

9

Checking the models II: the other three assumptions

9.1 Homogeneity of variance

Plotting the residuals against the fitted values is one of the standard techniques introduced in the main text to check the assumption of homogeneity of variance. It is illustrated here with the *diets* dataset. We use the standardised residuals rather than raw residuals for these model checking plots, as they are easier to interpret (see main text). Standardised residuals are referred to as type 2 in command language.

MINITAB COMMANDS FOR BOX 9.1 Weight change with diet

Commands

```
glm WGHTCH = DIET;  
brief 3;  
gfits;  
rtype 2.
```

Menu route

Stat > ANOVA > General Linear Model
WGHTCH → Response
DIET → Model

Results...

In addition, coefficients for all terms

Graphs...

Standardised residuals

Residuals versus fits

MINITAB OUTPUT FOR BOX 9.1 AND FIG. 9.1

Weight change with diet, with a graph of standardised residuals against fitted values

General Linear Model: WGHTCH versus DIET

Factor	Type	Levels	Values
DIET	fixed	3	1 2 3

Analysis of Variance for WGHTCH, using Adjusted SS for Tests

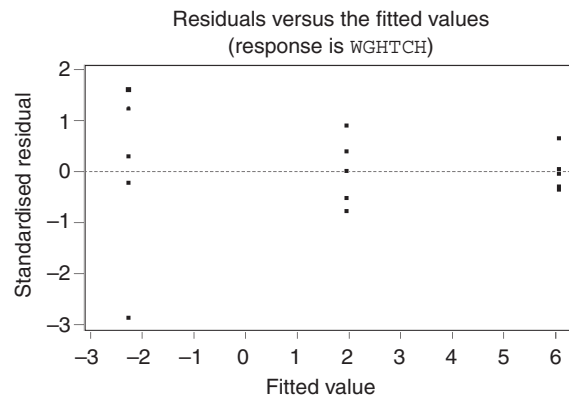
Source	DF	Seq SS	Adj SS	Adj MS	F	P
DIET	2	173.56	173.56	86.78	4.97	0.027
Error	12	209.42	209.42	17.45		
Total	14	382.99				

Term	Coef	SE Coef	T	P
Constant	1.924	1.079	1.78	0.100
DIET				
1	0.032	1.525	0.02	0.984
2	4.150	1.525	2.72	0.019

Unusual Observations for WGHTCH

Obs	WGHTCH	Fit	SE Fit	Residual	St Resid
15	-13.0400	-2.2580	1.8683	-10.7820	-2.89R

R denotes an observation with a large standardized residual

**9.4 Model criticism and solutions**

The Normality of error may be examined by plotting a histogram of residuals or a Normal order plot. Normal Order plots allow a more quantitative assessment of the Normality of the distribution of residuals. This method will first of all be described with some Normally distributed residuals. Using the *plantlets* dataset, the height of two species are compared.

MINITAB COMMANDS FOR BOX 9.2 AND FIG. 9.6 Analysis of height in the plantlets dataset

Commands `glm HGHT = SPECIES;`
 `brief 1;`
 `ghistogram;`
 `gnormal;`
 `rtype 2.`

Menu route Stat > ANOVA > General Linear Model
 HGHT → Response
 SPECIES → Model

Results...

Analysis of variance table.

Graphs...

Standardised residuals
 Histogram of residuals
 Normal plot of residuals

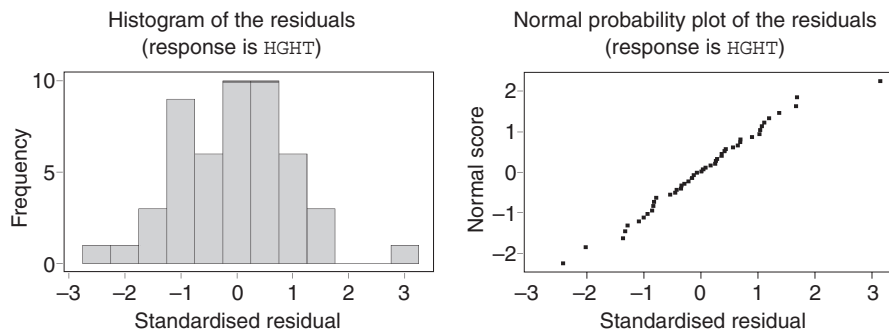
MINITAB OUTPUT FOR BOX 9.2 Analysis of height in the plantlets dataset

General Linear Model: HGHT versus SPECIES

Factor	Type	Levels	Values
SPECIES	fixed	2	1 2

Analysis of Variance for HGHT, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
SPECIES	1	260.83	260.83	260.83	46.28	0.000
Error	48	270.55	270.55	5.64		
Total	49	531.38				



Minitab output for Fig. 9.6 Normally distributed residual plots.

