

Create CDISC pilot tables

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Setup

This script creates RDF data cubes from .csv files.

```
library(rrdfancillary)
library(rrdfcdisc)
library(rrdfqb)
library(rrdfqbcrnd0)
devtools::load_all(pkg="../..")
```

```
## Loading rrdfqbcrndex
```

All files are stored in the directory

```
targetDir<- system.file("extdata/sample-rdf", package="rrdfqbcrndex")
(targetDir)
```

```
## [1] "/home/ma/projects/rrdfqbcrnd0/rrdfqbcrndex/inst/extdata/sample-rdf"
```

Create from demo data PhUSE scripting program

The files are generated by a SAS program - extdata/sample-workflow/adsl1.sas. The input files are read directly from .csv files instead of using the workbook, to avoid the extra step with the workbook, as the input files may be updated by running the SAS program.

```
tab1x01ObsDataCsvFn<- system.file("extdata/sample-cfg", "TAB1X01.csv", package="rrdfqbcindex")
# tab1x01ObsDataCsvFn<- "TAB1X01.csv"
tab1x01ObsData <- read.csv(tab1x01ObsDataCsvFn,stringsAsFactors=FALSE)

##TODO add measurefmt; quick hack - affects vignettes/cube-from-workbook.Rmd and
##TODO inst/data-raw/create-qb-examples-as-ttl.Rmd
if (!( "measurefmt" %in% names(tab1x01ObsData))) {
tab1x01ObsData$measurefmt<- "%6.1f"
tab1x01ObsData$measurefmt[ tab1x01ObsData$procedure %in% c("n", "nmiss", "count") ]<- "%6.0f"
## sprintf( tab1x01ObsData$measurefmt, tab1x01ObsData$measure)
}

tab1x01MetaDataCsvFn<- system.file("extdata/sample-cfg", "TAB1X01-Components.csv", package="rrdfqbcindex")
# tab1x01MetaDataCsvFn<- "TAB1X01-Components.csv"
tab1x01MetaData <- read.csv(tab1x01MetaDataCsvFn,stringsAsFactors=FALSE)

tab1x01.cube.fn<- BuildCubeFromDataFrames(tab1x01MetaData, tab1x01ObsData )
```

```
## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value
```

```
## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value
```

```
## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value
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## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
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## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
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## -- CODING ERROR- no decode value

```



```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

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## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
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## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

```



```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): N -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

```



```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --

```

```

## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Placebo --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## High Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Xanomeline
## Low Dose -- CODING ERROR- no decode value

```

```

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --

```

```

## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): count --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): quantity --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

```

```
## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): _ALL_ --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): Y -- CODING
## ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): percent --
## CODING ERROR- no decode value

## Warning in ph.recode(obsData[i, qbdim], recode.list[[qbdim]]): proportion
## -- CODING ERROR- no decode value
```

```
cat("TAB1X01 cube stored as ", normalizePath(tab1x01.cube.fn), "\n")
```

```
## TAB1X01 cube stored as /tmp/Rtmp5E1kxG/DC-TAB1X01-R-V-0-0-0.ttl
```

```
targetFile<- file.path(targetDir,"CDISC-pilot-TAB1X01.ttl")

if (file.copy( tab1x01.cube.fn, targetFile, overwrite=TRUE)) {
  cat("RDF data cube copied to ", normalizePath(targetFile), "\n")
}
```

```
## RDF data cube copied to /home/ma/projects/rrdfqbc rnd0/rrdfqbc rndex/inst/extdata/sample-rdf/CDISC-pi
```

Now look at the generated cubes by loading the turtle files.

```
dataCubeFile<- targetFile
```

The rest of the code only depends on the value of dataCubeFile.

```
checkCube <- new.rdf(ontology=FALSE) # Initialize
cat("Loading RDF data cube from ", normalizePath(dataCubeFile), "\n")
```

```
## Loading RDF data cube from /home/ma/projects/rrdfqbc rnd0/rrdfqbc rndex/inst/extdata/sample-rdf/CDISC
```

```
temp<- load.rdf(dataCubeFile, format="TURTLE", appendTo= checkCube)
summarize.rdf(checkCube)
```

```
## [1] "Number of triples: 1442"
```

Get the values in the cube

First set values for accessing the cube.

```
dsdName<- GetDsdNameFromCube( checkCube )
domainName<- GetDomainNameFromCube( checkCube )
forsparqlprefix<- GetForSparqlPrefix( domainName )
```

