

compareGroups: Descriptives by groups

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February 3, 2012

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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 5.

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.

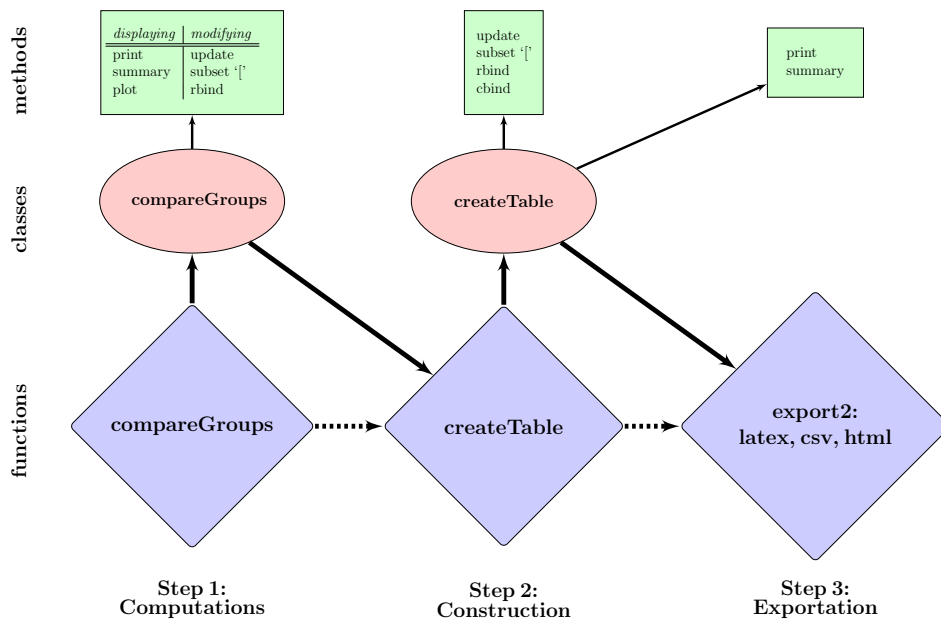


Figure 1: Diagram of the `compareGroups` package

3 Data used as example

To illustrate how this package works we used data from a cohort study aimed to establish risk factors related to coronary heart disease. Some variables have been partially modified to provide a better example for the use of this package.

```
> data(regicor)
> head(regicor)
```

```
      id year age  sex      smoker sbp dbp histhtn txhtn chol      hdl triglyc      ldl histchol txchol he
6101    2265 2005  70 Female      Never smoker 138  75      No      No  294 57.00000      93 218.40000      No      No
5762    1882 2005  56 Female      Never smoker 139  89      No      No  220 50.00000     160 138.00000      No      No
2992 3000105616 2000  37  Male Current or former < 1y 132  82      No      No  245 59.80429      89 167.39571      No      No
2611 3000103485 2000  69 Female      Never smoker 168  97      No      No  168 53.17571     116  91.62429      No      No
2762 3000103963 2000  70 Female      <NA>      NA  NA      No      No      NA      NA      NA      NA      <NA>      <NA>
1516 3000100883 2000  40 Female Current or former < 1y 108  70      No      No      NA 68.90000      94      NA      No      No
      phyact  pcs  mcs  cv  tocv death  todeath
6101 304.2000 54.455 58.918  No 1024.882  Yes 1299.16343
5762 160.3000 58.165 47.995  No 2756.849  No  39.32629
2992 552.7912 43.429 62.585  No 1905.969  No  858.42203
2611 522.0000 54.325 57.900  No 1055.380  No 1833.07619
2762      NA      NA      NA <NA>      NA <NA>      NA
1516 386.9505 57.315 47.869  No 3239.241  No  877.61155
```

Variables and labels in this data frame are:

Name	Label	Codes
id	Individual id	
year	Recruitment year	1995; 2000; 2005
age	Age	
sex	Sex	Male; Female
smoker	Smoking status	Never smoker; Current or former < 1y; Former \geq 1y
sbp	Systolic blood pressure	
dbp	Diastolic blood pressure	
histhtn	History of hypertension	Yes; No
txhtn	Hypertension treatment	No; Yes
chol	Total cholesterol	
hdl	HDL cholesterol	
triglyc	Triglycerides	
ldl	LDL cholesterol	
histchol	History of hyperchol.	Yes; No
txchol	Cholesterol treatment	No; Yes
height	Height (cm)	
weight	Weight (Kg)	
bmi	Body mass index	
phyact	Physical activity (Kcal/week)	
pcs	Physical component	
mcs	Mental component	
cv	Cardiovascular event	No; Yes
tocv	Days to cardiovascular event or end of follow-up	
death	Overall death	No; Yes
todeath	Days to overall death or end of follow-up	

OBSERVATIONS:

1. It is important to note that `compareGroups` is not aimed to perform quality control of the data.

Other useful packages such as `r2lh` [2] 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):

```
> regicor$tdeath <- with(regicor, Surv(todeath, death == 'Yes'))
> label(regicor$tdeath) <- "Mortality"
> regicor$tcv <- with(regicor, Surv(tocv, cv == 'Yes'))
> label(regicor$tcv) <- "Cardiovascular"
```

Note that variables *tdeath* and *tcv* are created as time-to-death and time-to-cardiovascular event, respectively; both take censoring into account (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 *regicor* data between *year* (“response” variable) and all other variables (“explanatory” variables), this formula is required:

```
> compareGroups(year ~ . , data=regicor)
```

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 *id* from the analysis:

```
> compareGroups(year ~ . -id, data=regicor)
```

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

```
> res<-compareGroups(year ~ age + sex + smoker + triglyc , data=regicor)
> res
```

```
----- Summary of results by groups of 'Recruitment year'-----
```

var	N	p.value	method	selection
1 Age	2294	0.078*	continuous normal	ALL
2 Sex	2294	0.506	categorical	ALL
3 Smoking status	2233	<0.001**	categorical	ALL
4 Triglycerides	2231	0.582	continuous normal	ALL

```
-----
```

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

Note: Although we have full data (n= 2294) for Age and Sex there are some missing data in Smoking status and Triglycerides.

Year groups have some differences in Age although these don't reach statistical significance (p-value=0.078); however, Smoking status is clearly different.

Age & Triglycerides has been used as continuous and normal distributed. Sex & Smoking status 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., "male" participants):

```
> compareGroups(year ~ age + smoker + triglyc, data=regicor, subset = sex=='Male')
```

```
----- Summary of results by groups of 'Recruitment year'-----
```

var	N	p.value	method	selection
1 Age	1101	0.212	continuous normal	sex == "Male"
2 Smoking status	1071	<0.001**	categorical	sex == "Male"
3 Triglycerides	1075	0.817	continuous normal	sex == "Male"

```
-----
```

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

Note that only results for male participants are shown.

To subset specific variable/s (e.g., *triglyc* and *sbp*):

```
> compareGroups(year ~ age + smoker + triglyc + sbp, data=regicor,
+               selec = list(triglyc=txchol=='No', sbp=txhtn=='No'))
```

```
----- Summary of results by groups of 'Recruitment year'-----
```

var	N	p.value	method	selection
1 Age	2294	0.078*	continuous normal	ALL
2 Smoking status	2233	<0.001**	categorical	ALL
3 Triglycerides	1963	0.882	continuous normal	txchol == "No"
4 Systolic blood pressure	1810	<0.001**	continuous normal	txhtn == "No"

```
-----
```

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

Combinations are also allowed, e.g.:

```
> compareGroups(year ~ age + smoker + triglyc + sbp, data=regicor,
+               selec = list(triglyc=txchol=='No', sbp=txhtn=='No'),
+               subset = sex=='Male')
```

```

----- Summary of results by groups of 'Recruitment year'-----

  var                N    p.value  method
1 Age                1101 0.212    continuous normal
2 Smoking status     1071 <0.001** categorical
3 Triglycerides       943 0.993    continuous normal
4 Systolic blood pressure 886 <0.001** continuous normal
  selection
1 sex == "Male"
2 sex == "Male"
3 (sex == "Male") & (txchol == "No")
4 (sex == "Male") & (txhtn == "No")
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1

```

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

```

> compareGroups(year ~ age + smoker + triglyc + triglyc, data=regicor,
+               selec = list(triglyc.1=txchol=='No'))

```

```

----- Summary of results by groups of 'Recruitment year'-----

  var                N    p.value  method      selection
1 Age                2294 0.078*    continuous normal ALL
2 Smoking status     2233 <0.001** categorical      ALL
3 Triglycerides      2231 0.582    continuous normal ALL
4 Triglycerides      1963 0.882    continuous normal txchol == "No"
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1

```

In this case results for *triglyc* will be reported for all participants ($n = 2231$) and also for only those not treated with anti-cholesterol drugs ($txchol == 'No'$). Note that “triglyc.1” in the **selec** statement refers to the second time that *triglyc* 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., Triglycerides used as non-normal distributed:

```

> compareGroups(year ~ age + smoker + triglyc + sbp, data=regicor, method = c(triglyc=2))

```

```

----- Summary of results by groups of 'Recruitment year'-----

  var                N    p.value  method      selection
1 Age                2294 0.078*    continuous normal    ALL
2 Smoking status     2233 <0.001** categorical      ALL
3 Triglycerides      2231 0.762    continuous non-normal ALL
4 Systolic blood pressure 2280 <0.001** continuous normal    ALL
-----
Signif. codes:  0 '**' 0.05 '*' 0.1 ' ' 1

```

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

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(year ~ age + smoker + triglyc + sbp, data=regicor,
+               method = c(triglyc=NA), alpha= 0.01)
```

```
----- Summary of results by groups of 'Recruitment year'-----
```

var	N	p.value	method	selection
1 Age	2294	0.078*	continuous normal	ALL
2 Smoking status	2233	<0.001**	categorical	ALL
3 Triglycerides	2231	0.762	continuous non-normal	ALL
4 Systolic blood pressure	2280	<0.001**	continuous normal	ALL

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

According to Shapiro-Wilk test, stating the cutpoint at 0.01 level, Triglycerides 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:40=1; 41:45=2; 46:50=3; 51:55=4; 56:60=5; 61:65=6; 66:hi=7"
> regicor$age7gr<-car::recode(regicor$age, cuts)
> compareGroups(year ~ age7gr, data=regicor, method = c(age7gr=NA))
```

```
----- Summary of results by groups of 'Recruitment year'-----
```

var	N	p.value	method	selection
1 Age	2294	0.049**	continuous non-normal	ALL

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

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

```
----- Summary of results by groups of 'Recruitment year'-----
```

var	N	p.value	method	selection
1 Age	2294	0.001**	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 ~ smoker + triglyc + sbp, data=regicor)
```

```
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 ~ smoker + triglyc + sbp, data=regicor, max.ylev=7)
```

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

	var	N	p.value	method	selection
1	Smoking status	2233	<0.001**	categorical	ALL
2	Triglycerides	2231	0.021**	continuous normal	ALL
3	Systolic blood pressure	2280	<0.001**	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(year ~ smoker + age7gr, method= (age7gr=3), data=regicor, max.xlev=5)
```

```
----- Summary of results by groups of 'Recruitment year'-----
```

	var	N	p.value	method	selection
1	Smoking status	2233	<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(year ~ smoker + triglyc + sbp, data=regicor, include.label= FALSE)
```

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

	var	N	p.value	method	selection
1	smoker	2233	<0.001**	categorical	ALL
2	triglyc	2231	0.582	continuous normal	ALL
3	sbp	2280	<0.001**	continuous normal	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(year ~ age + smoker + triglyc + sbp, data=regicor,
+                        method = c(triglyc=2))
> createTable(resu1)
```


-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Smoking status:				<0.001
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)	
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)	
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)	
Triglycerides	94.0 [71.0; 136]	98.0 [72.0; 133]	98.0 [72.0; 139]	0.762
Systolic blood pressure	133 (19.2)	133 (21.3)	129 (19.8)	<0.001

Note: percentiles 25 and 75 are calculated for *Triglycerides*.