The residuals in Fig. 9.6 appear to be Normally distributed and originate from a dataset size 50. Imagine these standardised residuals being ranked. If these 50 values have been drawn at random from a Standard Normal Distribution (see revision section), then we can calculate the expected value of the lowest residual—which in this case we would expect to be -2.24 standard deviations below the mean of zero. Corresponding expected residuals can be calculated for all 50 points. This can be calculated in Minitab by the use of the NSCORES command. For example, the following set of commands will produce the 50 ‘expected’ standardised residuals:

Producing the ‘expected’ standardised residuals

Commands	<pre> set c3 1:50 end nscores c3 c4 name c4 'NORMSCOR' </pre>
Menu route	<p>Calc > Make patterned data > simple set of numbers c3 → store patterned data in 1 → from the first value 50 → to the last value 1 → in steps of</p> <p>Calc > calculator NORMSCOR → store result in variable NSCOR (c3) → Expression</p>

Minitab can also store the actual standardised residuals produced by the fit of the data to the model you have specified. To do this, repeat the last analysis with the following additional commands.

Saving the standardised residuals from a fit

Commands	<pre>name c8 = 'SRES1' glm HGHT = SPECIES; brief 1; sresiduals SRES1.</pre>
Menu route	Stat > ANOVA > General Linear Model HGHT → Response SPECIES → Model <div style="border: 1px solid black; padding: 2px; display: inline-block; margin: 5px;">Results...</div> <input type="radio"/> Analysis of variance table <div style="border: 1px solid black; padding: 2px; display: inline-block; margin: 5px;">Storage...</div> <input checked="" type="checkbox"/> standardised residuals

When the analysis is executed, Minitab will place them in a separate column headed SRES1. These standardised residuals can then be sorted into order of ascending size.

Sorting the standardised residuals

Commands	<pre>sort SRES1 C5; by SRES1.</pre>
Menu route	Manip > Sort SRES1 → Sort column(s) C5 → Store sorted column(s) in SRES1 → Sort by column :

The lowest standardised residual from our dataset, now at the top of C5, is -2.41 ; not too far from the expected value of -2.24 . Our ordered standardised residuals can now be plotted against their expected values in NORMSCOR.

Plotting the expected against observed standardised residuals

Commands	<pre>Plot NORMSCOR*SRES1</pre>
Menu route	Graph > Plot NORMSCOR → Graph variables, Y SRES1 → Graph variables, X

This will finally produce the same Normal probability plot as in Fig. 9.6. This exercise illustrates precisely where this plot comes from. For the other two examples in this section, we return to requesting the Normal probability plot as part of the analysis.

MINITAB COMMANDS FOR BOX 9.3 AND FIG. 9.7 Analysing longevity in the *plantlets* dataset

Commands	<pre> glm LONGEV = SPECIES; brief 1; ghistogram; gnormal; rtype 2. </pre>
Menu route	<pre> Stat > ANOVA > General Linear Model LONGEV → Response SPECIES → Model </pre> <div style="border: 1px solid black; padding: 2px; width: fit-content; margin: 5px 0;">Results...</div> <ul style="list-style-type: none"> <input type="radio"/> Analysis of variance table <div style="border: 1px solid black; padding: 2px; width: fit-content; margin: 5px 0;">Graphs...</div> <ul style="list-style-type: none"> <input type="radio"/> Standardised residuals <input checked="" type="checkbox"/> Histogram of residuals <input checked="" type="checkbox"/> Normal plot of residuals

