Correlation and Regression

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1 Relationship between the two quantitative variables

Two well-known methods to examine the relationship between the two quantitative variables are calculating correlation and fitting the regression models.

First of all, you have to draw scattergram. Let's consider the relationship between height and the span of spread writing hand in `survey` data set.

In Rgui console, type `plot(Wr.Hnd ~ Height, data=survey)`. If you would like to see the relationship separately for males and females, use `pch=as.integer(Sex)` option.

In EZR, select [Tools], [Load package(s) ...], then select `MASS` and click [OK]. Next, select [File], [Read data set from an attached package], then double-click `MASS` in Package box and double-click `survey` in Data set box, then click [OK]. Next, select [Graphs and tables], [Scatterplot], then select `Height` as [x-variable] and `Wr.Hnd` as [y-variable], check off the box beside "Least-squares line", and click [OK]. If you like to plot with different markers for males and females, click the [Plot by groups...] button and select `Sex` and check off the box besides [Plot lines by group] and click [OK] before the clicking final [OK].

1.1 The difference between correlation and regression

The correlation means the strength of the relationship between 2 quantitative variables, and the regression means how much the variance of a variable can be explained by the variance of the other variable, by fitting the linear model.

1.2 Correlation analysis

The relationship shown as scatterplot may be apparent or spurious correlation. The researcher must always pay attention to it.

To show the strength of correlation, Pearson's product moment correlation coefficients are usually used. When one variable becomes larger and the other also becomes larger, the correlation is positive (The value of Pearson's correlation coefficient is also

positive). When one variable becomes larger and the other becomes smaller, the correlation is negative (The value of Pearson's correlation coefficient is also negative). As nonparametric (using rank) version, the Spearman's rank correlation coefficients are also used.

The definition of the Pearson's correlation coefficient r between the 2 variables X and Y is,

$$r = \frac{\sum_{i=1}^{n}(X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum_{i=1}^{n}(X_i - \bar{X})^2 \sum_{i=1}^{n}(Y_i - \bar{Y})^2}}$$

The null-hypothesis that the r is not different from 0 can be tested using t_0 value defined as follows and t-distribution with $n - 2$ degree of freedom.

$$t_0 = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$

In Rgui console, to calculate the Pearson's correlation coefficient between heights and spread writing hand spans with null-hypothesis testing, type as follows. For Spearman's rank correlation coeffients, `method="spearman"` option can be used.

```
cor.test(survey$Height, survey$Wr.Hnd)
```

The confidence intervals for Spearman's rank correlation can be obtained using `fmsb` package's `spearman.ci.sas()` function as follows.

```
library(fmsb)
spearman.ci.sas(survey$Height, survey$Wr.Hnd)
```

In EZR, select [Statistical analysis], [Continuous variables], [Test for Pearson's correlation], then select `Height` and `Wr.Hnd` (clicking with pressing Ctrl), and click [OK] (If you need Spearman's rank correlation, you need to use [Statistical analysis], [Nonparametric tests], [Spearman's rank correlation test] menu). The following result will appear in the Output Window. Scattergram with regression line is automatically drawn, but it should be igrnored. In EZR, confidence interbals for Spearman's rank correlation is not given.

```
        Pearson's product-moment correlation

data:  survey$Height and survey$Wr.Hnd
t = 10.7923, df = 206, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.5063486 0.6813271
sample estimates:
     cor
0.600991
(skip)
correlation coefficient = 0.601, 95% CI 0.506-0.681, p.value = 8.23e-22
```

Among the output of EZR, you only need to refer the bottom line as summary. The estimated Pearson's correlation coefficient r is 0.601 with 95% confidence interval of [0.506, 0.681]. The p-value of `8.23e-22` means that under the null hypothesis (no correlation), the probability to happen to get this or more related data is 8.23×10^{-22}. According to the traditional criteria to judge the strength of correlation (more than 0.7 'strong', 0.4-0.7 'moderate', 0.2-0.4 'weak'), there is a moderate correlation.

To calculate the correlations for males and females separately, you can specify subset. In Rgui console, it's easy to calculate those as follows.

```
males <- subset(survey, Sex=="Male")
cor.test(males$Height, males$Wr.Hnd)
females <- subset(survey, Sex=="Female")
cor.test(females$Height, females$Wr.Hnd)
```

In EZR, select [Statistical analysis], [Continuous variables], [Test for Pearson's correlation], and select `Height` and `Wr.Hnd` (clicking with pressing Ctrl), and type `Sex=="Male"` in the box below "Condition to limit samples for analysis ...", then click [OK] for males. For females, you can do almost similarly, but type `Sex=="Female"` instead of `Sex=="Male"` in the box.

