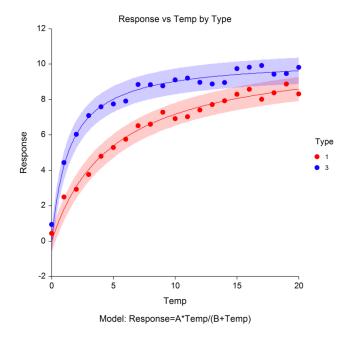
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Chapter 351

General (Custom and Preset) Model Fit – Y vs One X

Introduction

Curve fitting refers to finding an appropriate mathematical model that expresses the relationship between a dependent variable *Y* and a single independent variable *X* and estimating the values of its parameters using nonlinear regression. An introduction to curve fitting and nonlinear regression can be found in the chapter entitled Curve Fitting, so these details will not be repeated here. Here are some examples of the curve fitting that can be accomplished with this procedure.



This program is a general purpose curve fitting procedure providing many new technologies that have not been easily available. It is preprogrammed to fit over thirty common mathematical models including growth models like linear-growth and Michaelis-Menten. It also fits many approximating models such as regular polynomials and piecewise polynomials. In addition to these preprogrammed models, it also fits models that you write yourself.

This routine includes several innovative features. First, it can fit curves to several batches of data simultaneously. Second, it compares fitted models across groups using graphics and numerical tests such as an approximate F-test for curve coincidence and a computer-intensive randomization test that compares curve coincidence and individual parameter values. Third, it computes bootstrap confidence intervals for parameter values, predicted means, and predicted values using the latest computer-intensive bootstrapping technology.

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Preset Models

Below are the models that you may fit. Select "Custom Model" to enter a custom model. Whenever possible, use one of the preset models since reasonable starting values for the parameters will be calculated for you. The minimum, maximum, and starting values for each parameter in the preset models may be entered. The available preset models are

 $Y = (A + BX)^{(-1 / C)}$ Bleasdale-Nelder Exponential (Type 1) Y = exp(A(X - B))Exponential (Type 2) Y = A(exp(-BX))Exponential (Three Parameter) $Y = A(X^B)exp(-CX)$ Exponential (Four Parameter) Y = (A + BX)exp(-CX) + DExponential (Sum of Two) Y = A(exp(-BX)) + C(exp(-DX))Exponential (Sum of Three) Y = A(exp(-BX)) - C(exp(-DX)) + E(exp(-FX))Farazdaghi-Harris $Y = 1 / (A + BX^C)$ Gompertz (Two Parameter) $Y = \exp((A / B)(1 - \exp(BX)))$ Gompertz (Three Parameter) Y = A(exp(-exp(-B(X - C))))Hill $Y = AX^C / (B^C + X^C)$ Holliday $Y = 1 / (A + BX + CX^2)$ Joined (Linear, Linear) Y = A + BX + C(X - D)sign(X - D)Joined (Linear, Linear, Linear) Y = A + BX + C(X - D)sign(X - D) + E(X - F)sign(X - F)Joined (Linear, Quadratic) $Y = A + BX + CX^2 + (X - D)sign(X - D)(C(X + D) + E)$ Joined (Quadratic, Linear) $Y = A + BX + CX^2 + (X - D)sign(X - D)(E - C(X + D))$ Joined (Quadratic, Quadratic) $Y = A + BX + CX^2 + (X - D)sign(X - D)(E(X + D) + F)$ Logarithmic $Y = B(\ln(|X| - A))$ Logistic (Three Parameter) Y = A / (1 + B(exp(-CX)))Y = D + (A - D) / (1 + B(exp(-CX)))Logistic (Four Parameter) Lognormal $Y = A + (B / X)exp(-C(ln(X) - D)^2)$ Michaelis-Menten Y = AX / (B + X)Michaelis-Menten (Two Terms) Y = AX / (B + X) + CX / (D + X)Michaelis-Menten (Three Terms) Y = AX / (B + X) + CX / (D + X) + EX / (F + X)