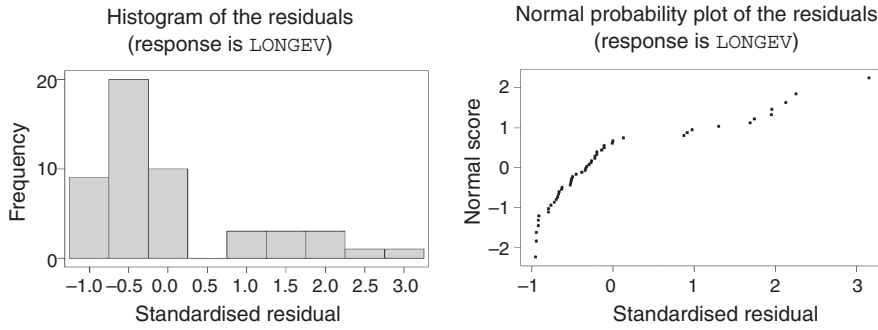
MINITAB OUTPUT FOR BOX 9.3 Analysing longevity in the *plantlets* dataset

General Linear Model: LONGEV versus SPECIES

Factor	Type	Levels	Values
SPECIES	fixed	2	1 2

Analysis of Variance for LONGEV, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
SPECIES	1	3300	3300	3300	0.30	0.585
Error	48	525103	525103	10940		
Total	49	528403				



Minitab output for Fig. 9.7 Residual plots for right hand skewed residuals.

MINITAB COMMANDS FOR BOX 9.4 AND FIG. 9.8 Analysing leaf size in the *plantlets* dataset

Commands `glm LEAFSIZE = SPECIES;`
`brief 1;`
`ghistogram;`
`gnormal;`
`rtype 2.`

Menu route Stat > ANOVA > General Linear Model
 LEAFSIZE → Response
 SPECIES → Model

Results...

- Analysis of variance table

Graphs...

- Standardised residuals
- Histogram of residuals
- Normal plot of residuals

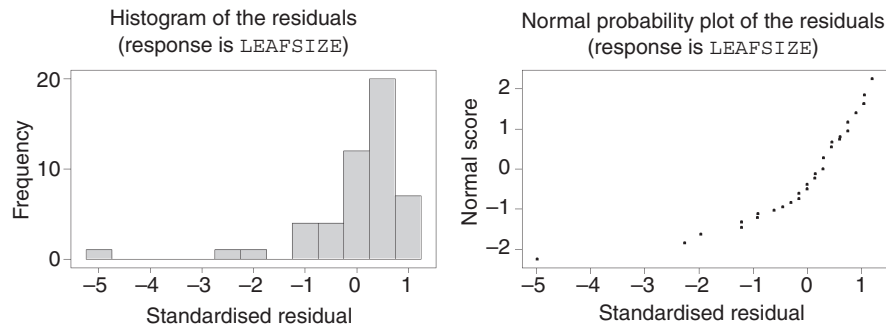
MINITAB OUTPUT FOR BOX 9.4 Analysing leaf size in the *plantlets* dataset

General Linear Model: LEAFSIZE versus SPECIES

Factor	Type	Levels	Values
SPECIES	fixed	2	1 2

Analysis of Variance for LEAFSIZE, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
SPECIES	1	0.1152	0.1152	0.1152	0.25	0.618
Error	48	21.9496	21.9496	0.4573		
Total	49	22.0648				



Minitab output for Fig. 9.8 Residual plots for left land skewed residuals.

Plotting residuals against fitted values

This technique was introduced earlier in this chapter as a means of checking for homogeneity of variance. It can also illustrate any problems with linearity, as illustrated with the 3Ys dataset.

MINITAB COMMANDS FOR BOX 9.5 AND FIG. 9.9 Dataset 3Ys, Y1	
Commands	<pre> glm Y1 = X; covariate X; brief 1; gfits; rtype 2. </pre>
Menu route	<pre> Stat > ANOVA > General Linear Model Y1 → Response X → Model Covariates... X → Covariates Results... ☉ Analysis of variance table Graphs... ☉ Standardised residuals ☑ Residuals versus fits </pre>

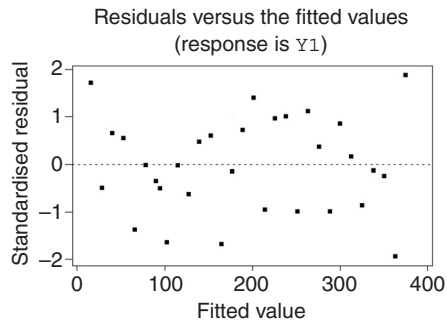
MINITAB OUTPUT FOR BOX 9.5 Dataset 3Ys, Y1

General Linear Model: Y1 versus

Factor Type Levels Values

Analysis of Variance for Y1, using Adjusted SS for Tests

Source	DF	Seq SS	Adj SS	Adj MS	F	P
X	1	345772	345772	345772	1.1E+05	0.000
Error	28	89	89	3		
Total	29	345861				



Minitab output for Fig. 9.9 Residuals with homogenous variance against fitted values.

