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Germán Rodríguez Introducing R

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4 Linear Models

Let us try some linear models, starting with multiple regression and analysis of covariance models, and then moving on to models using regression splines. In this section I will use the data read in Section 3, so make sure the fpe data frame is attached to your current session.

4.1 Fitting a Model

To fit an ordinary linear model with fertility change as the response and setting and effort as predictors, try

```
> lmfit = lm( change ~ setting + effort )
```

Note first that lm is a function, and we assign the result to an object that we choose to call lmfit (for linear model fit). This stores the results of the fit for later examination.

The argument to lm is a model formula, which has the response on the left of the tilde \sim (read "is modeled as") and a Wilkinson-Rogers model specification formula on the right. R uses

- + to combine elementary terms, as in A+B
- : for interactions, as in A:B;
- * for both main effects and interactions, so A*B = A+B+A:B

A nice feature of R is that it lets you create interactions between categorical variables, between categorical and continuous variables, and even between numeric variables (it just creates the cross-product).

4.2 Examining a Fit

Let us look at the results of the fit. One thing you can do with lmfit, as you can with any R object, is print it.

```
> lmfit

Call:
lm(formula = change ~ setting + effort)

Coefficients:
(Intercept) setting effort
   -14.4511 0.2706 0.9677
```

The output includes the model formula and the coefficients. You can get a bit more detail by requesting a summary:

```
> summary(lmfit)
Call:
lm(formula = change ~ setting + effort)
Residuals:
     Min
              10 Median
                                30
                                        Max
-10.3475 -3.6426 0.6384 3.2250 15.8530
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) -14.4511
                        7.0938 -2.037 0.057516 .
setting
             0.2706
                        0.1079 2.507 0.022629 *
effort
             0.9677
                        0.2250 4.301 0.000484 ***
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '.' 0.1 ' ' 1
Residual standard error: 6.389 on 17 degrees of freedom
Multiple R-Squared: 0.7381,
                               Adjusted R-squared: 0.7073
F-statistic: 23.96 on 2 and 17 DF, p-value: 1.132e-05
```

The output includes a more conventional table with parameter estimates and standard errors, as well the residual standard error and multiple R-squared. (By default S-Plus includes the matrix of correlations among parameter estimates, which is often bulky, while R sensibly omits it. If you really need it, add the option correlation=TRUE to the call to summary.)

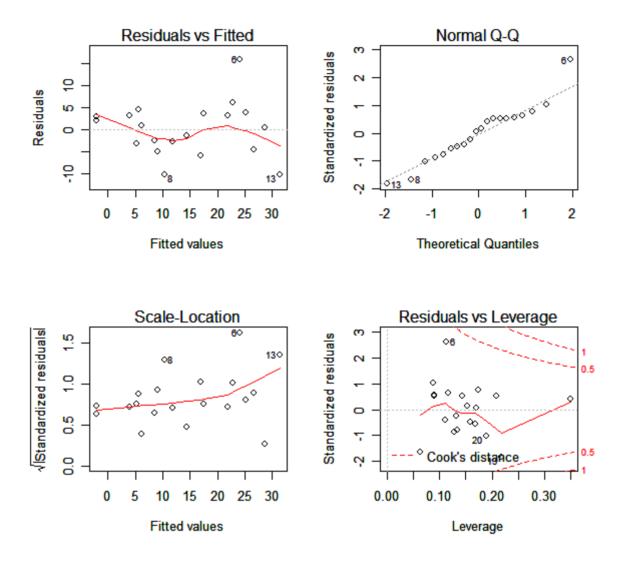
To get a hierarchical analysis of variance table corresponding to introducing each of the terms in the model one at a time, in the same order as in the model formula, try the anova function:

Alternatively, you can plot the results using

```
> plot(lmfit)
```

This will produce a set of four plots: residuals versus fitted values, a Q-Q plot of standardized residuals, a scale-location plot (square roots of standardized residuals versus fitted values, and a plot of residuals versus leverage that adds bands corresponding to Cook's distances of 0.5 and 1.

R will prompt you to click on the graph window or press Enter before showing each plot, but we can do better. Type par(mfrow=c(2,2)) to set your graphics window to show four plots at once, in a layout with 2 rows and 2 columns. Then redo the graph using plot(lmfit). To go back to a single graph per window use par(mfrow=c(1,1)). There are many other ways to customize your graphs by setting high-level parameters, type ?par to learn more.



Technical Note: You may have noticed that we have used the function plot with all kinds of arguments: one or two variables, a data frame, and now a linear model fit. In R jargon plot is a generic function. It checks for the kind of object that you are plotting and then calls the appropriate (more specialized) function to do the work. There are actually many plot functions in R, including plot.data.frame and plot.lm. For most purposes the generic function will do the right thing and you don't need to be concerned about its inner workings.

4.3 Extracting Results

There are some specialized functions that allow you to extract elements from a linear model fit. For example

```
> fitted(lmfit)

1 2 3 4 5 6 7 8

-2.004026 5.572452 25.114699 21.867637 28.600325 24.146986 17.496913 10.296380
... output edited ...
```

extracts the fitted values. In this case it will also print them, because we did not asign them to anything. (The longer form fitted.values is an alias.)