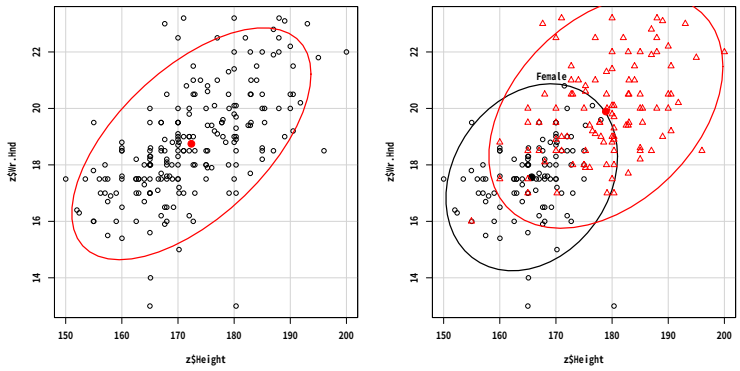
For males, the result is obtained below. The correlation coefficient is still significantly different from zero, but according to traditional judgement, it means weak correlation. The correlation for the data combining males and females may be exaggerated due to the different data ranges of both sexes being pooled.

```
correlation coefficient = 0.385, 95% CI 0.209-0.537, p.value = 4.99e-05
```

1.3 Probability ellipse and Hotelling's T^2

EZR does not support to draw, but probability ellipse is useful to see the correlation status. Using `car` package's `dataEllipse()` function, it's possible.

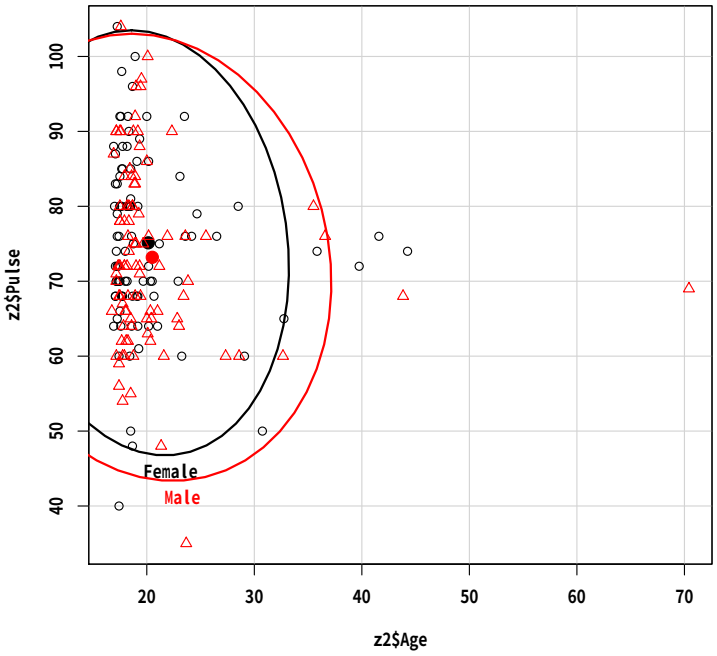
```
library(car)
z <- survey[, c("Height", "Wr.Hnd", "Sex")]
z <- subset(z, complete.cases(z)) # Missing values have to be omitted.
layout(t(1:2))
dataEllipse(z$Height, z$Wr.Hnd, levels=0.95)
dataEllipse(z$Height, z$Wr.Hnd, z$Sex, levels=0.95)
```



The difference between two probability ellipses can be tested by Hotelling's T^2.

```
if (require(Hotelling)==FALSE) {
 install.packages("Hotelling", dep=TRUE)
 library(Hotelling)
}
Z <- split(z[, c("Height", "Wr.Hnd")], z[, "Sex"])
print(hotelling.test(Z[[1]], Z[[2]]))
```

```
z2 <- survey[, c("Age", "Pulse", "Sex")]
z2 <- subset(z2, complete.cases(z2)) # Exclude missing values to draw probability ellipse
dataEllipse(z2$Age, z2$Pulse, z2$Sex, levels=0.95)
Z2 <- split(z2[, c("Age", "Pulse")], z2[, "Sex"])
print(hotelling.test(Z2[[1]], Z2[[2]]))
```



1.4 Fitting a regression model

The principle of fitting regression models to observed data is that the variance of a dependent variable can be mostly explained by the variance of independent variables. If the explanatory power is enough, substituting the independent variables by actual values will serve a corresponding projection or estimation of the dependet variable. Reverse calculation is also possible, as in the case of so-called "working curve". A working curve (but often line, sometimes with transformation) provides the equation as regression model for the series of observed absorptions for fixed concentrations. Usually a working line can be used when its explanatory power is more than 98%.