To get instead percentile 2.5 and 97.5:

```
> resu2<-compareGroups(year ~ age + smoker + triglyc + sbp, data=regicor,
+                        method = c(triglyc=2), Q1=0.025, Q3=0.975)
> createTable(resu2)
```

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Smoking status:				<0.001
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)	
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)	
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)	
Triglycerides	94.0 [47.0; 292]	98.0 [47.0; 278]	98.0 [42.0; 293]	0.762
Systolic blood pressure	133 (19.2)	133 (21.3)	129 (19.8)	<0.001

Note: percentiles 2.5 and 97.5 are calculated for Triglycerides.

To get minimum and maximum:

```
> compareGroups(year ~ age + smoker + triglyc + sbp, data=regicor,
+               method = c(triglyc=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”):

```
> regicor$smk<-regicor$smoker
> levels(regicor$smk)<- c("Never smoker", "Current or former < 1y",
+                        "Never or former >= 1y", "Unknown")
> cbind(table(regicor$smk))
```

```

      [,1]
Never smoker      1201
Current or former < 1y  593
Never or former >= 1y  439
Unknown              0
```

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

```
> compareGroups(year ~ age + smk + sbp, data=regicor)
```

```
Error in fisher.test(obj) : FEXACT error 6.
LDKEY is too small for this problem.
Try increasing the size of the workspace.
```

```
----- Summary of results by groups of 'Recruitment year'-----
```

var	N	p.value	method	selection
1 Age	2294	0.078*	continuous normal	ALL
2 Smoking status	2233	.	categorical	ALL
3 Systolic blood pressure	2280	<0.001**	continuous normal	ALL

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

Note that an “Error” message is printed and no p-values for *smk* are calculated.

To avoid using empty categories, `simplify` must be stated as `TRUE`

```
> compareGroups(year ~ age + smk + sbp, data=regicor, simplify=TRUE)
```

```
----- Summary of results by groups of 'Recruitment year'-----
```

var	N	p.value	method	selection
1 Age	2294	0.078*	continuous normal	ALL
2 Smoking status	2233	<0.001**	categorical	ALL
3 Systolic blood pressure	2280	<0.001**	continuous normal	ALL

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

4.1.5 Summary

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

```
> res<-compareGroups(year ~ age + sex + smoker + txchol + triglyc + sbp,
+                      method = c(triglyc=2), data=regicor)
> summary(res[c(1, 3, 4)])
```

```
--- Descriptives of each row-variable by groups of 'Recruitment year' ---
```

```
-----
row-variable: Age
```

	N	mean	sd	p.overall	p.trend	p.1995 vs 2000	p.1995 vs 2005	p.2000 vs 2005
[ALL]	2294	54.73627	11.04926					
1995	431	54.09745	11.7172	0.077837	0.031665	0.930249	0.143499	0.161195
2000	786	54.33715	11.21814					
2005	1077	55.28319	10.62606					

```
-----
row-variable: Smoking status
```

	Never smoker	Current or former < 1y	Former >= 1y	Never smoker (row%)	Current or former < 1y (row%)
[ALL]	1201	593	439	53.78415	26.5562
1995	234	109	72	56.38554	26.26506
2000	414	267	77	54.61741	35.22427
2005	553	217	290	52.16981	20.4717

	Former >= 1y (row%)	p.overall	p.trend	p.1995 vs 2000	p.1995 vs 2005	p.2000 vs 2005
[ALL]	19.65965					
1995	17.3494	0	2.4e-05	0.000144	0.000144	0
2000	10.15831					
2005	27.35849					

```
-----
row-variable: Cholesterol treatment
```

	No	Yes	No (row%)	Yes (row%)	p.overall	p.trend	p.1995 vs 2000	p.1995 vs 2005	p.2000 vs 2005
[ALL]	2011	228	89.81688	10.18312					
1995	403	28	93.50348	6.49652	0.000429	1e-04	0.193023	0.00196	0.014913
2000	705	68	91.2031	8.796895					
2005	903	132	87.24638	12.75362					

Note that because only variables 1, 3 & 4 are selected, only results for Age, Cholesterol treatment & Triglycerides are shown. Age is summarized by the mean and the standard deviation, Cholesterol treatment by frequencies and percentage, and Triglycerides (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="./univar/")
```

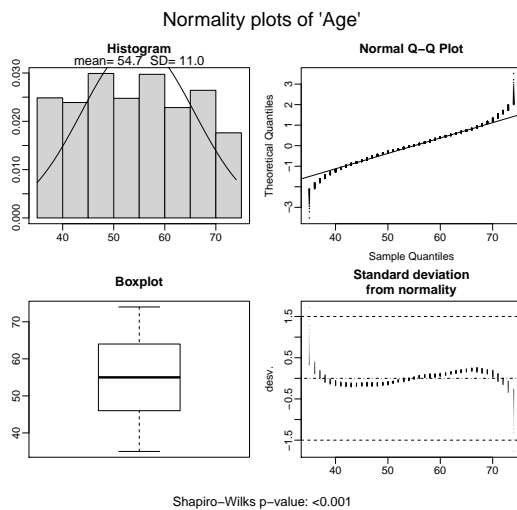


Figure 2: Plot of Age

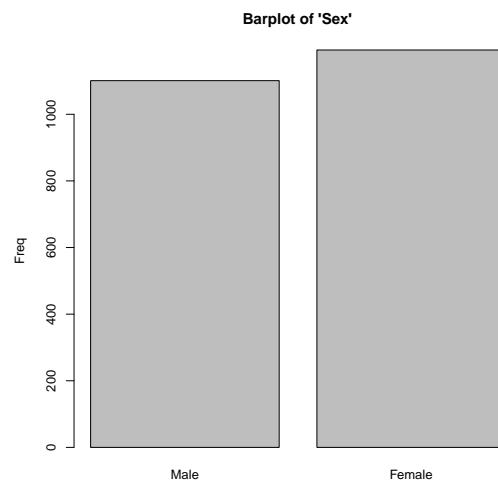


Figure 3: Plot of Sex

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="./bivar/")
```

4.1.7 Updating

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

```
> res<-compareGroups(year ~ age + sex + triglyc, data=regicor)
> res
```



Figure 4: Plot of Age



Figure 5: Plot of Sex

----- Summary of results by groups of 'Recruitment year'-----

var	N	p.value	method	selection
1 Age	2294	0.078*	continuous normal	ALL
2 Sex	2294	0.506	categorical	ALL
3 Triglycerides	2231	0.582	continuous normal	ALL

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

The object *res* is updated using:

```
> res<-update(res, . ~. - sex + smoker + chol, subset = sex=='Male',
+             method = c(triglyc=2, chol = 2),
+             selec = list(triglyc=txchol=='No', sbp=txhtn=='No'))
```

```
> res
```

----- Summary of results by groups of 'Recruitment year'-----

var	N	p.value	method	selection
1 Age	1101	0.212	continuous normal	sex == "Male"
2 Triglycerides	943	0.426	continuous non-normal	(sex == "Male") & (txchol == "No")
3 Smoking status	1071	<0.001**	categorical	sex == "Male"
4 Total cholesterol	1054	<0.001**	continuous non-normal	sex == "Male"

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

Note that “Sex” is removed as an explanatory variable but used as a filter, subsetting only “Male” participants. Variable “Triglycerides” has been changed to “continuous non-normal” and to show results only for non-treated male participants. Two new variables have been added: Smoking status and Total cholesterol.

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(sex ~ age + smoker + txchol + sbp, data=regicor, ref=1)
> createTable(res1, show.ratio=TRUE)
```

-----Summary descriptives table by 'Sex'-----

	Male N=1101	Female N=1193	OR	p.overall
Age	54.8 (11.1)	54.7 (11.0)	1.00 [0.99;1.01]	0.840
Smoking status:				<0.001
Never smoker	301 (28.1%)	900 (77.5%)	Ref.	
Current or former < 1y	410 (38.3%)	183 (15.7%)	0.15 [0.12;0.19]	
Former >= 1y	360 (33.6%)	79 (6.80%)	0.07 [0.06;0.10]	
Cholesterol treatment:				0.583
No	962 (89.4%)	1049 (90.2%)	Ref.	
Yes	114 (10.6%)	114 (9.80%)	0.92 [0.70;1.21]	
Systolic blood pressure	134 (18.9)	129 (21.2)	0.99 [0.98;0.99]	<0.001

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

```
> res2<-compareGroups(sex ~ age + smoker + txchol + sbp, data=regicor,
+                      ref=c(smoker=1, txchol=2))
> createTable(res2, show.ratio=TRUE)
```

-----Summary descriptives table by 'Sex'-----

	Male N=1101	Female N=1193	OR	p.overall
Age	54.8 (11.1)	54.7 (11.0)	1.00 [0.99;1.01]	0.840
Smoking status:				<0.001
Never smoker	301 (28.1%)	900 (77.5%)	Ref.	
Current or former < 1y	410 (38.3%)	183 (15.7%)	0.15 [0.12;0.19]	
Former >= 1y	360 (33.6%)	79 (6.80%)	0.07 [0.06;0.10]	
Cholesterol treatment:				0.583
No	962 (89.4%)	1049 (90.2%)	1.09 [0.83;1.43]	
Yes	114 (10.6%)	114 (9.80%)	Ref.	
Systolic blood pressure	134 (18.9)	129 (21.2)	0.99 [0.98;0.99]	<0.001

Note that the reference category for Smoking status is the first and for Cholesterol treatment 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(sex ~ age + smoker + txchol + sbp, data=regicor, ref.no='NO')
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Sex'-----

