinical trial unit project 05) data. This dataset has been fabricated for demonstration purposes only and is not real clinical data. Principally it is made up of eight forms. These are called "surgeries", "baseline", "outcome", "treatment", "allmedi", "studyterminat", "ae" and "sae". You will see these names again later when the data has been read into R. The project setup includes most data types implementable in secuTrial. It is, however, not exhaustive. Since the data is delivered with the installation of the `secuTrialR` package we can point to it via the `system.file()` function.

```
ctu05_data_location <- system.file("extdata", "sT_exports", "export_options",
                                   "s_export_CSV-xls_CTU05_20191003-144349_all_info.zip",
                                   package = "secuTrialR")
```

If you work on your own datasets you can specify a path as a regular character string without using `system.file()`.

secuTrial export options

Prior to reading your data into R you need to export it with the secuTrial ExportSearchTool. We suggest exporting **non-rectangular**, **zipped**, **English** data with **reference values** stored **in a separate table** including **Add-IDs**, **centre information**, **form status**, **project setup** and **without duplicated meta data**. Furthermore, it is important to use **"CSV format"/"CSV format for MS Excel"** and suggested to select **UTF-8** encoding. Most of these options are truly optional and reading your data should work even with differences from the above specifications.

Reading a secuTrial data export into R

There is one principle function to read your data (i.e. `read_secuTrial()`). Below you can see it in action with the `CTU05` dataset.

```
ctu05_data <- read_secuTrial(data_dir = ctu05_data_location)
#> Read export successfully.
```

If the "Read export successfully." message appears your data was correctly read.

The `secuTrialdata` object

If you inspect the `class()` of `ctu05_data` you will find that it is a `secuTrialdata` object.

```
class(ctu05_data)
#> [1] "secuTrialdata"
```

Really this is only a `list` containing all the information from your secuTrial export.

```
typeof(ctu05_data)
#> [1] "list"
```

The data tables in the `secuTrialdata` object

We have implemented a custom variation of the `print()` function for `secuTrialdata` objects.

```
print(ctu05_data)
#> secuTrial data imported from:
#> /home/wrightp/R/x86_64-pc-linux-gnu-library/3.6/secuTrialR/extdata/sT_exports/
#> export_options/s_export_CSV-xls_CTU05_20191003-144349_all_info.zip
#>             table nrow ncol  meta       original_name
#>                vp    4   12  TRUE              vp.xls
#>              vpfs    8    2  TRUE            vpfs.xls
#>                fs    8    8  TRUE              fs.xls
#>                qs   29    8  TRUE              qs.xls
#>                is   85    9  TRUE              is.xls
#>               ctr    3    3  TRUE             ctr.xls
#>                cn   11   15  TRUE              cn.xls
#>              atcn    0    9  TRUE            atcn.xls
#>             atcvp    0   16  TRUE           atcvp.xls
#>               qac    0   12  TRUE             qac.xls
#>               cts    0   10  TRUE             cts.xls
```

```
#>              miv    0   10  TRUE             miv.xls
#>            atmiv    0   15 FALSE           atmiv.xls
#>         baseline   17  107 FALSE        baseline.xls
#>       atbaseline    0   79 FALSE      atbaseline.xls
#>          outcome   13   48 FALSE         outcome.xls
#>        atoutcome    5   47 FALSE       atoutcome.xls
#>        treatment   11   44 FALSE       treatment.xls
#>      attreatment    0   45 FALSE     attreatment.xls
#>          allmedi   17   47 FALSE         allmedi.xls
#>        atallmedi    2   47 FALSE       atallmedi.xls
#>    studyterminat   10   41 FALSE   studyterminat.xls
#>  atstudyterminat    1   39 FALSE atstudyterminat.xls
#>               ae    1   66 FALSE              ae.xls
#>             atae    0   58 FALSE            atae.xls
#>              sae    2   64 FALSE             sae.xls
#>            atsae    0   57 FALSE           atsae.xls
#>       esurgeries   18   11 FALSE      esurgeries.xls
#>     atesurgeries    0    9 FALSE    atesurgeries.xls
#>               cl  205    3  TRUE              cl.xls
#>            atae1    0   20 FALSE           atae1.xls
```

It shows you where the export archive of your `secuTrialdata` object is located, tells you which tables (i.e. `table`) it contains, what the source files (i.e. `original_name`) are and specifies each table's dimensions (i.e. `ncol`, `nrow`).

