

compareGroups 2.0: Descriptives by groups

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1 Introduction

The `compareGroups` package allows users to create tables displaying results of univariate analyses, stratified or not by categorical variable groupings.

Tables can easily be exported to CSV, \LaTeX or HTML.

This package can be used from the  prompt or from a user-friendly GUI.

This document provides an overview of the usage of the `compareGroups` package.

To load the package using the  prompt, enter:

```
> library(compareGroups)
```

Once the package is loaded, non-R users can follow the GUI instructions in Section 7.

2 Design: classes and methods

The `compareGroups` package has three functions:

- `compareGroups` creates an object of class `compareGroups`. This object can be:
 - printed
 - summarized
 - plotted
 - updated
- `createTable` creates an object of class `createTable`. This object can be:
 - printed
 - summarized
- `export2latex`, `export2csv`, `export2html` will export results to CSV, \LaTeX or HTML, respectively.

Figure 1 shows the diagram of the package.

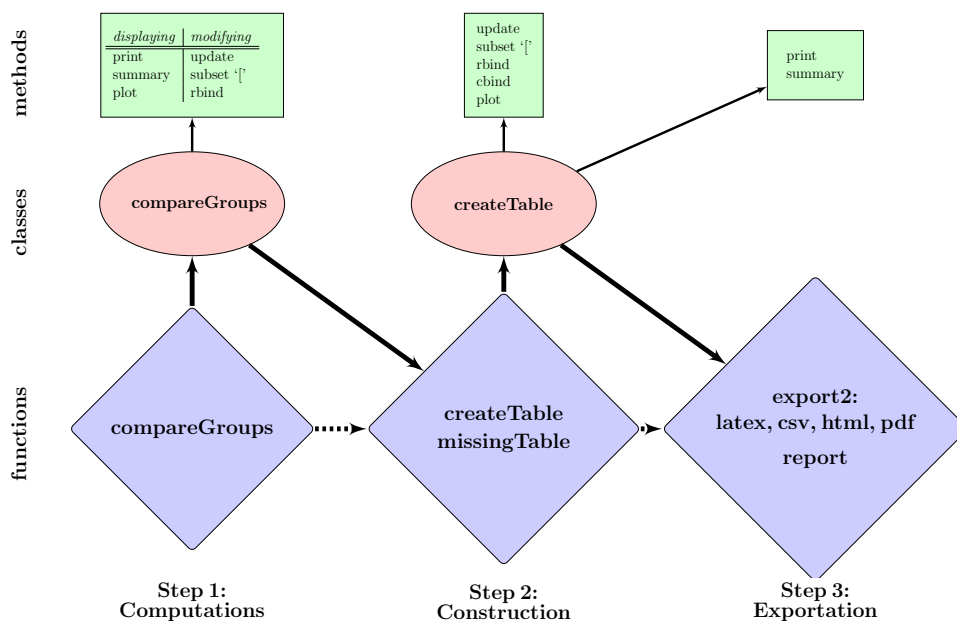


Figure 1: Diagram of the `compareGroups` package

3 Data used as example

To illustrate how this package works we sampled 85% data from the participants in the PREDIMED study (www.predimed.org) [2]. PREDIMED is a multicenter trial in Spain, where randomly assigned participants who were at high cardiovascular risk, but with no cardiovascular disease at enrolment, to one of three diets: a Mediterranean diet supplemented with extra-virgin olive oil (MedDiet+VOO), a Mediterranean diet supplemented with mixed nuts (MedDiet+Nuts), or a control diet (advice to reduce dietary fat). Participants received quarterly individual and group educational sessions and, depending on group assignment, free provision of extra-virgin olive oil, mixed nuts, or small non-food gifts. The primary end point was the rate of major cardiovascular events (myocardial infarction, stroke, or death from cardiovascular causes).

First of all, load PREDIMED data typing:

```
> data(predimed)
```

Variables and labels in this data frame are:

Name	Label	Codes
group	Intervention group	Control; MedDiet + Nuts; MedDiet + VOO
sex	Sex	Male; Female
age	Age	
smoke	Smoking	Never; Current; Former
bmi	Body mass index	
waist	Waist circumference	
wth	Waist-to-height ratio	
htn	Hypertension	No; Yes
diab	Type-2 diabetes	No; Yes
hyperchol	Dyslipidemia	No; Yes
famhist	Family history of premature CHD	No; Yes
hormo	Hormone-replacement therapy	No; Yes
p14	MedDiet Adherence score	
toevent	follow-up to main event (years)	
event	AMI, stroke, or CV Death	No; Yes

OBSERVATIONS:

1. It is important to note that `compareGroups` is not aimed to perform quality control of the data. Other useful packages such as `r21h` [3] are available for this purpose.
2. It is strongly recommended that the `data.frame` contain only the variables to be analyzed; the ones not needed in the present analysis should be removed from the list.
3. The nature of variables to be analyzed should be known, or at least which variables are to be used as categorical. It is important to code categorical variables as factors and the order of their levels is meaningful in this package.
4. The function `label` from the `Hmisc` package could be used to label the variables properly. The tables of results will contain the variable labels (by default).

3.1 Time-to-event variables

A variable of class `Surv` must be created to deal with time-to-event variables (i.e., time to Cardiovascular event/censored in our example):

```
> predimed$tmaint <- with(predimed, Surv(toevent, event == 'Yes'))
> label(predimed$tmaint) <- "AMI, stroke, or CV Death"
```

Note that variables *tmain* and *are* are created as time-to-death and time-to-cardiovascular event, respectively, both taking into account censoring (i.e. they are of class *Surv*).

4 Using R syntax

4.1 compareGroups

This is the main function. It does all the calculus. It is needed to store results in an object. Later, applying the function `createTable` (Section 4.2) to this object will create tables of the analysis results.

For example, to perform a univariate analysis with the *predimed* data between *group* (“response” variable) and all other variables (“explanatory” variables), this formula is required:

```
> compareGroups(group ~ . , data=predimed)
```

4.1.1 Selecting response variables

If only a dot occurs on the right side of the “~” all variables in the data frame will be used.

To remove the variable *toevent* and *event* from the analysis:

```
> compareGroups(group ~ . -toevent - event, data=predimed)
```

To select some explanatory variables (e.g., *age*, *sex*, and *waist*) and store results in an object of class `compareGroups`:

```
> res<-compareGroups(group ~ age + sex + smoke + waist + hormo, data=predimed)
> res
```

```
----- Summary of results by groups of 'Intervention group'-----

  var                N    p.value  method      selection
1 Age                6324 0.003** continuous normal ALL
2 Sex                6324 <0.001** categorical      ALL
3 Smoking            6324 0.444   categorical      ALL
4 Waist circumference 6324 0.045** continuous normal ALL
5 Hormone-replacement therapy 5661 0.850   categorical      ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 '.' 1
```

Note: Although we have full data (n= 6324) for Age, Sex and Waist circumference, there are some missing data in Hormone-replacement therapy (probably male participants).

Diet groups have some differences in Smoking and Hormone-replacement therapy although those don’t reach statistical significance (p-value=0.714 and 0.859, respectively); although Age, Sex and Waist circumference are clearly different.

Age & Waist circumference has been used as continuous and normal distributed. Sex, Smoking & Hormone-replacement therapy as categorical.

No filters have been used (e.g., selecting only treated patients); therefore, the *selection* column lists “ALL” (for all variables).

4.1.2 Subsetting

To perform the analysis in a subset of participants (e.g., “female” participants):

```
> compareGroups(group ~ age + smoke + waist + hormo, data=predimed,
+               subset = sex=="Female")
```

```
----- Summary of results by groups of 'Intervention group'-----
```

	var	N	p.value	method	selection
1	Age	3645	0.056*	continuous normal	sex == "Female"
2	Smoking	3645	0.907	categorical	sex == "Female"
3	Waist circumference	3645	0.016**	continuous normal	sex == "Female"
4	Hormone-replacement therapy	3459	0.898	categorical	sex == "Female"

```
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1
```

Note that only results for female participants are shown.

To subset specific variable/s (e.g., *hormo* and *waist*):

```
> compareGroups(group ~ age + sex + smoke + waist + hormo, data=predimed,
+               selec = list(hormo= sex=="Female", waist = waist>20 ))
```

```
----- Summary of results by groups of 'Intervention group'-----
```

	var	N	p.value	method	selection
1	Age	6324	0.003**	continuous normal	ALL
2	Sex	6324	<0.001**	categorical	ALL
3	Smoking	6324	0.444	categorical	ALL
4	Waist circumference	6324	0.045**	continuous normal	waist > 20
5	Hormone-replacement therapy	3459	0.898	categorical	sex == "Female"

```
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1
```

Combinations are also allowed, e.g.:

```
> compareGroups(group ~ age + smoke + waist + hormo, data=predimed,
+               selec = list(waist= !is.na(hormo)), subset = sex=="Female")
```

```
----- Summary of results by groups of 'Intervention group'-----
```

	var	N	p.value	method	selection
1	Age	3645	0.056*	continuous normal	sex == "Female"
2	Smoking	3645	0.907	categorical	sex == "Female"
3	Waist circumference	3459	0.007**	continuous normal	(sex == "Female") & (!is.na(hormo))
4	Hormone-replacement therapy	3459	0.898	categorical	sex == "Female"

```
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1
```

A variable can appear twice in the formula, e.g.:

```
> compareGroups(group ~ age + sex + bmi + bmi + waist + hormo, data=predimed,
+               selec = list(bmi.1=!is.na(hormo)))
```

```
----- Summary of results by groups of 'Intervention group'-----
```

	var	N	p.value	method	selection
1	Age	6324	0.003**	continuous normal	ALL
2	Sex	6324	<0.001**	categorical	ALL
3	Body mass index	6324	<0.001**	continuous normal	ALL
4	Body mass index	5661	<0.001**	continuous normal	!is.na(hormo)
5	Waist circumference	6324	0.045**	continuous normal	ALL
6	Hormone-replacement therapy	5661	0.850	categorical	ALL

```
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1
```

In this case results for *bmi* will be reported for all participants (n= 6324) and also for only those with no missing in Hormone-replacement therapy (!is.na(hormo)). Note that “bmi.1” in the **selec** statement refers to the second time that *bmi* appears in the formula.

4.1.3 Methods for continuous variables

By default continuous variables are analyzed as normal-distributed. When a table is built (see **createTable** function, Section 4.2), continuous variables will be described with mean and standard deviation. To change default options, e.g., “waist” used as non-normal distributed:

```
> compareGroups(group ~ age + smoke + waist + hormo, data=predimed,
+               method = c(waist=2))
```

```
----- Summary of results by groups of 'Intervention group'-----

  var                N    p.value method                selection
1 Age                6324 0.003** continuous normal          ALL
2 Smoking            6324 0.444   categorical              ALL
3 Waist circumference 6324 0.085*  continuous non-normal ALL
4 Hormone-replacement therapy 5661 0.850   categorical              ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 '.' 1
```

Note that “continuous non-normal” is shown in the *method* column for the variable Hormone-replacement therapy.

Possible values in methods statement are:

- 1: forces analysis as normal-distributed
- 2: forces analysis as continuous non-normal
- 3: forces analysis as categorical
- NA: performs a Shapiro-Wilks test to decide between normal or non-normal

If the **method** for a variable is stated as = **NA**, then a Shapiro-Wilk test for normality is used to decide if the variable is normal or non-normal distributed. To change the significance threshold:

```
> compareGroups(group ~ age + smoke + waist + hormo, data=predimed,
+               method = c(waist=NA), alpha= 0.01)
```

```
----- Summary of results by groups of 'Intervention group'-----

  var                N    p.value method                selection
1 Age                6324 0.003** continuous normal          ALL
2 Smoking            6324 0.444   categorical              ALL
3 Waist circumference 6324 0.085*  continuous non-normal ALL
4 Hormone-replacement therapy 5661 0.850   categorical              ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 '.' 1
```

According to Shapiro-Wilk test, stating the cutpoint at 0.01 level, Hormone-replacement therapy departed significantly from the normal distribution and therefore the method for this variable will be “continuous non-normal”.

All non factor variables are considered as continuous. Exception is made (by default) for those that have fewer than 5 different values. This threshold can be changed in the **min.dis** statement:

```
> cuts<-"lo:55=1; 56:60=2; 61:65=3; 66:70=4; 71:75=5; 76:80=6; 81:hi=7"
> predimed$age7gr<-car::recode(predimed$age, cuts)
> compareGroups(group ~ age7gr, data=predimed, method = c(age7gr=NA))
```

```
----- Summary of results by groups of 'Intervention group'-----
```

```

var N      p.value method      selection
1 Age 6324 0.007** continuous non-normal ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1

```

```
> compareGroups(group ~ age7gr, data=predimed, method = c(age7gr=NA), min.dis=8)
```

```
----- Summary of results by groups of 'Intervention group'-----
```

```

var N      p.value method      selection
1 Age 6324 0.009** categorical ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1

```

To avoid errors the maximum categories for the response variable is set at 5 in this example (default value). If this variable has more than 5 different values, the function `compareGroups` returns an error message. For example:

```
> compareGroups(age7gr ~ sex + bmi + waist , data=predimed)
```

```
Error en compareGroups.default(X = X, y = y, include.label = include.label, :
number of groups must be less or equal to 5
```

Defaults setting can be changed with the **max.ylev** statement:

```
> compareGroups(age7gr ~ sex + bmi + waist, data=predimed, max.ylev=7)
```

```
----- Summary of results by groups of 'Age'-----
```

```

var      N      p.value method      selection
1 Sex      6324 <0.001** categorical      ALL
2 Body mass index 6324 0.021** continuous normal ALL
3 Waist circumference 6324 0.034** continuous normal ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1

```

Similarly, by default there is a limit for the maximum number of levels for an explanatory variable. If this level is exceeded, the variable is removed from the analysis and a warning message is printed:

```
> compareGroups(group ~ sex + age7gr, method= (age7gr=3), data=predimed, max.xlev=5)
```

```
----- Summary of results by groups of 'Intervention group'-----
```

```

var N      p.value method      selection
1 Sex 6324 <0.001** categorical ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1

```

```
Warning in compareGroups.default(X = X, y = y, include.label = include.label, :
Variables 'age7gr' have been removed since some errors occurred
```


4.1.4 Dressing up the output

Although the options described in this section correspond to `compareGroups` function, results of changing/setting them won't be visible until the table is created with the `createTable` function (explained later).

include.label By default the variable labels are shown in the output (if there is no label the name will be printed). Changing the statement `include.label` from “= TRUE” (default) to “= FALSE” will cause variable names to be printed instead.

```
> compareGroups(group ~ age + smoke + waist + hormo, data=predimed,
+               include.label= FALSE)
```

```
----- Summary of results by groups of 'group'-----
```

```

var   N    p.value method      selection
1 age  6324 0.003** continuous normal ALL
2 smoke 6324 0.444  categorical      ALL
3 waist 6324 0.045** continuous normal ALL
4 hormo 5661 0.850  categorical      ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 '.' 1
```

Q1, Q3 When the method for a variable is stated as “2” (i.e., to be analyzed as continuous non-normal; see section 4.1.3), by default the median and quartiles 1 and 3 will be shown in the final results, after applying the function `createTable` (see Section 4.2).

```
> resu1<-compareGroups(group ~ age + waist, data=predimed,
+                      method = c(waist=2))
> createTable(resu1)
```

```
-----Summary descriptives table by 'Intervention group'-----
```

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Waist circumference	101 [94.0;108]	100 [93.0;107]	100 [93.0;107]	0.085

Note: percentiles 25 and 75 are calculated for *Waist circumference*.