	Male N=1101	Female N=1193	OR	p.overall
Age	54.8 (11.1)	54.7 (11.0)	1.00 [0.99;1.01]	0.840
Smoking status:				<0.001
Never smoker	301 (28.1%)	900 (77.5%)	Ref.	
Current or former < 1y	410 (38.3%)	183 (15.7%)	0.15 [0.12;0.19]	
Former >= 1y	360 (33.6%)	79 (6.80%)	0.07 [0.06;0.10]	
Cholesterol treatment:				0.583
No	962 (89.4%)	1049 (90.2%)	Ref.	
Yes	114 (10.6%)	114 (9.80%)	0.92 [0.70;1.21]	
Systolic blood pressure	134 (18.9)	129 (21.2)	0.99 [0.98;0.99]	<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(sex ~ age + txchol + sbp, data=regicor)
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Sex'-----

	Male N=1101	Female N=1193	OR	p.overall
Age	54.8 (11.1)	54.7 (11.0)	1.00 [0.99;1.01]	0.840
Cholesterol treatment:				0.583
No	962 (89.4%)	1049 (90.2%)	Ref.	
Yes	114 (10.6%)	114 (9.80%)	0.92 [0.70;1.21]	
Systolic blood pressure	134 (18.9)	129 (21.2)	0.99 [0.98;0.99]	<0.001

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

```
> res<-compareGroups(sex ~ age + txchol + sbp, data=regicor, fact.ratio= c(age=10, sbp=100))
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Sex'-----

	Male N=1101	Female N=1193	OR	p.overall
Age	54.8 (11.1)	54.7 (11.0)	0.99 [0.92;1.07]	0.840
Cholesterol treatment:				0.583
No	962 (89.4%)	1049 (90.2%)	Ref.	
Yes	114 (10.6%)	114 (9.80%)	0.92 [0.70;1.21]	
Systolic blood pressure	134 (18.9)	129 (21.2)	0.26 [0.17;0.39]	<0.001

Here the OR is for the increase of 10 years for Age and 100 mmHg for Systolic blood pressure.

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(sex ~ histchol + txchol + sbp, data=regicor)
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Sex'-----

	Male N=1098	Female N=1182	OR	p.overall
History of hyperchol.:				0.308
Yes	353 (32.3%)	356 (30.2%)	Ref.	
No	741 (67.7%)	823 (69.8%)	1.10 [0.92;1.32]	
Cholesterol treatment:				0.583
No	962 (89.4%)	1049 (90.2%)	Ref.	
Yes	114 (10.6%)	114 (9.80%)	0.92 [0.70;1.21]	
Systolic blood pressure	134 (18.9)	129 (21.2)	0.99 [0.98;0.99]	<0.001

Note: This output shows the OR of being female. Therefore, 'male' is the reference category.

```
> res<-compareGroups(sex ~ histchol + txchol + sbp, data=regicor, ref.y=2)
> createTable(res, show.ratio=TRUE)
```

-----Summary descriptives table by 'Sex'-----

	Male N=1098	Female N=1182	OR	p.overall
History of hyperchol.:				0.308
Yes	353 (32.3%)	356 (30.2%)	Ref.	
No	741 (67.7%)	823 (69.8%)	0.91 [0.76;1.08]	
Cholesterol treatment:				0.583
No	962 (89.4%)	1049 (90.2%)	Ref.	
Yes	114 (10.6%)	114 (9.80%)	1.09 [0.83;1.43]	
Systolic blood pressure	134 (18.9)	129 (21.2)	1.01 [1.02;1.01]	<0.001

Note: This output shows the OR of being male.

Note: This output shows the OR of being male, and 'female' 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(tcv ~ txchol, data=regicor), bivar=TRUE, file="./bivar/")
> plot(compareGroups(tcv ~ sbp, data=regicor), bivar=TRUE, file="./bivar/")
```

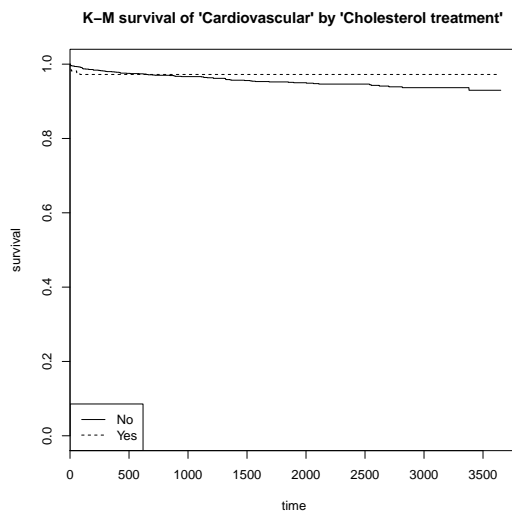


Figure 6: Categorical

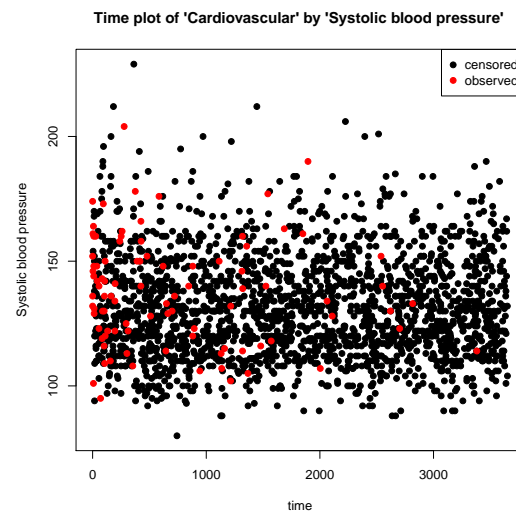


Figure 7: Continuous

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 + tdeath + tcv, timemax=c(tcv=365.25*5, tdeath=365.25*3),
+                    data=regicor)
> res
```

Note that *tdeath* is calculated at 5 years and *tcv* 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="./univar/")
> plot(res[2], bivar=TRUE, file="./bivar/")
```

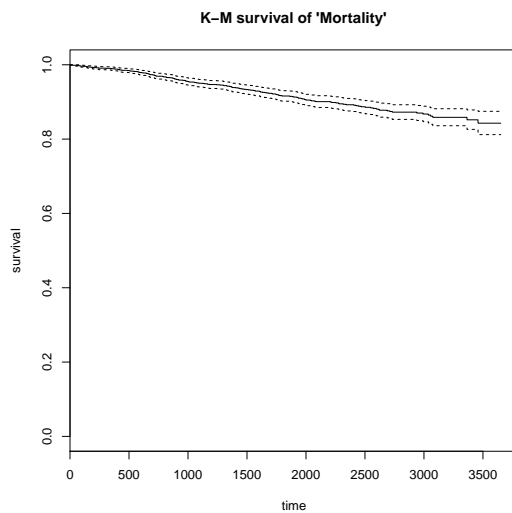


Figure 8: Univariate

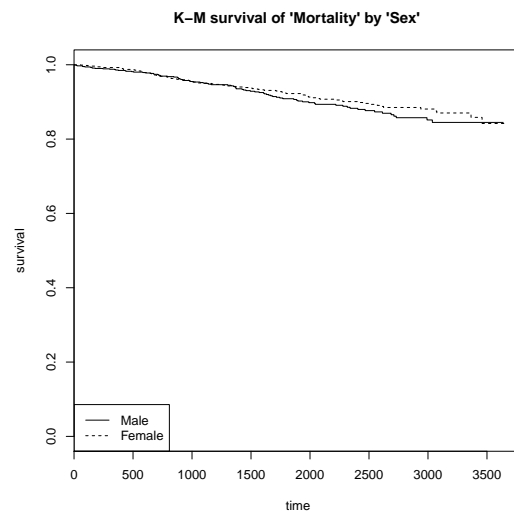


Figure 9: Stratified by *year*

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(year ~ age + sex + smoker + triglyc , method= c(triglyc=2),
+                    data=regicor)
> 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 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex:				0.506
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)	
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)	
Smoking status:				<0.001
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)	
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)	
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)	
Triglycerides	94.0 [71.0; 136]	98.0 [72.0; 133]	98.0 [72.0; 139]	0.762

Note that the option “descr” returns descriptives.

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

---Available data---

	[ALL]	1995	2000	2005	method	select
Age	2294	431	786	1077	continuous-normal	ALL
Sex	2294	431	786	1077	categorical	ALL
Smoking status	2233	415	758	1060	categorical	ALL
Triglycerides	2231	403	752	1076	continuous-non-normal	ALL

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 47.8% are male, obviously 52.2% are female). To hide some category, e.g., Male:

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

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex: Female	225 (52.2%)	396 (50.4%)	572 (53.1%)	0.506
Smoking status:				<0.001
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)	
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)	
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)	
Triglycerides	94.0 [71.0; 136]	98.0 [72.0; 133]	98.0 [72.0; 139]	0.762

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(year ~ age + sex + histhtn + txhtn, data=regicor)
> createTable(res, hide.no='no')
```

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex:				0.506
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)	
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)	
History of hypertension	111 (25.8%)	233 (29.6%)	379 (35.5%)	<0.001
Hypertension treatment	71 (16.5%)	127 (16.2%)	230 (22.2%)	0.002

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 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.10 (11.72)	54.34 (11.22)	55.28 (10.63)	0.078
Sex:				0.506
Male	206 (47.796%)	390 (49.618%)	505 (46.890%)	
Female	225 (52.204%)	396 (50.382%)	572 (53.110%)	
History of hypertension:				<0.001
Yes	111 (25.8%)	233 (29.6%)	379 (35.5%)	
No	320 (74.2%)	553 (70.4%)	690 (64.5%)	
Hypertension treatment:				0.002
No	360 (83.5%)	659 (83.8%)	804 (77.8%)	
Yes	71 (16.5%)	127 (16.2%)	230 (22.2%)	

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 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex:				0.506
Male	47.8%	49.6%	46.9%	
Female	52.2%	50.4%	53.1%	
History of hypertension:				<0.001
Yes	25.8%	29.6%	35.5%	
No	74.2%	70.4%	64.5%	
Hypertension treatment:				0.002
No	83.5%	83.8%	77.8%	
Yes	16.5%	16.2%	22.2%	

Note that only percentages are displayed.

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

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex:				0.506
Male	206	390	505	
Female	225	396	572	
History of hypertension:				<0.001
Yes	111	233	379	
No	320	553	690	
Hypertension treatment:				0.002
No	360	659	804	
Yes	71	127	230	

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 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall	N
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078	2294
Sex:				0.506	2294
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)		
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)		
History of hypertension:				<0.001	2286
Yes	111 (25.8%)	233 (29.6%)	379 (35.5%)		
No	320 (74.2%)	553 (70.4%)	690 (64.5%)		
Hypertension treatment:				0.002	2251
No	360 (83.5%)	659 (83.8%)	804 (77.8%)		
Yes	71 (16.5%)	127 (16.2%)	230 (22.2%)		

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

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

-----Summary descriptives table by 'Recruitment year'-----

	p.overall
Age	0.078
Sex:	
Male	0.506
Female	
History of hypertension:	
Yes	<0.001
No	
Hypertension treatment:	
No	0.002
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 'Recruitment year'-----

	[ALL] N=2294	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.7 (11.0)	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex:					0.506
Male	1101 (48.0%)	206 (47.8%)	390 (49.6%)	505 (46.9%)	
Female	1193 (52.0%)	225 (52.2%)	396 (50.4%)	572 (53.1%)	
History of hypertension:					<0.001
Yes	723 (31.6%)	111 (25.8%)	233 (29.6%)	379 (35.5%)	
No	1563 (68.4%)	320 (74.2%)	553 (70.4%)	690 (64.5%)	
Hypertension treatment:					0.002
No	1823 (81.0%)	360 (83.5%)	659 (83.8%)	804 (77.8%)	
Yes	428 (19.0%)	71 (16.5%)	127 (16.2%)	230 (22.2%)	

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 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)
Sex:			
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)
History of hypertension:			
Yes	111 (25.8%)	233 (29.6%)	379 (35.5%)
No	320 (74.2%)	553 (70.4%)	690 (64.5%)
Hypertension treatment:			
No	360 (83.5%)	659 (83.8%)	804 (77.8%)
Yes	71 (16.5%)	127 (16.2%)	230 (22.2%)

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 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall	p.trend
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078	0.032
Sex:				0.506	0.544
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)		
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)		
History of hypertension:				<0.001	<0.001
Yes	111 (25.8%)	233 (29.6%)	379 (35.5%)		
No	320 (74.2%)	553 (70.4%)	690 (64.5%)		
Hypertension treatment:				0.002	0.002
No	360 (83.5%)	659 (83.8%)	804 (77.8%)		
Yes	71 (16.5%)	127 (16.2%)	230 (22.2%)		

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 $1 - pchisq(cor(as.integer(x), as.integer(y))^2 * (length(x) - 1), 1)$

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 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall	p.1995 vs 2000	p.1995 vs 2005	p.2000 vs 2005
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078	0.930	0.143	0.161
Sex:				0.506	0.794	0.794	0.792
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)				
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)				
History of hypertension:				<0.001	0.169	0.001	0.015
Yes	111 (25.8%)	233 (29.6%)	379 (35.5%)				
No	320 (74.2%)	553 (70.4%)	690 (64.5%)				
Hypertension treatment:				0.002	0.951	0.023	0.004
No	360 (83.5%)	659 (83.8%)	804 (77.8%)				
Yes	71 (16.5%)	127 (16.2%)	230 (22.2%)				

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= year!=2005), show.ratio=TRUE)
```