If the zero-adjustment is done by standard solution with zero concentration, the regression line must go through the origin (therefore, intercept must be zero), otherwise (zero-adjustment is done by pure water) the regression line may not go through the origin.

For example, let the series of absorption for the standard solutions with fixed concentrations (0, 1, 2, 5, 10 $\mu g/\ell$) as (0.24, 0.33, 0.54, 0.83, 1.32), when the zero-adjustment was done by pure water. If we denote the absorption variable as y and the concentration variable as x, the regression model can be written as $y = bx + a$. The coefficients a and b (a is called as "intercept" and b is called as "regression coefficient")

should be estimated by the least square method to find the set of a and b minimizing the sum of square errors,

$$f(a,b) = \sum_{i=1}^{5} (y_i - bx_i - a)^2$$

Solving the equations that each partial diffential of $f(a,b)$ by a and b equals 0, then we can obtain the following 2 equations.

$$b = \frac{\sum_{i=1}^{5} x_i y_i/5 - \sum_{i=1}^{5} x_i/5 \cdot \sum_{i=1}^{5} y_i/5}{\sum_{i=1}^{5} {x_i}^2/5 - \left(\sum_{i=1}^{5} x_i/5\right)^2}$$

$$a = \sum_{i=1}^{5} y_i/5 - b \cdot \sum_{i=1}^{5} x_i/5$$

Using these a and b values and measured absorption (for example 0.67), we can estimate the unknown concentration of sample solution. To note, the measured absorption of any sample must range within the values for standard solutions. The regression model has no guarantee to stand outrange of standard solutions[1].

In Rgui console, we can apply `lm()` (linear model) to estimate the fitted regression model as follows.

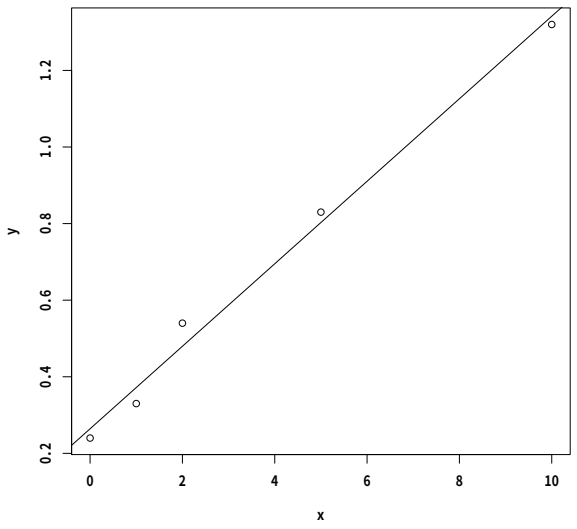
```
y <- c(0.24, 0.33, 0.54, 0.83, 1.32)
x <- c(0, 1, 2, 5, 10)
# apply linear model fitting
res <- lm(y ~ x)
# show the summary of result
summary(res)
# draw scattergram with regression line
plot(y ~ x)
abline(res)
# calculate the concentration corresponding to the absorption of 0.67
(0.67 - res$coef[1])/res$coef[2]
```

The summary of result is shown below.

[1] Such an extrapolation is not recommended. Usually concentrating or diluting the solutions to remeasure the absorption is recommended.

```
Call:
lm(formula = y ~ x)

Residuals:
       1        2        3        4        5
-0.02417 -0.04190  0.06037  0.02718 -0.02147

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.26417    0.03090   8.549 0.003363 **
x            0.10773    0.00606  17.776 0.000388 ***
---
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1  1

Residual standard error: 0.04894 on 3 degrees of freedom
Multiple R-squared: 0.9906,     Adjusted R-squared: 0.9875
F-statistic:   316 on 1 and 3 DF,  p-value: 0.0003882
```

We can see that the estimated intercept was $a = 0.26417$ and regression coefficient was $b = 0.10773$, and the model explains 98.75% (0.9875) of the data, which is shown in `Adjusted R-squared`. The `p-value` means the result (significant probability) of testing the null-hypothesis (the extent how the variance of absorption can be explained by the model is similar to error variance).



The concentration for the absorption of 0.67 is given at last as 3.767084. Therefore, we can conclude that the concentration of the solution, of which absorption was 0.67, was 3.8 $\mu g/\ell$.