By now you have possibly realized that all the forms specified earlier (i.e. "surgeries", "baseline", "outcome", "treatment", "allmedi", "studyterminat", "ae" and "sae") are present, but also that there are many tables which you do not recognize.

The majority of the unrecognizable tables are tagged as `TRUE` in the `meta` column. This means that they are structural data tables. Their names and data structures are fixed in secuTrial exports. In the following we will briefly explain which information the most relevant meta tables contain.

- `vp` - visitplan definition
- `vpfs` - visitplan form linkage
- `fs` - forms information
- `qs` - questions
- `is` - items i.e. variable definitions
- `ctr` - centre information
- `cn` - casenodes i.e. table of entered study participants
- `cl` - information how the data in the variables is coded

Furthermore, there is a set of tables whose names start with "at". These are audit trail tables and only relevant if you need to investigate changes in the data. Last but not least you may have also realized that the "surgeries" table is called `esurgeries`. This is because it is a so-called repetition form. Repetition forms are labelled with a leading "e" and are implemented as subforms in other forms. In this case, `esurgeries` is a subform in `baseline` and the linkage is defined by the `mnpdocid` column in both tables. If this sounds cryptic to you we suggest you talk so someone who has implemented a database in secuTrial and let them explain it with a specific example. It is pretty straight forward when you look at a concrete implementation.

Accessing the tables and values

Since the `secuTrialdata` object is a `list` and the data tables within this `list` are `data.frames` you can simply access the tables using `$`. Let's say you would like to have a look at the placebo to verum ratio in your `treatment` data or what types of other medication were entered in `allmedi`.

```
table(ctu05_data$treatment$rando_treatment)
#>
#> Placebo   Verum
#>       8       3
table(ctu05_data$allmedi$med_product)
#>
#> Amoxicillin Doxycycline    Importal
#>           2           1           3
```

Data transformations

During the loading process, coded categorical data is transformed. For example the `gender` variable in the `baseline` form is categorical. The raw data is accessible via `gender` and the transformed version of the data is added during the reading process and accessible via `gender.factor`. Thus, data is not overwritten but added with the `.factor` extension. If there are issues during factorization a `warning()` will inform you of this.

```
# raw gender data
ctu05_data$baseline$gender
#>  [1]  1 NA NA  2  1  2  1 NA NA  1  2 NA NA  1  2  2 NA
#> attr(,"label")
#> [1] "Gender"

# transformed gender data
ctu05_data$baseline$gender.factor
#>  [1] male   <NA>   <NA>   female male   female male   <NA>   <NA>   male
#> [11] female <NA>   <NA>   male   female female <NA>
#> attr(,"label")
#> [1] Gender
#> Levels: male female

# raw more meds
ctu05_data$allmedi$no_more_meds
#>  [1] 1 1 0 1 1 1 0 0 0 1 0 0 1 1 1 1 0
#> attr(,"label")
#> [1] "No further medication"

# transformed more meds
ctu05_data$allmedi$no_more_meds.factor
#>  [1] yes yes no  yes yes yes no  no  no  yes no  no  yes yes yes yes no
#> attr(,"label")
#> [1] No further medication
#> Levels: no yes
```

Note that descriptive labels have also been automatically added to the data.

```
label(ctu05_data$allmedi$no_more_meds.factor)
#> [1] "No further medication"
label(ctu05_data$baseline$gender.factor)
#> [1] "Gender"
label(ctu05_data$esurgeries$surgery_organ.factor)
#> [1] "Organ"
```

Datetime data is also transformed and similarly to the factorization process the names are concatenated with `.date` or `.datetime`.

```
# raw
ctu05_data$baseline$visit_date
#>  [1] 20190401 20190402 20190403 20190402 20190403 20190404 20190405
#>  [8] 20190406 20190407 20190411 20190412 20190413 20190414 20190413
#> [15] 20190414 20190415 20180501
#> attr(,"label")
#> [1] "Date of visit"

# processed
ctu05_data$baseline$visit_date.date
#>  [1] "2019-04-01" "2019-04-02" "2019-04-03" "2019-04-02" "2019-04-03"
#>  [6] "2019-04-04" "2019-04-05" "2019-04-06" "2019-04-07" "2019-04-11"
#> [11] "2019-04-12" "2019-04-13" "2019-04-14" "2019-04-13" "2019-04-14"
#> [16] "2019-04-15" "2018-05-01"

# raw only head
head(ctu05_data$baseline$hiv_date)
#> [1] 201903052356           NA           NA           NA           NA
#> [6]          NA

# processed only head
head(ctu05_data$baseline$hiv_date.datetime)
#> [1] "2019-03-05 23:56:00 CET" NA
#> [3] NA                        NA
#> [5] NA                        NA

# classes
class(ctu05_data$baseline$visit_date)
#> [1] "integer"
class(ctu05_data$baseline$visit_date.date)
#> [1] "Date"
class(ctu05_data$baseline$hiv_date)
#> [1] "numeric"
class(ctu05_data$baseline$hiv_date.datetime)
#> [1] "POSIXct" "POSIXt"
```

