Chapter 6

Linear regression and ANOVA

Regression and analysis of variance form the basis of many investigations. In this chapter we describe how to undertake many common tasks in linear regression (broadly defined), while Chapter 7 discusses many generalizations, including other types of outcome variables, longitudinal and clustered analysis, and survival methods.

Many SAS procedures and R commands can perform linear regression, as it constitutes a special case of which many models are generalizations. We present detailed descriptions for SAS `proc reg` and `proc glm` as well as for the R `lm()` command, as these offer the most flexibility and best output options tailored to linear regression in particular. While ANOVA can be viewed as a special case of linear regression, separate routines are available in SAS (`proc anova`) and R (`aov()`) to perform it. In addition, SAS `proc mixed` is needed for some calculations. We address these additional procedures only with respect to output that is difficult to obtain through the standard linear regression tools.

R supports a flexible modeling language implemented using formulas (see `help(formula)` and 6.1.1) for regression that is shared with the lattice graphics functions. Many of the routines available within R return or operate on `lm` class objects, which include objects such as coefficients, residuals, fitted values, weights, contrasts, model matrices, and the like (see `help(lm)`).

The CRAN statistics for the social sciences task view provides an excellent overview of methods described here and in Chapter 7.

6.1 Model fitting

6.1.1 Linear regression

SAS *Example:* 6.6.2

```
proc glm data=ds;
   model y = x1 ... xk;
run;
```

or

```
proc reg data=ds;
   model y = x1 ... xk;
run;
```

Note: Both `proc glm` and `proc reg` support linear regression models, while `proc reg` provides more regression diagnostics. The `glm` procedure more easily allows categorical covariates.

R

```
mod1 = lm(y ~ x1 + ... + xk, data=ds)
summary(mod1)
summary.aov(mod1)
```

or

```
form = as.formula(y ~ x1 + ... + xk)
mod1 = lm(form, data=ds)
summary(mod1)
coef(mod1)
```

Note: The first argument of the `lm()` function is a formula object, with the outcome specified followed by the $\sim$ operator then the predictors. It returns a linear model object. More information about the linear model `summary()` command can be found using `help(summary.lm)`. The `coef()` function extracts coefficients from a model (see also the `coefplot` package). The `biglm()` function in the `biglm` package can support model fitting to very large datasets. By default, stars are used to annotate the output of the `summary()` functions regarding significance levels: these can be turned off using the command `options(show.signif.stars=FALSE)`. The `biglm` package can be used to undertake estimation with larger datasets.

6.1.2 Linear regression with categorical covariates

Example: 6.6.2

See 6.1.4 (parameterization of categorical covariates).

SAS

```
proc glm data=ds;
   class x1;
   model y = x1 x2 ... xk;
run;
```

Note: The `class` statement specifies covariates that should be treated as categorical. The `glm` procedure uses reference cell coding; the reference category can be controlled using the `order` option to the `proc glm` statement, as in 7.10.11.

R

```
ds = transform(ds, x1f = as.factor(x1))
mod1 = lm(y ~ x1f + x2 + ... + xk, data=ds)
```

Note: The `as.factor()` command in R creates a categorical variable from a variable. By default, the lowest value (either numerically or lexicographically) is the reference value. The `levels` option for the `factor()` function can be used to select a particular reference value (see 2.2.19). Ordered factors can be constructed using the `ordered()` function.

6.1.3 Changing the reference category

SAS

```
proc sort data=ds;
   by classvar;
run;

proc glm data=ds order=data;
   class classvar;
   model y = classvar;
run;
```

or

```
proc genmod data=ds;
   class classvar (param=ref ref="level");
   model y = classvar;
run;
```

Note: The first code is necessary for procedures that use the more primitive `class` statement, as reviewed in 6.1.4. For these procedures, the default reference category is the last one. The `order` option can take other values, which may be useful. If the desired reference cell cannot be sorted to the end, it may be necessary to recode the category values to, e.g., `A. Brown`, `B. Blue`, and `C. Green` from `Blue`, `Brown`, and `Green`, before sorting. Sorting `by descending classvar` may also be useful. The second set of code will work in the `genmod`, `logistic`, and `surveylogistic` procedures.

R

```
ds = transform(ds, neworder = factor(classvar,
   levels=c("level", "otherlev1", "otherlev2"))
mod1 = lm(y ~ neworder, data=ds)
```

Note: The first level of a factor (by default that which appears first lexicographically) is the reference group. This can be modified through use of the `factor()` function.

6.1.4 Parameterization of categorical covariates

Example: 6.6.5

SAS and R handle this issue in different ways. In R, `as.factor()` can be applied within any model-fitting function. Parameterization of the covariate can be controlled as below. For SAS, some procedures accept a `class` statement to declare that a covariate is to be treated as categorical. The following procedures will not accept a class statement: `arima`, `catmod`, `factor`, `lifetest`, `loess`, `mcmc`, `nlin`, `nlmixed`, `reg`, and `varclus`. For these procedures, indicator (or "dummy") variables must be created in a data step, though this should be done with caution. The following procedures accept a class statement which applies reference cell or indicator variable coding (described as `contr.SAS()` in the R note below) to the listed variables: `proc anova`, `candisc`, `discrim`, `fmm`, `gam`, `glimmix`, `glm`, `mixed`, `quantreg`, `robustreg`, `stepdisc`, and `surveyreg`. The value used as the referent can often be controlled, usually as an `order` option to the controlling `proc`, as in 7.10.11. For these procedures, other parameterizations must be coded in a data step. The following procedures accept multiple parameterizations, using the syntax shown below for `proc logistic`: `proc genmod` (defaults to reference cell coding), `proc logistic` (defaults to effect coding), `proc phreg` (defaults to reference cell coding), and `proc surveylogistic` (defaults to effect coding).

SAS

```
proc logistic data=ds;
   class x1 (param=paramtype) x2 (param=paramtype);
   ...
run;
```

or

```
proc logistic data=ds;
   class x1 x2 / param=paramtype;
   ...
run;
```

Note: Available `paramtypes` include: 1) `orthpoly`, equivalent to `contr.poly()`; 2) `effect` (the default for `proc logistic` and `proc surveylogistic`), equivalent to `contr.sum()`; and 3) `ref`, equivalent to `contr.SAS()`. In addition, if the same parameterization is desired

for all of the categorical variables in the model, it can be added in a statement such as the second example. In this case, `param=glm` can be used to emulate the parameterization found in the other procedures which accept `class` statements and in `contr.SAS()` within R; this is the default for `proc genmod` and proc `phreg`.

R

```
ds = transform(ds, x1f = as.factor(x1))
mod1 = lm(y ~ x1f, contrasts=list(x1f="contr.SAS"), data=ds)
```

Note: The `as.factor()` function creates a factor object, akin to how SAS treats class variables in `proc glm`. The `contrasts` option for the `lm()` function specifies how the levels of that factor object should be used within the function. The `levels` option to the `factor()` function allows specification of the ordering of levels (the default is lexicographic). An example can be found in 6.6.

The specification of the design matrix for analysis of variance and regression models can be controlled using the `contrasts` option. Examples of options (for a factor with four equally spaced levels) are given below.

```
> contr.treatment(4)
  2 3 4
1 0 0 0
2 1 0 0
3 0 1 0
4 0 0 1
> contr.SAS(4)
  1 2 3
1 1 0 0
2 0 1 0
3 0 0 1
4 0 0 0
> contr.helmert(4)
  [,1] [,2] [,3]
1   -1   -1   -1
2    1   -1   -1
3    0    2   -1
4    0    0    3
```

```
> contr.poly(4)
              .L   .Q     .C
[1,] -0.671  0.5 -0.224
[2,] -0.224 -0.5  0.671
[3,]  0.224 -0.5 -0.671
[4,]  0.671  0.5  0.224
> contr.sum(4)
  [,1] [,2] [,3]
1    1    0    0
2    0    1    0
3    0    0    1
4   -1   -1   -1
```

See `options("contrasts")` for defaults, and `contrasts()` or `lm()` to apply a contrast function to a factor variable. Support for reordering factors is available within the `factor()` function.

6.1.5 Linear regression with no intercept

SAS

```
proc glm data=ds;
   model y = x1 ... xk / noint;
run;
```

Note: The `noint` option works with many `model` statements.

R

```
mod1 = lm(y ~ 0 + x1 + ... + xk, data=ds)
```

or

```
mod1 = lm(y ~ x1 + ... + xk - 1, data=ds)
```

6.1.6 Linear regression with interactions

Example: 6.6.2

SAS

```
proc glm data=ds;
   model y = x1 x2 x1*x2 x3 ... xk;
run;
```

or

```
proc glm data=ds;
   model y = x1|x2 x3 ... xk;
run;
```

Note: The `|` operator includes the product and all lower order terms, while the `*` operator includes only the specified interaction. So, for example, `model y = x1|x2|x3` and `model y = x1 x2 x3 x1*x2 x1*x3 x2*x3 x1*x2*x3` are equivalent statements. The syntax above also works with any covariates designated as categorical using the `class` statement (6.1.2). The `model` statement for many procedures accepts this syntax.