In Rcmdr, the data must be entered as a Data Set. Select [Data], [New data set] and type `workingcurve` in the box of "Enter name for data set:". After the "Data Editor" window appears, click [var1] and type `y` in the "variable name" box and check the radio button of "numeric" as type and press Enter key. Next, change [var2] to [x] similarly. Then enter the data into each cells, and close the window (usually select [File], [Close]).
To draw scattergram with regression line, select [Graphs], [Scatterplot...], then select `x` as "x-variable" and `y` as "y-variable". Check off the box beside "Smooth Line" and click [OK].
To apply a linear regression model fitting, select [Statistics], [Fit models], [Linear regression], then select `y` as "response variable" and `x` as "Explanatory variables". Clicking [OK] leads to the summary of results shown in the Output Window.

For other situations than working curves, linear regression models can be applied in a similar manner. Let's go back to the example of `survey` data set (Of course, the `MASS` package must be loaded before using `survey` data set). If we want to explain the variance of the span of writing hand by the height, we can apply the linear regression model to the `survey` data set by typing as follows in Rgui console.

```
res <- lm(Wr.Hnd ~ Height, data=survey)
summary(res)
```

In Rcmdr, after activating `survey` as already mentioned, select [Statistics], [Fit models], [Linear regression], then select `Wr.Hnd` as "response variable" and `Height` as "Explanatory variables". Clicking [OK] gives the summary result.

1.5 Testing the stability of estimated coefficients

When the response variable has virtually no relationship with the explanatory variable, the sums of squared residuals for many possible regression lines (any line on the centroid) may give almost same values. In other words, the estimated intercept and slope are very unstable in such situation. To evaluate the stability of parameters of regression line (regression coefficient b and intercept a), t_0 values are usually used. Let the relationship between y and x be expressed by the equation of $y = a_0 + b_0 x + e$, and assume the error term e obeying the normal distribution with mean 0 and variance σ^2, the estimated regression coefficient a would obey the normal distribution of mean a_0, variance $(\sigma^2/n)(1 + M^2/V)$, where M and V are the mean and the variance of x. Then the sum of squared residuals Q divided by the variance of error σ^2 (say, Q/σ^2) obeys the chi-square distribution with degree of freedom $(n-2)$. Therefore, the $t_0(a_0)$ defined as follows obeys the t-distribution with the degree of freedom $(n-2)$.

$$t_0(a_0) = \frac{\sqrt{n(n-2)}(a - a_0)}{\sqrt{(1 + M^2/V)Q}}$$

However, to calculate this value, a_0 must be known. Under the null hypothesis of $a_0 = 0$, $t_0(0)$ calculated from the observed data is almost matching with $t_0(a_0)$ and obeys the t-distribution with degree of freedom $(n-2)$. The absolute value of $t_0(0)$ is less than the 97.5% point of t-distribution at the 95% probability. We can also get the significance probability using the distribution function (cumulative probability density function).

Similarly, we can calculate $t_0(b)$ for regression coefficient as follows.

$$t_0(b) = \frac{\sqrt{n(n-2)V}b}{\sqrt{Q}}$$

Using the relationship that the $t_0(b)$ obeys the t-distribution with degree of freedom $(n-2)$, we can calculate the significance probability.

If the significant probability is very small (usually less than 5%, this criteria is called as the significance level of the test), we can say that a_0 or b_0 is significantly different from zero, which means the stability of estimated a_0 or b_0.

In both Rgui concole and Rcmdr, the significance probabilities are shown at the column of `Pr(>|t|)`.

2 Applied regression models

2.1 Multiple regression model

The explanatory variables can include two or more variables. In such case, the model is called as "multiple regression model". There are some points to pay attention, but basically the explanatory variables can be given as the right terms of linear model, connected by +. For example, for the same data previously described, if you would like to explain the variance of the span of writing hand (`Wr.Hnd`) by the variance of height (`Height`) and the variance of the span of non-writing hand (`NW.Hnd`), you may type as follows in Rgui console.

```
res <- lm(Wr.Hnd ~ Height + NW.Hnd, data=survey)
summary(res)
```

In Rcmdr, select [Statistics], [Fit models], [Linear regression], then select `Wr.Hnd` as "response variable", and `Height` and `NW.Hnd` with pressing Ctrl key as "Explanatory variables". Clicking [OK] leads to the summary of results shown in the Output Window. In EZR, [Statistical analysis], [Continuous variables], [Linear regression], then specify the variables similarly as the case of Rcmdr.