The same commands may be repeated for the other two variables in this dataset, in which the residuals show increasing and decreasing variance with the fitted values (see Figs 9.10 and 9.11 in the main text).

Plotting the residuals against each explanatory variable

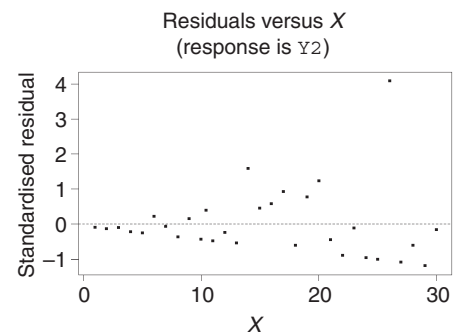
We will illustrate this with the second response variable in the 3Ys dataset. In this instance, plotting against the fitted values, and plotting against the explanatory variable (X) will result in the same graph, as there is only one explanatory variable. However, in models with several explanatory variables, the same technique may allow you to pinpoint which explanatory variable may be responsible for the non-linearity.

MINITAB COMMANDS FOR AN EXAMPLE OF FIG. 9.13

```
Commands          glm Y2 = X;
                  covariate X;
                  brief 1;
                  gvars X;
                  rtype 2.
```

Menu route	Stat > ANOVA > General Linear Model Y2 → Response X → Model <input type="checkbox"/> Covariates... X → Covariates <input type="checkbox"/> Results... <input checked="" type="radio"/> Analysis of variance table <input type="checkbox"/> Graphs... <input checked="" type="radio"/> Standardised residuals X → Residuals versus the variables
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Minitab output of an example of
Fig. 9.13.



These techniques may then be applied to the *bacteria* dataset, to resolve whether interactions or transformations are the better way of solving for non-linearity and heterogeneity of variance, as illustrated in the subsequent section of the main text.

9.5 Predicting the volume of merchantable wood: an example of model criticism

This example brings together both model criticism and basic data manipulation techniques, with an analysis based on the *merchantable timber* dataset. This case study starts off with an analysis of the untransformed data.

MINITAB COMMANDS FOR BOX 9.11 AND FIG. 9.19 Untransformed analysis of tree volume

Commands `glm VOLUME = DIAM;`
`covariate DIAM;`
`brief 3;`
`gfits;`
`rtype 2.`

Menu route Stat > ANOVA > General Linear Model
 VOLUME → Response
 DIAM → Model

 DIAM → Covariates

 In addition, coefficients for all terms

 Standardised residuals
 Residuals versus fits

MINITAB OUTPUT FOR BOX 9.11 Untransformed analysis of tree volume

General Linear Model: VOLUME versus

Factor	Type	Levels	Values
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Analysis of Variance for VOLUME, using Adjusted SS for Tests

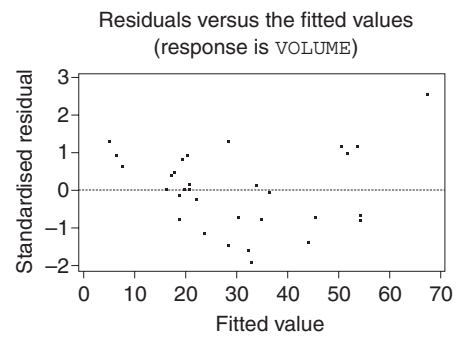
Source	DF	Seq SS	Adj SS	Adj MS	F	P
DIAM	1	7581.9	7581.9	7581.9	419.47	0.000
Error	29	524.2	524.2	18.1		
Total	30	8106.1				

Term	Coef	SE Coef	T	P
Constant	-36.945	3.365	-10.98	0.000
DIAM	60.791	2.968	20.48	0.000

Unusual Observations for VOLUME

Obs	VOLUME	Fit	SE Fit	Residual	St Resid
31	77.0000	67.4157	1.9723	9.5843	2.54RX

R denotes an observation with a large standardized residual.
 X denotes an observation whose X value gives it large influence.