R

```
mod1 = lm(y ~ x1 + x2 + x1:x2 + x3 + ... + xk, data=ds)
```

or

```
lm(y ~ x1*x2 + x3 + ... + xk, data=ds)
```

Note: The `*` operator includes all lower order terms (in this case main effects), while the `:` operator includes only the specified interaction. So, for example, the commands `y ~ x1*x2*x3` and `y ~ x1 + x2 + x3 + x1:x2 + x1:x3 + x2:x3 + x1:x2:x3` are equivalent. The syntax also works with any covariates designated as categorical using the `as.factor()` command (see 6.1.2).

6.1.7 One-way analysis of variance

Example: 6.6.5

SAS

```
proc glm data=ds;
   class x;
   model y = x / solution;
run;
```

Note: The `solution` option to the `model` statement requests that the parameter estimates be displayed. Other procedures which fit ANOVA models include `proc anova` and `proc mixed`.

R

```
ds = transform(ds, xf=as.factor(x))
mod1 = aov(y ~ xf, data=ds)
summary(mod1)
anova(mod1)
```

Note: The `summary()` command can be used to provide details of the model fit. More information can be found using `help(summary.aov)`. Note that `summary.lm(mod1)` will display the regression parameters underlying the ANOVA model.

6.1.8 Analysis of variance with two or more factors

Example: 6.6.5

Interactions can be specified using the syntax introduced in 6.1.6 (see interaction plots, 8.5.2).

SAS

```
proc glm data=ds;
   class x1 x2;
   model y = x1 x2;
run;
```

Note: Other procedures which fit ANOVA models include `proc anova` and `proc mixed`.

R

```
aov(y ~ as.factor(x1) + as.factor(x2), data=ds)
```

6.2 Tests, contrasts, and linear functions of parameters

6.2.1 Joint null hypotheses: several parameters equal 0

As an example, consider testing the null hypothesis $H_0 : \beta_1 = \beta_2 = 0$.

SAS

```
proc reg data=ds;
   model ...;
   nametest: test x1=0, x2=0;
run;
```

Note: In the above, `nametest` is an arbitrary label which will appear in the output. Multiple `test` statements are permitted.

R

```
mod1 = lm(y ~ x1 + ... + xk, data=ds)
mod2 = lm(y ~ x3 + ... + xk, data=ds)
anova(mod2, mod1)
```

6.2.2 Joint null hypotheses: sum of parameters

As an example, consider testing the null hypothesis $H_0 : \beta_1 + \beta_2 = 1$.

SAS

```
proc reg data=ds;
   model ...;
   nametest: test x1 + x2 = 1;
run;
```

Note: The `test` statement is prefixed with an arbitrary `nametest` which will appear in the output. Multiple `test` statements are permitted.

R

```
mod1 = lm(y ~ x1 + ... + xk, data=ds)
covb = vcov(mod1)
coeff.mod1 = coef(mod1)
t = (coeff.mod1[2] + coeff.mod1[3] - 1)/
   sqrt(covb[2,2] + covb[3,3] + 2*covb[2,3])
pvalue = 2*(1-pt(abs(t), df=mod1$df))
```

Note: The `I()` function inhibits the interpretation of operators, to allow them to be used as arithmetic operators.

6.2.3 Tests of equality of parameters

Example: 6.6.7

As an example, consider testing the null hypothesis $H_0 : \beta_1 = \beta_2$.

SAS

```
proc reg data=ds;
   model ...;
   nametest: test x1=x2;
run;
```

Note: The `test` statement is prefixed with an arbitrary `nametest` which will appear in the output. Multiple `test` statements are permitted.

R

```
mod1 = lm(y ~ x1 + ... + xk, data=ds)
mod2 = lm(y ~ I(x1+x2) + ... + xk, data=ds)
anova(mod2, mod1)
```

or

```
library(gmodels)
estimable(mod1, c(0, 1, -1, 0, ..., 0))
```

or

```
mod1 = lm(y ~ x1 + ... + xk, data=ds)
covb = vcov(mod1)
coeff.mod1 = coef(mod1)
t = (coeff.mod1[2]-coeff.mod1[3])/sqrt(covb[2,2]+covb[3,3]-2*covb[2,3])
pvalue = 2*(1-pt(abs(t), mod1$df))
```

Note: The `I()` function inhibits the interpretation of operators, to allow them to be used as arithmetic operators. The `estimable()` function calculates a linear combination of the parameters. The more general R code below utilizes the same approach introduced in 6.2.1 for the specific test of $\beta_1 = \beta_2$ (different coding would be needed for other comparisons).

6.2.4 Multiple comparisons

Example: 6.6.6

SAS

```
proc glm data=ds;
   class x1;
   model y = x1;
   lsmeans x1 / pdiff adjust=tukey;
run;
```

Note: The `pdiff` option requests p-values for the hypotheses involving the pairwise comparison of means. The `adjust` option adjusts these p-values for multiple comparisons. Other options available through `adjust` include `bon` (for Bonferroni) and `dunnett`, among others. SAS `proc mixed` also has an `adjust` option for its `lsmeans` statement. A graphical presentation of significant differences among levels can be obtained with the `lines` option to the `lsmeans` statement, as shown in 6.6.6.

R

```
mod1 = aov(y ~ x, data=ds)
TukeyHSD(mod1, "x")
```

Note: The `TukeyHSD()` function takes an `aov` object as an argument and calculates the pairwise comparisons of all of the combinations of the factor levels of the variable `x` (see the `multcomp` package).

6.2.5 Linear combinations of parameters

Example: 6.6.7

It is often useful to calculate predicted values for particular covariate values. Here, we calculate the predicted value $E[Y|X_1 = 1, X_2 = 3] = \hat{\beta}_0 + \hat{\beta}_1 + 3\hat{\beta}_2$.

SAS

```
proc glm data=ds;
   model y = x1 ... xk;
   estimate 'label' intercept 1 x1 1 x2 3;
run;
```

Note: The `estimate` statement is used to calculate a linear combination of parameters (and associated standard errors). The optional quoted text is a label which will be printed with the estimated function.

R

```
mod1 = lm(y ~ x1 + x2, data=ds)
newdf = data.frame(x1=c(1), x2=c(3))
predict(mod1, newdf, se.fit=TRUE, interval="confidence")
```

or

```
library(gmodels)
estimable(mod1, c(0, 1, 3))
```

or

```
library(mosaic)
myfun = makeFun(mod1)
myfun(x1=1, x2=3)
```

Note: The `predict()` command in R can generate estimates at any combination of parameter values, as specified as a dataframe that is passed as an argument. More information on this function can be found using `help(predict.lm)`.

6.3 Model diagnostics

6.3.1 Predicted values

Example: 6.6.2

SAS

```
proc reg data=ds;
   model ...;
   output out=newds predicted=predicted_varname;
run;
```

or

```
proc glm data=ds;
   model ...;
   output out=newds predicted=predicted_varname;
run;
```

Note: The `output` statement creates a new dataset and specifies variables to be included, of which the predicted values are an example. Others can be found using the on-line help: Contents; SAS Products; SAS Procedures; REG; OUTPUT.

R

```
mod1 = lm(y ~ x, data=ds)
predicted.varname = predict(mod1)
```

Note: The command `predict()` operates on any `lm` object and by default generates a vector of predicted values. Similar commands retrieve other regression output.

6.3.2 Residuals

Example: 6.6.2

SAS

```
proc glm data=ds;
   model ...;
   output out=newds residual=residual_varname;
run;
```

or

```
proc reg data=ds;
   model ...;
   output out=newds residual=residual_varname;
run;
```

Note: The `output` statement creates a new dataset and specifies variables to be included, of which the residuals are an example. Others can be found using the on-line help: Contents; SAS Products; SAS Procedures; REG; OUTPUT.

R

```
mod1 = lm(y ~ x, data=ds)
residual.varname = residuals(mod1)
```

Note: The command `residuals()` operates on any `lm` object and generates a vector of residuals. Other functions for `aov`, `glm`, or `lme` objects exist (see, for example, `help(residuals.glm)`).

6.3.3 Standardized and Studentized residuals

Example: 6.6.2

Standardized residuals are calculated by dividing the ordinary residual (observed minus expected, $y_i - \hat{y}_i$) by an estimate of its standard deviation. Studentized residuals are calculated in a similar manner, where the predicted value and the variance of the residual are estimated from the model fit while excluding that observation. In SAS `proc glm` the standardized residual is requested by the `student` option, while the `rstudent` option generates the studentized residual.