In the multiple regression model, the estimated regression coefficients are the "partial regression coefficients", which adjust the effects of other explanatory variables on the response variable to obtain each explanatory variable's own effect on the response variable. But the values of partial regression coefficients depend on the absolute scale

of each variable, so that those cannot show the relative strength of effect on the response variable for each explanatory variable. For such comparison, the **standardized partial regression coefficients** can be used. In Rgui console, type as follows, then you obtain the estimates as `stb` for the standardized partial regression coefficients.

```
sdd <- c(0,sd(res$model$Height),sd(res$model$NW.Hnd))
stb <- coef(res)*sdd/sd(res$model$Wr.Hnd)
stb
```

The Rcmdr does not provide this as a menu item, but you can do so by editing the commands in script window, selecting lines and click [Submit]. EZR also does not provide this. However, the model remains as the named object such as RegModel.1, which is shown at the top-right label of [Model:]. If the name of the model is `RegModel.1`, you can type `res <- RegModel.1` before the 3 line scripts shown above, then select 4 lines and click [Submit].

Instead of calculating standardized partial regression coefficients, **squared partial correlation coefficients** can be used to show the relative contribution of explanatory variables to the response variable. To get the squared partial correlation coefficients, you can type as below.

```
SS <- anova(res)["Sum Sq"]
SS/sum(SS)
```

2.2 Evaluation of the goodness of fit

It is always necessary to evaluate the goodness of fit of the regression model to the data.

After the least square estimation of a and b, we can define $z_i = a + bx_i$ for each x. Then $e_i = y_i - z_i$ can be considered as "residuals". The residuals is the remaining part of the variance of y_i, that could not be explained by the regression model. Thus, the greater the residuals are, the worse the goodness of fit is. We would like to treat the both plus and minus residuals in its absolute distance, so that we can define the sum of squared residuals, Q, as follows.

$$Q = \sum_{i=1}^{n} e_i^2 = \sum_{i=1}^{n} (y_i - z_i)^2$$

$$= \sum_{i=1}^{n} y_i^2 - (\sum_{i=1}^{n} y_i)^2/n - \frac{(n\sum_{i=1}^{n} x_i y_i - \sum_{i=1}^{n} x_i \sum_{i=1}^{n} y_i)^2}{n\sum_{i=1}^{n} x_i^2 - (\sum_{i=1}^{n} x_i)^2}/n$$

The sum of squared residuals Q is the scale to show badness of fit of the regression model. Q divided by n is called as residual variance (we will denote it as var(e)).

Among the values of var(e) and the variance of y (var(y)) and Pearson's product limit correlation coefficient r, the following equation always stands.

$$\mathrm{var}(e) = \mathrm{var}(y)(1 - r^2)$$

Therefore,

$$r^2 = 1 - \frac{\mathrm{var}(e)}{\mathrm{var}(y)}$$

Thus the closer to 1 r^2 is, the goodness of fit is higher. In that meaning, r^2 is called as "deterministic coefficient" or "the attributable proportion of x".

Since r^2 becomes larger depending on the number of explanatory variables, usually the r^2 will be adjusted for the degree of freedom. That is, `Adjusted R-Squared` in the summary of results.

As another indicator for the goodness of fit, the AIC (Akaike information criterion) is sometimes used (particularly in multiple regression models), which can be calculated in R, using the resulted object of linear model fitting (for example, `res` of the example above). In Rgui console, type `AIC(res)`, then you can get the AIC value. Here I don't explain any more, but many online materials and books can be found[2].

2.3 Paying attention in fitting regression model

The target variables may be measurements including error. In such situation, it is not valid to assume one as response variable and the other as explanatory variable. Generally speaking, if we can assume the direction of effect like the stature determining weight and not *vise versa*, the regression is possible where the stature is explanatory variable and the weight is response variable. However, when the explanatory variable includes measurement error, the explanatory power of the regression model become worse. In addition, the regression models with opposite combination of response variable and explanatory variable do not match. Thus, it is very important that the determination of which variable is response variable shoule be based on the direction of causal relationship, with enough reference to previous studies and clinical/biological knowledge.

Another point to be noticed is extrapolation of regression model for prediction. Especially the extrapolation should be avoided when you apply the working curve for prediction, because the linearity of the working curve is only confirmed within the range of standard material concentrations. The increase of absorbance tends to be smaller in higher concentration ranges due to saturation of molecules, the linearity is lost there. If you measure the samples with high concentration, you must dilute them into the ranges of standard materials.

[2] `http://en.wikipedia.org/wiki/Akaike_information_criterion` is the explanation in the Wikipedia.

Exercise

A built-in dataset `airquality` includes the air quaility data in New York from May to September 1973. The variables are `Ozone` for ozone gas concentration in ppb, `Solar.R` for solar radiation in lang, `Wind` for wind speed in mph, `Temp` for atomospheric temperature in degree F, `Month` in number (5-9) and `Day` in number (1-31).
Let's fit the regression model for this data with ozone gas concentration as response variable and solar radiation as explanatory variable.