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	OR	p.overall
Age	54.1 (11.7)	54.3 (11.2)	1.00 [0.99;1.01]	0.729
Sex:				0.583
Male	206 (47.8%)	390 (49.6%)	Ref.	
Female	225 (52.2%)	396 (50.4%)	0.93 [0.73;1.18]	
History of hypertension:				0.169
Yes	111 (25.8%)	233 (29.6%)	Ref.	
No	320 (74.2%)	553 (70.4%)	0.82 [0.63;1.07]	
Hypertension treatment:				0.951
No	360 (83.5%)	659 (83.8%)	Ref.	
Yes	71 (16.5%)	127 (16.2%)	0.98 [0.71;1.35]	

Note that category “2005” 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(tcv ~ age + sex, data=regicor), show.ratio=TRUE)
```

-----Summary descriptives table by 'Cardiovascular'-----

	No event N=2071	Event N=92	HR	p.overall
Age	54.6 (11.1)	57.5 (11.0)	1.02 [1.00;1.04]	0.011
Sex:				0.696
Male	996 (48.1%)	46 (50.0%)	Ref.	
Female	1075 (51.9%)	46 (50.0%)	0.92 [0.61;1.39]	

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(tcv ~ age + sex, data=regicor), show.ratio=TRUE,
+             digits.ratio= 3)
```

-----Summary descriptives table by 'Cardiovascular'-----

	No event N=2071	Event N=92	HR	p.overall
Age	54.6 (11.1)	57.5 (11.0)	1.022 [1.003;1.041]	0.011
Sex:				0.696
Male	996 (48.1%)	46 (50.0%)	Ref.	
Female	1075 (51.9%)	46 (50.0%)	0.922 [0.613;1.387]	

4.2.2 Combining tables by row

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

```
> restab1 <- createTable(compareGroups(year~ age + sex, data=regicor))
> restab2 <- createTable(compareGroups(year~ smoker + triglyc, data=regicor))
> rbind("Epidemiological"=restab1,"History"=restab2)
```

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Epidemiological:				
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex:				0.506
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)	
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)	
History:				
Smoking status:				<0.001
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)	
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)	
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)	
Triglycerides	114 (74.4)	114 (70.7)	117 (76.0)	0.582

Note how variables are grouped under “Epidemiological” and “History” 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 Triglycerides:

```
> rbind("Epidemiological"=restab1,"History"=restab2)[c(1,4)]
```

```
-----Summary descriptives table by 'Recruitment year'-----
-----
                1995      2000      2005      p.overall
                N=431      N=786      N=1077
-----
Epidemiological:
  Age          54.1 (11.7) 54.3 (11.2) 55.3 (10.6)    0.078
History:
  Triglycerides 114 (74.4) 114 (70.7) 117 (76.0)    0.582
-----
```

To change the order:

```
> rbind("Epidemiological"=restab1,"History"=restab2)[c(4,3,2,1)]
```

```
-----Summary descriptives table by 'Recruitment year'-----
-----
                1995      2000      2005      p.overall
                N=431      N=786      N=1077
-----
History:
  Triglycerides          114 (74.4) 114 (70.7) 117 (76.0)    0.582
  Smoking status:
    Never smoker          234 (56.4%) 414 (54.6%) 553 (52.2%)
    Current or former < 1y 109 (26.3%) 267 (35.2%) 217 (20.5%)
    Former >= 1y          72 (17.3%) 77 (10.2%) 290 (27.4%)
Epidemiological:
  Sex:
    Male          206 (47.8%) 390 (49.6%) 505 (46.9%)
    Female          225 (52.2%) 396 (50.4%) 572 (53.1%)
  Age          54.1 (11.7) 54.3 (11.2) 55.3 (10.6)    0.078
-----
```

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(year ~ age + smoker + sbp + histhtn +triglyc , data=regicor)
> 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		
	1995	2000	2005	1995	2000	2005	1995	2000	2005
	N=431	N=786	N=1077	N=225	N=396	N=572	N=206	N=390	N=505
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	54.1 (11.7)	54.4 (11.2)	55.2 (10.6)	54.1 (11.8)	54.3 (11.2)	55.4 (10.7)
Smoking status:									
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)	182 (83.1%)	302 (79.3%)	416 (74.0%)	52 (26.5%)	112 (29.7%)	137 (27.5%)
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)	32 (14.6%)	68 (17.8%)	83 (14.8%)	77 (39.3%)	199 (52.8%)	134 (26.9%)
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)	5 (2.28%)	11 (2.89%)	63 (11.2%)	67 (34.2%)	66 (17.5%)	227 (45.6%)
Systolic blood pressure	133 (19.2)	133 (21.3)	129 (19.8)	132 (19.8)	129 (22.6)	127 (20.5)	134 (18.4)	137 (19.3)	132 (18.7)
History of hypertension:									
Yes	111 (25.8%)	233 (29.6%)	379 (35.5%)	61 (27.1%)	123 (31.1%)	198 (34.8%)	50 (24.3%)	110 (28.2%)	181 (36.2%)
No	320 (74.2%)	553 (70.4%)	690 (64.5%)	164 (72.9%)	273 (68.9%)	371 (65.2%)	156 (75.7%)	280 (71.8%)	319 (63.8%)
Triglycerides	114 (74.4)	114 (70.7)	117 (76.0)	97.8 (47.9)	99.7 (55.1)	104 (57.6)	131 (91.5)	128 (81.1)	132 (90.3)

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

```

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

```

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

	By Recruitment year			By Recruitment year			By Recruitment year		
	1995	2000	2005	1995	2000	2005	1995	2000	2005
	N=431	N=786	N=1077	N=225	N=396	N=572	N=206	N=390	N=505
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	54.1 (11.7)	54.4 (11.2)	55.2 (10.6)	54.1 (11.8)	54.3 (11.2)	55.4 (10.7)
Smoking status:									
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)	182 (83.1%)	302 (79.3%)	416 (74.0%)	52 (26.5%)	112 (29.7%)	137 (27.5%)
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)	32 (14.6%)	68 (17.8%)	83 (14.8%)	77 (39.3%)	199 (52.8%)	134 (26.9%)
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)	5 (2.28%)	11 (2.89%)	63 (11.2%)	67 (34.2%)	66 (17.5%)	227 (45.6%)

Systolic blood pressure	133 (19.2)	133 (21.3)	129 (19.8)	132 (19.8)	129 (22.6)	127 (20.5)	134 (18.4)	137 (19.3)	132 (18.7)
History of hypertension:									
Yes	111 (25.8%)	233 (29.6%)	379 (35.5%)	61 (27.1%)	123 (31.1%)	198 (34.8%)	50 (24.3%)	110 (28.2%)	181 (36.2%)
No	320 (74.2%)	553 (70.4%)	690 (64.5%)	164 (72.9%)	273 (68.9%)	371 (65.2%)	156 (75.7%)	280 (71.8%)	319 (63.8%)
Triglycerides	114 (74.4)	114 (70.7)	117 (76.0)	97.8 (47.9)	99.7 (55.1)	104 (57.6)	131 (91.5)	128 (81.1)	132 (90.3)

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

`> cbind(alltab,femaletab,maletab)`

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

	alltab				femaletab				maletab			
	1995	2000	2005		1995	2000	2005		1995	2000	2005	
	N=431	N=786	N=1077		N=225	N=396	N=572		N=206	N=390	N=505	
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)		54.1 (11.7)	54.4 (11.2)	55.2 (10.6)		54.1 (11.8)	54.3 (11.2)	55.4 (10.7)	
Smoking status:												
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)		182 (83.1%)	302 (79.3%)	416 (74.0%)		52 (26.5%)	112 (29.7%)	137 (27.5%)	
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)		32 (14.6%)	68 (17.8%)	83 (14.8%)		77 (39.3%)	199 (52.8%)	134 (26.9%)	
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)		5 (2.28%)	11 (2.89%)	63 (11.2%)		67 (34.2%)	66 (17.5%)	227 (45.6%)	
Systolic blood pressure	133 (19.2)	133 (21.3)	129 (19.8)		132 (19.8)	129 (22.6)	127 (20.5)		134 (18.4)	137 (19.3)	132 (18.7)	
History of hypertension:												
Yes	111 (25.8%)	233 (29.6%)	379 (35.5%)		61 (27.1%)	123 (31.1%)	198 (34.8%)		50 (24.3%)	110 (28.2%)	181 (36.2%)	
No	320 (74.2%)	553 (70.4%)	690 (64.5%)		164 (72.9%)	273 (68.9%)	371 (65.2%)		156 (75.7%)	280 (71.8%)	319 (63.8%)	
Triglycerides	114 (74.4)	114 (70.7)	117 (76.0)		97.8 (47.9)	99.7 (55.1)	104 (57.6)		131 (91.5)	128 (81.1)	132 (90.3)	