SAS

```
proc glm data=ds;
   model ...;
   output out=newds student=standardized_resid_varname;
run;
```

or

```
proc reg data=ds;
   model ...;
   output out=newds rstudent=studentized_resid_varname;
run;
```

Note: The `output` statement creates a new dataset and specifies variables to be included, of which the Studentized residuals are an example. Both `proc reg` and `proc glm` include both types of residuals. Others can be found using the on-line help: Contents; SAS Products; SAS Procedures; REG; OUTPUT.

R

```
mod1 = lm(y ~ x, data=ds)
standardized.resid.varname = stdres(mod1)
studentized.resid.varname = studres(mod1)
```

Note: The `stdres()` and `studres()` functions operate on any `lm` object and generate a vector of studentized residuals (the former command includes the observation in the

calculation, while the latter does not). Similar commands retrieve other regression output (see `help(influence.measures)`).

6.3.4 Leverage

Example: 6.6.2

Leverage is defined as the diagonal element of the $(X(X^TX)^{-1}X^T)$ or "hat" matrix.

SAS

```
proc glm data=ds;
   model ...;
   output out=newds h=leverage_varname;
run;
```

or

```
proc reg data=ds;
   model ...;
   output out=newds h=leverage_varname;
run;
```

Note: The `output` statement creates a new dataset and specifies variables to be included, of which the leverage values are one example. Others can be found using the on-line help: Contents; SAS Products; SAS Procedures; REG; OUTPUT.

R

```
mod1 = lm(y ~ x, data=ds)
leverage.varname = hatvalues(mod1)
```

Note: The command `hatvalues()` operates on any `lm` object and generates a vector of leverage values. Similar commands can be utilized to retrieve other regression output (see `help(influence.measures)`).

6.3.5 Cook's D

Example: 6.6.2

Cook's distance (D) is a function of the leverage (see 6.3.4) and the residual. It is used as a measure of the influence of a data point in a regression model.

SAS

```
proc glm data=ds;
   model ...;
   output out=newds cookd=cookd_varname;
run;
```

or

```
proc reg data=ds;
   model ...;
   output out=newds cookd=cookd_varname;
run;
```

Note: The `output` statement creates a new dataset and specifies variables to be included, of which the Cook's distance values are an example. Others can be found using the on-line help: Contents; SAS Products; SAS Procedures; REG; OUTPUT.

R

```
mod1 = lm(y ~ x, data=ds)
cookd.varname = cooks.distance(mod1)
```

Note: The command `cooks.distance()` operates on any `lm` object and generates a vector of Cook's distance values. Similar commands retrieve other regression output.

6.3.6 DFFITS

Example: 6.6.2

DFFITS are a standardized function of the difference between the predicted value for the observation when it is included in the dataset and when (only) it is excluded from the dataset. They are used as an indicator of the observation's influence.

SAS

```
proc reg data=ds;
   model ...;
   output out=newds dffits=dffits_varname;
run;
```

or

```
proc glm data=ds;
   model ...;
   output out=newds dffits=dffits_varname;
run;
```

Note: The `output` statement creates a new dataset and specifies variables to be included, of which the DFFITS values are an example. Others can be found using the on-line help: Contents; SAS Products; SAS Procedures; REG; OUTPUT.

R

```
mod1 = lm(y ~ x, data=ds)
dffits.varname = dffits(mod1)
```

Note: The command `dffits()` operates on any `lm` object and generates a vector of DFFITS values. Similar commands retrieve other regression output.

6.3.7 Diagnostic plots

Example: 6.6.3

SAS

```
proc reg data=ds;
   model ...
   output out=newds predicted=pred_varname residual=resid_varname
          h=leverage_varname cookd=cookd_varname;
run;

proc gplot data=ds;
   plot resid_varname * pred_varname;
   plot resid_varname * leverage_varname;
run;
quit;
```

Note: To mimic R more closely, use a data step to generate the square root of residuals. QQ plots of residuals can be generated via `proc univariate`. It is not straightforward to plot lines of constant Cook's D on the residuals vs. leverage plot. The `reg` procedure will produce many diagnostic plots, as will `proc glm` with the `plots=diagnostics` option.

R

```
mod1 = lm(y ~ x, data=ds)
par(mfrow=c(2, 2)) # display 2 x 2 matrix of graphs
plot(mod1)
```

Note: The `plot.lm()` function (which is invoked when `plot()` is given a linear regression model as an argument) can generate six plots: 1) a plot of residuals against fitted values, 2) a Scale-Location plot of $\sqrt{(Y_i - \hat{Y}_i)}$ against fitted values, 3) a normal Q-Q plot of the

residuals, 4) a plot of Cook's distances (6.3.5) versus row labels, 5) a plot of residuals against leverages (6.3.4), and 6) a plot of Cook's distances against leverage/(1–leverage). The default is to plot the first three and the fifth. The `which` option can be used to specify a different set (see `help(plot.lm)`).

6.3.8 Heteroscedasticity tests

SAS

```
proc model data=ds;
   parms int slope;
   y = int + slope * x;
   fit y / pagan=(1 x) white;
run; quit;
```

Note: In SAS, White's test [192] and the Breusch–Pagan test [19] can be found in the `model` procedure in the `SAS/ETS` product. Note the atypical syntax of `proc model`.

R

```
library(lmtest)
bptest(y ~ x1 + ... + xk, data=ds)
```

Note: The `bptest()` function in the `lmtest` package performs the Breusch–Pagan test for heteroscedasticity [19].

6.4 Model parameters and results

6.4.1 Parameter estimates

Example: 6.6.2

SAS

```
ods output parameterestimates=newds;
proc glm data=ds;
   model ... / solution;
run;
```

or

```
proc reg data=ds outest=newds;
   model ...;
run;
```

Note: The `ods output` statement (A.7.1) can be used to save any piece of SAS output as a SAS dataset. The `outest` option is specific to `proc reg`, though many other procedures accept similar syntax.

R

```
mod1 = lm(y ~ x, data=ds)
coeff.mod1 = coef(mod1)
```

Note: The first element of the vector `coeff.mod1` is the intercept (assuming that a model with an intercept was fit).

6.4.2 Standardized regression coefficients

Standardized coefficients from a linear regression model are the parameter estimates obtained when the predictors and outcomes have been standardized to have a variance of 1 prior to model fitting.

SAS

```
proc reg data=ds;
   model ... / stb;
run;
```

R

```
library(QuantPsyc)
mod1 = lm(y ~ x)
lm.beta(lm1)
```

6.4.3 Standard errors of parameter estimates

See 6.4.9 (covariance matrix).

SAS

```
proc reg data=ds outest=newds;
   model .../ outseb ...;
run;
```

or

```
ods output parameterestimates=newds;
proc glm data=ds;
   model .../ solution;
run;
```

Note: The `ods output` statement (A.7.1) can be used to save any piece of SAS output as a SAS dataset.

R

```
mod1 = lm(y ~ x, data=ds)
sqrt(diag(vcov(mod1)))
```

or

```
coef(summary(mod1))[,2]
```

Note: The standard errors are the second column of the results from `coef()`.

6.4.4 Confidence interval for parameter estimates

Example: 6.6.2

SAS

```
proc reg data=ds;
   model ... / clb;
run;
```

R

```
mod1 = lm(y ~ x, data=ds)
confint(mod1)
```

6.4.5 Confidence limits for the mean

These are the lower (and upper) confidence limits for the mean of observations with the given covariate values, as opposed to the prediction limits for individual observations with those values (see prediction limits, 6.4.6).

SAS

```
proc glm data=ds;
   model ...;
   output out=newds lclm=lcl_mean_varname;
run;
```

or

```
proc reg data=ds;
   model ...;
   output out=newds lclm=lcl_mean_varname;
run;
```

Note: The `output` statement creates a new dataset and specifies output variables to be included, of which the lower confidence limit values are one example. The upper confidence limits can be generated using the `uclm` option to the `output` statement. Other possibilities can be found using the on-line help: Contents; SAS Products; SAS Procedures; REG; OUTPUT.

R

```
mod1 = lm(y ~ x, data=ds)
pred = predict(mod1, interval="confidence")
lcl.varname = pred[,2]
```

Note: The lower confidence limits are the second column of the results from `predict()`. To generate the upper confidence limits, the user would replace `lclm` with `uclm` for SAS and access the third column of the `predict()` object in R. The command `predict()` operates on any `lm()` object, and with these options generates confidence limit values. By default, the function uses the estimation dataset, but a separate dataset of values to be used to predict can be specified. The `panel=panel.lmbands` option from the `mosaic` package can be added to an `xyplot()` call to augment the scatterplot with confidence interval and prediction bands.

6.4.6 Prediction limits

These are the lower (and upper) prediction limits for "new" observations with the covariate values of subjects observed in the dataset, as opposed to confidence limits for the population mean (see confidence limits, 6.4.5).