In Rgui console, enter the following 4 lines.

```
plot(Ozone ~ Solar.R, data=airquality)
res <- lm(Ozone ~ Solar.R, data=airquality)
abline(res)
summary(res)
```

In Rcmdr, at first, the `airquality` must be activated by select [Data], [Data in packages], [Read data set from an attached packages ...], then double-click `datasets` in the left panel and double-click `airquality` in the right panel, then click [OK].
To draw scattergram, [Graphs], [Scatterplot ...], then select `Solar.R` as x-variable and `Ozone` as y-variable. Check the box beside "Smooth Line" off, and click [OK]. Then you will get the scattergram with a regression line. To obtain the numerical result of regression model fitting, select [Statistics], [Fit models ...], [Linear regression], then select `Ozone` as Response variable and `Solar.R` as Explanatory variables, and click [OK]. Then you will see the result in the Output window.

Both give the same results as follows.

```
Call:
lm(formula = Ozone ~ Solar.R, data = airquality)

Residuals:
    Min      1Q  Median      3Q     Max
-48.292 -21.361  -8.864  16.373 119.136

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 18.59873    6.74790   2.756 0.006856 **
Solar.R      0.12717    0.03278   3.880 0.000179 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Residual standard error: 31.33 on 109 degrees of freedom
  (42 observations deleted due to missingness)
Multiple R-Squared: 0.1213,Adjusted R-squared: 0.1133
F-statistic: 15.05 on 1 and 109 DF,  p-value: 0.0001793
```

The fitted regression model is Ozone = $18.599 + 0.127 \cdot$ Solar.R, and the `p-value` shown in the bottom line is 0.0001793, as the result of F-test. Therefore, the fitting of the model can be judged as significant. However, the `Adjusted R-squared` shown above line is 0.11, which means only about 10% of the variance of the Ozone concentration can be explained by this model. We should judge the model is not so good.

To improve fitting, it may be possible to add more variables (for example, `Wind` and/or `Temp`) as explanatory variables as the multiple regression model. In Rgui console, you can easily do so by typing the next 3 lines. Then you see about 60% of `Adjusted R-Squared` value.

```
mres <- lm(Ozone ~ Solar.R + Wind + Temp, data=airquality)
summary(mres)
AIC(mres)
```

In Rcmdr, select [Statistics], [Fit models ...], [Linear model], then type `Ozone` at the box to the left of ~ and type `Solar.R + Wind + Temp` at the box to the right of ~, and click [OK]. In EZR, select [Statistical analysis], [Continuous variables], [Linear models], then select `Ozone` as response variable and

2.4 Analysis of Covariance (ANACOVA/ANCOVA)

Let's consider the situation below.

- There are 2 continuous variables `X` and `Y`, and 1 binary varialbe `B`.
- The aim is to test the null hypothesis that no significant difference of `Y` between 2 groups indicated by `B`. However, there is a significant correlation between `X` and `Y`. The adjustment for `X` is needed to evaluate the difference of `Y` by `B`.
- The model is
$$\mathrm{Y} = \beta_0 + \beta_1 \mathrm{X} + \beta_2 \mathrm{B} + \beta_{12} \mathrm{XB} + \varepsilon$$
- If β_{12} is significantly different from 0, there is a significant interaction. The correlation between `X` and `Y` is different by `B`. (In this case, regression analysis should be separately conducted by the groups indicated by `B`.
- Otherwise, there is no significant interaction between `X` and `B` on `Y`. The model may change as below.
$$\mathrm{Y} = \beta_0 + \beta_1 \mathrm{X} + \beta_2 \mathrm{B} + \varepsilon$$
- β_2 shows the effect of `B` on `Y` with adjusting the effect of `X`.

An example is available from `https://minato.sip21c.org/grad/sample3.dat`. The data includes the following variables.

REGION East Japan or West Japan

PREF The names of prefectures in Japan

CAR1990 Number of cars for private property per 100 households in 1990

TA1989 Number of deaths by traffic accidets per 100,000 population in 1989

DIDP1985 Percentage of dwellers in DID (densely inhabiting disctrict) in 1985

The purpose of the analysis is to test the null-hypothesis that TA1989 is not significantly different by REGION. However, of course, CAR1990 should be correlated with TA1989, and thus the ANACOVA should be conducted. The R code is shown below.

```
x <- read.delim("https://minato.sip21c.org/grad/sample3.dat")
plot(TA1989 ~ CAR1990, pch=as.integer(REGION), data=x)
east <- lm(TA1989 ~ CAR1990, data=subset(x, REGION=="East"))
summary(east)
abline(east, lty=1)
west <- lm(TA1989 ~ CAR1990, data=subset(x, REGION=="West"))
summary(west)
abline(west, lty=2)
legend("bottomright", pch=1:2, lty=1:2, legend=c("East","West"))
summary(lm(TA1989 ~ REGION*CAR1990, data=x))
ac <- lm(TA1989 ~ REGION+CAR1990, data=x)
summary(ac)
cfs <- dummy.coef(ac)
cfs[[1]] + cfs$CAR1990 * mean(ac$model$CAR1990) + cfs$REGION # For adjusted means
```

