

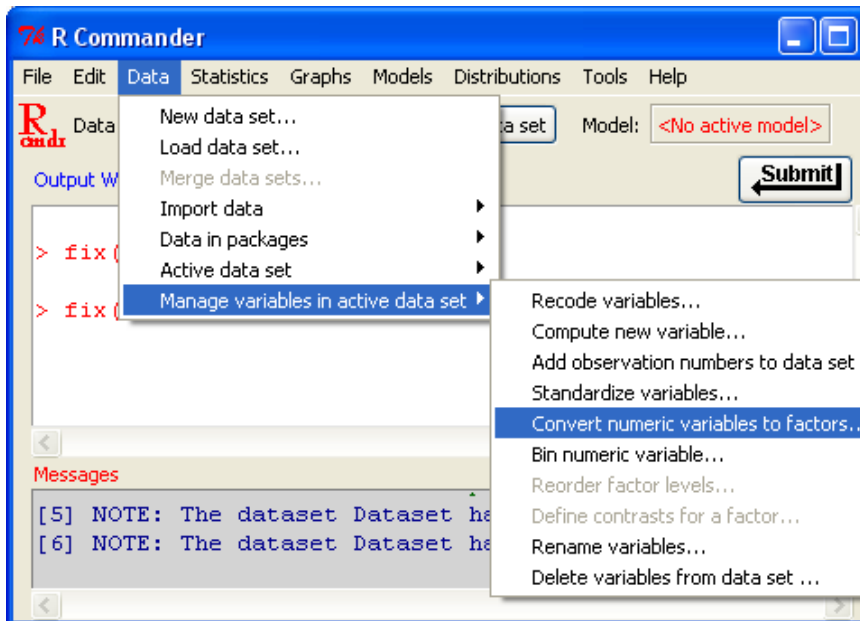
Two Independent Sample t-Test

Example: The following data is results from measuring the body mass index from two independent random samples from two populations.

Sample 1: 22, 23, 25, 26, 27, 19, 22, 28, 33, 24

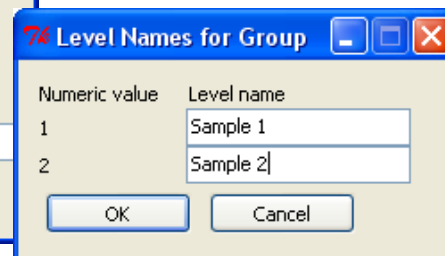
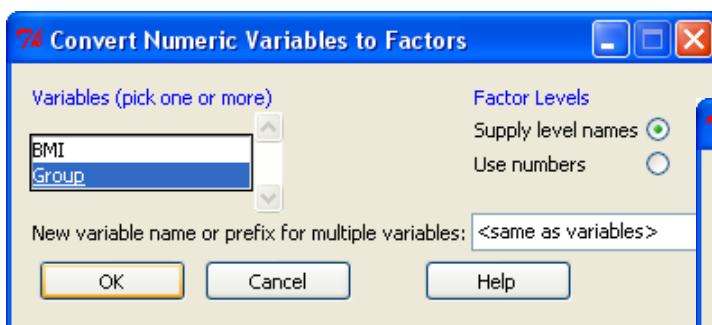
Sample 2: 21, 25, 36, 24, 33, 28, 29, 31, 30, 32, 33, 35

- 1) BMI data must be arranged in a single column and with Group variable takes on 1 or 2 placed in the column next to it denote which sample the value is from (See figure on the right).
- 2) Convert Group variable into factor variables by clicking on Data, Manage variables in active data set, and Convert numeric variables to factors.