Depending on the setup, incomplete dates can be valid entries in a secuTrial database. Thus they will also occasionally appear in your exports. The datetime conversion does not work in these cases and `NA`s are created. If this happens, `secuTrialR` will warn you accordingly and you should have a closer look into the affected datetime variables and whether you would like to perform so-called date imputation.

Export options

The `secuTrialdata` object also contains information on the export options.

```
ctu05_data$export_options
#> secuTrial version: 5.5.1.10
#> Time of export on server: 03.10.2019 - 14:43:49 (CEST)
#> Project version: (20.06.2019 - 11:22:04 (CEST))
#> Exported with short names
#> File extension: xls
#> Seperator: ' '
#> 32 files exported
#>   including 13 metadata elements
#> Reference values exported - factorize possible
#> Metadata elements:
#>              type exportname available
#>             forms         fs      TRUE
#>         casenodes         cn      TRUE
#>           centres        ctr      TRUE
#>             items         is      TRUE
#>         questions         qs      TRUE
#>           queries        qac      TRUE
#>         visitplan         vp      TRUE
#>    visitplanforms       vpfs      TRUE
#>       atcasenodes       atcn      TRUE
#>  atcasevisitplans      atcvp      TRUE
#>          comments        cts      TRUE
#>               miv        miv      TRUE
#>                cl         cl      TRUE
```

`export_options` itself is a `list`. If you are interested in more information than is printed you can also access it. Let's assume you would like to know the `project_name` and `encoding`.

```
ctu05_data$export_options$project_name
#> [1] "secuTrialR example CDMA"
ctu05_data$export_options$encoding
#> [1] "UTF-8"
```

Much more information is stored in the elements of `export_options`. The names of the elements should be descriptive enough to infer the contents.

```
names(ctu05_data$export_options)
#>  [1] "sep"                "date_format"        "datetime_format"
#>  [4] "date_format_meta"   "na.strings"         "short_names"
#>  [7] "is_zip"             "is_rectangular"     "audit_trail"
#> [10] "column_names"       "lang_not_supported" "dict_items"
#> [13] "refvals_separate"   "add_id"             "lab_id"
#> [16] "meta_names"         "meta_available"     "duplicate_meta"
#> [19] "all_files"          "data_files"         "data_names"
#> [22] "file_end"           "extension"          "data_dir"
#> [25] "secuTrial_version"  "project_version"    "project_name"
#> [28] "format_info"        "time_of_export"     "encoding"
#> [31] "form_status"        "centre_info"        "proj_setup"
#> [34] "factorized"         "dated"              "labelled"
```

Generic functions for `secuTrialdata` objects

Now that you understand the `secuTrialdata` object we will show you some generic functions you can use on objects of this class.

Show the study participants

First off you may be interested in a table of participants.

```
get_participants(ctu05_data)
#>    mnppid        mnpaid mnpctrid                      mnpctrname
#> 1    1204 RPACK-CBE-001      462           Charité Berlin (RPACK)
#> 2    1205 RPACK-CBE-002      462           Charité Berlin (RPACK)
#> 3    1206 RPACK-CBE-003      462           Charité Berlin (RPACK)
#> 4    1207 RPACK-CBE-004      462           Charité Berlin (RPACK)
#> 5    1208 RPACK-CBE-005      462           Charité Berlin (RPACK)
#> 6    1209 RPACK-INS-011      461         Inselspital Bern (RPACK)
#> 7    1210 RPACK-INS-012      461         Inselspital Bern (RPACK)
#> 8    1211 RPACK-INS-013      461         Inselspital Bern (RPACK)
#> 9    1212 RPACK-INS-014      461         Inselspital Bern (RPACK)
#> 10   1213 RPACK-INS-015      461         Inselspital Bern (RPACK)
#> 11   1214 RPACK-USB-123      441 Universitätsspital Basel (RPACK)
```

Recruitment over time

You can return recruitment per centre and year.