The next statement shows the first 10 triples in the cube.


```

observations1Rq<- paste( forsparqlprefix,
',
select *
where {?s ?p ?o .}
limit 10
',
"\n"
)
observations1<- sparql.rdf(checkCube, observations1Rq )
knitr::kable(head(observations1))

```

s	p	o
ds:obs50	rdf:type	qb:Observation
ds:obs50	crnd-dimension:ittfl	code:CODING ERROR- no decode value
ds:obs50	crnd-dimension:comp24fl	code:CODING ERROR- no decode value
ds:obs50	crnd-dimension:trt01p	code:CODING ERROR- no decode value
ds:obs50	crnd-dimension:procedure	code:CODING ERROR- no decode value
ds:obs50	crnd-dimension:efffl	code:CODING ERROR- no decode value

The next statement shows the first 10 triples in the cube, where the subject is a qb:Observation.

```

observations2Rq<- paste( forsparqlprefix,
',
select *
where { ?s a qb:Observation ; ?p ?o .}
limit 10
',
"\n"
)
observations2<- sparql.rdf(checkCube, observations2Rq)
knitr::kable(head(observations2, 10))

```

s	p	o
ds:obs49	rdfs:label	49
ds:obs49	crnd-dimension:disconfl	code:CODING ERROR- no decode value
ds:obs49	crnd-dimension:trt01p	code:CODING ERROR- no decode value
ds:obs49	crnd-dimension:procedure	code:CODING ERROR- no decode value
ds:obs49	qb:dataSet	ds:dataset-TAB1X01
ds:obs49	crnd-dimension:comp24fl	code:CODING ERROR- no decode value
ds:obs49	crnd-dimension:ittfl	code:CODING ERROR- no decode value
ds:obs49	crnd-attribute:denominator	
ds:obs49	crnd-dimension:efffl	code:CODING ERROR- no decode value
ds:obs49	crnd-attribute:unit	NA

Get cube components

The cube components are shown in the next output.

```

componentsRq<- GetComponentSparqlQuery( forsparqlprefix, dsdName )
components<- as.data.frame(sparql.rdf(checkCube, componentsRq), stringsAsFactors=FALSE)
components$vn<- gsub("crnd-dimension:|crnd-attribute:|crnd-measure:", "", components$p)
knitr::kable(components[,c("vn", "label")])

```

vn	label
comp24fl	comp24fl
disconfl	disconfl
efffl	efffl
factor	Type of procedure (quantity, proportion...)
ittfl	ittfl
procedure	Statistical Procedure
saffl	saffl
trt01p	Treatment Arm

The codelists are shown in the next output.

```

codelistsRq<- GetCodeListSparqlQuery( forsparqlprefix, dsdName )
codelists<- as.data.frame(sparql.rdf(checkCube, codelistsRq), stringsAsFactors=FALSE)
codelists$vn<- gsub("crnd-dimension:|crnd-attribute:|crnd-measure:", "", codelists$dimension)
codelists$clc<- gsub("code:", "", codelists$c1)
knitr::kable(codelists[,c("vn", "clc", "clprefLabel")])

```

vn	clc	clprefLabel
comp24fl	comp24fl-N	N
comp24fl	comp24fl-Y	Y
comp24fl	comp24fl- <i>ALL</i>	<i>ALL</i>
comp24fl	comp24fl- <i>NONMISS</i>	<i>NONMISS</i>
disconfl	disconfl-Y	Y
disconfl	disconfl- <i>ALL</i>	<i>ALL</i>
disconfl	disconfl- <i>NONMISS</i>	<i>NONMISS</i>
efffl	efffl-N	N
efffl	efffl-Y	Y
efffl	efffl- <i>ALL</i>	<i>ALL</i>
efffl	efffl- <i>NONMISS</i>	<i>NONMISS</i>
factor	factor- <i>ALL</i>	<i>ALL</i>
factor	factor- <i>NONMISS</i>	<i>NONMISS</i>
factor	factor-proportion	proportion
factor	factor-quantity	quantity
ittfl	ittfl-Y	Y
ittfl	ittfl- <i>ALL</i>	<i>ALL</i>
ittfl	ittfl- <i>NONMISS</i>	<i>NONMISS</i>
procedure	procedure-count	count
procedure	procedure-percent	percent
saffl	saffl-Y	Y
saffl	saffl- <i>ALL</i>	<i>ALL</i>
saffl	saffl- <i>NONMISS</i>	<i>NONMISS</i>
trt01p	trt01p-	
trt01p	trt01p-Placebo	Placebo
trt01p	trt01p-Xanomeline_High_Dose	Xanomeline High Dose

vn	clc	clprefLabel
trt01p	trt01p-Xanomeline_Low_Dose	Xanomeline Low Dose
trt01p	trt01p- <i>ALL</i>	<i>ALL</i>
trt01p	trt01p- <i>NONMISS</i>	<i>NONMISS</i>