To get instead percentile 2.5 and 97.5:

```
> resu2<-compareGroups(group ~ age + smoke + waist + hormo, data=predimed,
+                      method = c(waist=2), Q1=0.025, Q3=0.975)
> createTable(resu2)
```

```
-----Summary descriptives table by 'Intervention group'-----
```

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Smoking:				0.444

Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Waist circumference	101 [80.0;123]	100 [80.0;121]	100 [80.0;121]	0.085
Hormone-replacement therapy:				0.850
No	1811 (98.3%)	1835 (98.4%)	1918 (98.2%)	
Yes	31 (1.68%)	30 (1.61%)	36 (1.84%)	

Note: percentiles 2.5 and 97.5 are calculated for Follow-up.

To get minimum and maximum:

```
> compareGroups(group ~ age + smoke + waist + hormo, data=predimed,
+               method = c(waist=2), Q1=0, Q3=1)
```

simplify Sometimes a categorical variable has no individuals for a specific group. For example, *smoker* has 3 levels. As an example and to illustrate this problem, we have created a new variable *smk* with a new category (“Unknown”):

```
> predimed$smk<-predimed$smoke
> levels(predimed$smk)<- c("Never smoker", "Current or former < 1y", "Never or former >= 1y",
> label(predimed$smk)<-"Smoking 4 cat."
> cbind(table(predimed$smk))
```

```
      [,1]
Never smoker      3892
Current or former < 1y    858
Never or former >= 1y  1574
Unknown              0
```

Note that this new category (“unknown”) has no individuals:

```
> compareGroups(group ~ age + smk + waist + hormo, data=predimed)
```

```
----- Summary of results by groups of 'Intervention group'-----
```

var	N	p.value	method	selection
1 Age	6324	0.001**	continuous normal	ALL
2 Smoking 4 cat.	6324	0.714	categorical	ALL
3 Waist circumference	6324	0.019**	continuous normal	ALL
4 Hormone-replacement therapy	5650	0.859	categorical	ALL

```
-----
```

```
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1
```

```
Warning message:
```

```
In compare.i(X[, i], y = y, selec.i = selec[i], method.i = method[i], :
Some levels of 'smk' are removed since no observation in that/those levels
```

Note that an “Warning” message is printed related to the problem with *smk*.

To avoid using empty categories, **simplify** must be stated as TRUE (Default value).

```
> compareGroups(group ~ age + smk, data=predimed, simplify=FALSE)
```

----- Summary of results by groups of 'Intervention group'-----

	var	N	p.value	method	selection
1	Age	6324	0.001**	continuous	normal ALL
2	Smoking 4 cat.	6324	.	categorical	ALL

Signif. codes: 0 '**' 0.05 '*' 0.1 '.' 1

Warning messages:

```
1: In chisq.test(obj, simulate.p.value = TRUE) :
  cannot compute simulated p-value with zero marginals
2: In chisq.test(obj, simulate.p.value = TRUE) :
  Chi-squared approximation may be incorrect
```

Nota that a warning message is shown and no p-values are calculated for Smoking.

4.1.5 Summary

Applying the **summary** function to an object of class **createTable** will obtain a more detailed output:

```
> res<-compareGroups(group ~ age + sex + smoke + waist + hormo, method = c(waist=2),
+                     data=predimed)
> summary(res[c(1, 2, 4)])
```

--- Descriptives of each row-variable by groups of 'Intervention group' ---

row-variable: Age

	N	mean	sd	p.overall	p.trend	p.Control vs MedDiet + Nuts	p.Control vs MedDiet + V00
[ALL]	6324	67.0117	6.17499				
Control	2042	67.34231	6.27992	0.002666	0.101163	0.001672	0.20596
MedDiet + Nuts	2100	66.6819	6.016395				
MedDiet + V00	2182	67.01971	6.212578				
				p.MedDiet + Nuts vs MedDiet + V00			
[ALL]							
Control		0.172672					
MedDiet + Nuts							
MedDiet + V00							

row-variable: Sex

	Male	Female	Male (row%)	Female (row%)	p.overall	p.trend	p.Control vs MedDiet + Nuts
[ALL]	2679	3645	42.36243	57.63757			
Control	812	1230	39.76494	60.23506	8.1e-05	0.388386	0.000133
MedDiet + Nuts	968	1132	46.09524	53.90476			
MedDiet + V00	899	1283	41.20073	58.79927			
					p.Control vs MedDiet + V00	p.MedDiet + Nuts vs MedDiet + V00	
[ALL]							
Control		0.358324		0.002076			
MedDiet + Nuts							
MedDiet + V00							

row-variable: Waist circumference

	N	med	Q1	Q3	p.overall	p.trend	p.Control vs MedDiet + Nuts	p.Control vs MedDiet + V00
[ALL]	6324	100	93	107				
Control	2042	101	94	108	0.084601	0.039557	0.125792	0.110639
MedDiet + Nuts	2100	100	93	107				
MedDiet + V00	2182	100	93	107				
					p.MedDiet + Nuts vs MedDiet + V00			
[ALL]								
Control		0.743479						
MedDiet + Nuts								
MedDiet + V00								

Note that because only variables 1, 3 & 4 are selected, only results for Age, Sex & Waist circumference are shown. Age is summarized by the mean and the standard deviation, Sex by frequencies and percentage, and Waist circumference (method =2) by the median and quartiles.

4.1.6 Plotting

Variables can be plotted to see their distribution. Plots differ according to whether the variable is continuous or categorical. Plots can be seen on-screen or saved as PDF.

```
> plot(res[c(1,2)], file="./figures/univar/")
```

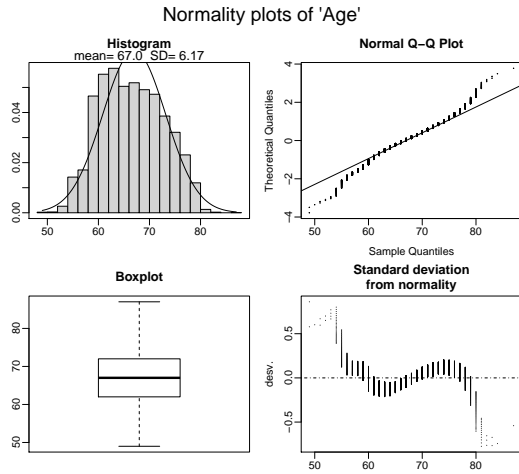


Figure 2: Plot of Age

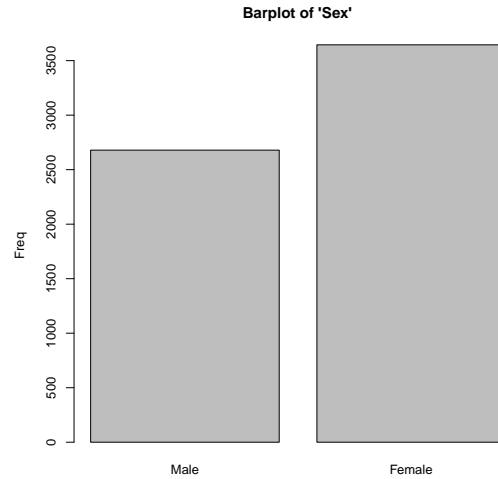


Figure 3: Plot of Sex

Plots also can be done according to grouping variable. In this case only a boxplot is shown for continuous variables:

```
> plot(res[c(1,2)], bivar=TRUE, file="./figures/bivar/")
```

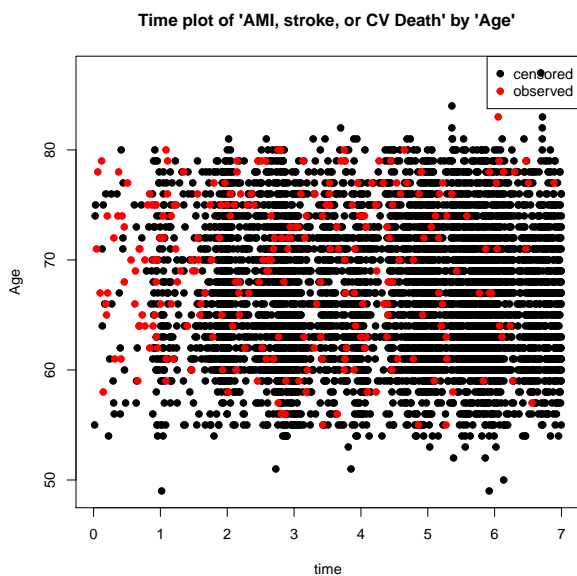


Figure 4: Plot of Age

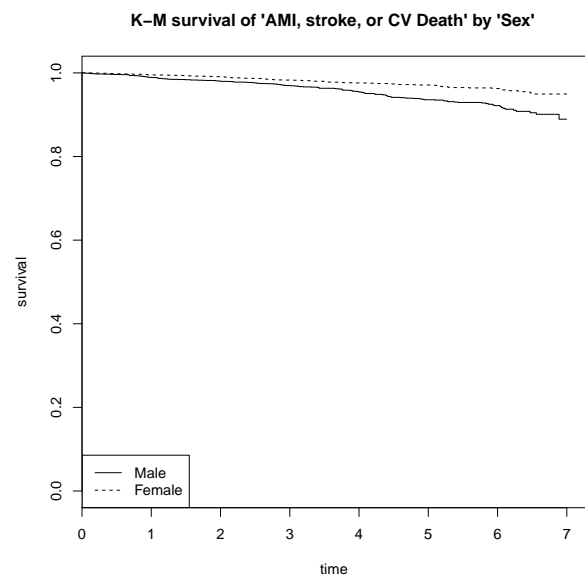


Figure 5: Plot of Sex

4.1.7 Updating

The object from `compareGroups` can later be updated. For example:

```
> res<-compareGroups(group ~ age + sex + smoke + waist + hormo, data=predimed)
> res
```

```
----- Summary of results by groups of 'Intervention group'-----
```

var	N	p.value	method	selection
1 Age	6324	0.003**	continuous normal	ALL
2 Sex	6324	<0.001**	categorical	ALL
3 Smoking	6324	0.444	categorical	ALL
4 Waist circumference	6324	0.045**	continuous normal	ALL
5 Hormone-replacement therapy	5661	0.850	categorical	ALL

```
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 '.' 1
```

The object *res* is updated using:

```
> res<-update(res, . ~. - sex + bmi + toevent, subset = sex=='Female',
+             method = c(waist=2, toevent=2), selec = list(bmi=!is.na(hormo)))
```

```
> res
```

```
----- Summary of results by groups of 'Intervention group'-----
```

var	N	p.value	method	selection
1 Age	3645	0.056*	continuous normal	sex == "Female"
2 Smoking	3645	0.907	categorical	sex == "Female"
3 Waist circumference	3645	0.037**	continuous non-normal	sex == "Female"
4 Hormone-replacement therapy	3459	0.898	categorical	sex == "Female"
5 Body mass index	3459	0.002**	continuous normal	(sex == "Female") & (!is.na(hormo))
6 follow-up to main event (years)	3645	<0.001**	continuous normal	sex == "Female"

```
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 '.' 1
```

Note that “Sex” is removed as an explanatory variable but used as a filter, subsetting only “Female” participants. Variable “Waist circumference” has been changed to “continuous non-normal”. Two new variables have been added: Body mass index and Follow-up (stated continuous non-normal). For Body mass index is stated to show only data of participants with non-missing values in Hormone-replacement therapy.