Minitab output for Fig. 9.19 Residual plot for analysis of untransformed data.

The second analysis transforms the data and includes two explanatory variables. To take the natural logs of VOLUME, HEIGHT and DIAM, follow the commands or menus in the next box. Notice that there are a number of different functions that may be chosen from the function pane, by double clicking on the expression of your choice. Minitab will then express the function for a *number*, and then you replace *number* with the variable you wish to transform. The second analysis is then performed on the transformed data.

MINITAB COMMANDS TO TRANSFORM DATA

Commands	<pre> name C4 = 'LVOL' let LVOL = LOGE (VOLUME) name C5 = 'LHGHT' let LHGHT = LOGE (HEIGHT) name C6 = 'LDIAM' let LDIAM = LOGE (DIAM) </pre>
Menu route	<pre> Calc > Calculator LVOL → Store result in variable LOGE (VOLUME) → Expression (alternatively, double click on Natural Log, which can be found by scrolling down the pane titled 'Functions') Calc > Calculator LHGHT → Store result in variable LOGE (HEIGHT) → Expression Calc > Calculator LDIAM → Store result in variable LOGE (DIAM) → Expression </pre>

MINITAB COMMANDS FOR BOX 9.12 AND FIG. 9.20 Comparing trees to cylinders

Commands glm LVOL = LHGHT + LDIAM;
 covariate LHGHT LDIAM;
 brief 3;
 gfits;
 rtype 2.

Menu route Stat > ANOVA > General Linear Model
 LVOL → Response
 LHGHT + LDIAM → Model
 Covariates...
 LHGHT LDIAM → Covariates
 Results...
 ⊙ In addition, coefficients for all terms
 Graphs...
 ⊙ Standardised residuals
 ☑ Residuals versus fits

MINITAB OUTPUT FOR BOX 9.12 Comparing trees to cylinders

General Linear Model: LVOL versus

Factor	Type	Levels	Values
--------	------	--------	--------

Analysis of Variance for LVOL, using Adjusted SS for Tests

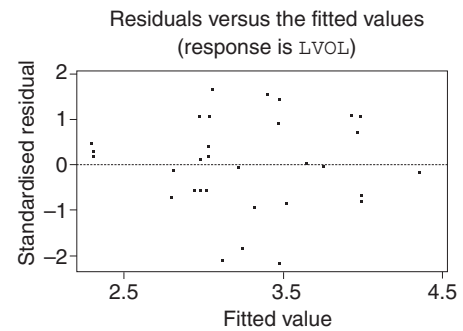
Source	DF	Seq SS	Adj SS	Adj MS	F	P
LHGHT	1	3.4957	0.1978	0.1978	29.86	0.000
LDIAM	1	4.6275	4.6275	4.6275	698.74	0.000
Error	28	0.1854	0.1854	0.0066		
Total	30	8.3087				

Term	Coef	SE Coef	T	P
Constant	-1.7047	0.8818	-1.93	0.063
LHGHT	1.1171	0.2044	5.46	0.000
LDIAM	1.98271	0.07501	26.43	0.000

Unusual Observations for LVOL

Obs	LVOL	Fit	SE Fit	Residual	St Resid
15	2.94969	3.11824	0.01535	-0.16855	-2.11R
18	3.31054	3.47500	0.02883	-0.16445	-2.16R

R denotes an observation with a large standardized residual.



Minitab output for Fig. 9.20 Residual plot for tree volume treated as a cylinder.

The third step in this case study is to estimate the mean deviation of the intercept from the expected cylinder intercept. This is done by creating a new variable, and requesting its mean and standard error, using the following commands:

MINITAB COMMANDS FOR BOX 9.13	
Estimating the mean deviation of the intercept from the expected cylinder intercept	
Commands	<pre>name C7 = 'LDEVINT' let LDEVINT = LVOL - LHGHT - 2*LDIAM describe LDEVINT</pre>
Menu route	<pre>Calc > Calculator LDEVINT → Store result in variable LVOL - LHGHT - 2*LDIAM → Expression Stat > Basic statistics > Display descriptive statistics LDEVINT → Variables</pre>

MINITAB OUTPUT FOR BOX 9.13						
Estimating the mean deviation of the intercept from the expected cylinder intercept						
Descriptive Statistics: LDEVINT						
Variable	N	Mean	Median	TrMean	StDev	SE Mean
LDEVINT	31	-1.1994	-1.2029	-1.1975	0.0791	0.0142
Variable	Minimum	Maximum	Q1	Q3		
LDEVINT	-1.3678	-1.0630	-1.2514	-1.1248		

Finally, we estimate the proportion of the cylinder that represents useable timber.