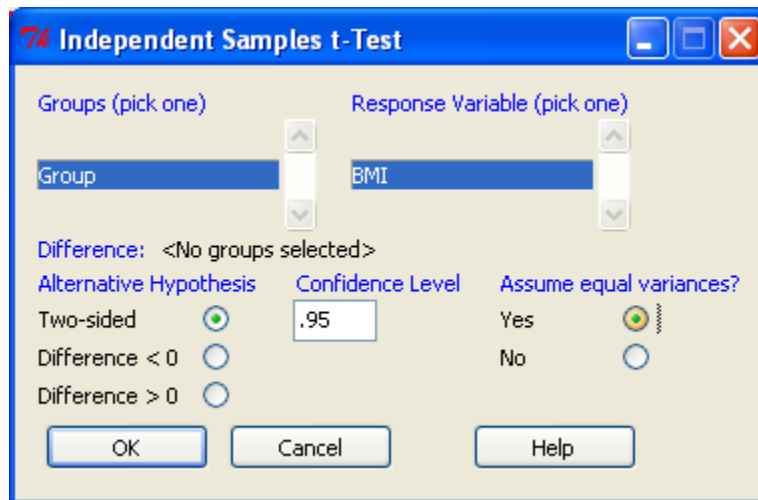
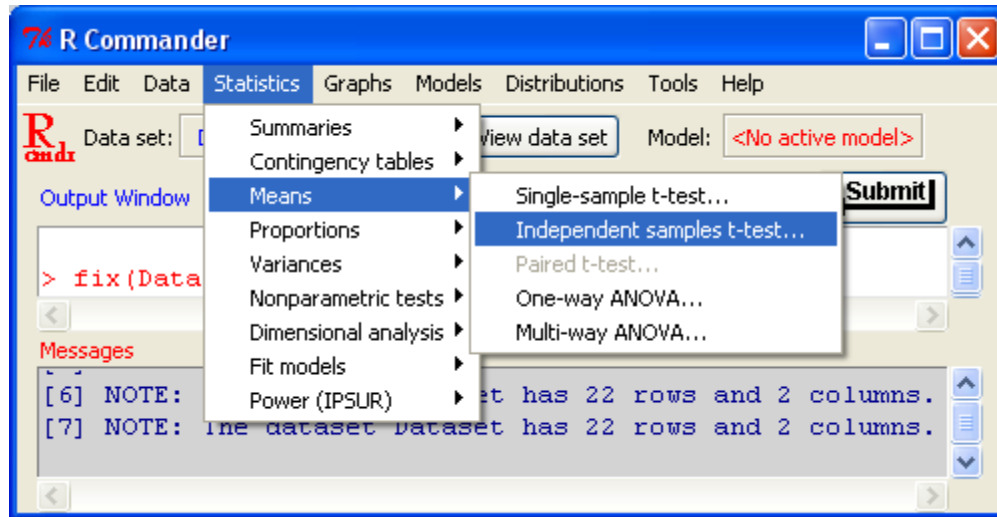


The screenshot shows the R Data Editor window with a data table. The table has two columns: 'BMI' and 'Group'. The 'Group' column contains values 1 and 2, representing the two samples.

	BMI	Group
1	22	1
2	23	1
3	25	1
4	26	1
5	27	1
6	19	1
7	22	1
8	28	1
9	33	1
10	24	1
11	21	2
12	25	2
13	36	2
14	24	2
15	33	2
16	28	2
17	29	2
18	31	2
19	30	2
20	32	2
21	33	2
22	35	2



- 4.) Perform test of equality of variances and check p-value (p-value = 0.6421, not shown in this instruction) to determine if equal variances assumption is acceptable. If p-value is greater than 0.05, the equal variances assumption would be acceptable at 5% level of significance.
- 5.) Click Statistics, Means, Independent sample t-test to perform two independent samples t-test with Assume equal variances Yes bullet checked.



R Commander Output:

Two Sample t-test

```
data: BMI by Group
t = -2.6437, df = 20, p-value = 0.01558
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -8.676786 -1.023214
sample estimates:
mean in group Sample 1 mean in group Sample 2
      24.90             29.75
```