4.1.8 Odds Ratios & Hazard Ratios

When the response variable is binary, the Odds Ratio (OR) can be printed in the final table. If the response variable is time-to-event (see Section 3.1), the Hazard Ratio (HR) can be printed instead.

ref This statement can be used to change the reference category:

```
> res1<-compareGroups(htn ~ age + sex + bmi + smoke, data=predimed, ref=1)
> createTable(res1, show.ratio=TRUE)
```

```
-----Summary descriptives table by 'Hypertension'-----
```

	No N=1089	Yes N=5235	OR	p.ratio	p.overall
Age	65.9 (6.19)	67.2 (6.15)	1.04 [1.03;1.05]	<0.001	<0.001

```

Sex:
  Male      595 (54.6%) 2084 (39.8%)      Ref.      Ref.
  Female    494 (45.4%) 3151 (60.2%) 1.82 [1.60;2.08] 0.000
Body mass index 28.9 (3.69) 30.2 (3.80) 1.10 [1.08;1.12] <0.001 <0.001
Smoking:
  Never     536 (49.2%) 3356 (64.1%)      Ref.      Ref.
  Current   233 (21.4%) 625 (11.9%) 0.43 [0.36;0.51] 0.000
  Former    320 (29.4%) 1254 (24.0%) 0.63 [0.54;0.73] <0.001

```

Note that for categorical response variables the reference category is the first one in the statement:

```

> res2<-compareGroups(htn ~ age + sex + bmi + smoke, data=predimed,
+                      ref=c(smoke=1, sex=2))
> createTable(res2, show.ratio=TRUE)

```

-----Summary descriptives table by 'Hypertension'-----

	No N=1089	Yes N=5235	OR	p.ratio	p.overall
Age	65.9 (6.19)	67.2 (6.15)	1.04 [1.03;1.05]	<0.001	<0.001
Sex:					<0.001
Male	595 (54.6%)	2084 (39.8%)	0.55 [0.48;0.63]	0.000	
Female	494 (45.4%)	3151 (60.2%)	Ref.	Ref.	
Body mass index	28.9 (3.69)	30.2 (3.80)	1.10 [1.08;1.12]	<0.001	<0.001
Smoking:					<0.001
Never	536 (49.2%)	3356 (64.1%)	Ref.	Ref.	
Current	233 (21.4%)	625 (11.9%)	0.43 [0.36;0.51]	0.000	
Former	320 (29.4%)	1254 (24.0%)	0.63 [0.54;0.73]	<0.001	

Note that the reference category for Smoking status is the first and for Sex the second.

ref.no Similarly to the “ref” statement, **ref.no** is used to state “no” as the reference category for all variables with this category:

```

> res<-compareGroups(htn ~ age + sex + bmi + hormo + hyperchol, data=predimed,
+                     ref.no='NO')
> createTable(res, show.ratio=TRUE)

```

-----Summary descriptives table by 'Hypertension'-----

	No N=1089	Yes N=5235	OR	p.ratio	p.overall
Age	65.9 (6.19)	67.2 (6.15)	1.04 [1.03;1.05]	<0.001	<0.001
Sex:					<0.001
Male	595 (54.6%)	2084 (39.8%)	Ref.	Ref.	
Female	494 (45.4%)	3151 (60.2%)	1.82 [1.60;2.08]	0.000	
Body mass index	28.9 (3.69)	30.2 (3.80)	1.10 [1.08;1.12]	<0.001	<0.001
Hormone-replacement therapy:					0.856
No	928 (98.4%)	4636 (98.3%)	Ref.	Ref.	
Yes	15 (1.59%)	82 (1.74%)	1.08 [0.64;1.97]	0.773	
Dyslipidemia:					<0.001
No	409 (37.6%)	1337 (25.5%)	Ref.	Ref.	
Yes	680 (62.4%)	3898 (74.5%)	1.75 [1.53;2.01]	<0.001	

Note: 'no', 'No' or 'NO' will produce the same results; the coding is not case sensitive.

fact.ratio By default OR or HR for continuous variables are calculated for each unit increase. It can be changed by the **fact.or** statement:

```
> res<-compareGroups(htn ~ age + bmi, data=predimed)
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Hypertension'-----

	No N=1089	Yes N=5235	OR	p.ratio	p.overall
Age	65.9 (6.19)	67.2 (6.15)	1.04 [1.03;1.05]	<0.001	<0.001
Body mass index	28.9 (3.69)	30.2 (3.80)	1.10 [1.08;1.12]	<0.001	<0.001

Here the OR is for the increase of one unit for Age and Systolic blood pressure.

```
> res<-compareGroups(htn ~ age + bmi, data=predimed,
+                     fact.ratio= c(age=10, bmi=2))
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Hypertension'-----

	No N=1089	Yes N=5235	OR	p.ratio	p.overall
Age	65.9 (6.19)	67.2 (6.15)	1.43 [1.28;1.59]	<0.001	<0.001
Body mass index	28.9 (3.69)	30.2 (3.80)	1.22 [1.17;1.26]	<0.001	<0.001

Here the OR is for the increase of 10 years for Age and 2 units for Body mass index.

ref.y By default when OR or HR are calculated, the reference category for the response variable is the first. The reference category could be changed using the **ref.y** statement:

```
> res<-compareGroups(htn ~ age + sex + bmi + hyperchol, data=predimed)
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Hypertension'-----

	No N=1089	Yes N=5235	OR	p.ratio	p.overall
Age	65.9 (6.19)	67.2 (6.15)	1.04 [1.03;1.05]	<0.001	<0.001
Sex:					<0.001
Male	595 (54.6%)	2084 (39.8%)	Ref.	Ref.	
Female	494 (45.4%)	3151 (60.2%)	1.82 [1.60;2.08]	0.000	
Body mass index	28.9 (3.69)	30.2 (3.80)	1.10 [1.08;1.12]	<0.001	<0.001
Dyslipidemia:					<0.001
No	409 (37.6%)	1337 (25.5%)	Ref.	Ref.	
Yes	680 (62.4%)	3898 (74.5%)	1.75 [1.53;2.01]	<0.001	

Note: This output shows the OR of having hypertension. Therefore, 'Non-hypertension' is the reference category.

```
> res<-compareGroups(htn ~ age + sex + bmi + hyperchol, data=predimed, ref.y=2)
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Hypertension'-----

	No N=1089	Yes N=5235	OR	p.ratio	p.overall
Age	65.9 (6.19)	67.2 (6.15)	0.96 [0.98;0.95]	<0.001	<0.001
Sex:					<0.001
Male	595 (54.6%)	2084 (39.8%)	Ref.	Ref.	
Female	494 (45.4%)	3151 (60.2%)	0.55 [0.48;0.63]	0.000	
Body mass index	28.9 (3.69)	30.2 (3.80)	0.91 [0.92;0.89]	<0.001	<0.001
Dyslipidemia:					<0.001
No	409 (37.6%)	1337 (25.5%)	Ref.	Ref.	
Yes	680 (62.4%)	3898 (74.5%)	0.57 [0.50;0.65]	<0.001	

Note: This output shows the OR of having No hypertension.

Note: This output shows the OR of having No hypertension, and 'Hypertension' is now the reference category.

When the response variable is of class **Surv**, the bivariate **plot** function returns a Kaplan-Meier figure if the explanatory variable is categorical. For continuous variables the function returns a line for each individual, ending with a circle for censored and with a plus sign for uncensored.

```
> plot(compareGroups(tmain ~ sex, data=predimed), bivar=TRUE, file="./figures/bivar/")
> plot(compareGroups(tmain ~ age, data=predimed), bivar=TRUE, file="./figures/bivar/")
```

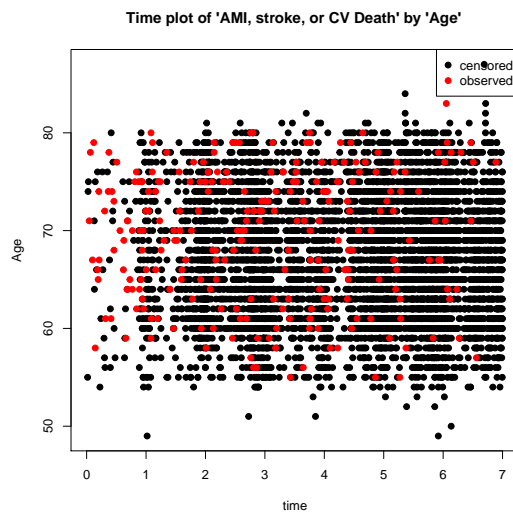


Figure 6: Categorical

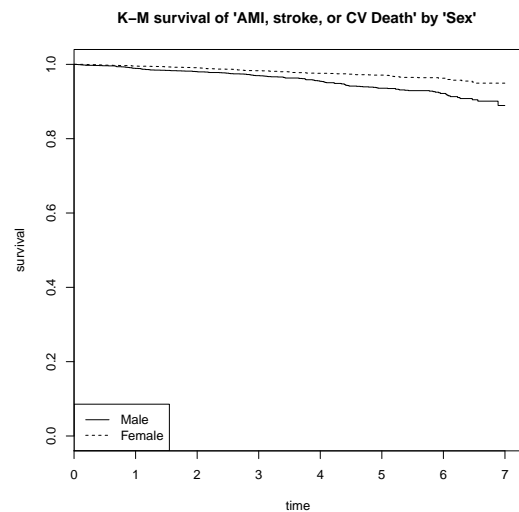


Figure 7: Continuous

4.1.9 Time-to-event explanatory variables

When a variable of class **Surv** (see Section 3.1) is used as explanatory it will be described with the probability of event, computed by Kaplan-Meier, up to a stated time.

timemax By default probability is calculated at the median of the follow-up period. **timemax** option allows us to change at what time probability is calculated.

```
> res<-compareGroups(sex ~ age + tmain, timemax=c(tmain=3),
+                    data=predimed)
> res
```

Note that *tmain* is calculated at 3 years (see section 3.1).

The **plot** function applied to a variable of class **Surv** returns a Kaplan-Meier figure. The figure can be stratified by the grouping variable.

```
> plot(res[2], file="./figures/univar/")
> plot(res[2], bivar=TRUE, file="./figures/bivar/")
```

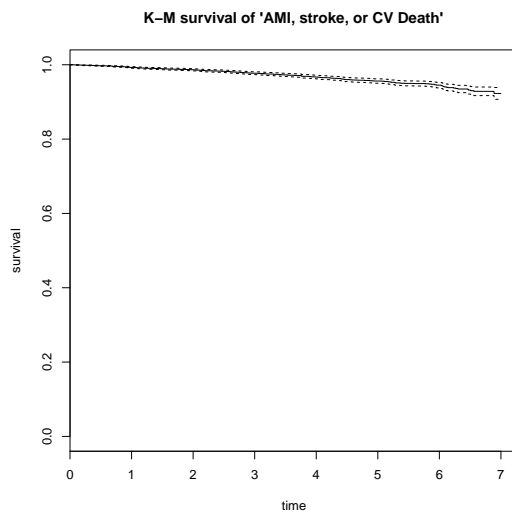


Figure 8: Univariate

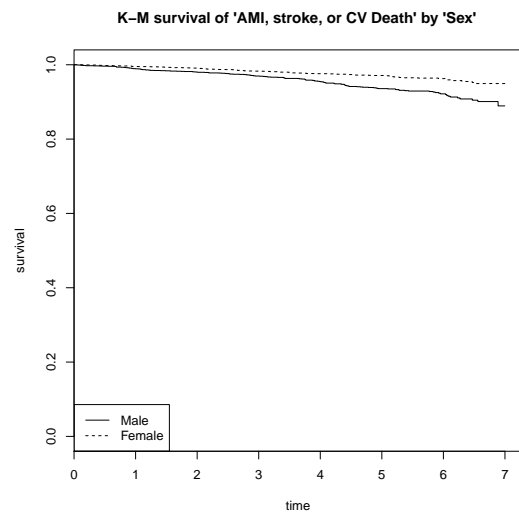


Figure 9: Stratified by *year*

4.2 createTable

createTable function, applied to an object of **compareGroups** class, returns tables with descriptives that can be displayed on-screen or exported to CSV, L^AT_EX or HTML.

```
> res<-compareGroups(group ~ age + sex + smoke + waist + hormo, data=predimed,
+                    selec = list(hormo=sex=="Female"))
> restab<-createTable(res)
```

Two tables are created with the **createTable** function: one with the descriptives and the other with the available data. The **print** command print applied to an object of class **createTable** returns one or both tables:

```
> print(restab,which.table='descr')
```

```
-----Summary descriptives table by 'Intervention group'-----
```

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Hormone-replacement therapy:				0.898
No	1143 (97.4%)	1036 (97.2%)	1183 (97.0%)	
Yes	31 (2.64%)	30 (2.81%)	36 (2.95%)	

Note that the option “descr” returns descriptives.

```
> print(restab, which.table='avail')
```

```
---Available data---
```

	[ALL]	Control	MedDiet + Nuts	MedDiet + V00	method	select
Age	6324	2042	2100	2182	continuous-normal	ALL
Sex	6324	2042	2100	2182	categorical	ALL
Smoking	6324	2042	2100	2182	categorical	ALL
Waist circumference	6324	2042	2100	2182	continuous-normal	ALL
Hormone-replacement therapy	3459	1174	1066	1219	categorical	sex == "Female"

Note that the option “avail” returns the available data, as well as methods and selections.

By default only the descriptives table is shown. Stating “both” in `which.table` options returns both tables.

4.2.1 Dressing up tables

hide If the explanatory variable is dichotomous, one of the categories often is hidden in the results displayed (i.e., if 42.4% are male, obviously 57.6% are female). To hide some category, e.g., Male:

```
> update(restab, hide = c(sex="Male"))
```

```
-----Summary descriptives table by 'Intervention group'-----
```

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex: Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	<0.001
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Hormone-replacement therapy:				0.898
No	1143 (97.4%)	1036 (97.2%)	1183 (97.0%)	
Yes	31 (2.64%)	30 (2.81%)	36 (2.95%)	

Note that the percentage of males is hidden.

hide.no Similarly, as explained above, if the category “no” is to be hidden for all variables:

```
> res<-compareGroups(group ~ age + sex + htn + diab, data=predimed)
> createTable(res, hide.no='no', hide = c(sex="Male"))
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex: Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	<0.001
Hypertension	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	0.249
Type-2 diabetes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	0.017

Note: 'no', 'No' or 'NO' will produce the same results; the coding is not case sensitive.

digits The number of digits that appear in the results can be changed, e.g:

```
> createTable(res, digits= c(age=2, sex = 3))
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.34 (6.28)	66.68 (6.02)	67.02 (6.21)	0.003
Sex:				<0.001
Male	812 (39.765%)	968 (46.095%)	899 (41.201%)	
Female	1230 (60.235%)	1132 (53.905%)	1283 (58.799%)	
Hypertension:				0.249
No	331 (16.2%)	362 (17.2%)	396 (18.1%)	
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	
Type-2 diabetes:				0.017
No	1072 (52.5%)	1150 (54.8%)	1100 (50.4%)	
Yes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	

Note that mean and standard deviation has two decimal places for age, while percentage in sex has been set to three decimal places.

type By default categorical variables are summarized by frequencies and percentages. This can be changed by the **type** command:

```
> createTable(res, type=1)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	39.8%	46.1%	41.2%	
Female	60.2%	53.9%	58.8%	
Hypertension:				0.249
No	16.2%	17.2%	18.1%	
Yes	83.8%	82.8%	81.9%	
Type-2 diabetes:				0.017
No	52.5%	54.8%	50.4%	
Yes	47.5%	45.2%	49.6%	

Note that only percentages are displayed.