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(year ~ age + smoker + sbp, data=regicor)),
+       which.table='both')
```

```
-----Summary descriptives table by 'Recruitment year'-----
-----
              1995      2000      2005      p.overall
              N=431      N=786      N=1077
-----
Age              54.1 (11.7) 54.3 (11.2) 55.3 (10.6)      0.078
Smoking status:
  Never smoker    234 (56.4%) 414 (54.6%) 553 (52.2%)
  Current or former < 1y 109 (26.3%) 267 (35.2%) 217 (20.5%)
  Former >= 1y    72 (17.3%) 77 (10.2%) 290 (27.4%)
Systolic blood pressure 133 (19.2) 133 (21.3) 129 (19.8)      <0.001
-----
```

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

```
-----
              [ALL] 1995 2000 2005      method      select
-----
Age              2294 431 786 1077 continuous-normal  ALL
Smoking status   2233 415 758 1060 categorical        ALL
Systolic blood pressure 2280 428 775 1077 continuous-normal  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(year ~ age + smoker + sbp, data=regicor)), nmax=FALSE)
```

```
-----Summary descriptives table by 'Recruitment year'-----
-----
              1995      2000      2005      p.overall
              N=431      N=786      N=1077
-----
Age              54.1 (11.7) 54.3 (11.2) 55.3 (10.6)      0.078
Smoking status:
  Never smoker    234 (56.4%) 414 (54.6%) 553 (52.2%)
  Current or former < 1y 109 (26.3%) 267 (35.2%) 217 (20.5%)
  Former >= 1y    72 (17.3%) 77 (10.2%) 290 (27.4%)
Systolic blood pressure 133 (19.2) 133 (21.3) 129 (19.8)      <0.001
-----
```

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

```
> summary(createTable(compareGroups(year ~ age + smoker + sbp, data=regicor)))
```

---Available data---

	[ALL]	1995	2000	2005	method	select
Age	2294	431	786	1077	continuous-normal	ALL
Smoking status	2233	415	758	1060	categorical	ALL
Systolic blood pressure	2280	428	775	1077	continuous-normal	ALL

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

```
> res<-compareGroups(year ~ age + smoker + sbp + txhtn, data=regicor)
> restab<-createTable(res, type=1, show.ratio=TRUE )
> restab
```

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Smoking status:				<0.001
Never smoker	56.4%	54.6%	52.2%	
Current or former < 1y	26.3%	35.2%	20.5%	
Former >= 1y	17.3%	10.2%	27.4%	
Systolic blood pressure	133 (19.2)	133 (21.3)	129 (19.8)	<0.001
Hypertension treatment:				0.002
No	83.5%	83.8%	77.8%	
Yes	16.5%	16.2%	22.2%	

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

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=431	2000 N=786	2005 N=1077	p.overall	N
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078	2294
Smoking status:				<0.001	2233
Never smoker	56.4%	54.6%	52.2%		
Current or former < 1y	26.3%	35.2%	20.5%		
Former >= 1y	17.3%	10.2%	27.4%		
Systolic blood pressure	133 (19.2)	133 (21.3)	129 (19.8)	<0.001	2280
Hypertension treatment:				0.002	2251
No	83.5%	83.8%	77.8%		
Yes	16.5%	16.2%	22.2%		

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

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

-----Summary descriptives table by 'Recruitment year'-----

	1995 N=206	2000 N=390	2005 N=505	p.overall	N
Age	54.1 (11.8)	54.3 (11.2)	55.4 (10.7)	0.212	1101
Smoking status:				<0.001	1071
Never smoker	26.5%	29.7%	27.5%		
Current or former < 1y	39.3%	52.8%	26.9%		
Former >= 1y	34.2%	17.5%	45.6%		
Systolic blood pressure	134 (18.4)	137 (19.3)	132 (18.7)	0.002	1098
Hypertension treatment:				<0.001	1078
No	85.0%	87.7%	77.2%		
Yes	15.0%	12.3%	22.8%		

Note that the `compareGroups` object (*res*) is updated, selecting only 'Male' 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(year~ age + sex + smoker +sbp, data=regicor))
```

```
-----Summary descriptives table by 'Recruitment year'-----
```

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex:				0.506
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)	
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)	
Smoking status:				<0.001
Never smoker	234 (56.4%)	414 (54.6%)	553 (52.2%)	
Current or former < 1y	109 (26.3%)	267 (35.2%)	217 (20.5%)	
Former >= 1y	72 (17.3%)	77 (10.2%)	290 (27.4%)	
Systolic blood pressure	133 (19.2)	133 (21.3)	129 (19.8)	<0.001

```
> createTable(compareGroups(year~ age + sex + smoker +sbp, data=regicor))[1:2, ]
```

```
-----Summary descriptives table by 'Recruitment year'-----
```

	1995 N=431	2000 N=786	2005 N=1077	p.overall
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.078
Sex:				0.506
Male	206 (47.8%)	390 (49.6%)	505 (46.9%)	
Female	225 (52.2%)	396 (50.4%)	572 (53.1%)	