SAS

```
proc glm data=ds;
   model ...;
   output out=newds lcl=lcl_varname;
run;
```

or

```
proc reg data=ds;
   model ...;
   output out=newds lcl=lcl_varname;
run;
```

Note: The `output` statement creates a new dataset and specifies variables to be included, of which the lower prediction limit values are an example. The upper limits can be requested with the `ucl` option to the `output` statement. Other possibilities can be found using the on-line help: Contents; SAS Products; SAS Procedures; REG; OUTPUT.

R

```
mod1 = lm(y ~ ..., data=ds)
pred.w.lowlim = predict(mod1, interval="prediction")[,2]
```

Note: This code saves the second column of the results from the `predict()` function into a vector. To generate the upper confidence limits, the user would access the third column of the `predict()` object in R. The command `predict()` operates on any `lm()` object, and with these options generates prediction limit values. By default, the function uses the estimation dataset, but a separate dataset of values to be used to predict can be specified.

6.4.7 R-squared

SAS

```
proc glm data=ds;
   model ...;
run;
```

Note: The coefficient of determination can be found as default output from `proc reg` or `proc glm`.

R

```
mod1 = lm(y ~ ..., data=ds)
summary(mod1)$r.squared
```

or

```
library(mosaic)
rsquared(mod1)
```

6.4.8 Design and information matrix

See 3.3 (matrices).

SAS

```
proc reg data=ds;
   model .../ xpx ...;
run;
```

or

```
proc glm data=ds;
   model .../ xpx ...;
run;
```

Note: A dataset containing the information ($X'X$) matrix can be created using `ODS` by specifying either `proc` statement or by adding the option `outsscp=newds` to the `proc reg` statement.

R

```
mod1 = lm(y ~ x1 + ... + xk, data=ds)
XpX = t(model.matrix(mod1)) %*% model.matrix(mod1)
```

or

```
X = cbind(rep(1, length(x1)), x1, x2, ..., xk)
XpX = t(X) %*% X
rm(X)
```

Note: The `model.matrix()` function creates the design matrix from a linear model object. Alternatively, this quantity can be built up using the `cbind()` function to glue together the design matrix `X`. Finally, matrix multiplication (3.3.6) and the transpose function are used to create the information ($X'X$) matrix.

6.4.9 Covariance matrix of parameter estimates

Example: 6.6.2

See 3.3 (matrices) and 6.4.3 (standard errors).

SAS

```
proc reg data=ds outest=newds covout;
run;
```

or

```
ods output covb=newds;
proc reg data=ds;
   model ... / covb ...;
```

R

```
mod1 = lm(y ~ x, data=ds)
vcov(mod1)
```

or

```
sumvals = summary(mod1)
covb = sumvals$cov.unscaled*sumvals$sigma^2
```

Note: Running `help(summary.lm)` provides details on return values.

6.4.10 Correlation matrix of parameter estimates

See 3.3 (matrices) and 6.4.3 (standard errors).

SAS

```
ods output covb=lmcov corrb=lmcorr ;
proc reg data=ds;
   model ... / covb corrb ...;
```

or

```
proc reg data=ds outest=newds covout;
   model ...;
   outest=outds;
run;
```

Note: the former can be used to generate either the covariance or correlation matrix, or both. The demonstrated `ODS` command will save the matrix or matrices as datasets. The latter uses the older method of generating SAS output as a dataset, but does not allow the generation of the correlation matrix.

R

```
mod1 = lm(y ~ x, data=ds)
mod1.cov = vcov(mod1)
mod1.cor = cov2cor(mod1.cov)
```

Note: The `cov2cor()` function is a convenient way to convert a covariance matrix into a correlation matrix.

6.5 Further resources

Accessible guides to linear regression in R and SAS can be found in [38] and [108], respectively. Cook [29] reviews regression diagnostics. Frank Harrell's `rms` (regression modeling strategies) package [63] features extensive support for regression modeling. The CRAN statistics for the social sciences task view provides an excellent overview of methods described here and in Chapter 7.

6.6 Examples

To help illustrate the tools presented in this chapter, we apply many of the entries to the HELP data. SAS and R code can be downloaded from `http://www.amherst.edu/~nhorton/sasr2/examples`.

We begin by reading in the dataset and keeping only the female subjects. In R, we prepare for later analyses by creating a version of `substance` as a factor variable (see 6.1.4).

```
proc import datafile='c:/book/help.dta'
   out=help_a dbms=dta;
run;

data help;
set help_a;
   if female;
run;
```

```
> options(digits=3)
> # read in Stata format
> library(foreign)
> ds = read.dta("help.dta", convert.underscore=FALSE)
> ds = transform(ds, sub = factor(substance,
    levels=c("heroin", "alcohol", "cocaine")))
> newds = subset(ds, female==1)
```

6.6.1 Scatterplot with smooth fit

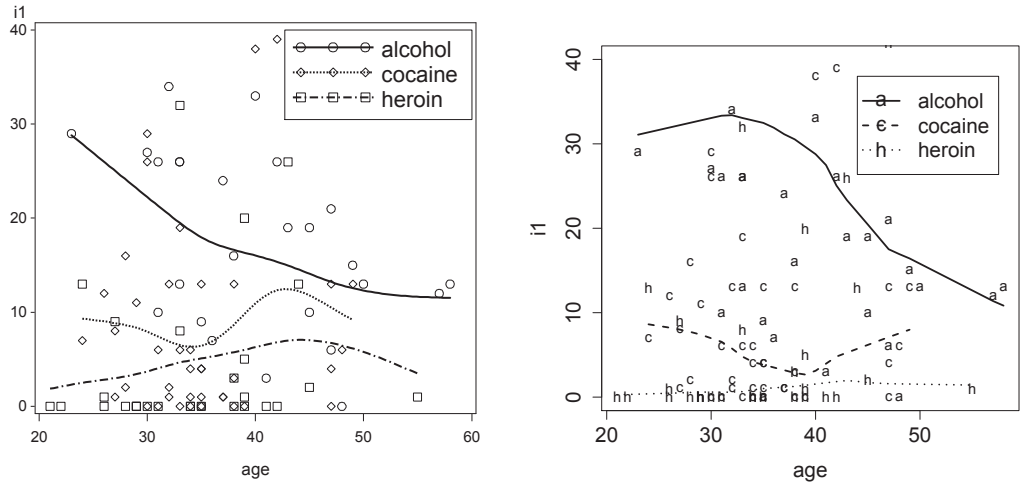
As a first step to help guide fitting a linear regression, we create a scatterplot (8.3.1) displaying the relationship between age and the number of alcoholic drinks consumed in the period before entering detox (variable name: `i1`), as well as primary substance of abuse (alcohol, cocaine, or heroin).

Figure 6.1 displays a scatterplot of observed values for `i1` (along with separate smooth fits by primary substance). To improve legibility, the plotting region is restricted to those with number of drinks between 0 and 40 (see plotting limits, 9.2.9).

```
axis1 order = (0 to 40 by 10) minor=none;
axis2 minor=none;
legend1 label=none value=(h=1.5) shape=symbol(10,1.2)
   down=3 position=(top right inside) frame mode=protect;
symbol1 v=circle i=sm70s c=black l=1 h=1.1 w=5;
symbol2 v=diamond i=sm70s c=black l=33 h=1.1 w=5;
symbol3 v=square i=sm70s c=black l=8 h=1.1 w=5;
proc gplot data=help;
   plot i1*age = substance / vaxis=axis1 haxis=axis2 legend=legend1;
run; quit;
```

```
> with(newds, plot(age, i1, ylim=c(0,40), type="n", cex.lab=1.4,
    cex.axis=1.4))
> with(newds, points(age[substance=="alcohol"], i1[substance=="alcohol"],
    pch="a"))
> with(newds, lines(lowess(age[substance=="alcohol"],
    i1[substance=="alcohol"]), lty=1, lwd=2))
> with(newds, points(age[substance=="cocaine"], i1[substance=="cocaine"],
    pch="c"))
> with(newds, lines(lowess(age[substance=="cocaine"],
    i1[substance=="cocaine"]), lty=2, lwd=2))
> with(newds, points(age[substance=="heroin"], i1[substance=="heroin"],
    pch="h"))
> with(newds, lines(lowess(age[substance=="heroin"],
    i1[substance=="heroin"]), lty=3, lwd=2))
> legend(44, 38, legend=c("alcohol", "cocaine", "heroin"), lty=1:3,
    cex=1.4, lwd=2, pch=c("a", "c", "h"))
```

The `pch` option to the `legend()` command can be used to insert plot symbols in R legends (Figure 6.1 displays the different line styles).



(a) SAS (b) R

Figure 6.1: Scatterplot of observed values for age and I1 (plus smoothers by substance)

Not surprisingly, Figure 6.1 suggests that there is a dramatic effect of primary substance, with alcohol users drinking more than others. There is some indication of an interaction with age. It is important to note that SAS uses only the points displayed (i.e., within the specified axes) when smoothing, while R uses all points, regardless of whether they appear in the plot.

