Testing reportRmd Labels

Install the new version - this is on a separate branch, so that if you want to revert you the development or CRAN versions you can simply delete the reportRmd package folder and re-install.

# if you don't have devtools installed:  
#install("devtools")  
  
# otherwise the variable label version is here:  
#devtools::install\_github("biostatsPMH/reportRmd", ref="varLabs")  
  
# For the most recent stable version  
# devtools::install\_github("biostatsPMH/reportRmd", ref="development")  
library(reportRmd)

# Labels & reportRmd

I’ve tried not to alter the basic workings of the package. The labels are added (and removed) from the variable attributes within data frames. **There is no longer an option for a default lookup table.**

# Worked Example

Get some descriptive stats for the ctDNA data that comes with the package. The nicenames argument is TRUE by default so underscores are replaced by spaces

data(ctDNA)  
rm\_covsum(data=ctDNA,  
 covs=c('cohort','ctdna\_status','size\_change'))

|  | n=270 |
| --- | --- |
| **cohort** |  |
| A | 50 (19) |
| B | 14 (5) |
| C | 18 (7) |
| D | 88 (33) |
| E | 100 (37) |
| **ctdna status** |  |
| Clearance | 137 (51) |
| No clearance, decrease from baseline | 44 (16) |
| No clearance, increase from baseline | 89 (33) |
| **size change** |  |
| Mean (sd) | -29.7 (52.8) |
| Median (Min,Max) | -32.5 (-100.0, 197.1) |
| Missing | 8 |

If we have a lookup table of variable names and labels that we imported from a data dictionary we can set the variable labels for the data frame and these will be used in the rm\_ functions

ctDNA\_names <- data.frame(var=names(ctDNA),  
 label=c('Patient ID',  
 'Study Cohort',  
 'Change in ctDNA since baseline',  
 'Number of weeks on treatment',  
 'Percentage change in tumour measurement'))  
ctDNA <- set\_labels(ctDNA,ctDNA\_names)  
  
rm\_covsum(data=ctDNA,  
 covs=c('cohort','ctdna\_status','size\_change'))

|  | n=270 |
| --- | --- |
| **Study Cohort** |  |
| A | 50 (19) |
| B | 14 (5) |
| C | 18 (7) |
| D | 88 (33) |
| E | 100 (37) |
| **Change in ctDNA since baseline** |  |
| Clearance | 137 (51) |
| No clearance, decrease from baseline | 44 (16) |
| No clearance, increase from baseline | 89 (33) |
| **Percentage change in tumour measurement** |  |
| Mean (sd) | -29.7 (52.8) |
| Median (Min,Max) | -32.5 (-100.0, 197.1) |
| Missing | 8 |

We can change individual labels with the set\_var\_labels command

ctDNA <- set\_var\_labels(ctDNA,  
 cohort="A new cohort label")  
rm\_covsum(data=ctDNA,  
 covs=c('cohort','ctdna\_status','size\_change'))

|  | n=270 |
| --- | --- |
| **A new cohort label** |  |
| A | 50 (19) |
| B | 14 (5) |
| C | 18 (7) |
| D | 88 (33) |
| E | 100 (37) |
| **Change in ctDNA since baseline** |  |
| Clearance | 137 (51) |
| No clearance, decrease from baseline | 44 (16) |
| No clearance, increase from baseline | 89 (33) |
| **Percentage change in tumour measurement** |  |
| Mean (sd) | -29.7 (52.8) |
| Median (Min,Max) | -32.5 (-100.0, 197.1) |
| Missing | 8 |

We can extract the variable labels to a data frame

var\_labels <- extract\_labels(ctDNA)  
var\_labels

variable label  
1 id Patient ID  
2 cohort A new cohort label  
3 ctdna\_status Change in ctDNA since baseline  
4 time Number of weeks on treatment  
5 size\_change Percentage change in tumour measurement

Or clear them all

ctDNA <- clear\_labels(ctDNA)