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 L^AT_EX

A special case of exporting is when tables are exported to L^AT_EX. 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 L^AT_EX document chunk to be processed with Sweave.

```
> restab<-createTable(compareGroups(year~ age + sex, data=regicor))
> export2latex(restab)
```

```
\begin{longtable}{lcccc}
\caption{Summary descriptives table by groups of 'Recruitment year'}\\
\hline
& 1995 & & 2000 & & 2005 & & \multirow{2}{*}{ p.overall }\\
& N=431 & & N=786 & & N=1077 & & \\
\hline
\hline
\endfirsthead
\multicolumn{5}{l}{\tablename\ \thetable\ \textit{-- continued from previous page}}\\
\hline
& 1995 & & 2000 & & 2005 & & \multirow{2}{*}{ p.overall }\\
& N=431 & & N=786 & & N=1077 & & \\
\hline
\hline
\endhead
\hline
\multicolumn{5}{l}{\textit{continued on next page}} \\
\endfoot
\multicolumn{5}{l}{} \\
\endlastfoot
Age & 54.1 (11.7) & & 54.3 (11.2) & & 55.3 (10.6) & & 0.078 \\
Sex: & & & & & & & 0.506 \\
$\quad$Male & 206 (47.8\%) & & 390 (49.6\%) & & 505 (46.9\%) & & \\
$\quad$Female & 225 (52.2\%) & & 396 (50.4\%) & & 572 (53.1\%) & & \\
\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. 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 \LaTeX 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.


5 Using GUI

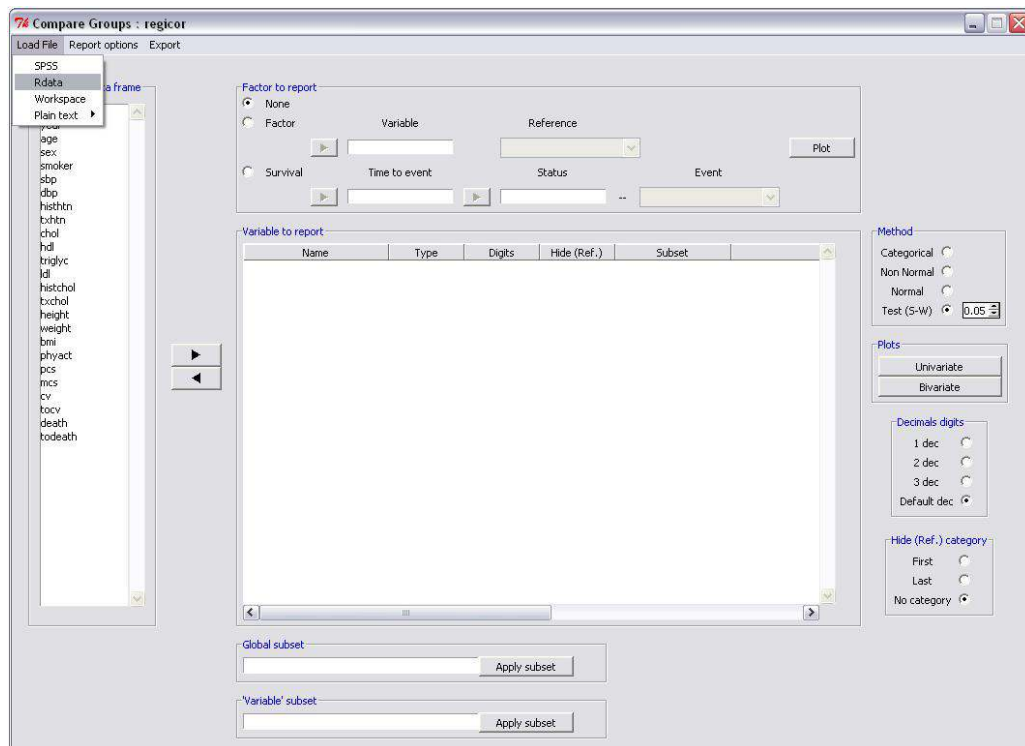
Once the `compareGroups` package is loaded, a Graphical User Interface (GUI) is displayed in response to typing `cGroupsGUI`. The GUI is meant to make it feasible for users who are unfamiliar with  to construct bivariate tables.

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

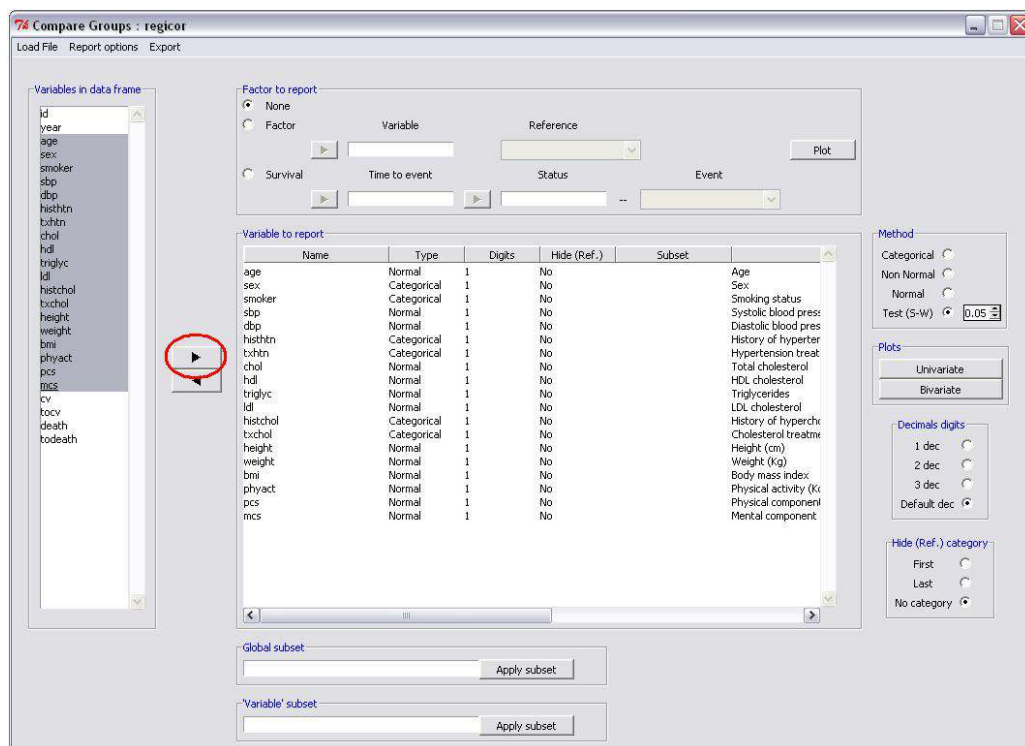
Table 2: Summary descriptives table by groups of 'Recruitment year'

	1995 N=431	2000 N=786	2005 N=1077	p.trend
Age	54.1 (11.7)	54.3 (11.2)	55.3 (10.6)	0.032
Gender: Female	52.2%	50.4%	53.1%	0.544
Smoking status:				<0.001
Never smoker	56.4%	54.6%	52.2%	
Current or former < 1y	26.3%	35.2%	20.5%	
Former \geq 1y	17.3%	10.2%	27.4%	
Systolic blood pressure	132.6 (19.2)	133.0 (21.3)	129.3 (19.8)	<0.001
Diastolic blood pressure	77.0 (10.5)	80.8 (10.3)	79.9 (10.6)	<0.001
History of hypertension: Yes	25.8%	29.6%	35.5%	<0.001
Hypertension treatment: Yes	16.5%	16.2%	22.2%	0.002
Total cholesterol	223.5 (43.2)	223.6 (44.5)	212.9 (46.4)	<0.001
HDL cholesterol	52.0 (14.5)	52.6 (15.8)	53.3 (14.2)	0.126
Triglycerides	92.0 [70.0; 131.0]	97.0 [72.0; 132.0]	93.0 [70.0; 132.0]	0.723
LDL cholesterol	151.7 (38.4)	149.0 (38.6)	136.3 (39.7)	<0.001
History of hyperchol.: Yes	22.5%	33.2%	33.2%	<0.001
Cholesterol treatment: Yes	6.5%	8.8%	12.8%	<0.001
Height (cm)	163.5 (9.2)	162.0 (9.4)	163.3 (9.0)	0.527