MINITAB COMMANDS FOR BOX 9.14 Estimating the proportion of the cylinder that represents useable timber

Commands name C8 = 'LUSEFRAC'
 let LUSEFRAC = LVOL - (-0.242 + LHGHT +2*LDIAM)
 describe LUSEFRAC

Menu route Calc > Calculator
 LUSEFRAC → Store result in variable
 LVOL - (-0.242 + LHGHT +2*LDIAM) → Expression

 Stat > Basic Statistics > Display Descriptive Statistics
 LUSEFRAC → Variables

MINITAB OUTPUT FOR BOX 9.14 Estimating the proportion of the cylinder that represents useable timber**Descriptive Statistics: LUSEFRAC**

Variable	N	Mean	Median	TrMean	StDev	SE Mean
LUSEFRAC	31	-0.9574	-0.9609	-0.9555	0.0791	0.0142
Variable	Minimum	Maximum	Q1	Q3		
LUSEFRAC	-1.1258	-0.8210	-1.0094	-0.8828		

9.8 Exercises

Stabilising the variance

The Minitab commands used in this exercise fall into three parts.

(1) Transforming the data

MINITAB COMMANDS TO TRANSFORM DATA

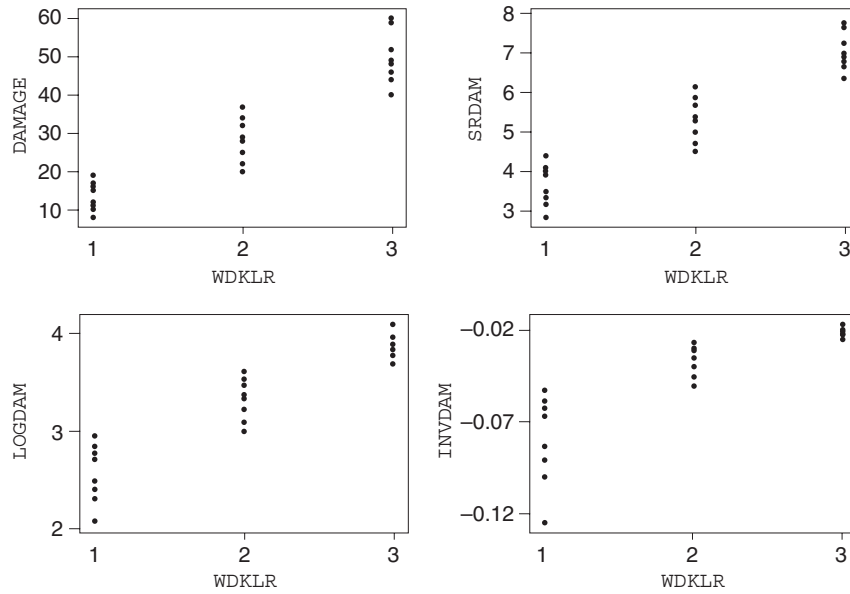
Commands name C3 = 'SRDAM'
 let SRDAM = SQRT(DAMAGE)
 name C4 = 'LOGDAM'
 let LOGDAM = LOGE(DAMAGE)
 name C5 = 'INVDAM'
 LET INVDAM = -1/DAMAGE

Menu route	Calc > Calculator SRDAM → Store result in variable SQRT (DAMAGE) → Expression Calc > Calculator LOGDAM → Store result in variable LOGE (DAMAGE) → Expression Calc > Calculator INVDAM → Store result in variable -1/DAMAGE → Expression
------------	---

(2) Plotting the graphs

Minitab commands for Fig. 9.21

Commands	<pre>plot DAMAGE*WDKLR plot SRDAM*WDKLR plot LOGDAM*WDKLR plot INVDAM*WDKLR</pre>
Menu route	Graph > Plot DAMAGE → Graph variables, Y, row 1 WDKLR → Graph variables, X, row 1 SRDAM → Graph variables, Y, row 2 WDKLR → Graph variables, X, row 2 LOGDAM → Graph variables, Y, row 3 WDKLR → Graph variables, X, row 3 INVDAM → Graph variables, Y, row 4 WDKLR → Graph variables, X, row 4



Minitab output for Fig. 9.21.