Monomolecular $Y = A(1 - \exp(-B(X - C)))$

Morgan-Mercer-Floding $Y = A - (A - B) / (1 + (C|X|)^D)$ Normal $Y = A + B(exp(-C(X - D)^2))$

Polynomial (Linear) Y = A + BX

Polynomial (Quadratic) $Y = A + BX + CX^2$

Polynomial (Cubic) $Y = A + BX + CX^2 + DX^3$

Power $Y = A(1 - B^X)$ Power^Power $Y = AX^(BX^C)$ Reciprocal Y = 1 / (A + BX)

Richards $Y = A(1 + (B - 1)exp(-C(X - D)))^{(1 / (1 - B))}$

Weibull $Y = A - (A - B)exp(-(C|X|)^D)$

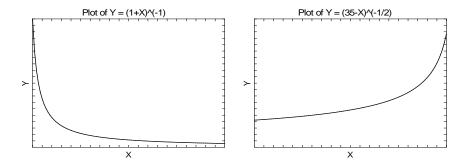
Selecting a Preset Model

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Over thirty preset models are available. These models provide a variety of curve shapes. Several of the models were developed for quite different physical processes but yield similar results. We now present examples and details of several of the preset models available.

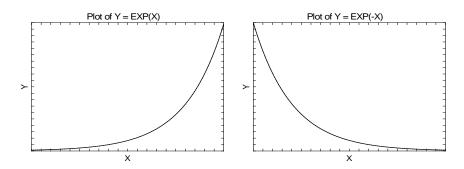
Bleasdale-Nelder: $Y = (A + BX)^{-1/C}$

This model, known as the Bleasdale-Nelder model, is mentioned in Ratkowsky (1989, page 103) and Seber (1989, page 362).

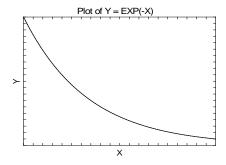


Exponential (Type 1): $Y = \exp(A(X - B))$

This model, known as the exponential model, is mentioned in Seber (1989, page 327). Note that taking the log of both sides reduces this equation to a linear model.



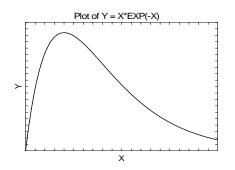
Exponential (Type 2): Y = A(exp(-BX))

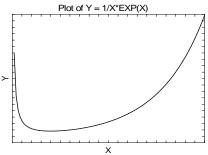


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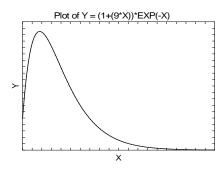
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Exponential (Three Parameter): Y = A(X^B)exp(-CX)

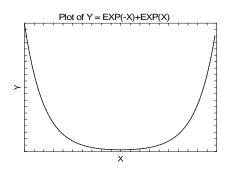


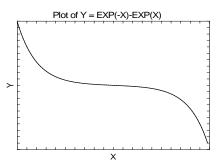


Exponential (Four Parameter): Y = (A + BX)exp(-CX) + D



Exponential (Sum of Two): Y = A(exp(-BX)) + C(exp(-DX))

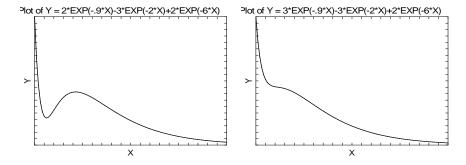




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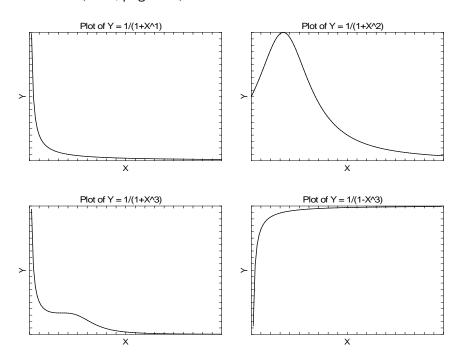
Exponential (Sum of Three): Y = A(exp(-BX)) - C(exp(-DX)) + E(exp(-FX))

This model is intended for the case when all parameters are positive. Note that the default starting values may not work for this model. You should be prepared to try different starting values.