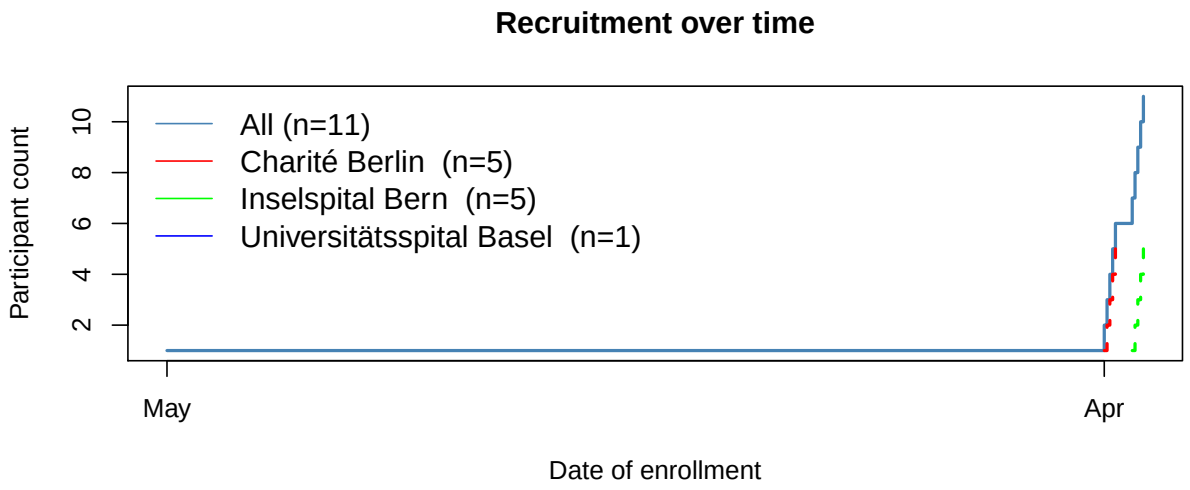
```
annual_recruitment(ctu05_data)
#>                             Center Total 2018 2019
#> 1                              All    11    1   10
#> 2           Charité Berlin (RPACK)     5    0    5
#> 3         Inselspital Bern (RPACK)     5    0    5
#> 4 Universitätsspital Basel (RPACK)     1    1    0
```

Since the centre names often have a systematic addition (e.g. (RPACK)) we have enabled the option to remove certain parts of the centre descriptions via regular expressions (i.e. `rm_regex` argument). In this case the regular expression removes trailing parentheses and everything they enclose.

```
annual_recruitment(ctu05_data, rm_regex = "\\(.*\\)$")
#>                       Center Total 2018 2019
#> 1                        All    11    1   10
#> 2           Charité Berlin      5    0    5
#> 3         Inselspital Bern      5    0    5
#> 4 Universitätsspital Basel      1    1    0
```

It is also possible to plot the recruitment over time.

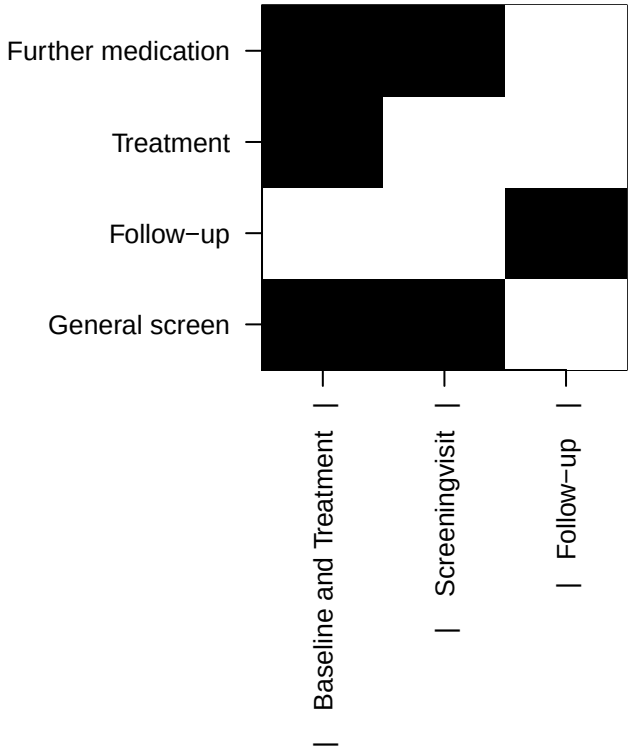
```
plot_recruitment(ctu05_data, cex = 1.2, rm_regex = "\\(.*\\)$")
```