The dimensions are shown in the next output.

```
dimensionsRq <- GetDimensionsSparqlQuery( forsparqlprefix )
dimensions<- sparql.rdf(checkCube, dimensionsRq)
knitr::kable(dimensions)
```

p

```
crnd-dimension:disconfl
crnd-dimension:saffl
crnd-dimension:trt01p
crnd-dimension:factor
crnd-dimension:procedure crnd-dimension:comp24fl
crnd-dimension:ittfl
crnd-dimension:efffl
```

Then the attributes as shown in the next output.

```
attributesRq<- GetAttributesSparqlQuery( forsparqlprefix )
attributes<- sparql.rdf(checkCube, attributesRq)
knitr::kable(attributes)
```

p

```
crnd-attribute:denominator crnd-attribute:unit
```

Get observations

And finally the SPARQL query for observations, showing only the first 10 observations.

```
observationsRq<- GetObservationsSparqlQuery( forsparqlprefix, domainName, dimensions, attributes )
cat(observationsRq)
```

```
## prefix rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
## prefix skos: <http://www.w3.org/2004/02/skos/core#>
## prefix prov: <http://www.w3.org/ns/prov#>
## prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#>
## prefix dcat: <http://www.w3.org/ns/dcat#>
## prefix owl: <http://www.w3.org/2002/07/owl#>
## prefix xsd: <http://www.w3.org/2001/XMLSchema#>
## prefix pav: <http://purl.org/pav>
## prefix dc: <http://purl.org/dc/elements/1.1/>
## prefix dct: <http://purl.org/dc/terms/>
## prefix mms: <http://rdf.cdisc.org/mms#>
```

```

## prefix cts: <http://rdf.cdisc.org/ct/schema#>
## prefix cdiscs: <http://rdf.cdisc.org/std/schema#>
## prefix cdash-1-1: <http://rdf.cdisc.org/std/cdash-1-1#>
## prefix cdashct: <http://rdf.cdisc.org/cdash-terminology#>
## prefix sdtmct: <http://rdf.cdisc.org/sdtm-terminology#>
## prefix sdtm-1-2: <http://rdf.cdisc.org/std/sdtm-1-2#>
## prefix sdtm-1-3: <http://rdf.cdisc.org/std/sdtm-1-3#>
## prefix sdtms-1-3: <http://rdf.cdisc.org/sdtm-1-3/schema#>
## prefix sdtmig-3-1-2: <http://rdf.cdisc.org/std/sdtmig-3-1-2#>
## prefix sdtmig-3-1-3: <http://rdf.cdisc.org/std/sdtmig-3-1-3#>
## prefix sendct: <http://rdf.cdisc.org/send-terminology#>
## prefix sendig-3-0: <http://rdf.cdisc.org/std/sendig-3-0#>
## prefix adamct: <http://rdf.cdisc.org/adam-terminology#>
## prefix adam-2-1: <http://rdf.cdisc.org/std/adam-2-1#>
## prefix adamig-1-0: <http://rdf.cdisc.org/std/adamig-1-0#>
## prefix adamvr-1-2: <http://rdf.cdisc.org/std/adamvr-1-2#>
## prefix qb: <http://purl.org/linked-data/cube#>
## prefix rrdqbcrnd0: <http://www.example.org/rrdqbcrnd0/>
## prefix code: <http://www.example.org/dc/code/>
## prefix dccs: <http://www.example.org/dc/tab1x01/dccs/>
## prefix ds: <http://www.example.org/dc/tab1x01/ds/>
## prefix crnd-dimension: <http://www.example.org/dc/dimension#>
## prefix crnd-attribute: <http://www.example.org/dc/attribute#>
## prefix crnd-measure: <http://www.example.org/dc/measure#>
##
## select * where {
##   ?s a qb:Observation ;
##     qb:dataSet ds:dataset-TAB1X01 ;
##     crnd-dimension:disconfl ?disconfl;
##     crnd-dimension:saffl ?saffl;
##     crnd-dimension:trt01p ?trt01p;
##     crnd-dimension:factor ?factor;
##     crnd-dimension:procedure ?procedure;
##     crnd-dimension:comp24fl ?comp24fl;
##     crnd-dimension:ittfl ?ittfl;
##     crnd-dimension:efffl ?efffl;
##     crnd-attribute:denominator ?denominator;
##     crnd-attribute:unit ?unit;
##     crnd-measure:measure ?measure .
## optional{ ?disconfl skos:prefLabel ?disconflvalue . }
## optional{ ?saffl skos:prefLabel ?safflvalue . }
## optional{ ?trt01p skos:prefLabel ?trt01pvalue . }
## optional{ ?factor skos:prefLabel ?factorvalue . }
## optional{ ?procedure skos:prefLabel ?procedurevalue . }
## optional{ ?comp24fl skos:prefLabel ?comp24flvalue . }
## optional{ ?ittfl skos:prefLabel ?ittflvalue . }
## optional{ ?efffl skos:prefLabel ?effflvalue . }
## }
## order by ?s