(3) Obtaining descriptive statistics

MINITAB COMMANDS FOR BOX 9.15	
Commands	describe DAMAGE SRDAM LOGDAM INVDAM; by WDKLR.
Menu route	Stat > Basic Statistics > Display Descriptive Statistics DAMAGE SRDAM LOGDAM INVDAM → Variables <input checked="" type="checkbox"/> By variable: WDKLR → By variable

MINITAB OUTPUT FOR BOX 9.15						
Descriptive Statistics: DAMAGE, SRDAM, LOGDAM, INVDAM by WDKLR						
Variable	WDKLR	N	Mean	Median	TrMean	StDev
DAMAGE	1	8	13.50	13.50	13.50	3.82
	2	8	28.38	28.50	28.38	5.88
	3	8	49.75	48.50	49.75	6.98
SRDAM	1	8	3.641	3.669	3.641	0.529
	2	8	5.301	5.338	5.301	0.558
	3	8	7.038	6.964	7.038	0.492
LOGDAM	1	8	2.565	2.596	2.565	0.297
	2	8	3.3260	3.3498	3.3260	0.2133
	3	8	3.8985	3.8815	3.8985	0.1393

INVDAM	1	8	-0.07998	-0.07500	-0.07998	0.02460
	2	8	-0.03667	-0.03510	-0.03667	0.00799
	3	8	-0.02044	-0.02062	-0.02044	0.00282
Variable	WDKLR	SE Mean	Minimum	Maximum	Q1	Q3
DAMAGE	1	1.35	8.00	19.00	10.25	16.75
	2	2.08	20.00	37.00	22.75	33.50
	3	2.47	40.00	60.00	44.50	57.25
SRDAM	1	0.187	2.828	4.359	3.201	4.092
	2	0.197	4.472	6.083	4.768	5.787
	3	0.174	6.325	7.746	6.671	7.564
LOGDAM	1	0.105	2.079	2.944	2.326	2.818
	2	0.0754	2.9957	3.6109	3.1230	3.5112
	3	0.0493	3.6889	4.0943	3.7953	4.0460
INVDAM	1	0.00870	-0.12500	-0.05263	-0.09773	-0.05974
	2	0.00282	-0.05000	-0.02703	-0.04409	-0.02987
	3	0.00100	-0.02500	-0.01667	-0.02248	-0.01752

Stabilising the variance in a blocked experiment

The Minitab output for this exercise may be found in the answers to exercises.

Lizard skulls

The first analysis is with the raw data (note how Minitab flags up a number of unusual observations).

MINITAB COMMANDS FOR BOX 9.16 AND FIG. 9.22

Commands

```
glm BVOL = JAWL;
covariate JAWL;
brief 3;
gfits;
rtype 2.
```

Menu route

Stat > ANOVA > General Linear Model

BVOL → Response

JAWL → Model

Covariates...

JAWL → Covariates

Results...

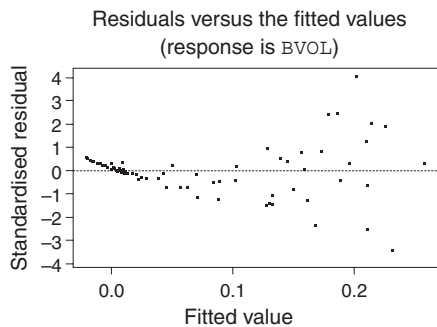
In addition, coefficients for all terms

Graphs...