Visit plan visualization

`secuTrialR` can provide a depiction of the visit structure, although only where the visit plan is fixed.

```
vs <- visit_structure(ctu05_data)
plot(vs)
```



Completeness of forms

If you are not sure about how complete the data in your export is, it may be useful to get a quick overview of how well the forms have been filled. The below table shows both absolute and relative numbers for a few forms.

```
fss <- form_status_summary(ctu05_data)
tail(fss, n = 5)
#>        form_name partly_filled completely_filled empty with_warnings
#> 6       baseline             3               14     0             0
#> 7        outcome             1               12     0             0
#> 8            sae             0                2     0             0
#> 9  studyterminat             0               10     0             0
#> 10     treatment             0               11     0             0
#>    with_errors partly_filled.percent completely_filled.percent
#> 6            0            0.17647059                0.8235294
#> 7            0            0.07692308                0.9230769
#> 8            0            0.00000000                1.0000000
#> 9            0            0.00000000                1.0000000
#> 10           0            0.00000000                1.0000000
#>    empty.percent with_warnings.percent with_errors.percent form_count
#> 6              0                    0                   0         17
#> 7              0                    0                   0         13
#> 8              0                    0                   0          2
#> 9              0                    0                   0         10
#> 10             0                    0                   0         11
```

Please note that a form is only complete if all required fields have been filled. Thus, a whole study may have 99% completeness on variable basis while showing 0% completeness on form basis. It is currently not technically possible to assess completeness on variable basis in a generic way. Hence, high completeness on form basis implies high completeness on variable basis but **NOT** vice versa.

For a more participant id centred statistic you can perform the following.

```
fsc <- form_status_counts(ctu05_data)
# show the top
head(fsc)
#>          pat_id form_name completely_filled partly_filled empty
#> 1 RPACK-CBE-001  baseline                3             0     0
#> 2 RPACK-CBE-002  baseline                1             0     0
#> 3 RPACK-CBE-003  baseline                1             0     0
#> 4 RPACK-CBE-004  baseline                1             0     0
#> 5 RPACK-CBE-005  baseline                1             2     0
#> 6 RPACK-INS-011  baseline                1             0     0
#>   with_warnings with_errors
#> 1             0           0
#> 2             0           0
#> 3             0           0
#> 4             0           0
#> 5             0           0
#> 6             0           0
```

Form linkage

Linkages amongst forms can be explored with the `links_secuTrial()` function. This relies on the `igraph` package to create a network. It is possible to interact with the network, e.g. move nodes around in order to read the labels better. The device ID is returned to the console, but can be ignored. Forms are plotted in deep yellow, variables in light blue.

```
links_secuTrial(ctu05_data)
```

The output can not be shown within this vignette but you should give it a try.

Sampling random participants

During study monitoring it is common practice to check random participants from a study database. These participants should be retrieved in a reproducible fashion. The below function allows this for a loaded secuTrial data export.

```
# retrieve at least 25 percent of participants recorded after March 18th 2019
# from the centres "Inselspital Bern" and "Charité Berlin"
return_random_participants(ctu05_data,
                           percent = 0.25,
                           seed = 1337,
                           date = "2019-03-18",
                           centres = c("Inselspital Bern (RPACK)",
                                       "Charité Berlin (RPACK)"))
#> $participants
#>          mnpaid                   centre mnpvisstartdate
#> 2 RPACK-INS-012 Inselspital Bern (RPACK)      2019-04-12
#> 4 RPACK-INS-014 Inselspital Bern (RPACK)      2019-04-14
#> 5 RPACK-CBE-005   Charité Berlin (RPACK)      2019-04-05
#> 3 RPACK-CBE-003   Charité Berlin (RPACK)      2019-04-03
#>
#> $rng_config
#> [1] "Mersenne-Twister" "Inversion"        "Rejection"
```

Please note that earlier R versions may return different results because there is a different `rng_config`. For this reason we have added the `rng_config` to the output.