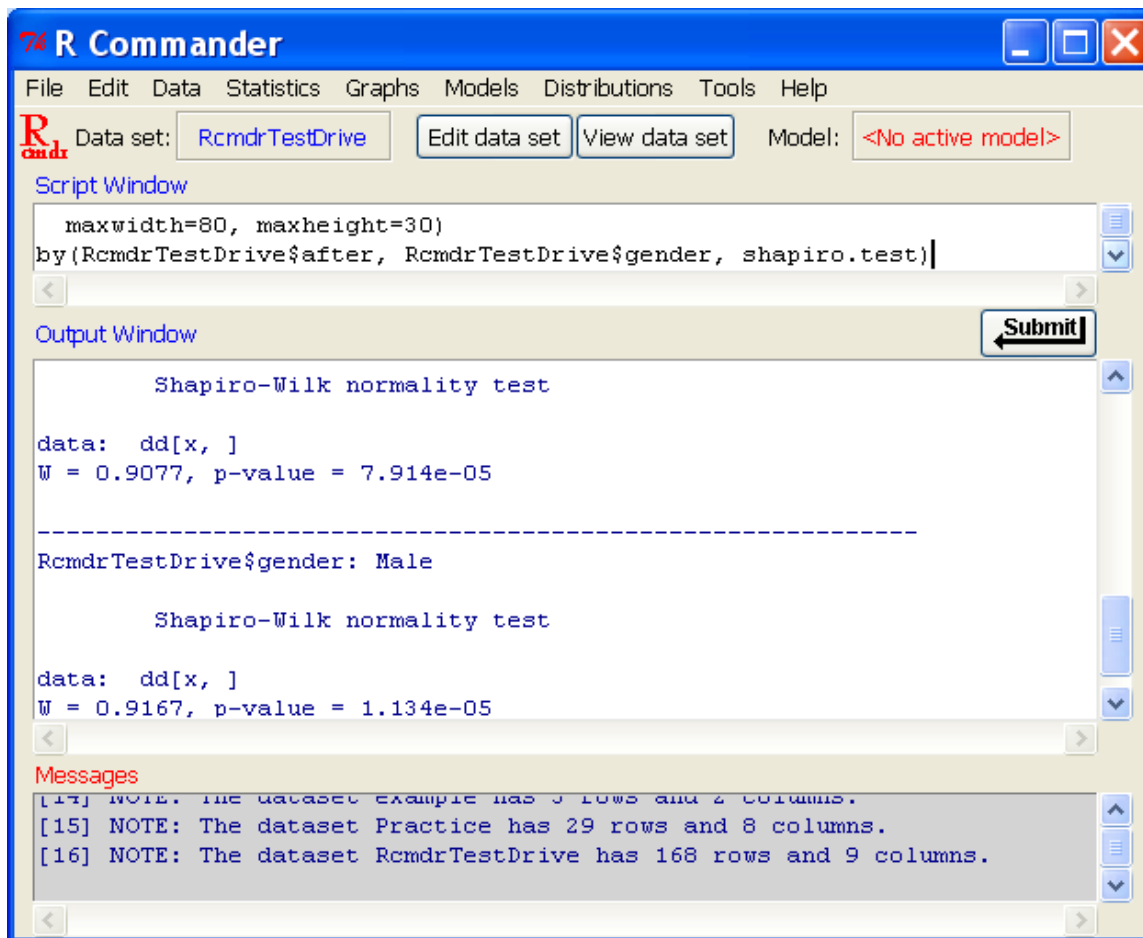
Interpretation: Since p-value = 0.01558 for the test is less than 0.05. One can conclude that the null hypothesis is rejected. There is sufficient evidence to support the alternative hypothesis that the average between the two populations is statistically significantly different.

Normality Tests for Subgroups in a Data File

If you have a quantitative variable **after** (in RcmdrTestDrive file) in a data file and you wish to test for normality for after variable for male and female subjects separately, the following is the R command to do it.

Assume the RcmdrTestDrive has the quantitative variable "after" and the qualitative variable "gender", the R command to do normality test on "after" variable for each gender is using a **by** command as the following: (You may enter this command in the Script Window and click on **Submit** button in the R Commander window)

```
by(RcmdrTestDrive$after, RcmdrTestDrive$gender, shapiro.test)
```



Use the following two lines with `ATTACH` function would have the same result:

```
attach(RcmdrTestDrive)  
by(after, gender, shapiro.test)
```