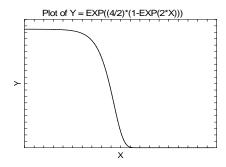


Farazdaghi and Harris: Y = 1 / (A + BX^C)

This model, known as the Farazdaghi and Harris model, is mentioned in Ratkowsky (1989, pages 99 and 104) and Seber (1989, page 362).

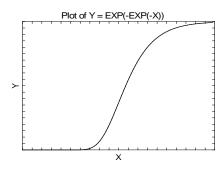


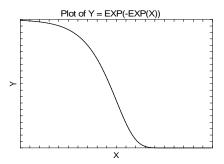
Gompertz (Two Parameter): Y = exp((A / B)(1 - exp(BX)))



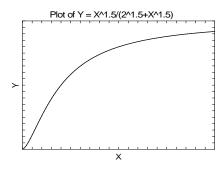
Gompertz (Three Parameter): Y = A(exp(-exp(-B(X - C))))

This model, known as the Gompertz model, is mentioned in Seber (1989, page 331).



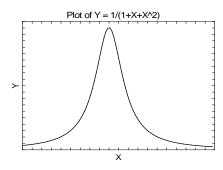


Hill: $Y = AX^C / (B^C + X^C)$



Holliday: $Y = 1 / (A + BX + CX^2)$

This model, known as the Holliday model, is mentioned in Seber (1989, page 362).



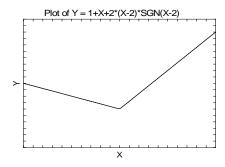
Joined (Linear, Linear): Y = A + BX + C(X - D)sign(X - D)

Common Equation

 $Y = a1 + b1X, X \le J$ Y = a2 + b2X, X > J

Parameter Identities

A = (a1 + a2)/2 B = (b1 + b2)/2 a1 = A + DC b1 = B - C J = D C = (b2 - b1)/2 D = J a2 = A - DC b2 = B + C



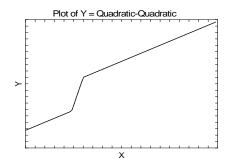
Joined (Linear, Linear): Y = A + BX + C(X - D)sign(X - D) + E(X - F)sign(X - F)

Common Equation

Y = a1 + b1X, $X \le J1$ Y = a2 + b2X, $J1 < X \le J2$ Y = a3 + b3X, X > J2

Parameter Identities

A = (a1 + a3)/2 B = (b1 + b3)/2 C = (b2 - b1)/2 D = J1 E = (b3 - b2)/2 F = J2 a1 = A + CD + EF b1 = B - C - E J1 = D a2 = A - CD - EF b2 = B + C - E J2 = Fa3 = A - CD + EF b3 = B + C + E



Joined (Linear, Quadratic): $Y = A + BX + CX^2 + (X - D)sign(X - D)(C(X + D) + E)$

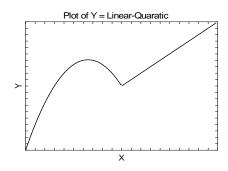
Common Equation

Y = a1 + b1X, $X \le a$ $Y = a2 + b2X + c2X^{2},$ X > a

Parameter Identities

A = (a1 + a2)/2 B = (b1 + b2)/2 C = c2/2 D = a E = (b2 - b1)/2a1 = A + CD2 + DE b1 = B - E a = D

a1 = A + CD2 + DE b1 = B - E a = Da2 = A - CD2 - DE b2 = B + E c2 = 2C



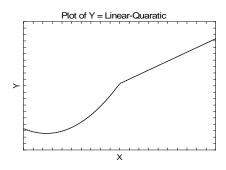
Joined (Quadratic, Linear): $Y = A + BX + CX^2 + (X - D)sign(X - D)(E - C(X + D))$