```
> createTable(res, type=3)
```

```
-----Summary descriptives table by 'Intervention group'-----
```

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	812	968	899	
Female	1230	1132	1283	
Hypertension:				0.249
No	331	362	396	
Yes	1711	1738	1786	
Type-2 diabetes:				0.017
No	1072	1150	1100	
Yes	970	950	1082	

Note that only frequencies are displayed.

Values 2 or “NA” return the same results, i.e., the default option.

show.n If option **show.n** is set to “TRUE” a column with available data for each variable appears in the results:

```
> createTable(res, show.n=TRUE)
```

```
-----Summary descriptives table by 'Intervention group'-----
```

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall	N
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003	6324
Sex:				<0.001	6324
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)		
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)		
Hypertension:				0.249	6324
No	331 (16.2%)	362 (17.2%)	396 (18.1%)		
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)		
Type-2 diabetes:				0.017	6324
No	1072 (52.5%)	1150 (54.8%)	1100 (50.4%)		
Yes	970 (47.5%)	950 (45.2%)	1082 (49.6%)		

show.descr If option **show.descr** is set to “FALSE” only p-values are displayed:

```
> createTable(res, show.descr=FALSE)
```

```
-----Summary descriptives table by 'Intervention group'-----
```

	p.overall
Age	0.003
Sex:	
Male	<0.001
Female	
Hypertension:	

```

      No      0.249
      Yes
Type-2 diabetes:
      No      0.017
      Yes
-----

```

show.all If `show.all` option is set to “TRUE” a column is displayed with descriptives for all data:

```
> createTable(res, show.all=TRUE)
```

```

-----Summary descriptives table by 'Intervention group'-----

-----
      [ALL]      Control      MedDiet + Nuts      MedDiet + V00      p.overall
      N=6324      N=2042      N=2100      N=2182
-----
Age      67.0 (6.17)  67.3 (6.28)  66.7 (6.02)  67.0 (6.21)  0.003
Sex:
  Male    2679 (42.4%)  812 (39.8%)  968 (46.1%)  899 (41.2%)  <0.001
  Female   3645 (57.6%) 1230 (60.2%) 1132 (53.9%) 1283 (58.8%)
Hypertension:
  No       1089 (17.2%) 331 (16.2%) 362 (17.2%) 396 (18.1%)  0.249
  Yes      5235 (82.8%) 1711 (83.8%) 1738 (82.8%) 1786 (81.9%)
Type-2 diabetes:
  No       3322 (52.5%) 1072 (52.5%) 1150 (54.8%) 1100 (50.4%)  0.017
  Yes      3002 (47.5%) 970 (47.5%) 950 (45.2%) 1082 (49.6%)
-----

```

show.p.overall If option `show.p.overall` is set to “FALSE” p-values are omitted from the table:

```
> createTable(res, show.p.overall=FALSE)
```

```

-----Summary descriptives table by 'Intervention group'-----

-----
      Control      MedDiet + Nuts      MedDiet + V00
      N=2042      N=2100      N=2182
-----
Age      67.3 (6.28)  66.7 (6.02)  67.0 (6.21)
Sex:
  Male    812 (39.8%)  968 (46.1%)  899 (41.2%)
  Female  1230 (60.2%) 1132 (53.9%) 1283 (58.8%)
Hypertension:
  No       331 (16.2%) 362 (17.2%) 396 (18.1%)
  Yes      1711 (83.8%) 1738 (82.8%) 1786 (81.9%)
Type-2 diabetes:
  No       1072 (52.5%) 1150 (54.8%) 1100 (50.4%)
  Yes      970 (47.5%) 950 (45.2%) 1082 (49.6%)
-----

```

show.p.trend If the response variable has more than two categories a p-value for trend can be calculated. Results are displayed if the `show.p.trend` option is set to “TRUE”:

```
> createTable(res, show.p.trend=TRUE)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall	p.trend
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003	0.101
Sex:				<0.001	0.388
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)		
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)		
Hypertension:				0.249	0.096
No	331 (16.2%)	362 (17.2%)	396 (18.1%)		
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)		
Type-2 diabetes:				0.017	0.160
No	1072 (52.5%)	1150 (54.8%)	1100 (50.4%)		
Yes	970 (47.5%)	950 (45.2%)	1082 (49.6%)		

Note: The p-value for trend is computed from the Pearson test when row-variable is normal and from the Spearman test when it is continuous non-normal. If row-variable is of class **Surv**, the test score is computed from a Cox model where the grouping variable is introduced as an integer variable predictor. If the row-variable is categorical, the p-value for trend is computed as $1 - pchisq(\text{cor}(\text{as.integer}(x), \text{as.integer}(y))^2 * (\text{length}(x) - 1), 1)$

show.p.mul For a response variable with more than two categories a pairwise comparison of p-values, corrected for multiple comparisons, can be calculated. Results are displayed if the **show.p.mul** option is set to “TRUE”:

```
> createTable(res, show.p.mul=TRUE)
```

```
-----Summary descriptives table by 'Intervention group'-----
```

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall	p.Control vs MedDiet + Nuts	p.Control vs MedDiet + V00	p.MedDiet + Nuts vs MedDiet + V00
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003	0.002	0.206	0.173
Sex:				<0.001	<0.001	0.358	0.002
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)				
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)				
Hypertension:				0.249	0.459	0.311	0.459
No	331 (16.2%)	362 (17.2%)	396 (18.1%)				
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)				
Type-2 diabetes:				0.017	0.185	0.185	0.014
No	1072 (52.5%)	1150 (54.8%)	1100 (50.4%)				
Yes	970 (47.5%)	950 (45.2%)	1082 (49.6%)				

Note: Tukey method is used when explanatory variable is normal-distributed and Benjamini & Hochberg [1] method otherwise.

show.ratio If response variable is dichotomous or has been defined as class **survival** (see Section 3.1), Odds Ratios and Hazard Ratios can be displayed in the results by stating “TRUE” at the **show.ratio** option:

```
> createTable(update(res, subset= group!="Control diet"), show.ratio=TRUE)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Hypertension:				0.249
No	331 (16.2%)	362 (17.2%)	396 (18.1%)	
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	
Type-2 diabetes:				0.017
No	1072 (52.5%)	1150 (54.8%)	1100 (50.4%)	
Yes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	

Note that category “Control diet” of the response variable has been omitted in order to have only two categories (i.e., a dichotomous variable). No Odds Ratios would be calculated if response variable has more than two categories.

```
> createTable(compareGroups(tmain ~ group + age + sex, data=predimed),
+             show.ratio=TRUE)
```

-----Summary descriptives table by 'AMI, stroke, or CV Death'-----

	No event N=6072	Event N=252	HR	p.ratio	p.overall
Intervention group:					0.011
Control	1945 (32.0%)	97 (38.5%)	Ref.	Ref.	
MedDiet + Nuts	2030 (33.4%)	70 (27.8%)	0.66 [0.48;0.89]	0.008	
MedDiet + V00	2097 (34.5%)	85 (33.7%)	0.70 [0.53;0.94]	0.018	
Age	66.9 (6.14)	69.4 (6.65)	1.06 [1.04;1.09]	<0.001	<0.001
Sex:					<0.001
Male	2528 (41.6%)	151 (59.9%)	Ref.	Ref.	
Female	3544 (58.4%)	101 (40.1%)	0.49 [0.38;0.63]	<0.001	

Note that when response variable is of class **Surv**, Hazard Ratios are calculated instead of Odds Ratios.

digits.ratio The number of decimal places for Odds/Hazard ratios can be changed by the **digits.ratio** option:

```
> createTable(compareGroups(tmain ~ group + age + sex, data=predimed),
+             show.ratio=TRUE, digits.ratio= 3)
```

-----Summary descriptives table by 'AMI, stroke, or CV Death'-----

	No event N=6072	Event N=252	HR	p.ratio	p.overall
Intervention group:					0.011
Control	1945 (32.0%)	97 (38.5%)	Ref.	Ref.	
MedDiet + Nuts	2030 (33.4%)	70 (27.8%)	0.658 [0.484;0.894]	0.008	
MedDiet + V00	2097 (34.5%)	85 (33.7%)	0.703 [0.525;0.941]	0.018	
Age	66.9 (6.14)	69.4 (6.65)	1.065 [1.043;1.086]	<0.001	<0.001
Sex:					<0.001
Male	2528 (41.6%)	151 (59.9%)	Ref.	Ref.	
Female	3544 (58.4%)	101 (40.1%)	0.488 [0.379;0.628]	<0.001	

4.2.2 Combining tables by row

Tables made with the same response variable can be combined by row:

```
> restab1 <- createTable(compareGroups(group ~ age + sex, data=predimed))
> restab2 <- createTable(compareGroups(group ~ bmi + smoke, data=predimed))
> rbind("Non-modifiable risk factors"=restab1, "Modifiable risk factors"=restab2)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Non-modifiable risk factors:				
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Modifiable risk factors:				
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	

Note how variables are grouped under “Non-modifiable” and “Modifiable” risk factors because of an epigraph defined in the `rbind` command in the example.

The resulting object is of class `rbind.createTable`, which can be subset but not updated. It inherits the class `'createTable'`. Therefore, columns and other arguments from the `createTable` function cannot be modified:

To select only Age and Smoking:

```
> rbind("Non-modifiable"=restab1,"Modifiable"=restab2)[c(1,4)]
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Non-modifiable:				
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Modifiable:				
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	

To change the order:

```
> rbind("Modifiable"=restab1,"Non-modifiable"=restab2)[c(4,3,2,1)]
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Non-modifiable:				
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001
Modifiable:				
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003

4.2.3 Combining tables by column

Columns from tables built with the same explanatory and response variables but done with a different subset (i.e. ALL, Male and Female) can be combined:

```

> res<-compareGroups(group ~ age + smoke + bmi + htn , data=predimed)
> alltab <- createTable(res, show.p.overall = FALSE)
> femaletab <- createTable(update(res,subset=sex=='Female'), show.p.overall = FALSE)
> maletab <- createTable(update(res,subset=sex=='Male'), show.p.overall = FALSE)
> cbind("ALL"=alltab,"FEMALE"=femaletab,"MALE"=maletab)

```

-----Summary descriptives table -----

	ALL			FEMALE			MALE		
	By Intervention group			By Intervention group			By Intervention group		
	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	Control N=1230	MedDiet + Nuts N=1132	MedDiet + V00 N=1283	Control N=812	MedDiet + Nuts N=968	MedDiet + V00 N=899
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	68.0 (5.96)	67.4 (5.57)	67.7 (5.84)	66.4 (6.62)	65.8 (6.40)	66.1 (6.61)
Smoking:									
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	1077 (87.6%)	993 (87.7%)	1115 (86.9%)	205 (25.2%)	266 (27.5%)	236 (26.3%)
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	66 (5.37%)	54 (4.77%)	71 (5.53%)	204 (25.1%)	242 (25.0%)	221 (24.6%)
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	87 (7.07%)	85 (7.51%)	97 (7.56%)	403 (49.6%)	460 (47.5%)	442 (49.2%)
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	30.8 (4.20)	30.2 (4.08)	30.4 (3.91)	29.6 (3.45)	29.1 (3.28)	29.2 (3.28)
Hypertension:									
No	331 (16.2%)	362 (17.2%)	396 (18.1%)	168 (13.7%)	147 (13.0%)	179 (14.0%)	163 (20.1%)	215 (22.2%)	217 (24.1%)
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	1062 (86.3%)	985 (87.0%)	1104 (86.0%)	649 (79.9%)	753 (77.8%)	682 (75.9%)

With the argument *caption* set to NULL no name is displayed for columns.

```

> cbind(alltab,femaletab,maletab,caption=NULL)

```

-----Summary descriptives table -----

	By Intervention group			By Intervention group			By Intervention group		
	By Intervention group			By Intervention group			By Intervention group		
	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	Control N=1230	MedDiet + Nuts N=1132	MedDiet + V00 N=1283	Control N=812	MedDiet + Nuts N=968	MedDiet + V00 N=899
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	68.0 (5.96)	67.4 (5.57)	67.7 (5.84)	66.4 (6.62)	65.8 (6.40)	66.1 (6.61)
Smoking:									
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	1077 (87.6%)	993 (87.7%)	1115 (86.9%)	205 (25.2%)	266 (27.5%)	236 (26.3%)
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	66 (5.37%)	54 (4.77%)	71 (5.53%)	204 (25.1%)	242 (25.0%)	221 (24.6%)
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	87 (7.07%)	85 (7.51%)	97 (7.56%)	403 (49.6%)	460 (47.5%)	442 (49.2%)
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	30.8 (4.20)	30.2 (4.08)	30.4 (3.91)	29.6 (3.45)	29.1 (3.28)	29.2 (3.28)

Hypertension:									
No	331 (16.2%)	362 (17.2%)	396 (18.1%)	168 (13.7%)	147 (13.0%)	179 (14.0%)	163 (20.1%)	215 (22.2%)	217 (24.1%)
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	1062 (86.3%)	985 (87.0%)	1104 (86.0%)	649 (79.9%)	753 (77.8%)	682 (75.9%)

By default the name of the table is displayed for each set of columns.