In EZR, select [File], [Import Data], [Read Data from File, Clipboard, or URL]. In the dialogue, type x to [Enter name for data set:], check Internet URL for [Location of Data File], check Tabs for [Field Separator], then click [OK]. Then type http://minato.sip21c.org/grad/sample3.dat to [Internet URL] dialogue and click [OK].
Then select [Statistical analysis], [Continuous variables], [ANCOVA]. In the next dialogue, select TA1989 as [Response Variable (pick one)], REGION as [Grouping variable (pick one)], and CAR1990 as [Numeric variable for adjustment (pick one)] and click [OK]. The result doesn't include adjusted means, but the graph and the result of significance test for each variable are automatically obtained.

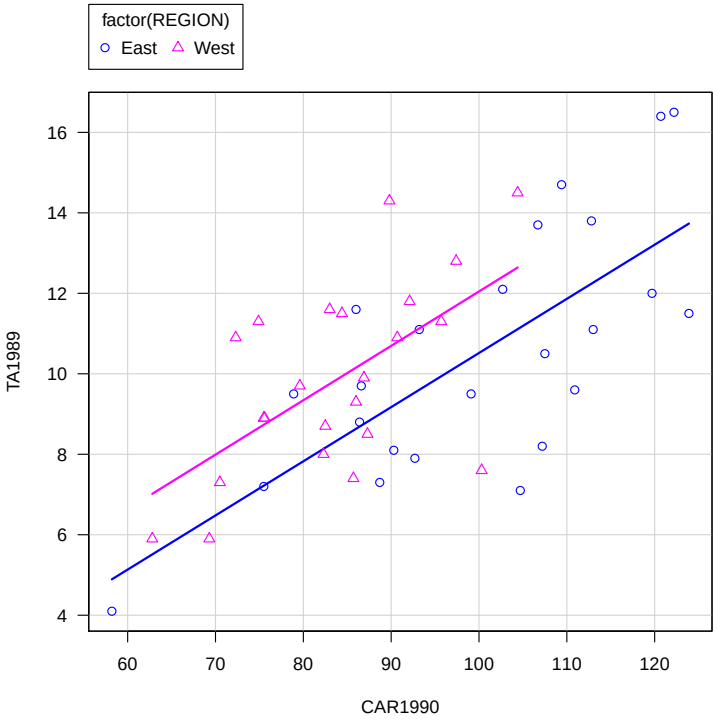
```
Anova Table (Type III tests)

Response: TA1989
               Sum Sq Df F value       Pr(>F)
(Intercept)     7.349  1  1.7857      0.18832
factor(REGION) 20.202  1  4.9091      0.03194 *
CAR1990       157.640  1 38.3061 0.0000001778 ***
Residuals     181.072 44
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

If the model name is `AnovaModel.1`, you can type `summary(AnovaModel.1)` to [R Script] window and press [Submit], them get the following result.

```
Call:
lm(formula = TA1989 ~ 1 + factor(REGION) + CAR1990, data = TempDF,
    na.action = na.omit)

Residuals:
    Min      1Q  Median      3Q     Max
-4.4792 -1.1700 -0.0155  1.5609  3.6357