6.6.2 Linear regression with interaction

Next we fit a linear regression model (6.1.1) for the number of drinks as a function of age, substance, and their interaction (6.1.6). To assess the need for the interaction, we use the F test from the Type III sums of squares in SAS. In R, we additionally fit the model with

no interaction and use the `anova()` function to compare the models (the `drop1()` function could also be used). To save space, some results of `proc glm` have been suppressed using the `ods select` statement (see A.7).

```
options ls=74;  /* reduces width of output to make it fit in gray area */
ods select overallanova modelanova parameterestimates;
proc glm data=help;
class substance;
   model i1 = age substance age * substance / solution;
   output out=helpout cookd=cookd_ch4 dffits=dffits_ch4
   student=sresids_ch4 residual=resid_ch4
   predicted=pred_ch4 h=lev_ch4;
run; quit;
ods select all;
```

```
The GLM Procedure

Dependent Variable: i1   i1

                                  Sum of
Source                     DF       Squares   Mean Square  F Value  Pr > F

Model                       5   12275.17570    2455.03514     9.99  <.0001

Error                     101   24815.36635     245.69670

Corrected Total           106   37090.54206
```

```
The GLM Procedure

Dependent Variable: i1   i1

Source                     DF     Type I SS   Mean Square  F Value  Pr > F

age                         1     384.75504     384.75504     1.57  0.2137
substance                   2   10509.56444    5254.78222    21.39  <.0001
age*substance               2    1380.85622     690.42811     2.81  0.0649


Source                     DF   Type III SS   Mean Square  F Value  Pr > F

age                         1     27.157727     27.157727     0.11  0.7402
substance                   2   3318.992822   1659.496411     6.75  0.0018
age*substance               2   1380.856222    690.428111     2.81  0.0649
```

```
The GLM Procedure

Dependent Variable: i1   i1

                                          Standard
Parameter                    Estimate        Error  t Value  Pr > |t|

Intercept                -7.77045212 B   12.87885672    -0.60    0.5476
age                       0.39337843 B    0.36221749     1.09    0.2801
substance     alcohol    64.88044165 B   18.48733701     3.51    0.0007
substance     cocaine    13.02733169 B   19.13852222     0.68    0.4976
substance     heroin      0.00000000 B     .              .       .
age*substance alcohol    -1.11320795 B    0.49135408    -2.27    0.0256
age*substance cocaine    -0.27758561 B    0.53967749    -0.51    0.6081
age*substance heroin      0.00000000 B     .              .       .
```

```
> options(show.signif.stars=FALSE)
> lm1 = lm(i1 ~ sub * age, data=newds)
> lm2 = lm(i1 ~ sub + age, data=newds)
> anova(lm2, lm1)

Analysis of Variance Table

Model 1: i1 ~ sub + age
Model 2: i1 ~ sub * age
  Res.Df   RSS Df Sum of Sq    F Pr(>F)
1    103 26196
2    101 24815  2      1381 2.81  0.065

> summary.aov(lm1)

             Df Sum Sq Mean Sq F value  Pr(>F)
sub           2  10810    5405   22.00 1.2e-08
age           1     84      84    0.34   0.559
sub:age       2   1381     690    2.81   0.065
Residuals   101  24815     246
```

There is some indication of a borderline significant interaction between age and substance group (p=0.065).

In SAS, the `ods output` statement can be used to save any printed result as a SAS dataset. In the following code, all printed output from `proc glm` is suppressed, but the parameter estimates are saved as a SAS dataset, then printed using `proc print`. In addition, various diagnostics are saved via the the `output` statement.

```
ods select none;
ods output parameterestimates=helpmodelanova;
proc glm data=help;
class substance;
model i1 = age|substance / solution;
output out=helpout cookd=cookd_ch4 dffits=dffits_ch4
   student=sresids_ch4 residual=resid_ch4
   predicted=pred_ch4 h=lev_ch4;
run; quit;
ods select all;
```

```
proc print data=helpmodelanova;
   var parameter estimate stderr tvalue probt;
   format _numeric_ 6.3;
run;

Obs    Parameter                Estimate    StdErr    tValue     Probt

 1     Intercept                 -7.770     12.879    -0.603     0.548
 2     age                        0.393      0.362     1.086     0.280
 3     substance     alcohol     64.880     18.487     3.509     0.001
 4     substance     cocaine     13.027     19.139     0.681     0.498
 5     substance     heroin       0.000       .         .         .
 6     age*substance alcohol     -1.113      0.491    -2.266     0.026
 7     age*substance cocaine     -0.278      0.540    -0.514     0.608
 8     age*substance heroin       0.000       .         .         .
```

In R, the `summary()` function provides similar information.

```
> summary(lm1)

Call:
lm(formula = i1 ~ sub * age, data = newds)

Residuals:
   Min     1Q Median     3Q    Max
-31.92  -8.25  -4.18   3.58  49.88

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)     -7.770     12.879   -0.60  0.54763
subalcohol      64.880     18.487    3.51  0.00067
subcocaine      13.027     19.139    0.68  0.49763
age              0.393      0.362    1.09  0.28005
subalcohol:age  -1.113      0.491   -2.27  0.02561
subcocaine:age  -0.278      0.540   -0.51  0.60813

Residual standard error: 15.7 on 101 degrees of freedom
Multiple R-squared:  0.331,        Adjusted R-squared:  0.298
F-statistic: 9.99 on 5 and 101 DF,  p-value: 8.67e-08
```

```
> confint(lm1)

                 2.5 %  97.5 %
(Intercept)    -33.319  17.778
subalcohol      28.207 101.554
subcocaine     -24.938  50.993
age             -0.325   1.112
subalcohol:age  -2.088  -0.138
subcocaine:age  -1.348   0.793
```

It may also be useful to produce the table in LaTeX format. In SAS, we can do this using the `latex` destination for the `ODS` system. When compiled, the resulting table is displayed in Figure 6.2.

```
ods latex file="c:\book\table.tex" style=styles.printer;
proc print data = helpmodelanova; run;
ods latex close;
```

Obs	Dependent	Parameter	Estimate	Biased	StdErr	tValue	Probt
1	I1	Intercept	5.31216647	1	6.87095132	0.77	0.4399
2	I1	AGE	0.10665333	1	0.19987433	0.53	0.5939
3	I1	SUBSTANCE alcohol	2.60085179	1	9.66168958	0.27	0.7879
4	I1	SUBSTANCE cocaine	10.45473101	1	10.21750929	1.02	0.3068
5	I1	SUBSTANCE heroin	0.00000000	1	.	.	.
6	I1	AGE*SUBSTANCE alcohol	0.45042340	1	0.26525085	1.70	0.0902
7	I1	AGE*SUBSTANCE cocaine	−0.21204498	1	0.29373772	−0.72	0.4707
8	I1	AGE*SUBSTANCE heroin	0.00000000	1	.	.	.

Figure 6.2: SAS table produced with `latex` destination in `ODS`

In R, we can use the `xtable` package to display the regression results in LaTeX, as shown in Table 6.1.

```
> library(xtable)
> lmtab = xtable(lm1, digits=c(0,3,3,2,4), label="better",
    caption="Formatted results using the {\\tt xtable} package")
> print(lmtab)  # output the LaTeX
```

Table 6.1: Formatted results using the `xtable` package

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	-7.770	12.879	-0.60	0.5476
subalcohol	64.880	18.487	3.51	0.0007
subcocaine	13.027	19.139	0.68	0.4976
age	0.393	0.362	1.09	0.2801
subalcohol:age	-1.113	0.491	-2.27	0.0256
subcocaine:age	-0.278	0.540	-0.51	0.6081

There are many quantities of interest stored in the linear model object `lm1`, and these can be viewed or extracted for further use.

```
> names(summary(lm1))

 [1] "call"          "terms"         "residuals"     "coefficients"
 [5] "aliased"       "sigma"         "df"            "r.squared"
 [9] "adj.r.squared" "fstatistic"    "cov.unscaled"

> summary(lm1)$sigma

[1] 15.7
```

```
> names(lm1)

 [1] "coefficients"  "residuals"     "effects"       "rank"
 [5] "fitted.values" "assign"        "qr"            "df.residual"
 [9] "contrasts"     "xlevels"       "call"          "terms"
[13] "model"
```

```
> coef(lm1)

   (Intercept)     subalcohol     subcocaine            age subalcohol:age
        -7.770         64.880         13.027          0.393         -1.113
subcocaine:age
        -0.278
```

```
> vcov(lm1)

               (Intercept) subalcohol subcocaine    age subalcohol:age
(Intercept)         165.86    -165.86    -165.86 -4.548          4.548
subalcohol         -165.86     341.78     165.86  4.548         -8.866
subcocaine         -165.86     165.86     366.28  4.548         -4.548
age                  -4.55       4.55       4.55  0.131         -0.131
subalcohol:age        4.55      -8.87      -4.55 -0.131          0.241
subcocaine:age        4.55      -4.55     -10.13 -0.131          0.131
               subcocaine:age
(Intercept)             4.548
subalcohol             -4.548
subcocaine            -10.127
age                    -0.131
subalcohol:age          0.131
subcocaine:age          0.291
```