Retrieve score variables

Generally, it is advisable to recalculate score variables before data analysis. A rule of thumb: The more complex a score is and the more data from different forms is necessary for its calculation the more likely its value should be recalculated. The below function will allow you to detect which variables this concerns.

```
return_scores(ctu05_data)
#>   name                  itemtype label
#> 1  age Years y (calculated only)   Age
```

Finding changes/differences in exports

In ongoing studies it is possible that changes to the secuTrial data entry interface (i.e. the electronic case report forms) are made. Sometimes these changes may call for adjustments in analysis code. It is considered good practice to run `diff_secuTrial()` on the last export and the current export of a project to at least make yourself aware of potential changes in the setup. If there are differences, the results of this function should be interpreted as a first indicator since they may not cover all alterations. Information is returned on new forms and variables. A detailed list of changes can be produced in the secuTrial FormBuilder with "Compare project setup".

```
# load second export from the same project
export_location <- system.file("extdata", "sT_exports", "longnames",
                               "s_export_CSV-xls_CTU05_long_ref_miss_en_utf8.zip",
                               package = "secuTrialR")
# read all export data
ctu05_data_new <- read_secuTrial_raw(data_dir = export_location)

# show diff
diff_secuTrial(ctu05_data, ctu05_data_new)
#> $new_forms
#> character(0)
#>
#> $new_variables
#> character(0)
#>
#> $removed_forms
#> character(0)
#>
#> $removed_variables
#> character(0)
```

This `list` contains only empty entries. Thus, you can conclude that nothing has changed.

Conversion to SPSS, STATA, SAS

Given that you are working with R it is unlikely that you need such conversions for yourself. However, collaborators may ask for data which is readily importable into SPSS, STATA or SAS. For this you can use `write_secuTrial()`.

```
# retrieve path to a temporary directory
tdir <- tempdir()
# write spss
write_secuTrial(ctu05_data, format = "sav", path = tdir)
```

Since this has not been heavily tested or used there may be issues and you might prefer doing this manually with the `haven` package.

Subsetting `secuTrialdata`

In some cases it may be useful to subset your `secuTrialdata` object. For example if you have cohort data and would like to supply a subset of the data for a retrospective study. We have implemented this option with `subset_secuTrial()`. It will truncate your `secuTrialdata` object and return a new `secuTrialdata` object which is a subset of the original data. It is possible to subset by including or excluding specific participant ids or centres.

```
# initialize some subset identifiers
participants <- c("RPACK-INS-011", "RPACK-INS-014", "RPACK-INS-015")
centres <- c("Inselspital Bern (RPACK)", "Universitätsspital Basel (RPACK)")

# exclude Bern and Basel
ctu05_data_berlin <- subset_secuTrial(ctu05_data, centre = centres, exclude = TRUE)
# exclude Berlin
ctu05_data_bern_basel <- subset_secuTrial(ctu05_data, centre = centres)
# keep only subset of participants
ctu05_data_pids <- subset_secuTrial(ctu05_data, participant = participants)

class(ctu05_data_berlin)
#> [1] "secuTrialdata"
class(ctu05_data_bern_basel)
#> [1] "secuTrialdata"
class(ctu05_data_pids)
#> [1] "secuTrialdata"
```