> cbind(alltab,femaletab,maletab)

-----Summary descriptives table -----

	alltab			femalatab			maletab		
	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	Control N=1230	MedDiet + Nuts N=1132	MedDiet + V00 N=1283	Control N=812	MedDiet + Nuts N=968	MedDiet + V00 N=899
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	68.0 (5.96)	67.4 (5.57)	67.7 (5.84)	66.4 (6.62)	65.8 (6.40)	66.1 (6.61)
Smoking:									
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	1077 (87.6%)	993 (87.7%)	1115 (86.9%)	205 (25.2%)	266 (27.5%)	236 (26.3%)
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	66 (5.37%)	54 (4.77%)	71 (5.53%)	204 (25.1%)	242 (25.0%)	221 (24.6%)
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	87 (7.07%)	85 (7.51%)	97 (7.56%)	403 (49.6%)	460 (47.5%)	442 (49.2%)
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	30.8 (4.20)	30.2 (4.08)	30.4 (3.91)	29.6 (3.45)	29.1 (3.28)	29.2 (3.28)
Hypertension:									
No	331 (16.2%)	362 (17.2%)	396 (18.1%)	168 (13.7%)	147 (13.0%)	179 (14.0%)	163 (20.1%)	215 (22.2%)	217 (24.1%)
Yes	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	1062 (86.3%)	985 (87.0%)	1104 (86.0%)	649 (79.9%)	753 (77.8%)	682 (75.9%)

NOTE: The resulting object is of class `cbind.createTable` and inherits also the class `createTable`. This cannot be updated. It can be nicely printed on the R console and also exported to L^AT_EX but it cannot be exported to CSV or HTML.

4.2.4 createTable miscellaneous

print By default only the table with the descriptives is printed. With the `which.table` command it can be changed: 'avail' returns data available and 'both' returns both tables:

```
> print(createTable(compareGroups(group ~ age + sex + smoke + waist + hormo,
+                               data=predimed)), which.table='both')
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Hormone-replacement therapy:				0.850
No	1811 (98.3%)	1835 (98.4%)	1918 (98.2%)	
Yes	31 (1.68%)	30 (1.61%)	36 (1.84%)	

---Available data---

	[ALL]	Control	MedDiet + Nuts	MedDiet + V00	method	select
Age	6324	2042	2100	2182	continuous-normal	ALL
Sex	6324	2042	2100	2182	categorical	ALL
Smoking	6324	2042	2100	2182	categorical	ALL
Waist circumference	6324	2042	2100	2182	continuous-normal	ALL
Hormone-replacement therapy	5661	1842	1865	1954	categorical	ALL

With the `print` command setting `nmax` option = FALSE, the total maximum “n” in the available data is omitted in the first row.

```
> print(createTable(compareGroups(group ~ age + sex + smoke + waist + hormo,
+                               data=predimed)), nmax=FALSE)
```

-----Summary descriptives table by 'Intervention group'-----

	Control	MedDiet + Nuts	MedDiet + V00	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Hormone-replacement therapy:				0.850
No	1811 (98.3%)	1835 (98.4%)	1918 (98.2%)	
Yes	31 (1.68%)	30 (1.61%)	36 (1.84%)	

summary returns the same table as that generated with **print** command setting **which.table='avail'**:

```
> summary(createTable(compareGroups(group ~ age + sex + smoke + waist + hormo,
+                               data=predimed)))
```

---Available data---

	[ALL]	Control	MedDiet + Nuts	MedDiet + V00	method	select
Age	6324	2042	2100	2182	continuous-normal	ALL
Sex	6324	2042	2100	2182	categorical	ALL
Smoking	6324	2042	2100	2182	categorical	ALL
Waist circumference	6324	2042	2100	2182	continuous-normal	ALL
Hormone-replacement therapy	5661	1842	1865	1954	categorical	ALL

update An object of class **createTable** can be updated:

```
> res<-compareGroups(group ~ age + sex + smoke + waist + hormo, data=predimed)
> restab<-createTable(res, type=1, show.ratio=TRUE )
> restab
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	39.8%	46.1%	41.2%	
Female	60.2%	53.9%	58.8%	
Smoking:				0.444
Never	62.8%	60.0%	61.9%	
Current	13.2%	14.1%	13.4%	
Former	24.0%	26.0%	24.7%	
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Hormone-replacement therapy:				0.850
No	98.3%	98.4%	98.2%	
Yes	1.68%	1.61%	1.84%	

```
> update(restab, show.n=TRUE)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall	N
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003	6324
Sex:				<0.001	6324
Male	39.8%	46.1%	41.2%		
Female	60.2%	53.9%	58.8%		
Smoking:				0.444	6324
Never	62.8%	60.0%	61.9%		
Current	13.2%	14.1%	13.4%		
Former	24.0%	26.0%	24.7%		
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045	6324
Hormone-replacement therapy:				0.850	5661
No	98.3%	98.4%	98.2%		
Yes	1.68%	1.61%	1.84%		

In just one statement it is possible to update an object of class **compareGroups** and **createTable**:

```
> update(restab, x = update(res, subset=c(sex=='Female')), show.n=TRUE)
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=1230	MedDiet + Nuts N=1132	MedDiet + V00 N=1283	p.overall	N
Age	68.0 (5.96)	67.4 (5.57)	67.7 (5.84)	0.056	3645
Sex: Female	100%	100%	100%	.	3645
Smoking:				0.907	3645
Never	87.6%	87.7%	86.9%		
Current	5.37%	4.77%	5.53%		
Former	7.07%	7.51%	7.56%		
Waist circumference	99.0 (11.0)	97.8 (11.0)	98.0 (10.5)	0.016	3645
Hormone-replacement therapy:				0.898	3459
No	97.4%	97.2%	97.0%		
Yes	2.64%	2.81%	2.95%		

Note that the `compareGroups` object (*res*) is updated, selecting only 'Female' participants, and the `createTable` object (*restab*) is updated to add a column with the maximum available data for each explanatory variable.

subsetting Objects from `createTable` function can also be subsetted using “[”:

```
> createTable(compareGroups(group ~ age + sex + smoke + waist + hormo, data=predimed))
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Hormone-replacement therapy:				0.850
No	1811 (98.3%)	1835 (98.4%)	1918 (98.2%)	
Yes	31 (1.68%)	30 (1.61%)	36 (1.84%)	

```
> createTable(compareGroups(group ~ age + sex + bmi, data=predimed))[1:2, ]
```

-----Summary descriptives table by 'Intervention group'-----

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + V00 N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex:				<0.001
Male	812 (39.8%)	968 (46.1%)	899 (41.2%)	
Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	

4.3 Exporting tables

Tables can be exported to CSV, HTML or \LaTeX :

- `export2csv(restab, file="table1")`, exports to CSV format

- `export2html(restab, file="table1")`, exports to HTML format
- `export2latex(restab, file="table1")`, exports to \LaTeX format

File extensions are added automatically. Only the filename is needed (and the path if necessary) without the extension.

4.3.1 General exporting options

which.table By default only the table with the descriptives is exported. This can be changed with the `which.table` command: `'avail'` exports only available data and `'both'` both tables.

nmax By default a first row with the maximum “n” for available data (i.e. the number of participants minus the least missing data) is exported. Stating `nmax = FALSE` this first row is omitted.

sep Only relevant when table is exported to csv. Stating, for example, `sep = “;”` table will be exported to csv with columns separated by “;”

4.3.2 Exporting to \LaTeX

A special case of exporting is when tables are exported to \LaTeX . The function `export2latex` returns an object with the tex code as a character that can be changed in the \R session.

file If the `file` argument in `export2latex` is missing, the code is printed in the \R console. This can be useful when \R code is inserted in a \LaTeX document chunk to be processed with `Sweave`.

```
> restab<-createTable(compareGroups(group ~ age + sex + smoke + waist + hormo,
+                                   data=predimed))
> export2latex(restab)
```

```
\begin{longtable}{lcccc}\caption{Summary descriptives table by groups of `Intervention group'}\\
\hline
& Control & MedDiet + Nuts & MedDiet + VOO & \multirow{2}{*}{p.overall}\\
& N=2042 & N=2100 & N=2182 & \\
\hline
\hline
\endfirsthead
\multicolumn{5}{l}{\tablename\ \thetable\ \textit{-- continued from previous page}}\\
\hline
& Control & MedDiet + Nuts & MedDiet + VOO & \multirow{2}{*}{p.overall}\\
& N=2042 & N=2100 & N=2182 & \\
\hline
\hline
\endhead
\multicolumn{5}{l}{\textit{continued on next page}} \\
\endfoot
\multicolumn{5}{l}{} \\
\endlastfoot
Age & 67.3 (6.28) & 66.7 (6.02) & 67.0 (6.21) & 0.003 \\
Sex: & & & & <$0.001 \\
$\quad$Male & 812 (39.8\%) & 968 (46.1\%) & 899 (41.2\%) & \\
$\quad$Female & 1230 (60.2\%) & 1132 (53.9\%) & 1283 (58.8\%) & \\
Smoking: & & & & 0.444 \\
$\quad$Never & 1282 (62.8\%) & 1259 (60.0\%) & 1351 (61.9\%) & \\
$\quad$Current & 270 (13.2\%) & 296 (14.1\%) & 292 (13.4\%) & \\
$\quad$Former & 490 (24.0\%) & 545 (26.0\%) & 539 (24.7\%) & \\
Waist circumference & 101 (10.8) & 100 (10.6) & 100 (10.4) & 0.045
```



```

Hormone-replacement therapy: & & & 0.850 \\
$\quad$No & 1811 (98.3\%) & 1835 (98.4\%) & 1918 (98.2\%) & \\
$\quad$Yes & 31 (1.68\%) & 30 (1.61\%) & 36 (1.84\%) & \\
\hline
\end{longtable}

```

size The font size of exported tables can be changed by this option. Possible values are 'tiny', 'script-size', 'footnotesize', 'small', 'normalsize', 'large', 'Large', 'LARGE', 'huge', 'Huge' or 'same'. Default is 'same', which means that font size of the table is the same as specified in the main L^AT_EX document where the table will be inserted.

caption The table caption for descriptives table and available data table. If `which.table='both'` the first element of 'caption' will be assigned to descriptives table and the second to available data table. If it is set to "", no caption is inserted. Default value is NULL, which writes 'Summary descriptives table by groups of 'y'' for descriptives table and 'Available data by groups of 'y'' for the available data table.

loc.caption Table caption location. Possible values are 'top' or 'bottom'. Default value is 'top'.

label Used to cite tables in a L^AT_EX document. If `which.table='both'` the first element of 'label' will be assigned to the descriptives table and the second to the available data table. Default value is NULL, which assigns no label to the table/s.

landscape Table is placed in horizontal way. This option is specially usefull when table contains many columns and/or they are too wide to be placed vertically.

4.3.3 Generating an exhaustive report

In the version 2.0 of `compareGroups` package, a new function called 'report' has been created. This function automatically generates a PDF document with the descriptive table as well as the corresponding 'available' table. In addition, plots of all analysed variables are shown.

In order to make easier to 'navigate' throught the document, an index with hyperlinks is inserted in the document.

See the help file of this function where you can find an example with the REGICOR data (the other example data set contained in the `compareGroups` package)

```

> ?report # to know more about report function
> ?regicor # info about REGICOR data set

```

5 Missing values

Many times, it is important to be aware of the missingness contained in each variable, possibly by groups. Although ‘available’ table shows the number of the non-missing values for each row-variable and in each group, it would be desirable to test whether the frequency of non-available data is different between groups. For this purpose, a new function has been implemented in the `compareGroups` package, which is called ‘missingTable’. This function applies to both `compareGroups` and `createTable` class objects. This last option is useful when the table is already created. To illustrate it, we will use the REGICOR data set, comparing missing rates of all variables by year:

```
> # from a compareGroups object
> data(regicor)
> res <- compareGroups(year ~ .-id, regicor)
> missingTable(res)
```

-----Missingness table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	0 (0.00%)	0 (0.00%)	0 (0.00%)	1.000
Sex	0 (0.00%)	0 (0.00%)	0 (0.00%)	1.000
Smoking status	16 (3.71%)	28 (3.56%)	17 (1.58%)	0.010
Systolic blood pressure	3 (0.70%)	11 (1.40%)	0 (0.00%)	<0.001
Diastolic blood pressure	3 (0.70%)	11 (1.40%)	0 (0.00%)	<0.001
History of hypertension	0 (0.00%)	0 (0.00%)	8 (0.74%)	0.015
Hypertension treatment	0 (0.00%)	0 (0.00%)	43 (3.99%)	<0.001
Total cholesterol	28 (6.50%)	71 (9.03%)	2 (0.19%)	<0.001
HDL cholesterol	30 (6.96%)	38 (4.83%)	1 (0.09%)	<0.001
Triglycerides	28 (6.50%)	34 (4.33%)	1 (0.09%)	<0.001
LDL cholesterol	43 (9.98%)	98 (12.5%)	27 (2.51%)	<0.001
History of hyperchol.	0 (0.00%)	15 (1.91%)	6 (0.56%)	0.001
Cholesterol treatment	0 (0.00%)	13 (1.65%)	42 (3.90%)	<0.001
Height (cm)	8 (1.86%)	15 (1.91%)	12 (1.11%)	0.318
Weight (Kg)	8 (1.86%)	15 (1.91%)	12 (1.11%)	0.318
Body mass index	8 (1.86%)	15 (1.91%)	12 (1.11%)	0.318
Physical activity (Kcal/week)	64 (14.8%)	22 (2.80%)	2 (0.19%)	<0.001
Physical component	34 (7.89%)	123 (15.6%)	83 (7.71%)	<0.001
Mental component	34 (7.89%)	123 (15.6%)	83 (7.71%)	<0.001
Cardiovascular event	33 (7.66%)	45 (5.73%)	53 (4.92%)	0.118
Days to cardiovascular event or end of follow-up	33 (7.66%)	45 (5.73%)	53 (4.92%)	0.118
Overall death	44 (10.2%)	48 (6.11%)	54 (5.01%)	0.001
Days to overall death or end of follow-up	44 (10.2%)	48 (6.11%)	54 (5.01%)	0.001

```
> # or from createTable objects
> restab <- createTable(res, hide.no = 'no')
> missingTable(restab)
```

Perhaps a NA value of a categorical variable may mean something different from just non available. For example, patients admitted for Coronary Acute Syndrome with NA in ST elevation may have a higher risk of in-hospital death than the ones with available data, i.e. ST elevation yes or not. If these kind of variables are introduced in the data set as NA, they are removed from the analysis. To avoid the user having to recode NA as a new category for all categorical variables, new argument called ‘include.miss’ in `compareGroups` has been implemented which does it automatically. Let’s see an example with all variables from REGICOR data set by cardiovascular event.