6.6.3 Regression diagnostics

Assessing the model is an important part of any analysis. We begin by examining the residuals (6.3.2). First, we calculate the quantiles of their distribution (5.1.4), then display the smallest residual.

```
options ls=74;
proc means data=helpout min q1 median q3 max maxdec=2;
   var resid_ch4;
run;

The MEANS Procedure

                    Analysis Variable : resid_ch4

                     Lower                          Upper
     Minimum       Quartile         Median       Quartile         Maximum
------------------------------------------------------------------------
      -31.92          -8.31          -4.18           3.69           49.88
------------------------------------------------------------------------
```

```
> newds = transform(newds, pred = fitted(lm1))
> newds = transform(newds, resid = residuals(lm1))
> with(newds, quantile(resid))

    0%    25%    50%    75%   100%
-31.92  -8.25  -4.18   3.58  49.88
```

We could examine the output, then condition to find the value of the residual that is less than −31. Instead the dataset can be sorted so the smallest observation is first and then print one observation.

```
proc sort data=helpout;
   by resid_ch4;
run;

proc print data=helpout (obs=1);
   var id age i1 substance pred_ch4 resid_ch4;
run;

                                                      resid_
Obs     id    age    i1    substance    pred_ch4       ch4

  1    325     35     0     alcohol      31.9160    -31.9160
```

One way to print the largest value is to sort the dataset in the reverse order (2.3.10), then print just the first observation.

```
proc sort data=helpout;
   by descending resid_ch4;
run;

proc print data=helpout (obs=1);
   var id age i1 substance pred_ch4 resid_ch4;
run;

                                                    resid_
Obs    id    age    i1    substance    pred_ch4      ch4

  1     9     50    71     alcohol      21.1185    49.8815
```

```
> tmpds = with(newds,
     data.frame(id, age, i1, sub, pred, resid, rstandard(lm1)))
> subset(tmpds, resid==max(resid))

  id age i1     sub pred resid rstandard.lm1.
9  9  50 71 alcohol 21.1  49.9           3.32
```

Graphical tools are one of the best ways to examine residuals. Figure 6.3 displays the default diagnostic plots (6.3) from the model (for R) and the Q-Q plot generated from the saved diagnostics (for SAS).

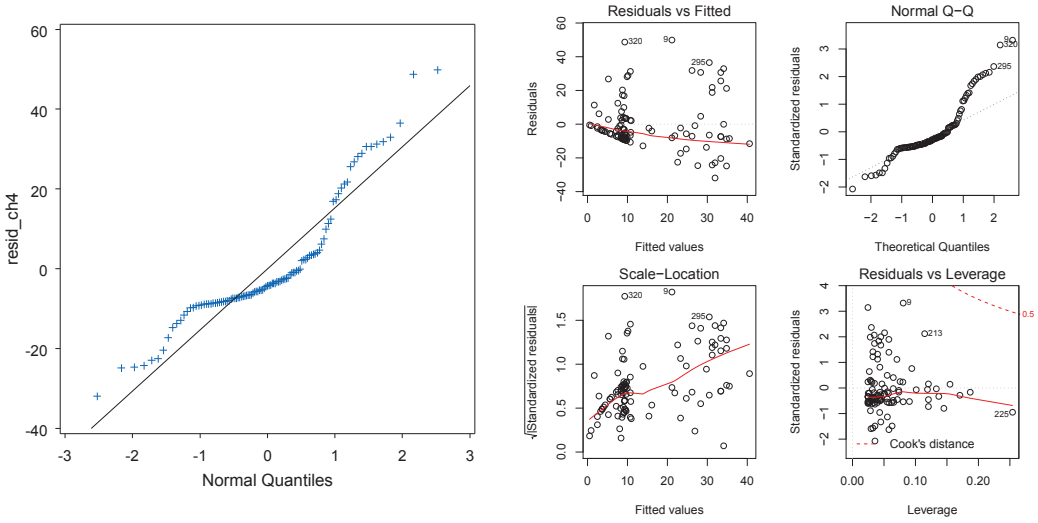
Sometimes in SAS it is necessary to clear out old graphics settings. This is easiest to do with the `goptions reset=all` statement (9.2.8).

```
goptions reset=all;
```

```
ods select univar;
proc univariate data=helpout;
   qqplot resid_ch4 / normal(mu=est sigma=est color=black);
run;
ods select all;
```

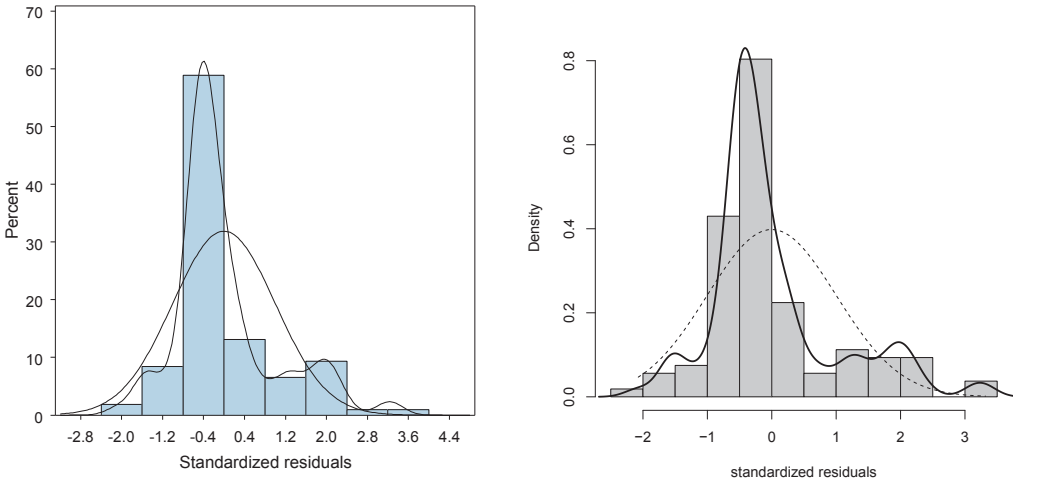
```
> oldpar = par(mfrow=c(2, 2), mar=c(4, 4, 2, 2)+.1)
> plot(lm1)
> par(oldpar)
```

In SAS, we get assorted diagnostic plots by default, but here we demonstrate a manual approach using the previously saved diagnostics. Figure 6.4 displays the empirical density of the standardized residuals, along with an overlaid normal density. The assumption that the residuals are approximately Gaussian does not appear to be tenable.



(a) SAS (b) R

Figure 6.3: Q-Q plot from SAS, default diagnostics from R



(a) SAS (b) R

Figure 6.4: Empirical density of residuals, with superimposed normal density

```
axis1 label=("Standardized residuals");
ods select "Histogram 1";
proc univariate data=helpout;
   var sresids_ch4;
   histogram sresids_ch4 / normal(mu=est sigma=est color=black)
      kernel(color=black) haxis=axis1;
run;
ods select all;
```

```
> library(MASS)
> std.res = rstandard(lm1)
> hist(std.res, breaks=seq(-2.5, 3.5, by=.5), main="",
     xlab="standardized residuals", col="gray80", freq=FALSE)
> lines(density(std.res), lwd=2)
> xvals = seq(from=min(std.res), to=max(std.res), length=100)
> lines(xvals, dnorm(xvals, mean(std.res), sd(std.res)), lty=2)
```

The residual plots indicate some potentially important departures from model assumptions, and further exploration should be undertaken.

6.6.4 Fitting the regression model separately for each value of another variable

One common task is to perform identical analyses in several groups. Here, as an example, we consider separate linear regressions for each substance abuse group. In SAS, we show only the parameter estimates, using `ODS`.

```
ods select none;
proc sort data=help;
   by substance;
run;

ods output parameterestimates=helpsubstparams;
proc glm data=help;
   by substance;
   model i1 = age / solution;
run;
ods select all;
```

```
options ls=74;
proc print data=helpsubstparams;
run;

Obs substance Dependent Parameter     Estimate       StdErr  tValue  Probt

 1   alcohol     i1     Intercept  57.10998953  18.00474934    3.17 0.0032
 2   alcohol     i1     age        -0.71982952   0.45069028   -1.60 0.1195
 3   cocaine     i1     Intercept   5.25687957  11.52989056    0.46 0.6510
 4   cocaine     i1     age         0.11579282   0.32582541    0.36 0.7242
 5   heroin      i1     Intercept  -7.77045212   8.59729637   -0.90 0.3738
 6   heroin      i1     age         0.39337843   0.24179872    1.63 0.1150
```

For R, a matrix of the correct size is created, then a `for` loop is run for each unique value of the grouping variable.

```
> uniquevals = unique(newds$substance)
> numunique = length(uniquevals)
> formula = as.formula(i1 ~ age)
> p = length(coef(lm(formula, data=newds)))
> res = matrix(rep(0, numunique*p), p, numunique)
> for (i in 1:length(uniquevals)) {
     res[,i] = coef(lm(formula,
        data=subset(newds, substance==uniquevals[i])))
  }
> rownames(res) = c("intercept","slope")
> colnames(res) = uniquevals
> res

          heroin cocaine alcohol
intercept -7.770   5.257   57.11
slope      0.393   0.116   -0.72
```

6.6.5 Two-way ANOVA

Is there a statistically significant association between gender and substance abuse group with depressive symptoms? In SAS, we can make an interaction plot (8.5.2) by hand, as below, or `proc glm` will make a similar one automatically.