```

```

observations<- as.data.frame(sparql.rdf(checkCube, observationsRq ), stringsAsFactors=FALSE)
knitr::kable(observations[ 1:10 ,
  c(paste0(sub("crnd-dimension:|crnd-attribute:|crnd-measure:", "", dimensions), "value"), sub("crnd-dim

```

disconflvalue	safflvalue	trt01pvalue	factorvalue	procedurevalue	comp24flvalue	ittflvalue	effflvalue	denominator
NA	NA	NA	NA	NA	NA	NA	NA	
NA	NA	NA	NA	NA	NA	NA	NA	ittfl
NA	NA	NA	NA	NA	NA	NA	NA	
NA	NA	NA	NA	NA	NA	NA	NA	ittfl
NA	NA	NA	NA	NA	NA	NA	NA	
NA	NA	NA	NA	NA	NA	NA	NA	ittfl
NA	NA	NA	NA	NA	NA	NA	NA	
NA	NA	NA	NA	NA	NA	NA	NA	ittfl
NA	NA	NA	NA	NA	NA	NA	NA	
NA	NA	NA	NA	NA	NA	NA	NA	saffl

Get observations with labels

The SPARQL query for observations with labels for variables, showing only the first 10 observations.

```
observationsDescriptionRq<- GetObservationsWithDescriptionSparqlQuery( forsparqlprefix, domainName, dimensionName,
cat(observationsDescriptionRq)
```

```
## prefix rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#>
## prefix skos: <http://www.w3.org/2004/02/skos/core#>
## prefix prov: <http://www.w3.org/ns/prov#>
## prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#>
## prefix dcat: <http://www.w3.org/ns/dcat#>
## prefix owl: <http://www.w3.org/2002/07/owl#>
## prefix xsd: <http://www.w3.org/2001/XMLSchema#>
## prefix pav: <http://purl.org/pav>
## prefix dc: <http://purl.org/dc/elements/1.1/>
## prefix dct: <http://purl.org/dc/terms/>
## prefix mms: <http://rdf.cdsc.org/mms#>
## prefix cts: <http://rdf.cdsc.org/ct/schema#>
## prefix cdiscs: <http://rdf.cdsc.org/std/schema#>
## prefix cdash-1-1: <http://rdf.cdsc.org/std/cdash-1-1#>
## prefix cdashct: <http://rdf.cdsc.org/cdash-terminology#>
## prefix sdtmct: <http://rdf.cdsc.org/sdtm-terminology#>
## prefix sdtm-1-2: <http://rdf.cdsc.org/std/sdtm-1-2#>
## prefix sdtm-1-3: <http://rdf.cdsc.org/std/sdtm-1-3#>
## prefix sdtms-1-3: <http://rdf.cdsc.org/sdtm-1-3/schema#>
## prefix sdtmig-3-1-2: <http://rdf.cdsc.org/std/sdtmig-3-1-2#>
## prefix sdtmig-3-1-3: <http://rdf.cdsc.org/std/sdtmig-3-1-3#>
## prefix sendct: <http://rdf.cdsc.org/send-terminology#>
## prefix sendig-3-0: <http://rdf.cdsc.org/std/sendig-3-0#>
## prefix adamct: <http://rdf.cdsc.org/adam-terminology#>
## prefix adam-2-1: <http://rdf.cdsc.org/std/adam-2-1#>
## prefix adamig-1-0: <http://rdf.cdsc.org/std/adamig-1-0#>
## prefix adamvr-1-2: <http://rdf.cdsc.org/std/adamvr-1-2#>
## prefix qb: <http://purl.org/linked-data/cube#>
## prefix rrdqbcrnd0: <http://www.example.org/rrdqbcrnd0/>
## prefix code: <http://www.example.org/dc/code/>
## prefix dccc: <http://www.example.org/dc/tab1x01/dccc/>
## prefix ds: <http://www.example.org/dc/tab1x01/ds/>
## prefix crnd-dimension: <http://www.example.org/dc/dimension#>
```

```