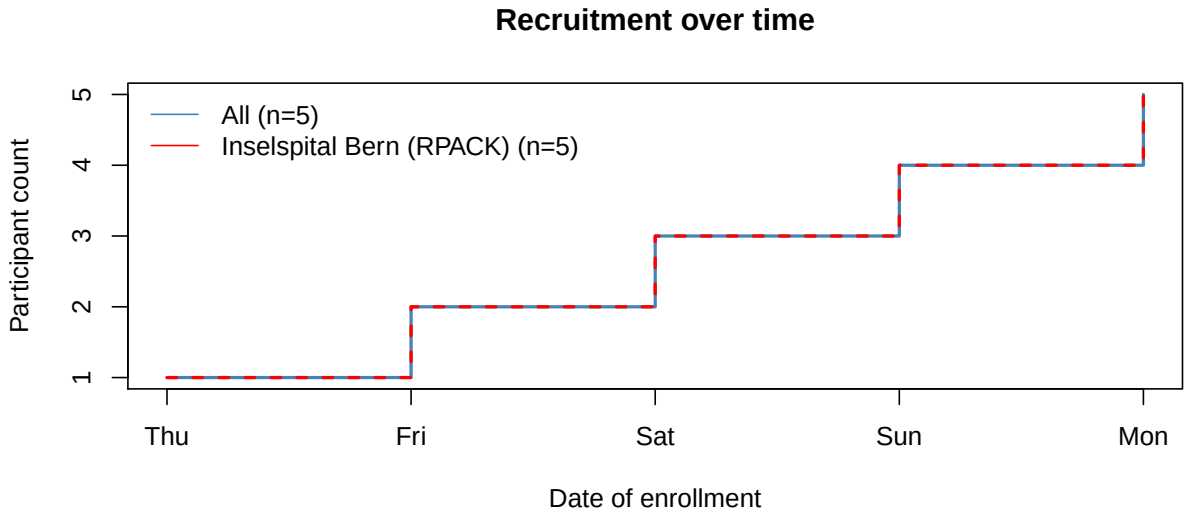
If you subset based on centres all traces of deleted centres will be removed. If you remove based on participant ids all traces of deleted participants will be removed.

```
# only Berlin remains
ctu05_data_berlin$ctr
#>   mnpctrid             mnpctrname mnpcname
#> 1      462 Charité Berlin (RPACK)       NA

# all centres remain eventhough all three ids are from Bern
ctu05_data_pids$ctr
#>   mnpctrid                       mnpctrname mnpcname
#> 1      462           Charité Berlin (RPACK)       NA
#> 2      461         Inselspital Bern (RPACK)       NA
#> 3      441 Universitätsspital Basel (RPACK)       NA
```

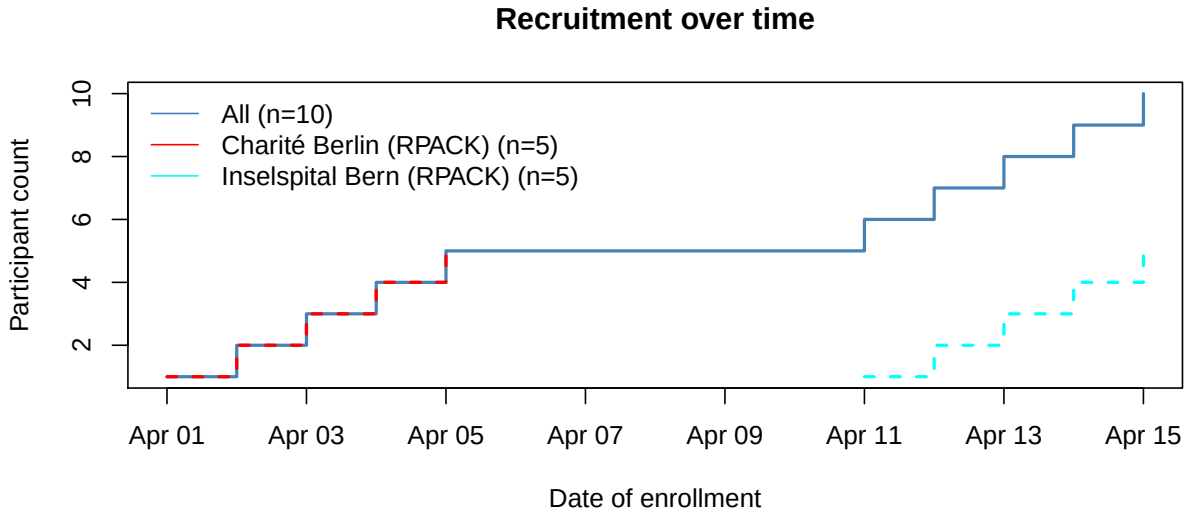
Since the truncated object's class remains unchanged (i.e. `secuTrialdata`) you can still use the generic functions on it. Let's say you would only like to look at the recruitment plot for Bern alone.

```
# keep only Bern
ctu05_data_bern <- subset_secuTrial(ctu05_data, centre = "Inselspital Bern (RPACK)")
# plot
plot_recruitment(ctu05_data_bern)
```



. . . or Bern and Berlin.

```
# keep only Bern and Berlin
ctu05_data_bern_berlin <- subset_secuTrial(ctu05_data,
                                           centre = c("Inselspital Bern (RPACK)",
                                                      "Charité Berlin (RPACK)"))
# plot
plot_recruitment(ctu05_data_bern_berlin)
```



The `as.data.frame` function

This vignette has been working with the `secuTrialdata` object as a `list`. For some users, working with a `list` can be tiresome so `secuTrialR` provides an `as.data.frame()` method to save the `data.frames` in the `secuTrialdata` object to an environment of your choice.