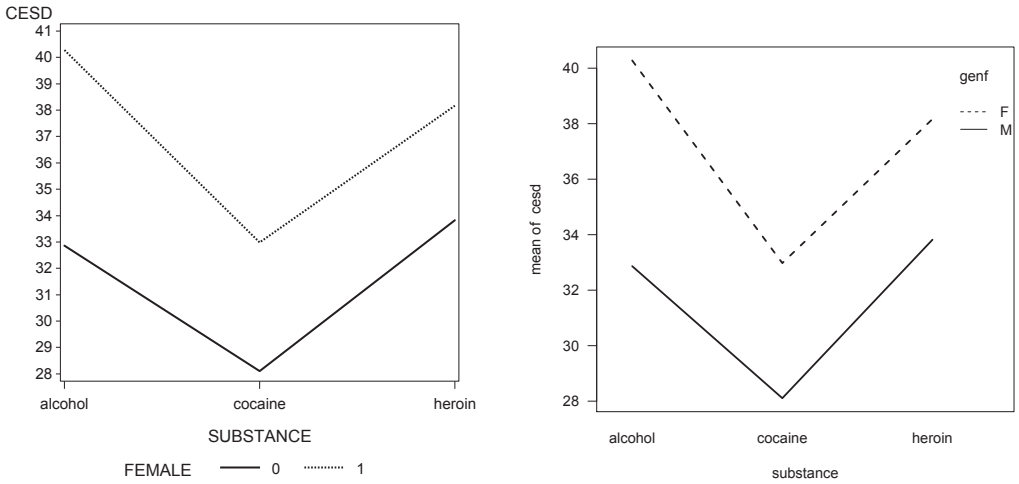
```
libname k 'c:/book';

proc sort data=k.help;
   by substance female;
run;

ods select none;
proc means data=k.help;
   by substance female;
   var cesd;
   output out=helpmean mean=;
run;
ods select all;
```

```
axis1 minor=none;
symbol1 i=j v=none l=1 c=black w=5;
symbol2 i=j v=none l=2 c=black w=5;
proc gplot data=helpmean;
   plot cesd*substance = female / haxis=axis1 vaxis=axis1;
run; quit;
```

R has a function `interaction.plot()` to carry out this task. Figure 6.5 displays an interaction plot for CESD as a function of substance group and gender.

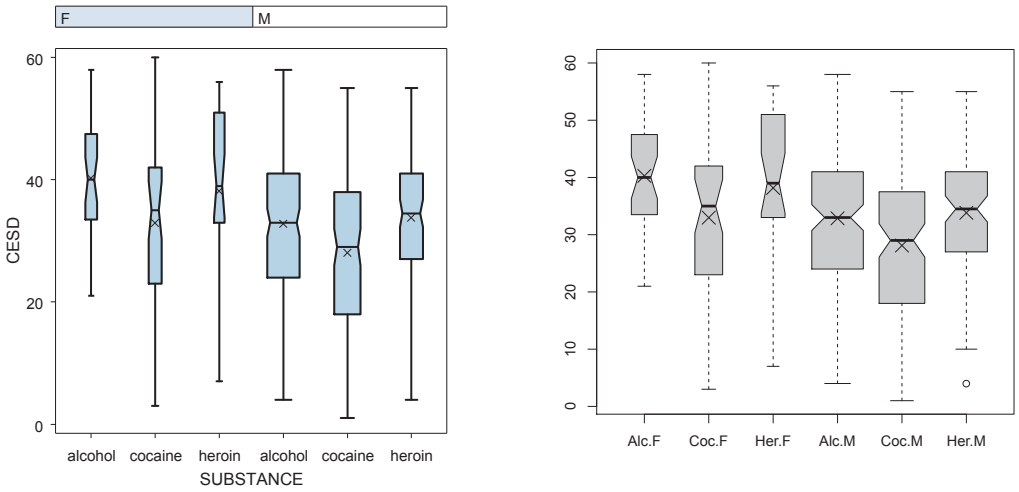
```
> ds = transform(ds, genf = as.factor(ifelse(female, "F", "M")))
> with(ds, interaction.plot(substance, genf, cesd,
     xlab="substance", las=1, lwd=2))
```

There are indications of large effects of gender and substance group, but little suggestion of interaction between the two. The same conclusion is reached in Figure 6.6, which displays boxplots by substance group and gender.



(a) SAS (b) R

Figure 6.5: Interaction plot of CESD as a function of substance group and gender



(a) SAS (b) R

Figure 6.6: Boxplot of CESD as a function of substance group and gender

```
data h2; set k.help;
   if female eq 1 then sex='F';
   else sex='M';
run;
proc sort data=h2; by sex; run;

symbol1 v='x' c=black;
proc boxplot data=h2;
   plot cesd * substance(sex) / notches boxwidthscale=1;
run;
```

```
> library(memisc)
> ds = transform(ds, subs = cases(
     "Alc" = substance=="alcohol",
     "Coc" = substance=="cocaine",
     "Her" = substance=="heroin"))
> boxout = with(ds,
     boxplot(cesd ~ subs + genf, notch=TRUE, varwidth=TRUE,
        col="gray80"))
> boxmeans = with(ds, tapply(cesd, list(subs, genf), mean))
> points(seq(boxout$n), boxmeans, pch=4, cex=2)
```

The width of each box is proportional to the size of the sample, with the notches denoting confidence intervals for the medians and X's marking the observed means. Next, we proceed to formally test whether there is a significant interaction through a two-way analysis of variance (6.1.8). In SAS, the Type III sums of squares table can be used to assess the interaction; we restrict output to this table to save space. In R we fit models with and without an interaction, and then compare the results. We also construct the likelihood ratio test manually.

```
options ls=74;
ods select modelanova;
proc glm data=k.help;
   class female substance;
   model cesd = female substance female*substance / ss3;
run;

The GLM Procedure

Dependent Variable: CESD

Source                    DF   Type III SS   Mean Square  F Value  Pr > F

FEMALE                     1   2463.232928   2463.232928    16.84  <.0001
SUBSTANCE                  2   2540.208432   1270.104216     8.69  0.0002
FEMALE*SUBSTANCE           2    145.924987     72.962494     0.50  0.6075
```

```
> aov1 = aov(cesd ~ sub * genf, data=ds)
> aov2 = aov(cesd ~ sub + genf, data=ds)
> resid = residuals(aov2)
> anova(aov2, aov1)

Analysis of Variance Table

Model 1: cesd ~ sub + genf
Model 2: cesd ~ sub * genf
  Res.Df   RSS Df Sum of Sq   F Pr(>F)
1    449 65515
2    447 65369  2       146 0.5   0.61
```

```
> options(digits=6)
> logLik(aov1)

'log Lik.' -1768.92 (df=7)

> logLik(aov2)

'log Lik.' -1769.42 (df=5)

> lldiff = logLik(aov1)[1] - logLik(aov2)[1]
> lldiff

[1] 0.505055

> 1 - pchisq(2*lldiff, df=2)

[1] 0.603472

> options(digits=3)
```

```
> summary(aov2)

             Df Sum Sq Mean Sq F value  Pr(>F)
sub           2   2704    1352    9.27 0.00011
genf          1   2569    2569   17.61 3.3e-05
Residuals   449  65515     146
```

There is little evidence (p=0.61) of an interaction, so this term can be dropped. For SAS, this means estimating the reduced model.

```
options ls=74; /* stay in gray box */
ods select overallanova parameterestimates;
proc glm data=k.help;
   class female substance;
   model cesd = female substance / ss3 solution;
run;
```

```
The GLM Procedure

Dependent Variable: CESD

                                   Sum of
Source                      DF       Squares   Mean Square  F Value  Pr > F

Model                        3    5273.13263    1757.71088    12.05  <.0001

Error                      449   65515.35744     145.91394

Corrected Total            452   70788.49007
```

```
The GLM Procedure

Dependent Variable: CESD

                                          Standard
Parameter               Estimate             Error   t Value   Pr > |t|

Intercept             39.13070331 B     1.48571047     26.34     <.0001
FEMALE    0           -5.61922564 B     1.33918653     -4.20     <.0001
FEMALE    1            0.00000000 B      .               .         .
SUBSTANCE alcohol     -0.28148966 B     1.41554315     -0.20     0.8425
SUBSTANCE cocaine     -5.60613722 B     1.46221461     -3.83     0.0001
SUBSTANCE heroin       0.00000000 B      .               .         .
```