## prefix crnd-attribute: <http://www.example.org/dc/attribute#>
## prefix crnd-measure: <http://www.example.org/dc/measure#>
## select * where {
##   ?s a qb:Observation ;
##   qb:dataSet ds:dataset-TAB1X01 ;
##   crnd-dimension:disconfl ?disconfl;
##   crnd-dimension:saffl ?saffl;
##   crnd-dimension:trt01p ?trt01p;
##   crnd-dimension:factor ?factor;
##   crnd-dimension:procedure ?procedure;
##   crnd-dimension:comp24fl ?comp24fl;
##   crnd-dimension:ittfl ?ittfl;
##   crnd-dimension:efffl ?efffl;
##   crnd-attribute:denominator ?denominator;
##   crnd-attribute:unit ?unit;
##   crnd-measure:measure ?measure .
##   optional{ ?disconfl skos:prefLabel ?disconflvalue . }
##   optional{ ?saffl skos:prefLabel ?safflvalue . }
##   optional{ ?trt01p skos:prefLabel ?trt01pvalue . }
##   optional{ ?factor skos:prefLabel ?factorvalue . }
##   optional{ ?procedure skos:prefLabel ?procedurevalue . }
##   optional{ ?comp24fl skos:prefLabel ?comp24flvalue . }
##   optional{ ?ittfl skos:prefLabel ?ittflvalue . }
##   optional{ ?efffl skos:prefLabel ?effflvalue . }
##   optional{ crnd-dimension:disconfl rdfs:label ?disconfllabel . }
##   optional{ crnd-dimension:saffl rdfs:label ?saffllabel . }
##   optional{ crnd-dimension:trt01p rdfs:label ?trt01plabel . }
##   optional{ crnd-dimension:factor rdfs:label ?factorlabel . }
##   optional{ crnd-dimension:procedure rdfs:label ?procedurelabel . }
##   optional{ crnd-dimension:comp24fl rdfs:label ?comp24fllabel . }
##   optional{ crnd-dimension:ittfl rdfs:label ?ittfllabel . }
##   optional{ crnd-dimension:efffl rdfs:label ?efffllabel . }
##   BIND( IRI(crnd-dimension:disconfl) as ?disconflIRI)
##   BIND( IRI(crnd-dimension:saffl) as ?safflIRI)
##   BIND( IRI(crnd-dimension:trt01p) as ?trt01pIRI)
##   BIND( IRI(crnd-dimension:factor) as ?factorIRI)
##   BIND( IRI(crnd-dimension:procedure) as ?procedureIRI)
##   BIND( IRI(crnd-dimension:comp24fl) as ?comp24flIRI)
##   BIND( IRI(crnd-dimension:ittfl) as ?ittflIRI)
##   BIND( IRI(crnd-dimension:efffl) as ?effflIRI)
##   BIND( IRI( ?s ) AS ?measureIRI)
## }
```

```
observationsDesc<- as.data.frame(sparql.rdf(checkCube, observationsDescriptionRq ), stringsAsFactors=FALSE)
knitr::kable(observationsDesc[ 1:10 ,
  c(paste0(rep(sub("crnd-dimension:|crnd-attribute:|crnd-measure:", "", dimensions),each=3),
    c("label", "value", "IRI")),
    sub("crnd-dimension:|crnd-attribute:|crnd-measure:", "", attributes), "measure", "measureIRI"
  )])
```

disconfllabel	disconflvalue	disconflIRI	saffllabel	safflvalue	safflIRI	trt01plabel	trt01pvalue
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA

disconfllabel	disconflvalue	disconflIRI	saffllabel	safflvalue	safflIRI	trt01plabel	trt01value
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA
disconfl	NA	crnd-dimension:disconfl	saffl	NA	crnd-dimension:saffl	Treatment Arm	NA

Reproduce the metadata for the workbook from cube

Here is an example of roundtripping: make the metadata used for the workbook from RDF data cube.