```
> # first create time-to-cardiovascular event
> regicor$tcv<-with(regicor, Surv(tocv, cv=='Yes'))
> # create the table
> res <- compareGroups(tcv ~ . -id-tocv-cv-todeath-death, regicor, include.miss = TRUE)
> restab <- createTable(res, hide.no = 'no')
> restab
```

-----Summary descriptives table by 'tcv'-----

	No event N=2071	Event N=92	p.overall
Recruitment year:			0.157
1995	388 (18.7%)	10 (10.9%)	
2000	706 (34.1%)	35 (38.0%)	
2005	977 (47.2%)	47 (51.1%)	
Age	54.6 (11.1)	57.5 (11.0)	0.021
Sex:			0.696
Male	996 (48.1%)	46 (50.0%)	
Female	1075 (51.9%)	46 (50.0%)	
Smoking status:			<0.001
Never smoker	1099 (53.1%)	37 (40.2%)	
Current or former < 1y	506 (24.4%)	47 (51.1%)	
Former >= 1y	419 (20.2%)	8 (8.70%)	
<Missing>	47 (2.27%)	0 (0.00%)	
Systolic blood pressure	131 (20.3)	138 (21.5)	0.001
Diastolic blood pressure	79.5 (10.4)	82.9 (12.3)	0.002
History of hypertension:			0.118
Yes	647 (31.2%)	38 (41.3%)	
No	1418 (68.5%)	54 (58.7%)	
<Missing>	6 (0.29%)	0 (0.00%)	
Hypertension treatment:			0.198
No	1657 (80.0%)	70 (76.1%)	
Yes	382 (18.4%)	22 (23.9%)	
<Missing>	32 (1.55%)	0 (0.00%)	
Total cholesterol	218 (44.5)	224 (50.4)	0.207
HDL cholesterol	52.8 (14.8)	50.4 (13.3)	0.114
Triglycerides	113 (68.2)	123 (52.4)	0.190
LDL cholesterol	143 (39.6)	149 (45.6)	0.148
History of hyperchol.:			0.470
Yes	639 (30.9%)	25 (27.2%)	
No	1414 (68.3%)	67 (72.8%)	
<Missing>	18 (0.87%)	0 (0.00%)	
Cholesterol treatment:			0.190
No	1817 (87.7%)	86 (93.5%)	
Yes	213 (10.3%)	6 (6.52%)	
<Missing>	41 (1.98%)	0 (0.00%)	
Height (cm)	163 (9.21)	163 (9.34)	0.692
Weight (Kg)	73.4 (13.7)	74.9 (12.8)	0.294
Body mass index	27.6 (4.56)	28.1 (4.48)	0.299
Physical activity (Kcal/week)	405 (397)	338 (238)	0.089
Physical component	49.7 (8.95)	47.4 (9.03)	0.023
Mental component	48.1 (10.9)	46.3 (12.2)	0.122

6 Analysis of genetic data

In the version 2.0 of `compareGroups`, it is possible to analyse genetic data, more concretely Single Nucleotide Polymorphisms (SNPs), using the function `compareSNPs`. This function takes advantage of `SNPassoc`[4] and `HardyWeinberg` [5] packages to perform quality control of genetic data displaying the Minor Allele Frequencies, Missingness, Hardy Weinberg Equilibrium, etc. of the whole data set or by groups. When groups are considered, it also performs a test to check whether missingness rates is the same among groups.

Following, we illustrate this by an example taking a data set from `SNPassoc` package.

First of all, load the SNPs data from `SNPassoc`, and visualize the first rows. Notice how are the SNPs coded, i.e. by the alleles. The alleles separator can be any character. If so, this must be specified in the 'sep' argument of `compareSNPs` function (see `?compareSNPs` for more details).

```
> data(SNPs)
> head(SNPs)
```

```
  id casco    sex blood.pre  protein snp10001 snp10002 snp10003 snp10004 snp10005 snp10006 snp10007
1  1      1 Female    13.7 75640.52      TT      CC      GG      GG      GG      GG      AA      CC
2  2      1 Female    12.7 28688.22      TT      AC      GG      GG      AG      AA      CC
3  3      1 Female    12.9 17279.59      TT      CC      GG      GG      GG      AA      CC
4  4      1 Male     14.6 27253.99      CT      CC      GG      GG      GG      AA      CC
5  5      1 Female    13.4 38066.57      TT      AC      GG      GG      GG      AA      CC
6  6      1 Female    11.3 9872.46      TT      CC      GG      GG      GG      AA      CC
  snp10008 snp10009 snp10010 snp10011 snp10012 snp10013 snp10014 snp10015 snp10016 snp10017
1      CC      AA      TT      GG      GG      AA      AA      GG      GG      TT
2      CC      AG      TT      GG      CG      AA      AC      GG      GG      CT
3      CC      AA      TT      CC      GG      AA      CC      GG      GG      TT
4      CC      AA      TT      GG      GG      AA      AC      GG      GG      TT
5      CC      AG      TT      GG      GG      AA      AC      GG      GG      CT
6      CC      AA      TT      GG      GG      AA      AA      GG      GG      TT
  snp10018 snp10019 snp10020 snp10021 snp10022 snp10023 snp10024 snp10025 snp10026
1      TT      CC      GG      GG      AA      TT      TT      CC      CC
2      CT      CG      GG      GG      AA      AT      TT      CC      GG
3      TT      CC      GG      GG      AA      TT      TT      CC      GG
4      TT      CG      GG      GG      AA      TT      CT      CC      GG
5      CT      CG      GG      GG      AA      AT      TT      CC      GG
6      TT      CC      GG      GG      AA      TT      TT      CC      GG
  snp10027 snp10028 snp10029 snp10030 snp10031 snp10032 snp10033 snp10034 snp10035
1      CC      CC      GG      AA      TT      AA      AA      TT      TT
2      CG      CT      GG      AA      TT      AG      AG      TT      TT
3      CC      CC      GG      AA      TT      AA      AA      TT      TT
4      CC      CT      AG      AA      TT      AG      AG      CT      TT
5      CG      CT      GG      AA      TT      AG      AG      TT      TT
6      CC      CC      GG      AA      TT      AA      AA      TT      <NA>
```

In this data frame there are some genetic and non-genetic data. Genetic variables are those whose names begin with 'snp'. If we want to summarize the first three SNPs by case control status:

```
> res<-compareSNPs(casco ~ snp10001 + snp10002 + snp10003, data=SNPs)
> res
```

```
***** Summary of genetic data (SNPs) by groups *****
```

```
*** casco = '0' ***
```

```
-----
SNP      Ntyped    MAF Genotypes    Genotypes.p HWE.p
-----
snp10001    47  26.6% TT|TC|CC  51.1|44.7|4.3 0.487
snp10002    47  26.6% CC|CA|AA  46.8|53.2|0.0 0.029
snp10003    44 100.0%      GG 100.0| 0.0|0.0 1.000
-----
```

```
*** casco = '1' ***
```

```
-----
SNP      Ntyped    MAF Genotypes    Genotypes.p HWE.p
-----
snp10001   110  23.6% TT|TC|CC  61.8|29.1|9.1 0.069
snp10002   110  28.6% CC|CA|AA  47.3|48.2|4.5 0.091
snp10003   100 100.0%      GG 100.0| 0.0|0.0 1.000
-----
```

*** Missingness test ***

```
-----
snps      p.value
-----
snp10001   1.000
snp10002   1.000
snp10003   0.756
-----
```

Note that all variables specified in the right hand side of the formula must be SNPs, i.e. variables whose levels or codes can be interpreted as genotypes (see `setupSNPs` function from `SNPassoc` package for more information). Separated summary tables by groups of cases and controls are displayed, and the last table corresponds to missingness test comparing non-available rates among groups.


If summarizing SNPs in the whole data set is desired, without separating by groups, leave the left side of formula in blank, as in `compareGroups` function. In this case, a single table is displayed and no missingness test is performed.

```
> res<-compareSNPs(~ snp10001 + snp10002 + snp10003, data=SNPs)
> res
```

***** Summary of genetic data (SNPs) *****