Coefficients:
                      Estimate Std. Error t value    Pr(>|t|)
(Intercept)           -2.95787    2.21349  -1.336      0.1883
factor(REGION)[T.West]  1.52190    0.68689   2.216      0.0319 *
CAR1990                 0.13475    0.02177   6.189 0.000000178 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.029 on 44 degrees of freedom
Multiple R-squared:  0.4728,Adjusted R-squared:  0.4488
F-statistic: 19.73 on 2 and 44 DF,  p-value: 0.0000007654
```

According to the result showing that the `Estimate` of `factor(REGION)[T.West]` is 1.522 with p-value less than 0.05 and the `Estimate` of `CAR1990` is 0.135 with p-value less than 0.05, we can say the following 2 things.

- If the number of cars per household is same, the western region has 1.522 per 100,000 higher death rate than the eastern region.
- If the difference of the region is controlled, the increase of 1 car per 100 households leads the increase of 0.135 per 100,000 death rate due to traffic accident.



2.5 Logistic regression analysis

The situation of the logistic regression is, the response variable is binary (occurrence of the event or not), not continuous. Therefore, the response variable obeys binary distribution, not normal distribution. For that purpose, `glm()` function with options of `family=binomial()` is used.

Let's consider an example of the presence of the bacteria *H. influenzae* in children with otitis media in the Northern Territory of Australia. The data is included in `bacteria` data set of `MASS` library. Included variables are shown below.

y presence or absence: a factor with levels n and y.

ap active/placebo: a factor with levels a and p.

hilo hi/low compliance: a factor with levels hi amd lo.

week numeric: week of test.

ID subject ID: a factor.

trt a factor with levels placebo, drug and drug+, a re-coding of ap and hilo.

To evaluate the effects of drugs, compliance and duration on the presense or absence of bacteria, the following R code can be used.

```
library(MASS)
data(bacteria)
res <- glm(y ~ ap + hilo + week, data=bacteria, family=binomial())
summary(res)
exp(coef(res))
exp(confint(res))
library(fmsb)
NagelkerkeR2(res)
```

The results can be obtained as follows.

summary(res)

```
Call:
glm(formula = y ~ ap + hilo + week, family = binomial(), data = bacteria)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.3763   0.3813   0.5212   0.6576   1.1194

Coefficients:
            Estimate Std. Error z value    Pr(>|z|)
(Intercept)   1.9278     0.3762   5.124 0.000000299 ***
ap[T.p]       0.8343     0.3816   2.186     0.02879 *
hilo[T.lo]   -0.5066     0.3546  -1.428     0.15317
week         -0.1167     0.0443  -2.633     0.00845 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 217.38  on 219  degrees of freedom
Residual deviance: 202.90  on 216  degrees of freedom
AIC: 210.9

Number of Fisher Scoring iterations: 4
```

exp(coef(res))

```
(Intercept)     ap[T.p]  hilo[T.lo]        week
  6.8743391   2.3032551   0.6025587   0.8898975
```

exp(confint(res))

```
                2.5 %     97.5 %
(Intercept) 3.3962571 14.9415826
ap[T.p]     1.1138918  5.0266682
hilo[T.lo]  0.2979555  1.2048297
week        0.8149128  0.9702764
```

NagelkerkeR2(res)

```
$N
[1] 220

$R2
[1] 0.1014725
```

The result means that the active drug and longer duration of drug administration have significantly lower odds ratio than 1 (`ap[T.p]`'s odds ratio is significantly higher than 1, which means placebo having higher risk of otitis media than active drug).

The result should be shown as below.

		95% C.I.		
Variables	Odds Ratio	Lower	Upper	p-value
Placebo	2.30	1.11	5.03	0.029
Low compliance	0.60	0.29	1.21	0.153
Duration (week)	0.89	0.81	0.98	0.008

In EZR, select [Statistical analysis], [Discrete variables], [Logistic regression]. Set `y` as [Objective variable], `ap[factor] + hilo[factor] + week` as [Explanatory variables] and check the appropriate check boxes, then click [OK].

3 Furthur Readings

- Armitage P, Berry G, Matthews JNS (2002) *Statistical Methods in Medical Research, 4th ed.*, Blackwell Publishing.
- Bull K, Spiegelhalter DJ (1997) Tutorial in biostatistics: Survival analysis in observational studies. *Statistics in Medicine*, 16: 1041-1074.
- Faraway JJ (2006) *Extending the linear models with R: Generalized linear, mixed effects and nonparametric regression models.* Chapman and Hall.
- `http://socserv.mcmaster.ca/jfox/Misc/Rcmdr/Getting-Started-with-the-Rcmdr.pdf` (The introductory textbook for R Commander, provided by Prof. John Fox (McMaster Univ.), the developper of Rcmdr package.)

- Maindonald J, Braun J (2003) *Data analysis and graphics using R*, Cambridge Univ. Press.
- Nagelkerke N (1991) A note on a general definition of the coefficient of determination. *Biometrika*, 78: 691-692.
- R Development Core Team (2010). *R: A language and environment for statistical computing. R Foundation for Statistical Computing*, Vienna, Austria. ISBN 3-900051-07-0, URL `http://www.R-project.org`.
- Venables WN, Ripley BD (1999) *Modern Applied Statistics with S-PLUS. Third Edition.* Springer.
- EZR on Rcmdr: `http://www.jichi.ac.jp/saitama-sct/SaitamaHP.files/statmedEN.html`