To extract the coefficients use the coef function (or the longer form coefficients)

```
> coef(lmfit)
(Intercept) setting effort
-14.4510978 0.2705885 0.9677137
```

To get the residuals, use the residuals function (or the abbreviation resid):

If you are curious to see exactly what a linear model fit produces, try the function

```
> names(lmfit)
[1] "coefficients" "residuals" "effects" "rank"
[5] "fitted.values" "assign" "qr" "df.residual"
[9] "xlevels" "call" "terms" "model"
```

which lists the named components of a linear fit. All of these objects may be extracted using the \$ operator. However, whenever there is a special extractor function you are encouraged to use it.

4.4 Factors and Covariates

So far our predictors have been continuous variables or *covariates*. We can also use categorical variables or *factors*. Let us group family planning effort into three categories:

```
> effortg = cut(effort, breaks = c(-1, 4, 14, 100),
+ label=c("weak","moderate","strong"))
```

The function cut creates a factor or categorical variable. The first argument is an input vector, the second is a vector of breakpoints, and the third is a vector of category labels. Note that there is one more breakpoint than there are categories. All values greater than the i-th breakpoint and less than or equal to the (i+1)-st breakpoint go into the i-th category. Any values below the first breakpoint or above the last one are coded NA (a special R code for missing values). If the labels are omitted, R generates a suitable default of the form "(a,b]". By default the intervals are closed on the right, so our intervals are ≤ 4 ; 5-14; 15+. To change this use the option right=FALSE.

Try fitting the analysis of covariance model:

As you can see, family planning effort has been treated automatically as a factor, and R has generated the necessary dummy variables for moderate and strong programs treating weak as the reference cell.

Choice of Contrasts: R codes unordered factors using the reference cell or "treatment contrast" method. The reference cell is always the first category which, depending on how the factor was created, is usually the first in alphabetical order. If you don't like this choice, R provides a special function to re-order levels, check out help(relevel).

S codes unordered factors using the *Helmert* contrasts by default, a choice that is useful in designed experiments because it produces orthogonal comparisons, but has baffled many a new user. Both R and S-Plus code ordered factors using polynomials. To change to the reference cell method for unordered factors use the following call

```
> options(contrasts=c("contr.treatment","contr.poly"))
```

Back on to our analysis of covariance fit. You can obtain a hierarchical anova table for the analysis of covariance model using the anova function:

Type ?anova to learn more about this function.

4.5 Regression Splines

The real power of R begins to shine when you consider some of the other functions you can include in a model formula. First, you can include mathematical functions, for example log(setting) is a perfectly legal term in a model formula. You don't have to create a variable representing the log of setting and then use it, R will create it 'on the fly', so you can type

```
> lm( change ~ log(setting) + effort)
```

If you wanted to use orthogonal polynomials of degree 3 on setting, you could include a term of the form poly(setting, 3)

You can also get R to calculate a well-conditioned basis for regression splines. First you must load the splines library (this step is not needed in S-Plus):

```
> library(splines)
```

This makes available the function bs to generate B-splines. For example the call

```
> setting.bs <- bs(setting, knots = c(66,74,84)) + effort )
```

will generate cubic B-splines with interior knots placed at 66, 74 and 84. This basis will use seven degrees of freedom, four corresponding to the constant, linear, quadratic and cubic terms, plus one for each interior knot. Alternatively, you may specify the number of degrees of freedom you are willing to spend on the fit using the parameter df. For cubic splines R will choose df-4 interior knots placed at suitable quantiles. You can also control the degree of the spline using the parameter degree, the default being cubic.

If you like *natural* cubic splines, you can obtain a well-conditioned basis using the function ns, which has exactly the same arguments as bs except for degree, which is always three. To fit a natural spline with five degrees of freedom, use the call

```
> setting.ns <- ns(setting, df=5)</pre>
```

Natural cubic splines are better behaved than ordinary splines at the extremes of the range. The restrictions mean that you save four degrees of freedom. You will probably want to use two of them to place additional knots at the extremes, but you can still save the other two.

To fit an additive model to fertility change using natural cubic splines on setting and effort with only one interior knot each, placed exactly at the median of each variable, try the following call:

```
> splinefit = lm( change ~ ns(setting, knot=median(setting)) +
+    ns(effort, knot=median(effort)) )
```

Here we used the parameter knot to specify where we wanted the knot placed, and the function median to calculate the median of setting and effort.

Do you think the linear model was a good fit? Natural cubic splines with exactly one interior knot require the same number of parameters as an ordinary cubic polynomial, but are much better behaved at the extremes.

4.6 Other Options

The 1m function has several additional parameters that we have not discussed. These include

data to specify a dataset, in case it is not attached subset to restrict the analysis to a subset of the data weights to do weighted least squares

and many others; see help(lm) for further details. The args function lists the arguments used by any function, in case you forget them. Try args(lm).

The fact that R has powerful matrix manipulation routines means that one can do many of these calculations from first principles. The next couple of lines create a model matrix to represent the constant, setting and effort, and then calculate the OLS estimate of the coefficients as (X'X)⁻¹X'y:

Compare these results with coef(lmfit).

Continue with Generalized Linear Models (glms)

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