Weight (Kg)	72.3 (12.6)	73.8 (14.0)	73.6 (13.9)	0.185
Body mass index	27.0 (4.1)	28.1 (4.6)	27.6 (4.6)	0.300
Physical activity (Kcal/week)	390.0 [225.5; 617.0]	347.5 [185.1; 573.7]	261.8 [126.6; 442.6]	<0.001
Physical component	49.3 (8.1)	49.0 (9.6)	50.1 (8.9)	0.043
Mental component	49.2 (11.3)	48.9 (11.0)	46.9 (10.8)	<0.001

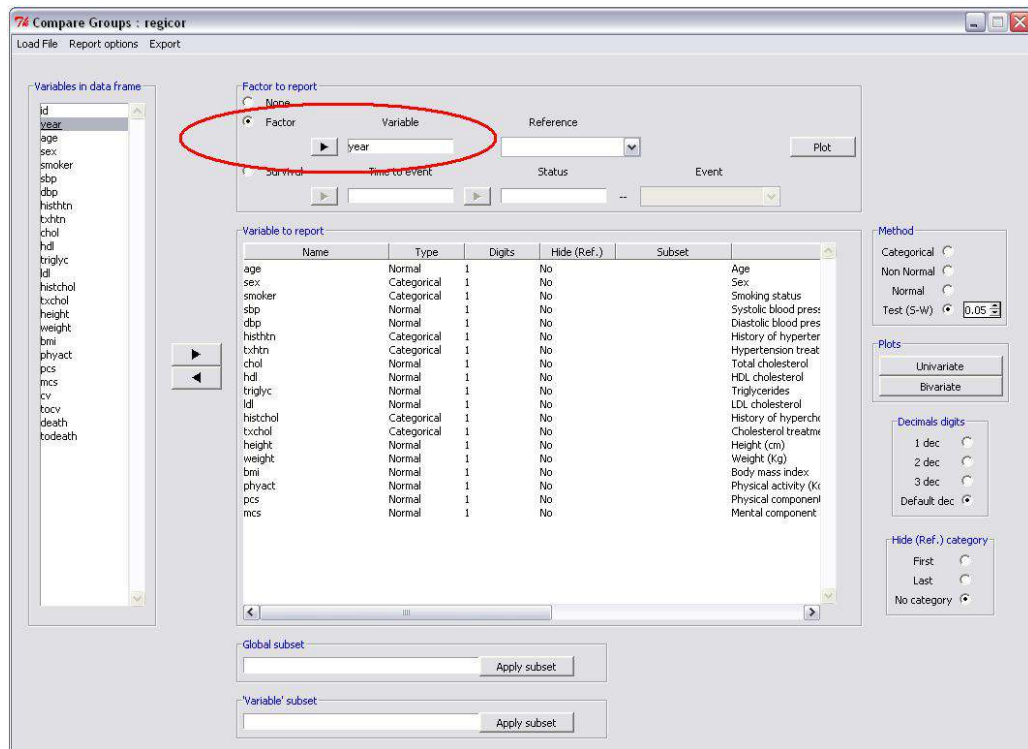
Step 1. Browse for and select the data to be loaded. Valid file types include SPSS or  format, CSV plain text file or a *data.frame* already existing in the Workspace. By default, the *regicor* example data is loaded when the GUI is opened.



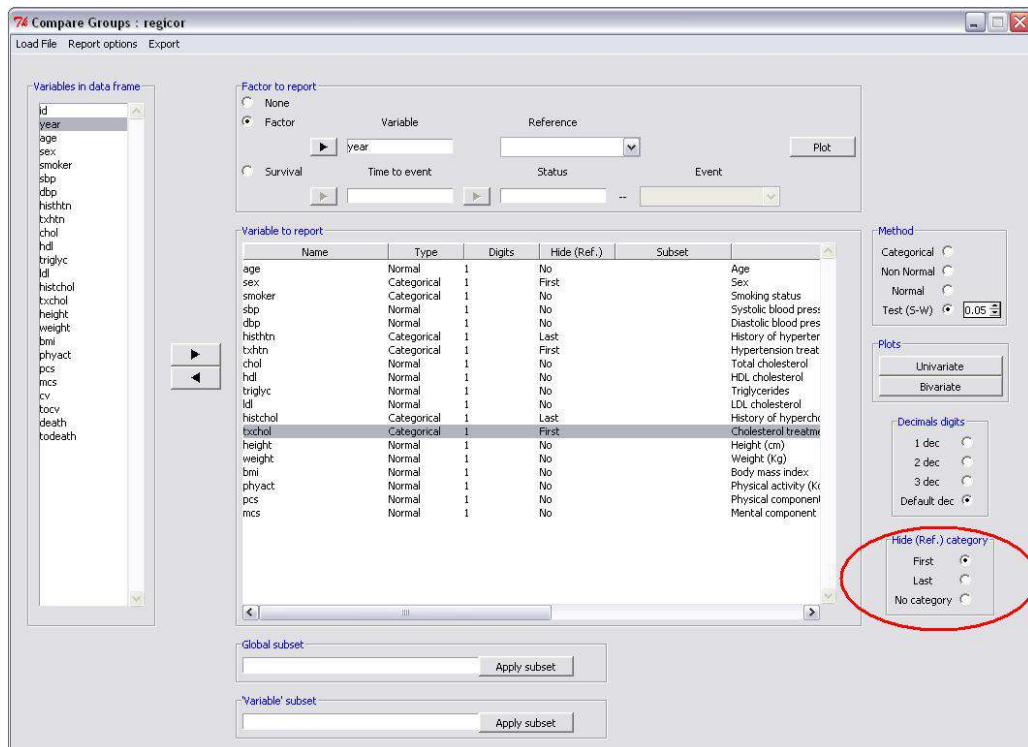
Step 2. Choose the variables to be described (row-variables).



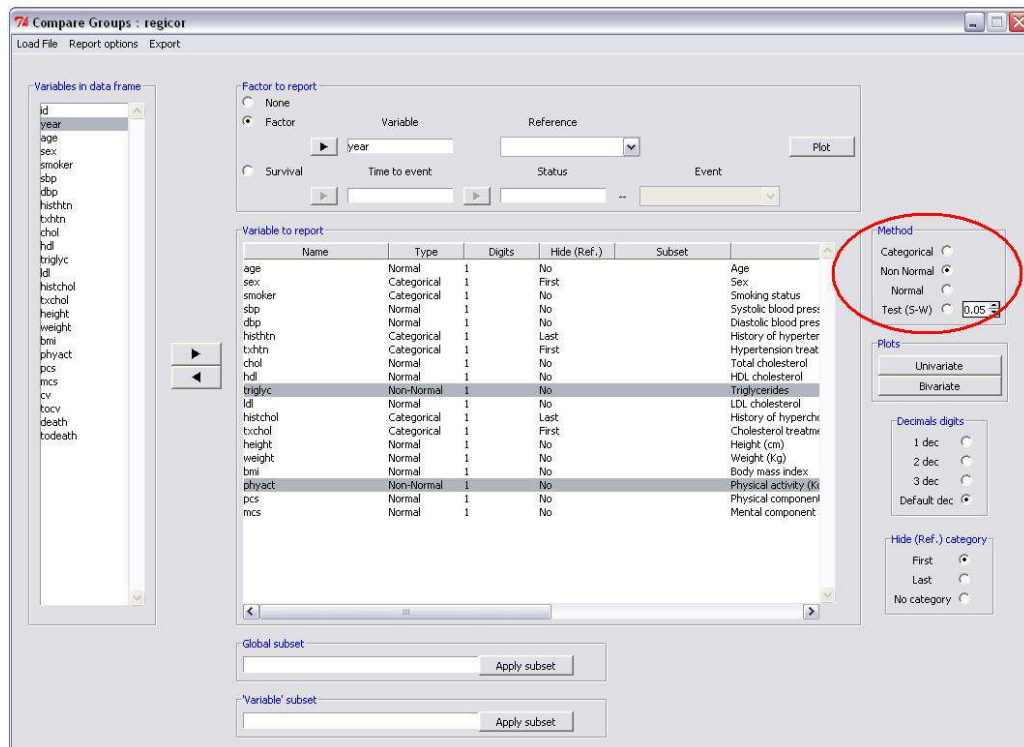
Step 3. If descriptives by year are desired (for example), move the variable *year* to the GUI top frame, making it the factor variable. To report descriptives for the whole sample (i.e., no groups), click on the 'none' button.



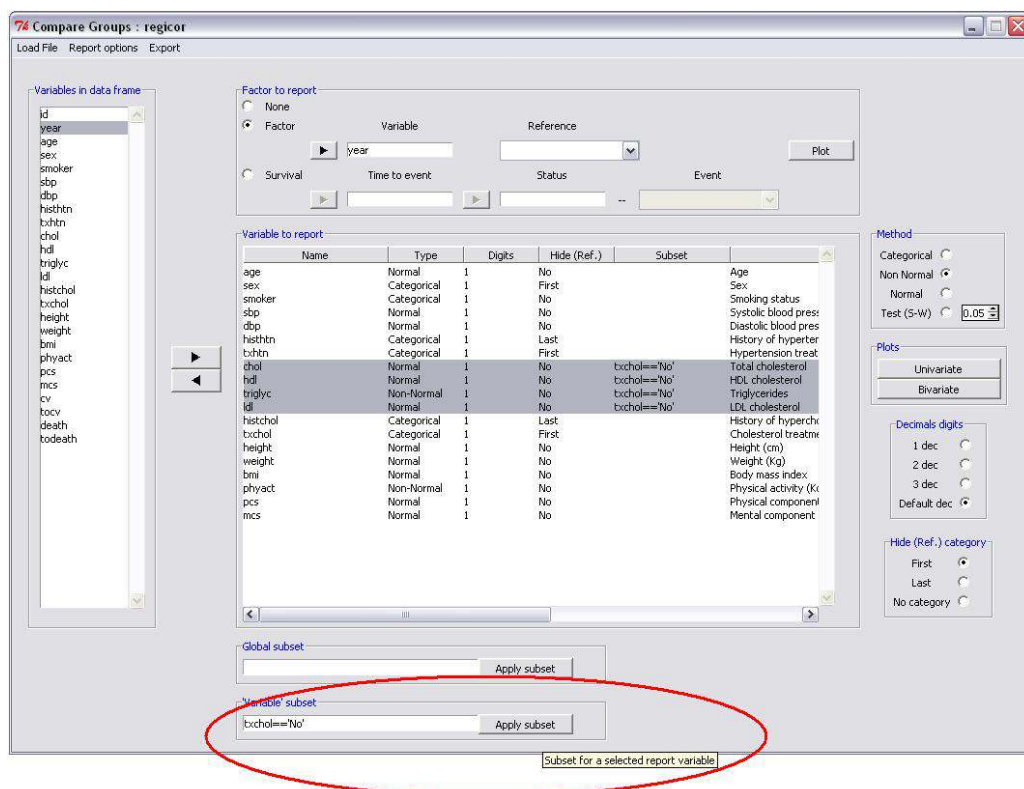
Step 4. It is possible to hide the first, last or no categories of a categorical row-variable. In this example, 'no' levels will be hidden for History of hypertension, Hypertension treatment, History of hypercholesterolemia and Cholesterol treatment; conversely, all categories will be shown for smoking.



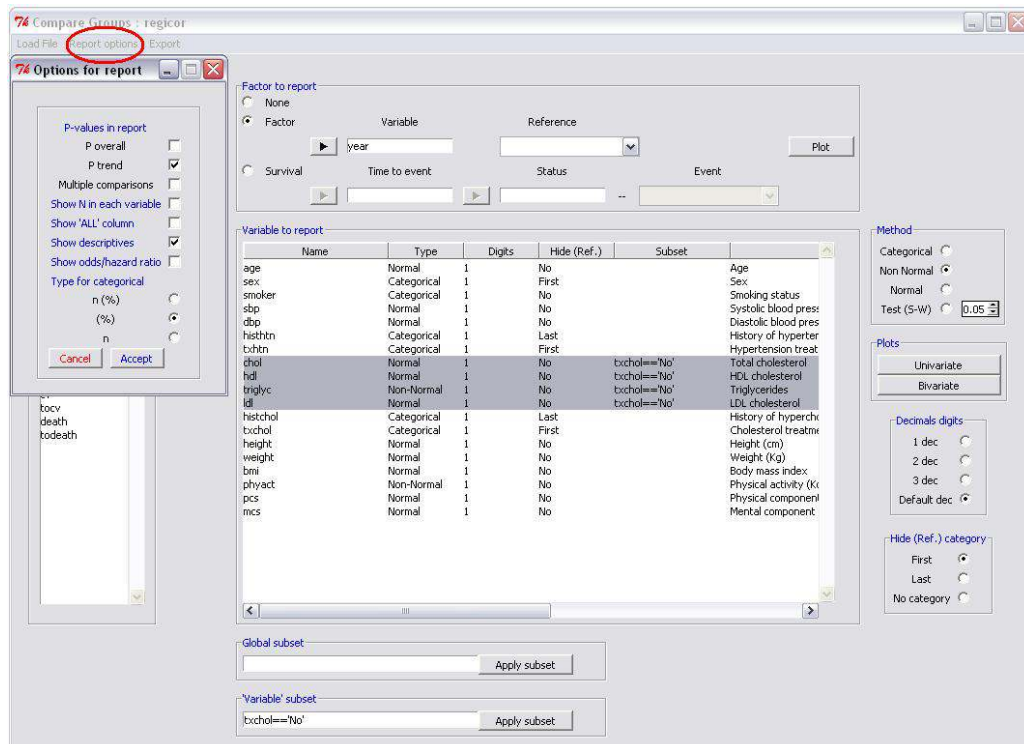
Step 5. For each continuous variable, it is possible to specify whether to treat it as normal or non-normal or to transform a numerical variable into a categorical one. This last option can be interesting if a categorical variable has been coded as numerical. By default, all continuous variables are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



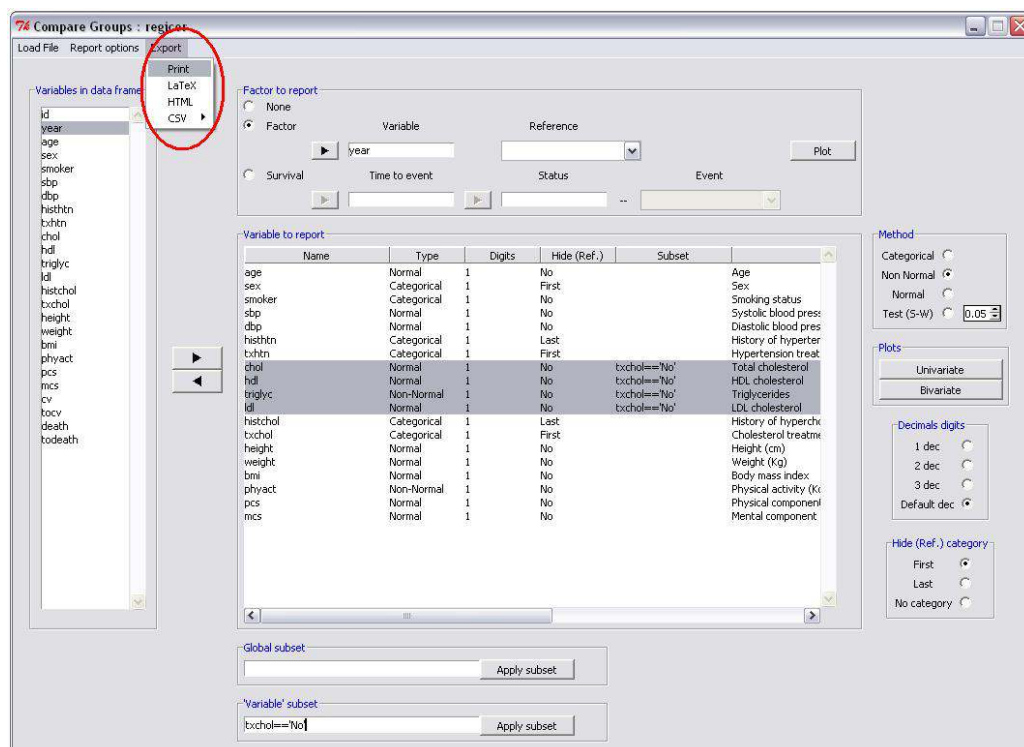
Step 6. For each row-variable, it is possible to select a subset of individuals from the data set to be included. In this example, descriptives of cholesterol, HDL-cholesterol, triglycerides and LDL-cholesterol will be reported only for non-treated individuals. Also, it is possible to specify criteria 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.



5.1 Computing Odds Ratio

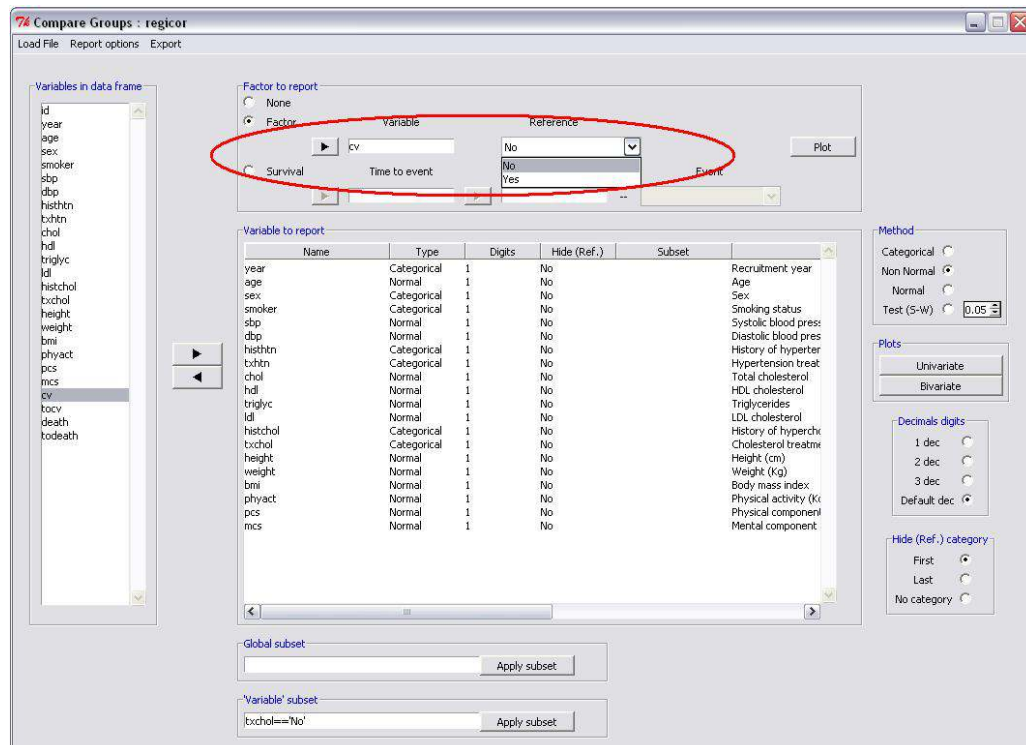
For a case-control study, it may be necessary to report the Odds Ratio between cases and controls for each variable. The table below contains Odds Ratios for each row-variable by cardiovascular disease status.

Table 3: Summary descriptives table by groups of 'Cardiovascular event'

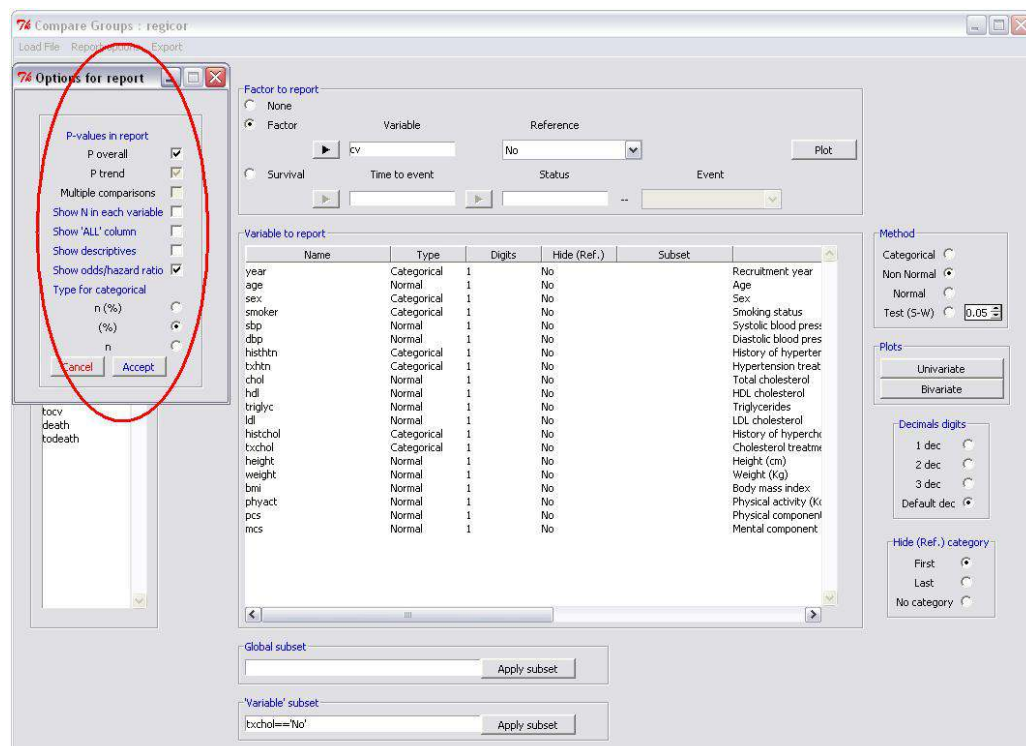
	OR
Recruitment year:	
1995	Ref.
2000	1.90 [0.96;4.12]
2005	1.84 [0.96;3.92]
Age	1.02 [1.00;1.04]
Gender: Female	0.93 [0.61;1.41]
Smoking status:	