Standardised residuals

Residuals versus fits

MINITAB OUTPUT FOR BOX 9.16 Analysis of lizard skulls						
General Linear Model: BVOL versus						
Factor	Type	Levels	Values			
Analysis of Variance for BVOL, using Adjusted SS for Tests						
Source	DF	Seq SS	Adj SS	Adj MS	F	P
JAWL	1	0.52278	0.52278	0.52278	284.65	0.000
Error	78	0.14325	0.14325	0.00184		
Total	79	0.66603				
Term		Coef	SE Coef	T		P
Constant		-0.041583	0.008060	-5.16		0.000
JAWL		0.52456	0.03109	16.87		0.000
Unusual Observations for BVOL						
Obs	BVOL	Fit	SE Fit	Residual	St Resid	
2	0.070000	0.168400	0.007651	-0.098400	-2.33R	
7	0.299300	0.214247	0.009916	0.085053	2.04R	
8	0.281400	0.179311	0.008165	0.102089	2.43R	
58	0.370000	0.201605	0.009267	0.168395	4.02R	
61	0.107000	0.211519	0.009775	-0.104519	-2.50R	
66	0.288900	0.186445	0.008511	0.102455	2.44R	
70	0.269800	0.257680	0.012234	0.012120	0.30 X	
71	0.090100	0.231347	0.010815	-0.141247	-3.41R	
R denotes an observation with a large standardized residual.						
X denotes an observation whose X value gives it large influence.						



Minitab output for Fig. 9.22 Residual plot of lizard skulls.

The second analysis is performed on the transformed allometric measurements, and includes SITE as an extra explanatory variable.

MINITAB COMMANDS FOR BOX 9.17 AND FIG. 9.23 **Alternative analysis for lizard skulls**

Commands

```

name C4 = 'LBVOL'
let LBVOL = LOGE(BVOL)
name C5 = 'LJAWL'
let LJAWL = LOGE(JAWL)
glm LBVOL = SITE + LJAWL;
covariate LJAWL;
brief 3;
gfits;
rtype 2.

```

Menu route

```

Calc > Calculator
  LBVOL → Store result in variable
  LOGE(BVOL) → Expression
Calc > Calculator
  LJAWL → Store result in variable
  LOGE(JAWL) → Expression

Stat > ANOVA > General Linear Model
  LBVOL → Response
  SITE + LJAWL → Model

  Covariates...
    LJAWL → Covariates

  Results...
    Ⓐ In addition, coefficients for all terms

  Graphs...
    Ⓐ Standardised residuals
    ☑ Residuals versus fits

```

MINITAB OUTPUT FOR BOX 9.17 **Transformed lizard skulls**

General Linear Model: LBVOL versus SITE

Factor	Type	Levels	Values
SITE	fixed	9	1 2 3 4 5 6 7 8 9

Analysis of Variance for LBVOL, using Adjusted SS for Tests

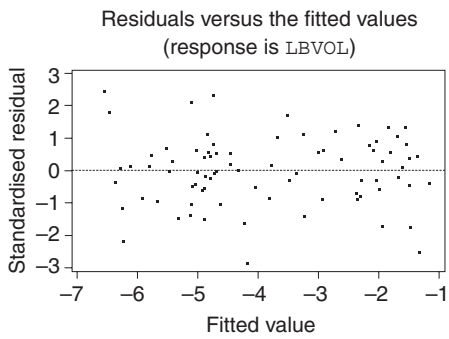
Source	DF	Seq SS	Adj SS	Adj MS	F	P
SITE	8	193.445	0.301	0.038	0.19	0.992
LJAWL	1	10.405	10.405	10.405	52.52	0.000
Error	70	13.867	13.867	0.198		
Total	79	217.717				

Term	Coef	SE Coef	T	P
Constant	-0.1302	0.5556	-0.23	0.815
SITE				
1	0.0267	0.3156	0.08	0.933
2	0.0644	0.1816	0.35	0.724
3	0.0836	0.1505	0.56	0.580
4	-0.0871	0.1487	-0.59	0.560
5	-0.0164	0.2107	-0.08	0.938
6	0.0099	0.2232	0.04	0.965
7	-0.1204	0.2486	-0.48	0.630
8	0.1036	0.3393	0.31	0.761
LJAWL	1.9904	0.2747	7.25	0.000

Unusual Observations for LBVOL

Obs	LBVOL	Fit	SE Fit	Residual	St Resid
11	-4.21313	-5.09052	0.15062	0.87739	2.09R
14	-3.76360	-4.73426	0.15017	0.97066	2.32R
71	-2.40684	-1.32702	0.12332	-1.07982	-2.52R
76	-5.54678	-6.53774	0.17726	0.99096	2.43R
80	-7.13090	-6.22199	0.16868	-0.90891	-2.21R

R denotes an observation with a large standardized residual.



Minitab output for Fig. 9.23 Residual plot for alternative analysis of lizard skulls.

Checking the perfect model

The Minitab output for this exercise may be found in the answers to exercises in Chapter 14.