The model was already fit in R to allow assessment of the interaction.

```
> aov2

Call:
   aov(formula = cesd ~ sub + genf, data = ds)

Terms:
                  sub  genf Residuals
Sum of Squares   2704  2569     65515
Deg. of Freedom     2     1       449

Residual standard error: 12.1
Estimated effects may be unbalanced
```

If results with the same referent categories used by SAS are desired, the default R design matrix (see 6.1.4) can be changed and the model re-fit.

```
> contrasts(ds$sub) = contr.SAS(3)
> aov3 = lm(cesd ~ sub + genf, data=ds)
> summary(aov3)

Call:
lm(formula = cesd ~ sub + genf, data = ds)

Residuals:
   Min     1Q Median     3Q    Max
-32.13  -8.85   1.09   8.48  27.09

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)    33.52       1.38   24.22  < 2e-16
sub1            5.61       1.46    3.83  0.00014
sub2            5.32       1.34    3.98  8.1e-05
genfM          -5.62       1.34   -4.20  3.3e-05

Residual standard error: 12.1 on 449 degrees of freedom
Multiple R-squared:  0.0745,        Adjusted R-squared:  0.0683
F-statistic:   12 on 3 and 449 DF,  p-value: 1.35e-07
```

The AIC criteria (7.8.3) can also be used to compare models. In SAS it is available in `proc reg` and `proc mixed`. Here we use `proc mixed`, omitting other output.

```
ods select fitstatistics;
proc mixed data=k.help method=ml;
   class female substance;
   model cesd = female|substance;
run; quit;

The Mixed Procedure

           Fit Statistics

-2 Log Likelihood              3537.8
AIC (smaller is better)        3551.8
AICC (smaller is better)       3552.1
BIC (smaller is better)        3580.6
```

```
ods select fitstatistics;
proc mixed data=k.help method=ml;
   class female substance;
   model cesd = female substance;
run; quit;
ods select all;

The Mixed Procedure

           Fit Statistics

-2 Log Likelihood              3538.8
AIC (smaller is better)        3548.8
AICC (smaller is better)       3549.0
BIC (smaller is better)        3569.4
```

```
> AIC(aov1)

[1] 3552

> AIC(aov2)

[1] 3549
```

The AIC criterion also suggests that the model without the interaction is most appropriate.

6.6.6 Multiple comparisons

We can also carry out multiple comparison (6.2.4) procedures to test each of the pairwise differences between substance abuse groups. In SAS this utilizes the `lsmeans` statement within `proc glm`.

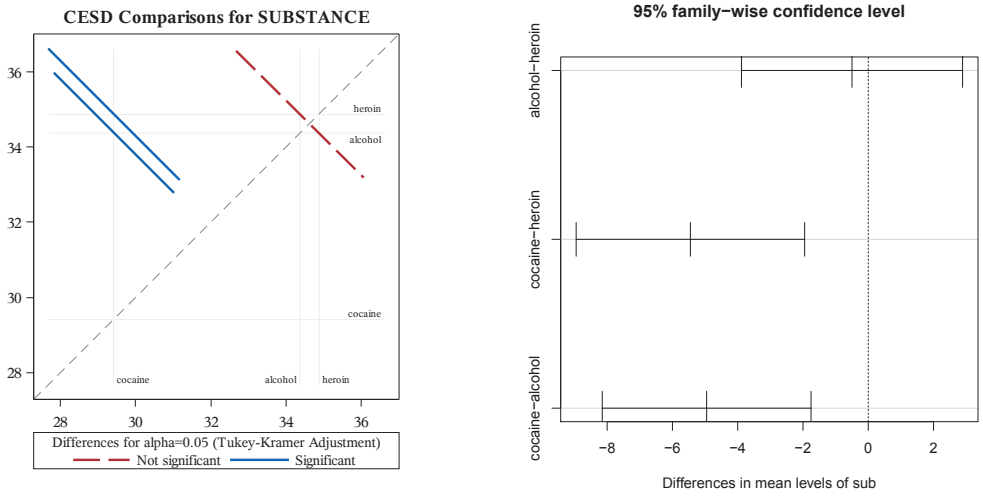
```
ods select diff lsmeandiffcl lsmlines diffplot;
proc glm data=k.help;
   class substance;
   model cesd = substance;
   lsmeans substance / pdiff adjust=tukey cl lines;
run; quit;
ods select all;
```

```
The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer

   Least Squares Means for effect SUBSTANCE
     Pr > |t| for H0: LSMean(i)=LSMean(j)

           Dependent Variable: CESD

i/j              1             2             3

   1                       0.0009        0.9362
   2        0.0009                        0.0008
   3        0.9362        0.0008
```

```
The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer

      Least Squares Means for Effect SUBSTANCE

             Difference         Simultaneous 95%
                Between      Confidence Limits for
i    j            Means       LSMean(i)-LSMean(j)

1    2         4.951829        1.753296     8.150362
1    3        -0.498086       -3.885335     2.889162
2    3        -5.449915       -8.950037    -1.949793
```

```
The GLM Procedure
Least Squares Means
Adjustment for Multiple Comparisons: Tukey-Kramer

Tukey-Kramer Comparison Lines for Least Squares Means of SUBSTANCE

LS-means with the same letter are not significantly different.

          CESD                 LSMEAN
        LSMEAN    SUBSTANCE    Number

A     34.87097    heroin            3
A
A     34.37288    alcohol           1

B     29.42105    cocaine           2
```

The above output demonstrates the results of the `lines` option using the `lsmeans` statement. The letter `A` shown on the left connecting the `heroin` and `alcohol` substances implies that there is not a statistically significant difference between these two groups. Since the `cocaine` substance has the letter `B` and no other group has one, the cocaine group is significantly different from each of the other groups. If instead the `cocaine` and `alcohol` substances **both** had a letter `B` attached, while the `heroin` and `alcohol` substances retained the letter `A` they have in the actual output, only the heroin and cocaine groups would differ significantly, while the alcohol group would differ from neither. This presentation becomes



(a) SAS (b) R

Figure 6.7: Pairwise comparisons

particularly useful as the number of groups increases. A graphical version called a `diffplot` is also produced; it is shown in Figure 6.7.

In R, we use the `TukeyHSD()` function.

```
> mult = TukeyHSD(aov(cesd ~ sub, data=ds), "sub")
> mult

  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = cesd ~ sub, data = ds)

$sub
                   diff   lwr   upr p adj
alcohol-heroin   -0.498 -3.89  2.89 0.936
cocaine-heroin   -5.450 -8.95 -1.95 0.001
cocaine-alcohol -4.952 -8.15 -1.75 0.001
```

The alcohol group and heroin group both have significantly higher CESD scores than the cocaine group, but the alcohol and heroin groups do not significantly differ from each other (95% CI for the difference ranges from −3.9 to 2.9). Figure 6.7 provides a graphical display of the pairwise comparisons.

```
> plot(mult)
```

6.6.7 Contrasts

We can also fit contrasts (6.2.3) to test hypotheses involving multiple parameters. In this case, we can compare the CESD scores for the alcohol and heroin groups to the cocaine group. In SAS, to allow checking the contrast, we use the `e` option to the `estimate` statement.

```
ods select contrastcoef estimates;
proc glm data=k.help;
   class female substance;
   model cesd = female substance;
   output out=outanova residual=resid_ch4anova;
   estimate 'A+H = C?' substance 1 -2 1 / e;
run; quit;
ods select all;
```

```
The GLM Procedure

Coefficients for Estimate A+H = C?

                            Row 1

Intercept                       0

FEMALE    0                     0
FEMALE    1                     0

SUBSTANCE alcohol               1
SUBSTANCE cocaine              -2
SUBSTANCE heroin                1
```

```
The GLM Procedure

Dependent Variable: CESD

                                        Standard
Parameter                 Estimate          Error   t Value   Pr > |t|

A+H = C?                10.9307848     2.42008987      4.52     <.0001
```

```
> library(gmodels)
> levels(ds$sub)

[1] "heroin"  "alcohol" "cocaine"

> fit.contrast(aov2, "sub", c(1,1,-2), conf.int=0.95 )

                 Estimate Std. Error t value Pr(>|t|) lower CI upper CI
sub c=( 1 1 -2 )     10.9       2.42    4.52 8.04e-06     6.17     15.7
```

As expected from the interaction plot (Figure 6.5), there is a statistically significant difference in this 1 degree of freedom comparison (p <0.0001).