Never smoker	Ref.
Current or former < 1y	2.75 [1.77;4.32]
Former ≥ 1y	0.58 [0.25;1.19]
Systolic blood pressure	1.02 [1.01;1.02]
Diastolic blood pressure	1.03 [1.01;1.05]
History of hypertension: Yes	1.54 [1.00;2.36]
Hypertension treatment: Yes	1.37 [0.82;2.21]
Total cholesterol	1.00 [1.00;1.01]
HDL cholesterol	0.99 [0.98;1.01]
Triglycerides	1.00 [1.00;1.00]
LDL cholesterol	1.00 [1.00;1.01]
History of hyperchol.: Yes	0.83 [0.51;1.31]
Cholesterol treatment: Yes	0.61 [0.23;1.30]
Height (cm)	1.00 [0.98;1.03]
Weight (Kg)	1.01 [0.99;1.02]
Body mass index	1.02 [0.98;1.07]
Physical activity (Kcal/week)	1.00 [1.00;1.00]
Physical component	0.97 [0.95;1.00]
Mental component	0.99 [0.97;1.00]

To build this table, as illustrated in the screens below, you would select *cv* variable (cardiovascular disease 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.

Select *cv* variable and define the reference.



Mark 'Show odds/hazard ratio' in the 'Report options' menu and click on 'Accept'.



Finally, choose the desired output mode from the 'Export' options.

5.2 Computing Hazard Ratio

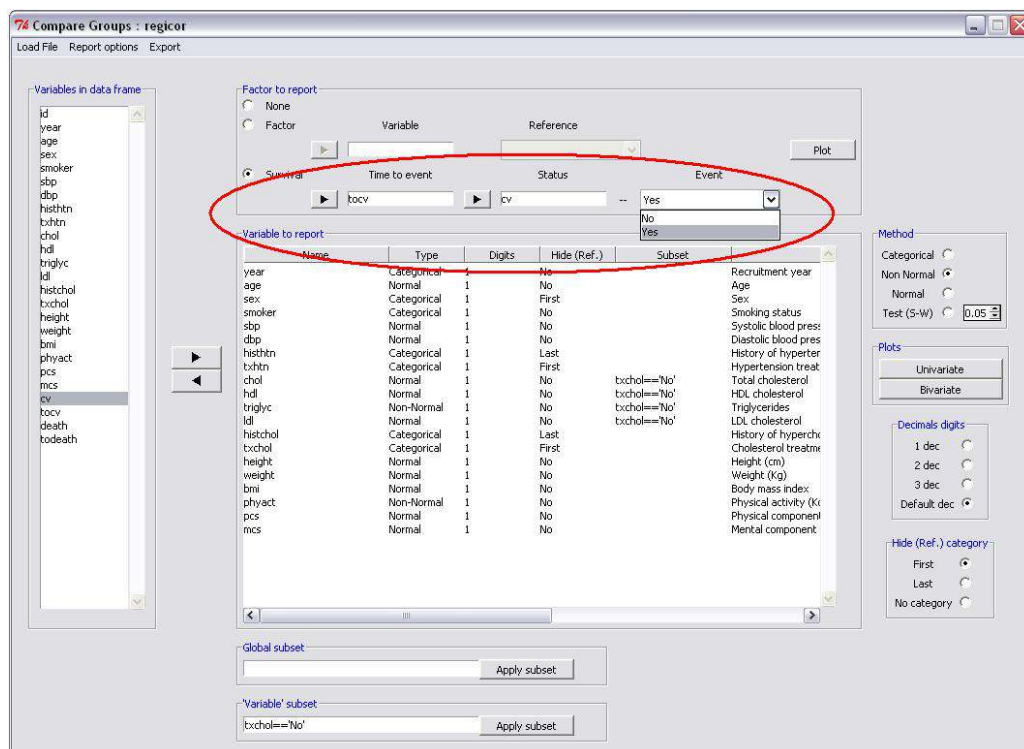
In a cohort study, it may be more informative to compute Hazard Ratios taking into account time-to-event.

Table 4: Summary descriptives table by groups of 'Cardiovascular event'

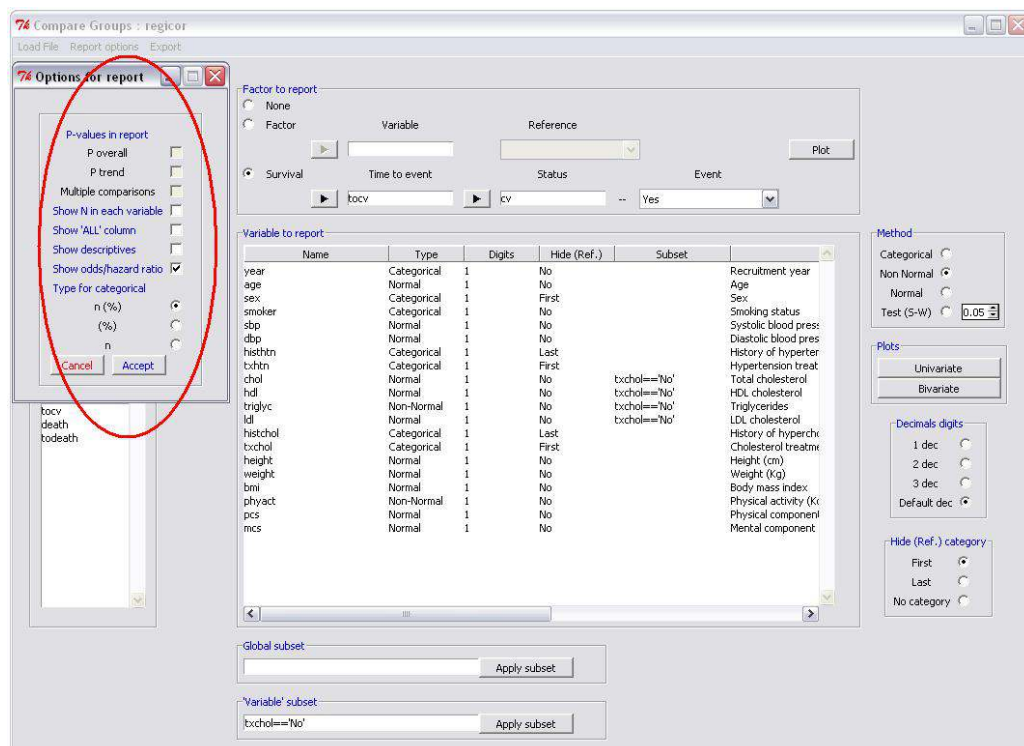
	HR
Recruitment year:	
1995	Ref.
2000	1.95 [0.96;3.93]
2005	1.82 [0.92;3.59]
Age	1.02 [1.00;1.04]
Gender: Female	0.92 [0.61;1.39]
Smoking status:	
Never smoker	Ref.
Current or former < 1y	2.67 [1.74;4.11]
Former \geq 1y	0.55 [0.26;1.18]
Systolic blood pressure	1.02 [1.01;1.02]
Diastolic blood pressure	1.03 [1.01;1.05]
History of hypertension: Yes	1.52 [1.01;2.31]
Hypertension treatment: Yes	1.37 [0.85;2.22]
Total cholesterol	1.00 [1.00;1.01]
HDL cholesterol	0.99 [0.98;1.00]
Triglycerides	1.00 [1.00;1.00]
LDL cholesterol	1.00 [1.00;1.01]
History of hyperchol.: Yes	0.82 [0.52;1.30]
Cholesterol treatment: Yes	0.61 [0.27;1.39]
Height (cm)	1.00 [0.98;1.03]
Weight (Kg)	1.01 [0.99;1.02]
Body mass index	1.02 [0.98;1.07]
Physical activity (Kcal/week)	1.00 [1.00;1.00]
Physical component	0.98 [0.96;1.00]
Mental component	0.99 [0.97;1.00]

To generate this table, select *tocv* variable and *cv*, 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.


Select *cv* variable and *tocv*.



Mark 'Show odds/hazard ratio' in the 'Report options' menu.



Finally, choose the Export option.

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

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.
- [2] C. Genolini, B Desgraupes, and Lionel-Riou Franca. *r2lh: R to LaTeX and HTML*, 2011. R package version 0.7.