First get the dimensions, measure and attribute

```
workbookDimAttrMeasRq<- GetDimAttrMeasInWorkbookFormatSparqlQuery( forsparqlprefix )
dimensionsattr<- sparql.rdf(checkCube, workbookDimAttrMeasRq )
knitr::kable(dimensionsattr)
```

compType	compName	codeType	nciDomainValue
dimension	crnd-dimension:disconfl	NA	NA
dimension	crnd-dimension:saffl	NA	NA
dimension	crnd-dimension:trt01p	NA	NA
dimension	crnd-dimension:factor	NA	NA
dimension	crnd-dimension:procedure	NA	NA
dimension	crnd-dimension:comp24fl	NA	NA
dimension	crnd-dimension:ittfl	NA	NA
dimension	crnd-dimension:efffl	NA	NA
attribute	crnd-attribute:denominator	NA	NA
attribute	crnd-attribute:unit	NA	NA
measure	crnd-measure:measure	NA	NA

Secondly, get the metadata for the workbook. To get the metadata element “cubeVersion” a workaround is needed. The cubeversion is not directly available but from dcat:distribution derived as the result of paste0(“DC-”, domainName,“-R-V-”,cubeVersion,“.ttl”).

```
workbookMetadataRq<- GetMetaDataInWorkbookFormatSparqlQuery( forsparqlprefix )
metadata<- sparql.rdf(checkCube, workbookMetadataRq)
cubeVersion<- gsub("-", ".", gsub("DC-.*-R-V-([^\.\.]+).ttl", "\\1", metadata[ metadata[,2]=="distribution",1]))
metadataX<- rbind(metadata, cbind(compType="metadata", compName="cubeVersion", compLabel=cubeVersion))
knitr::kable(metadataX)
```

compType	compName	compLabel
metadata	title	Demographics Analysis Results
metadata	distribution	DC-TAB1X01-R-V-0-0-0.ttl
metadata	comment	
metadata	label	Table 14-1.01 Summary of Populations

	compType	compName	compLabel
	metadata	description	Data from adsl1.sas program
	metadata	obsFileName	tab1x01.csv
compLabel	metadata	cubeVersion	0.0.0

Session information

```
sessionInfo()
```

```
## R version 3.2.3 (2015-12-10)
## Platform: x86_64-redhat-linux-gnu (64-bit)
## Running under: Fedora 23 (Workstation Edition)
##
## locale:
##  [1] LC_CTYPE=en_GB.UTF-8          LC_NUMERIC=C
##  [3] LC_TIME=en_GB.UTF-8          LC_COLLATE=en_GB.UTF-8
##  [5] LC_MONETARY=en_GB.UTF-8      LC_MESSAGES=en_GB.UTF-8
##  [7] LC_PAPER=en_GB.UTF-8         LC_NAME=en_GB.UTF-8
##  [9] LC_ADDRESS=en_GB.UTF-8       LC_TELEPHONE=en_GB.UTF-8
## [11] LC_MEASUREMENT=en_GB.UTF-8   LC_IDENTIFICATION=en_GB.UTF-8
##
## attached base packages:
## [1] methods      stats      graphics  grDevices  utils      datasets  base
##
## other attached packages:
##  [1] rrdqbcindex_0.2.3  rrdqbcindex_0.2.3  rrdqbc_0.2.3
##  [4] xlsx_0.5.7         xlsxjars_0.6.1     rrdqdisc_0.2.3
##  [7] devtools_1.11.0    RCurl_1.95-4.8     bitops_1.0-6
## [10] rrdqancillary_0.2.3 rrdq_2.1.2         rrdqlibs_1.4.0
## [13] rJava_0.9-8
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_0.12.4      knitr_1.12.3      magrittr_1.5      roxygen2_5.0.1
##  [5] highr_0.5.1      stringr_1.0.0     tools_3.2.3       withr_1.0.1
##  [9] htmltools_0.3.5  yaml_2.1.13       digest_0.6.9      formatR_1.3
## [13] memoise_1.0.0    evaluate_0.8.3    rmarkdown_0.9.5   stringi_1.0-1
```