```
-----
SNP      Ntyped    MAF Genotypes    Genotypes.p HWE.p
-----
snp10001   157  24.5% TT|TC|CC  58.6|33.8|7.6 0.353
snp10002   157  28.0% CC|CA|AA  47.1|49.7|3.2 0.006
snp10003   144 100.0%      GG 100.0| 0.0|0.0 1.000
-----
```


7 Using GUI

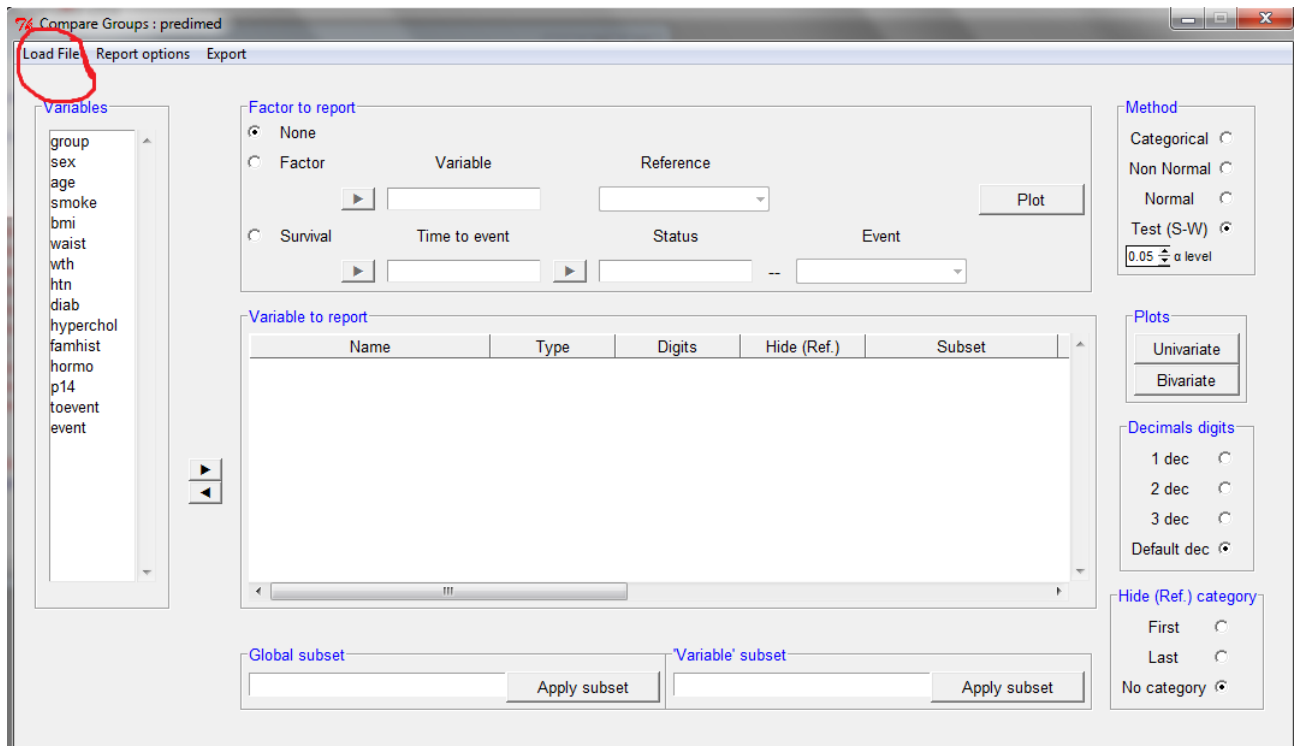
Once the `compareGroups` package is loaded, a Graphical User Interface (GUI) is displayed in response to typing `cGroupsGUI()`. The GUI is meant to make it feasible for users who are unfamiliar with  to construct bivariate tables.

In this section we illustrate, step by step, how to construct a bivariate table containing descriptives by groups from the *predimed* data using the GUI:

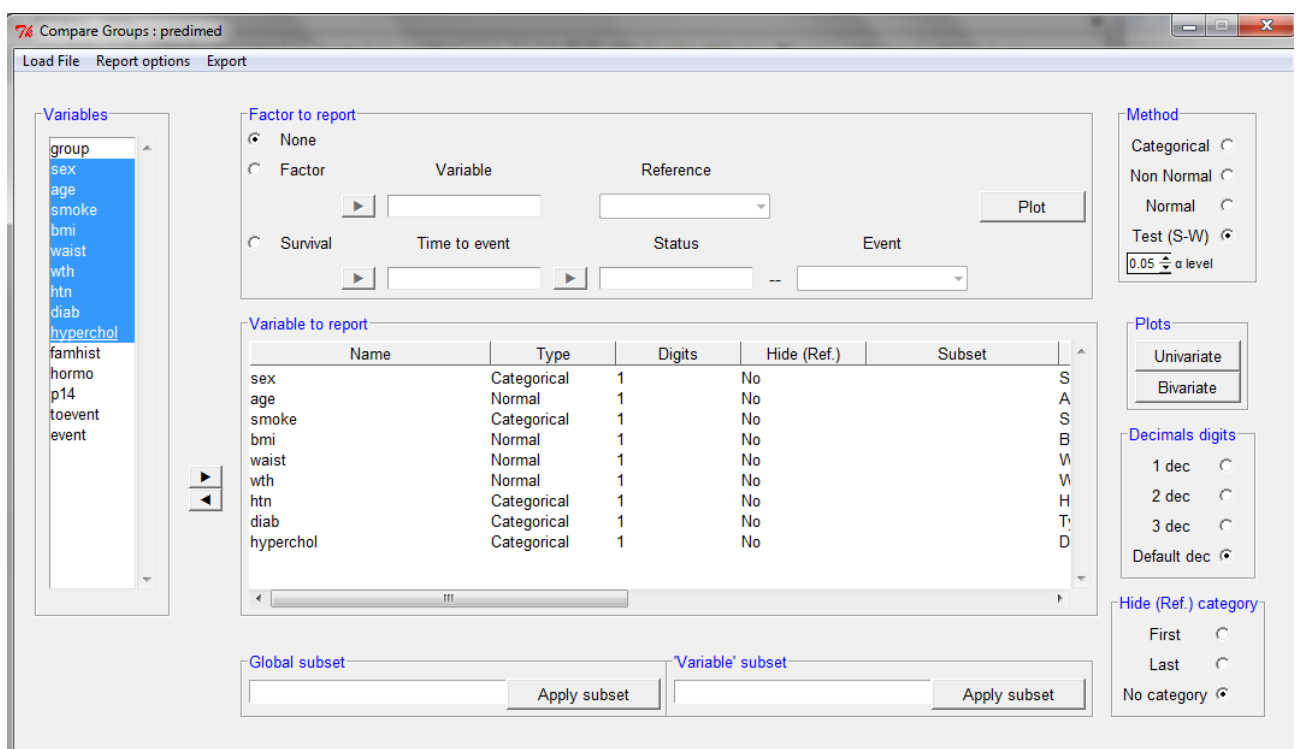
Table 2: Summary descriptives table by groups of ‘Intervention group’

	Control N=2042	MedDiet + Nuts N=2100	MedDiet + VOO N=2182	p.overall
Age	67.3 (6.28)	66.7 (6.02)	67.0 (6.21)	0.003
Sex: Female	1230 (60.2%)	1132 (53.9%)	1283 (58.8%)	<0.001
Smoking:				0.444
Never	1282 (62.8%)	1259 (60.0%)	1351 (61.9%)	
Current	270 (13.2%)	296 (14.1%)	292 (13.4%)	
Former	490 (24.0%)	545 (26.0%)	539 (24.7%)	
Body mass index	30.3 (3.96)	29.7 (3.77)	29.9 (3.71)	<0.001
Waist circumference	101 (10.8)	100 (10.6)	100 (10.4)	0.045
Waist-to-height ratio	0.63 (0.07)	0.62 (0.06)	0.63 (0.06)	<0.001
Hypertension	1711 (83.8%)	1738 (82.8%)	1786 (81.9%)	0.249
Type-2 diabetes	970 (47.5%)	950 (45.2%)	1082 (49.6%)	0.017
Dyslipidemia	1479 (72.4%)	1539 (73.3%)	1560 (71.5%)	0.423
Family history of premature CHD	462 (22.6%)	460 (21.9%)	507 (23.2%)	0.581
Hormone-replacement therapy	31 (1.68%)	30 (1.61%)	36 (1.84%)	0.850
MeDiet Adherence score	8.44 (1.94)	8.81 (1.90)	8.77 (1.97)	<0.001
follow-up to main event (years)	4.09 (1.74)	4.31 (1.70)	4.64 (1.60)	<0.001
AMI, stroke, or CV Death	97 (4.75%)	70 (3.33%)	85 (3.90%)	0.064

Step 1. Browse for and select the data to be loaded. Valid file types include SPSS or  format, CSV plain text file or a *data.frame* already existing in the Workspace. By default, the *predimed* example data is loaded when the GUI is opened.



Step 2. Choose the variables to be described (row-variables).



Step 3. If descriptives by group are desired (for example), move the variable *group* to the GUI top frame, making it the factor variable. To report descriptives for the whole sample (i.e., no groups), click on the 'none' button.

Compare Groups : predimed

Load File Report options Export

Variables

- group
- sex
- age
- smoke
- bmi
- waist
- wth
- htn
- diab
- hyperchol
- famhist
- hormo
- p14
- toevent
- event

Factor to report

☐ None

☒ Factor Variable Reference

group

☐ Survival Time to event Status Event

Variable to report

Name	Type	Digits	Hide (Ref.)	Subset
sex	Categorical	1	No	S
age	Normal	1	No	A
smoke	Categorical	1	No	S
bmi	Normal	1	No	B
waist	Normal	1	No	V
wth	Normal	1	No	V
htn	Categorical	1	No	H
diab	Categorical	1	No	T
hyperchol	Categorical	1	No	D

Method

☐ Categorical

☐ Non Normal

☐ Normal

☒ Test (S-W)

0.05 α level

Plots

Decimals digits

☐ 1 dec

☐ 2 dec

☐ 3 dec

☒ Default dec

Hide (Ref.) category

☐ First

☐ Last

☒ No category

Global subset

'Variable' subset

Step 4. It is possible to hide the first, last or no categories of a categorical row-variable. In this example, 'Male' levels will be hidden for Sex; conversely, all categories will be shown for other categorical variables.

Compare Groups : predimed

Load File Report options Export

Variables

- group
- sex
- age
- smoke
- bmi
- waist
- wth
- htn
- diab
- hyperchol
- famhist
- hormo
- p14
- toevent
- event

Factor to report

☐ None

☒ Factor Variable Reference

group

☐ Survival Time to event Status Event

Variable to report

Name	Type	Digits	Hide (Ref.)	Subset
sex	Categorical	1	No	S
age	Normal	1	No	A
smoke	Categorical	1	No	S
bmi	Normal	1	No	B
waist	Normal	1	No	V
wth	Normal	1	No	V
htn	Categorical	1	No	H
diab	Categorical	1	No	T
hyperchol	Categorical	1	No	D

Method

☐ Categorical

☐ Non Normal

☐ Normal

☒ Test (S-W)

0.05 α level

Plots

Decimals digits

☐ 1 dec

☐ 2 dec

☐ 3 dec

☒ Default dec

Hide (Ref.) category

☒ First

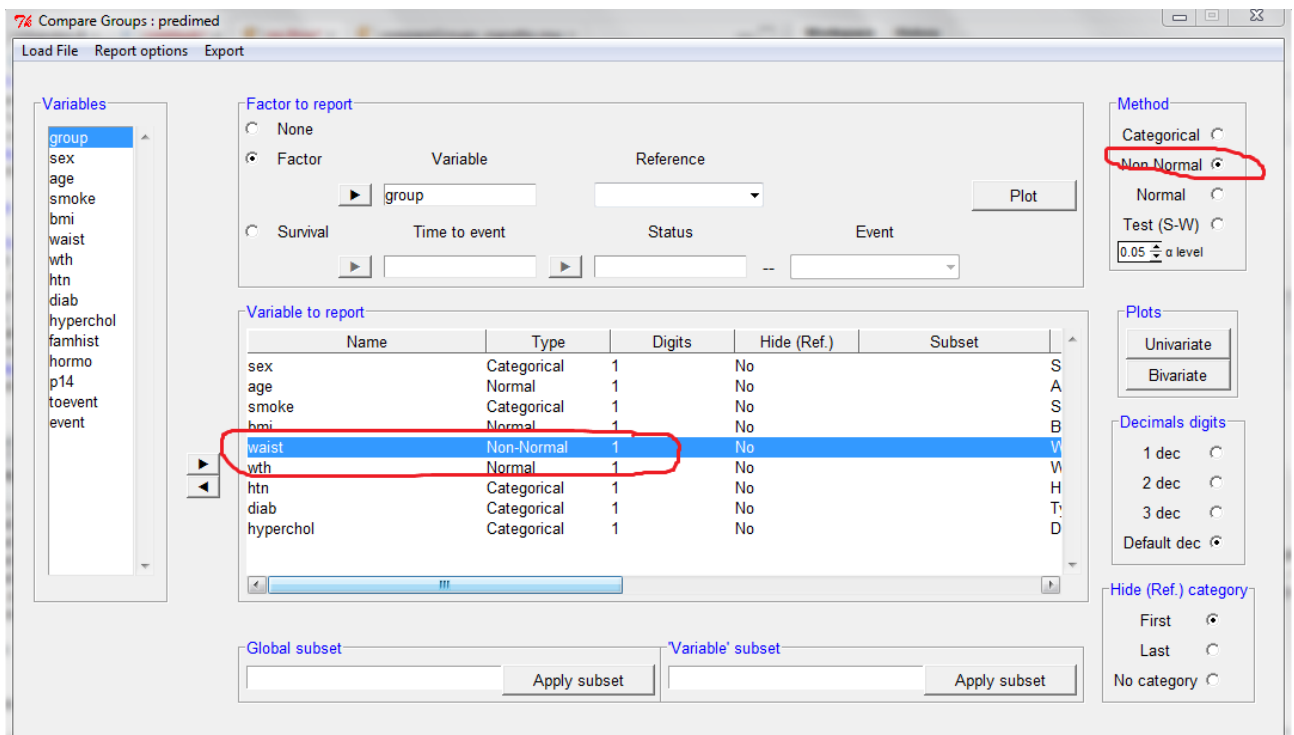
☐ Last

☐ No category

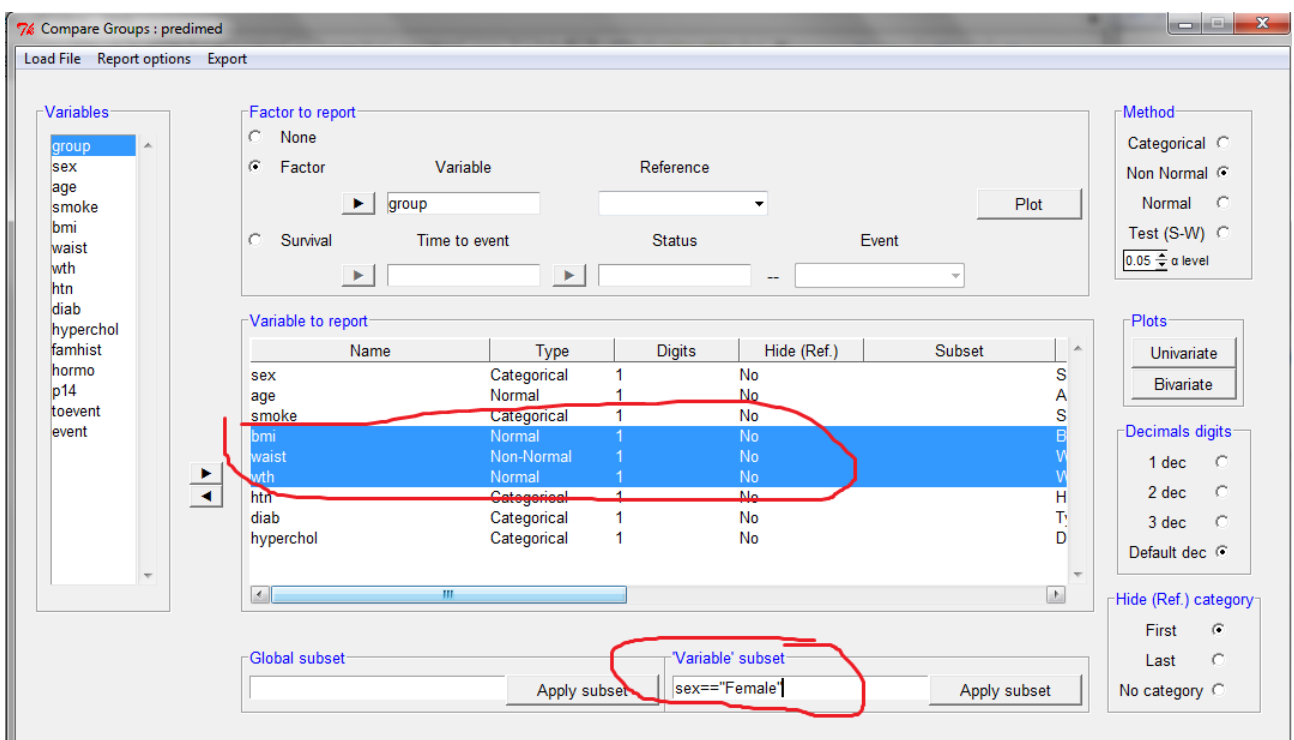
Global subset