Let's have a look at the state of your `globalenv()` before running `as.data.frame()`...

```
ls(globalenv())
#>  [1] "centres"                "ctu05_data"
#>  [3] "ctu05_data_berlin"      "ctu05_data_bern"
#>  [5] "ctu05_data_bern_basel"  "ctu05_data_bern_berlin"
#>  [7] "ctu05_data_location"    "ctu05_data_new"
#>  [9] "ctu05_data_pids"        "export_location"
#> [11] "fsc"                    "fss"
#> [13] "participants"           "vs"
```

```
# add files to global environment
as.data.frame(ctu05_data)
```

... and afterwards.

```
ls(globalenv())
#>  [1] "ae"                     "allmedi"
#>  [3] "atae"                   "atae1"
#>  [5] "atallmedi"              "atbaseline"
#>  [7] "atesurgeries"           "atmiv"
#>  [9] "atoutcome"              "atsae"
#> [11] "atstudyterminat"        "attreatment"
#> [13] "baseline"               "centres"
#> [15] "ctu05_data"             "ctu05_data_berlin"
#> [17] "ctu05_data_bern"        "ctu05_data_bern_basel"
#> [19] "ctu05_data_bern_berlin" "ctu05_data_location"
#> [21] "ctu05_data_new"         "ctu05_data_pids"
#> [23] "esurgeries"             "export_location"
#> [25] "fsc"                    "fss"
#> [27] "outcome"                "participants"
#> [29] "sae"                    "studyterminat"
#> [31] "treatment"              "vs"
```

A note on `mnp*` variables

There is a plethora of variables in the tables of secuTrial exports whose names start with `mnp`. These are meta variables which are e.g. important to logically link the different tables. Explaining them all is beyond the scope of this vignette. For detailed explanations please refer to the secuTrial user manual.

Disclaimer

The descriptions of the export data and the logic within are our understanding of them and come with no warranty. For in depth details please refer to the original secuTrial manuals.

The `sessionInfo()` of the vignette

```
sessionInfo()
#> R version 3.6.1 (2019-07-05)
#> Platform: x86_64-pc-linux-gnu (64-bit)
#> Running under: Ubuntu 18.04.3 LTS
#>
#> Matrix products: default
#> BLAS:   /usr/lib/x86_64-linux-gnu/blas/libblas.so.3.7.1
#> LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.7.1
#>
#> locale:
#>  [1] LC_CTYPE=C.UTF-8       LC_NUMERIC=C           LC_TIME=C.UTF-8
#>  [4] LC_COLLATE=C.UTF-8     LC_MONETARY=C.UTF-8    LC_MESSAGES=C.UTF-8
#>  [7] LC_PAPER=C.UTF-8       LC_NAME=C              LC_ADDRESS=C
#> [10] LC_TELEPHONE=C         LC_MEASUREMENT=C.UTF-8 LC_IDENTIFICATION=C
#>
#> attached base packages:
#> [1] tcltk     stats     graphics  grDevices utils     datasets  methods
#> [8] base
#>
#> other attached packages:
#>  [1] secuTrialR_0.8.3 lubridate_1.7.4  dplyr_0.8.3      tidyr_1.0.0
#>  [5] purrr_0.3.3      tibble_2.1.3     stringr_1.4.0    readxl_1.3.1
#>  [9] readr_1.3.1      igraph_1.2.4.1   haven_2.2.0      rmarkdown_1.16
#>
#> loaded via a namespace (and not attached):
#>  [1] Rcpp_1.0.3       knitr_1.25       magrittr_1.5     hms_0.5.2
#>  [5] tidyselect_0.2.5 R6_2.4.0         rlang_0.4.1      tools_3.6.1
#>  [9] packrat_0.5.0    xfun_0.10        htmltools_0.4.0  assertthat_0.2.1
#> [13] yaml_2.2.0       digest_0.6.22    lifecycle_0.1.0  crayon_1.3.4
#> [17] vctrs_0.2.0      zeallot_0.1.0    glue_1.3.1       evaluate_0.14
#> [21] stringi_1.4.3    compiler_3.6.1   pillar_1.4.2     cellranger_1.1.0
#> [25] forcats_0.4.0    backports_1.1.5  tufte_0.5        pkgconfig_2.0.3
```