'Variable' subset

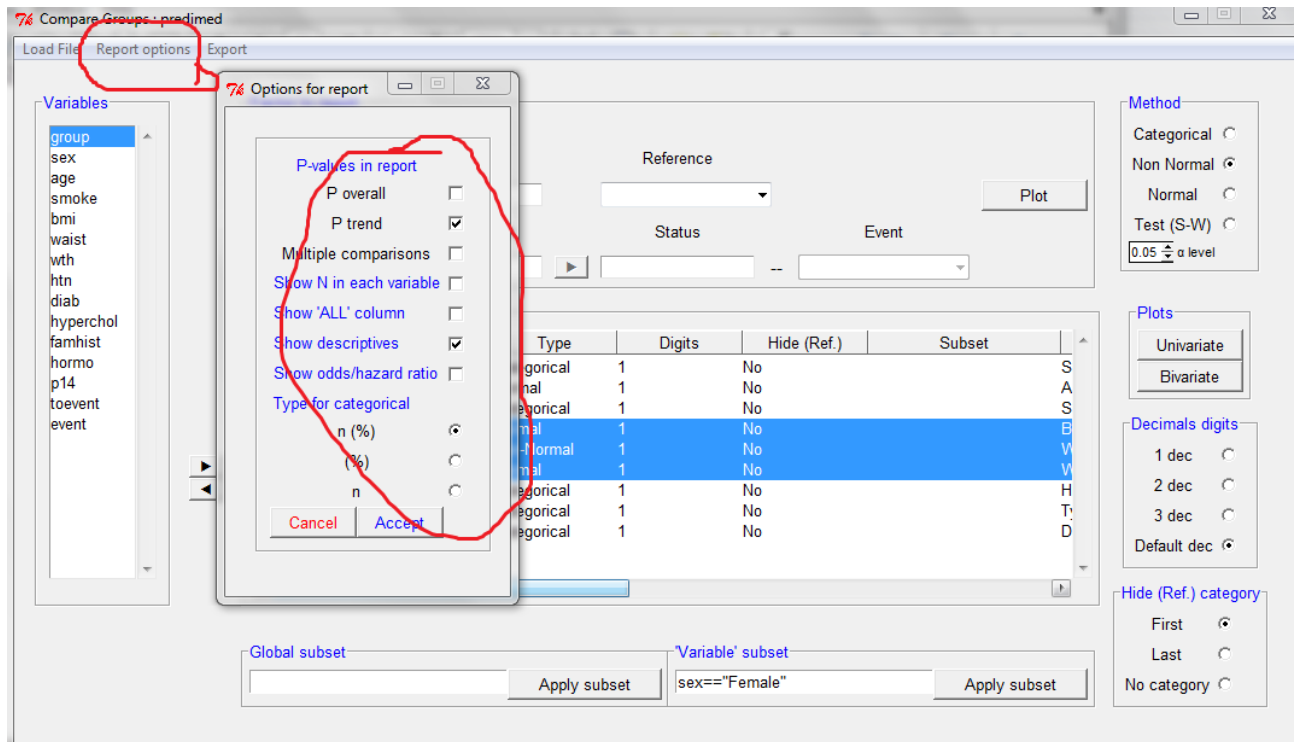
Step 5. For each continuous variable, it is possible to specify whether to treat it as normal or non-normal or to transform a numerical variable into a categorical one. This last option can be interesting if a categorical variable has been coded as numerical. By default, all continuous variables are treated as normal. In this example, Waist circumference will be treated as non-normal, i.e., median and quartiles will be reported instead of mean and standard deviation.



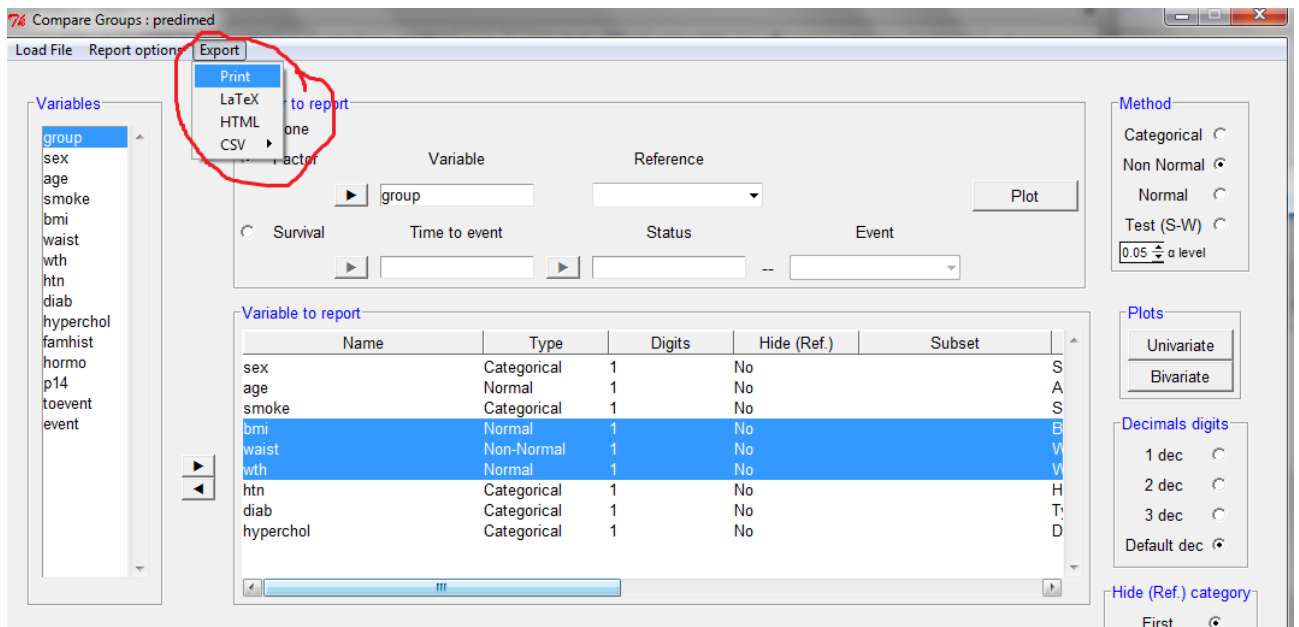
Step 6. For each row-variable, it is possible to select a subset of individuals from the data set to be included. In this example, descriptives of Body mass index, Waist circumference and Waist-to-height ratio will be reported only for Female participants. Also, it is possible to specify criteria to select a subset of individuals to be included for all row-variables: type the logical condition (selection criteria of individuals) on the 'Global subset' window instead of 'Variable subset'.



Step 7. Some bivariate table characteristics can be set by clicking on 'Report options' from the main menu, such as to report descriptives (mean, frequencies, medians, etc.), display the p-trend, and show only relative frequencies.



Step 8. Finally, specify the bivariate table format (L^AT_EX, CVS plain text or HTML). Clicking on 'print' will then display the bivariate table, as well as a summary (available data, etc.), on the R console. The table can also be exported to the file formats listed.



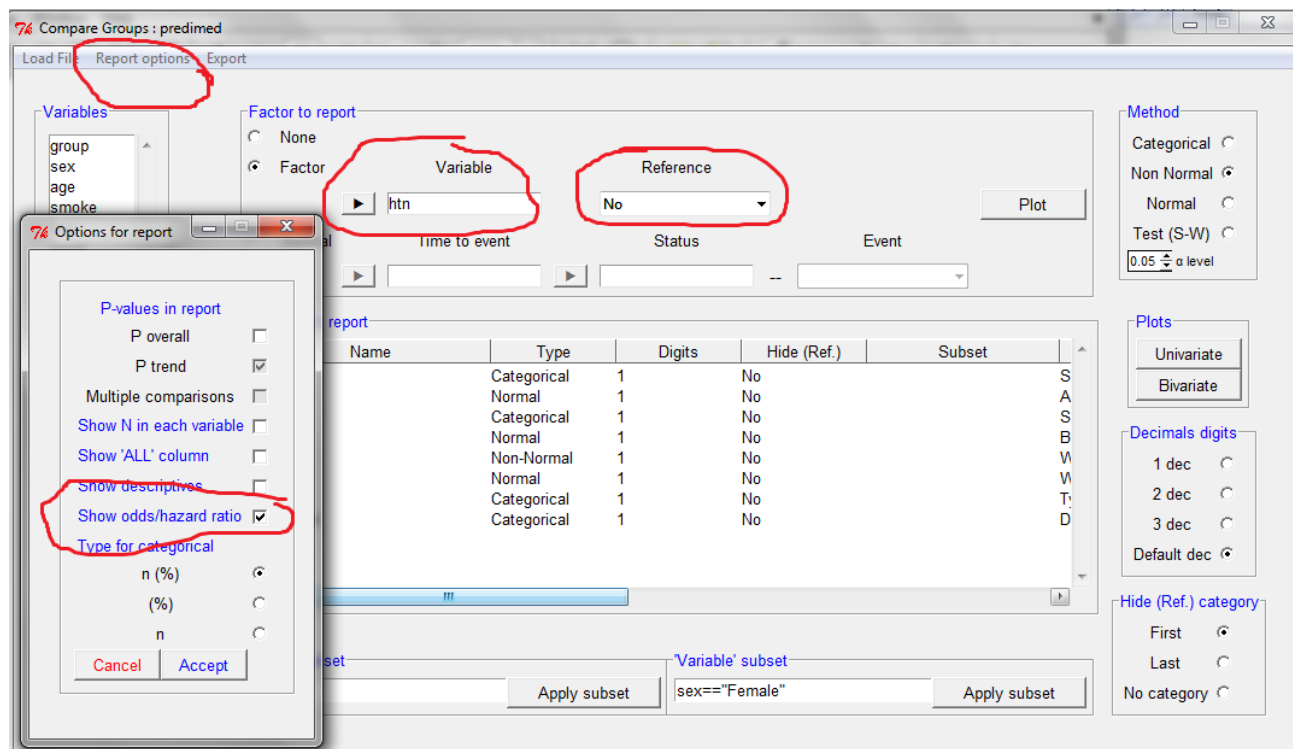
7.1 Computing Odds Ratio

For a case-control study, it may be necessary to report the Odds Ratio between cases and controls for each variable. The table below contains Odds Ratios for each row-variable by hypertension status.

Table 3: Summary descriptives table by groups of 'Hypertension'

	OR	p.ratio	p.overall
Age	1.04 [1.03;1.05]	<0.001	<0.001
Sex: Female	1.82 [1.60;2.08]	0.000	<0.001
Smoking:			<0.001
Never	Ref.	Ref.	
Current	0.43 [0.36;0.51]	0.000	
Former	0.63 [0.54;0.73]	<0.001	
Body mass index	1.10 [1.08;1.12]	<0.001	<0.001
Waist circumference	1.01 [1.01;1.02]	<0.001	<0.001
Waist-to-height ratio	71.5 [25.6;199]	<0.001	<0.001
Type-2 diabetes	0.25 [0.22;0.29]	0.000	<0.001
Dyslipidemia	1.75 [1.53;2.01]	<0.001	<0.001
Family history of premature CHD	0.87 [0.75;1.01]	0.070	0.074
Hormone-replacement therapy	1.08 [0.64;1.97]	0.773	0.856
MeDiet Adherence score	0.96 [0.93;1.00]	0.028	0.029
follow-up to main event (years)	0.94 [0.90;0.98]	0.002	0.001
AMI, stroke, or CV Death	1.04 [0.75;1.48]	0.826	0.879

To build this table, as illustrated in the screens below, you would select *htn* variable (Hypertension status) as the factor variable, indicate 'no' category on the 'reference' pull-down menu, and mark 'Show odds/hazard ratio' in the 'Report Options' menu before exporting the table.



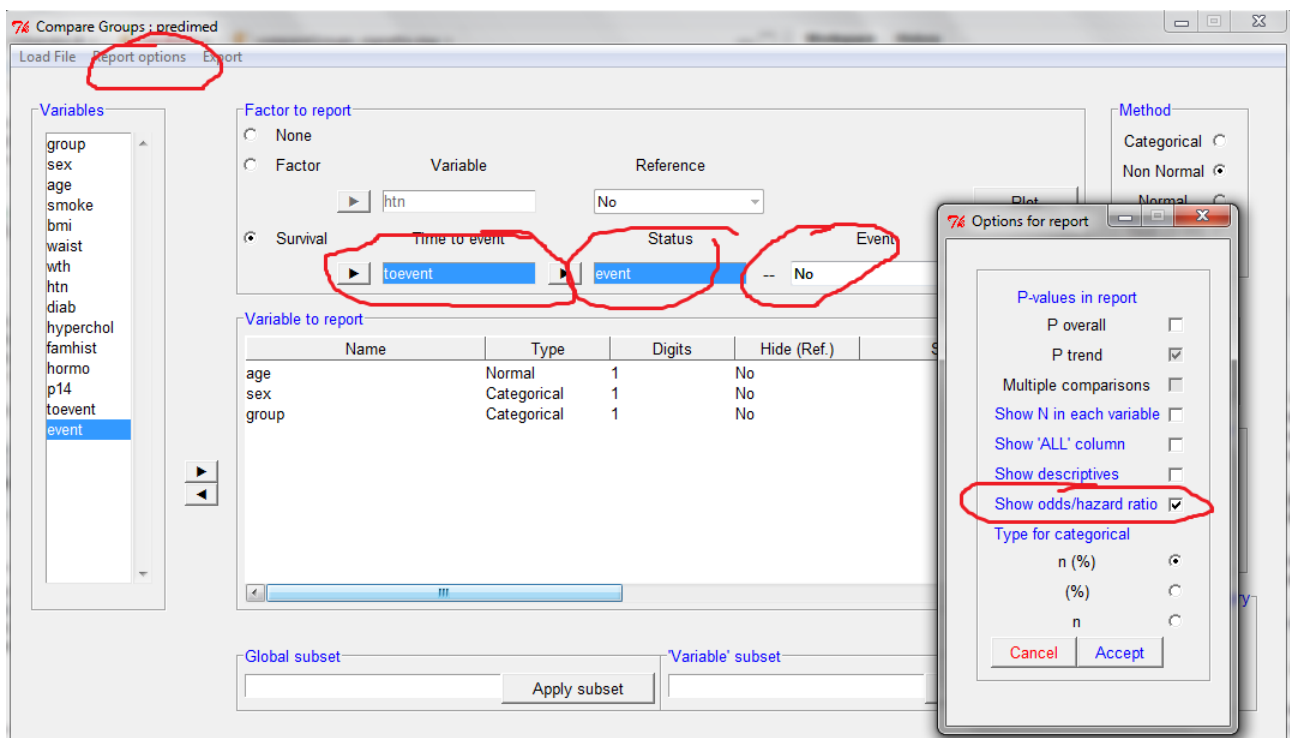
7.2 Computing Hazard Ratio


In a cohort study, it may be more informative to compute hazard ratio taking into account time-to-event.

Table 4: Summary descriptives table by groups of ‘AMI, stroke, or CV Death’

	No event N=6072	Event N=252	HR	p.ratio	p.overall
Intervention group:					0.011
Control	1945 (32.0%)	97 (38.5%)	Ref.	Ref.	
MedDiet + Nuts	2030 (33.4%)	70 (27.8%)	0.66 [0.48;0.89]	0.008	
MedDiet + VOO	2097 (34.5%)	85 (33.7%)	0.70 [0.53;0.94]	0.018	
Age	66.9 (6.14)	69.4 (6.65)	1.06 [1.04;1.09]	<0.001	<0.001
Sex:					<0.001
Male	2528 (41.6%)	151 (59.9%)	Ref.	Ref.	
Female	3544 (58.4%)	101 (40.1%)	0.49 [0.38;0.63]	<0.001	

To generate this table, select *toevent* variable and *event*, indicating the time-to-event and the status, respectively, and select the event category for the status variable. Finally, as for Odds Ratios, mark ‘Show odds/hazard ratio’ in the ‘Report Options’ menu before exporting the table.



To return to the  console, just close the GUI window.

Bibliography

References

- [1] Y. Benjamini and Y. Hochberg. Controlling the false discovery rate: A practical and powerful approach to multiple testing. *J. Roy. Statist. Soc. Ser. B*, 57:289–300, 1995.
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