Common Equation

 $Y = a1 + b1X + c1X^{2}, X \le a$ Y = a2 + b2X, X > a

Parameter Identities

A = (a1 + a2)/2 B = (b1 + b2)/2 C = c1/2 E = (b2 - b1)/2 a1 = A - CD2 + DE b1 = B - E a = D a2 = A + CD2 - DE b2 = B + E c1 = 2C



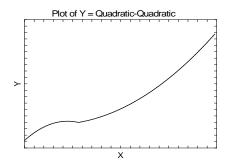
Joined (Quadratic, Quadratic): $Y = A + BX + CX^2 + (X - D)sign(X - D)(E(X + D) + F)$

Common Equation

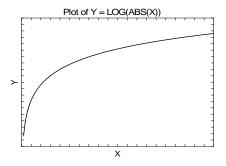
 $Y = a1 + b1X + c1X^{2},$ $X \le a$ $Y = a2 + b2X + c2X^{2},$ X > a

Parameter Identities

A = (a1 + a2)/2	B = (b1 + b2)/2	C = (c1 + c2)/2
D = a	E = (c2 - c1)/2	F = (b2 - b1)/2
a1 = A - ED2 + DF	b1 = B - F	a = D
a2 = A + ED2 - DF	b2 = B + F	
c1 = C - F	c2 = C + F	

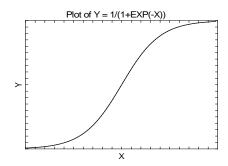


Logarithmic: Y = B(ln(|X| - A))



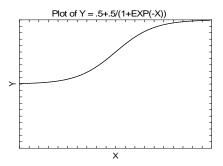
Logistic (Three Parameter): Y = A / (1 + B(exp(-CX)))

This model, known as the three-parameter logistic model, is mentioned in Seber (1989, page 330).

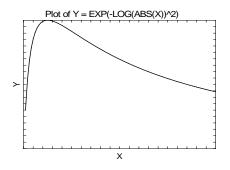


Logistic (Four Parameter): Y = D + (A - D) / (1 + B(exp(-CX)))

This model, known as the four-parameter logistic model, is mentioned in Seber (1989, page 338). Note that the extra parameter, D, has the effect of shifting the graph vertically. Otherwise, this plot is the same as the three-parameter logistic.

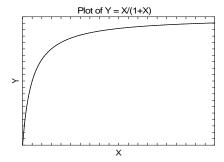


Lognormal: $Y = A + (B / X)exp(-C(ln(X) - D)^2)$

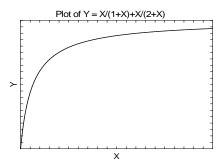


Michaelis-Menten: Y = AX / (B + X)

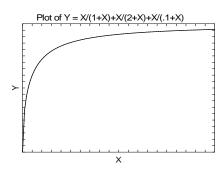
This is a popular growth model.



Michaelis-Menten (Two Terms): Y = AX / (B + X) + CX / (D + X)

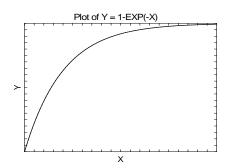


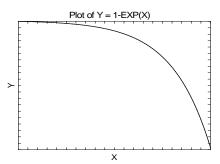
Michaelis-Menten (Three Terms): Y = AX / (B + X) + CX / (D + X) + EX / (F + X)



Monomolecular: Y = A(1 - exp(-B(X - C)))

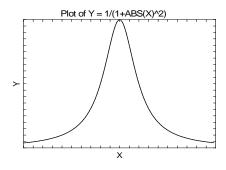
This model, known as the monomolecular model, is mentioned in Seber (1989, page 328).

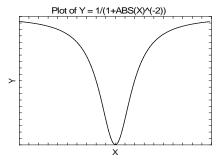




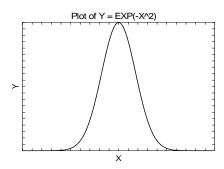
Morgan-Mercer-Floding: $Y = A - (A - B) / (1 + (C|X|)^D)$

This model, known as the Morgan-Mercer-Floding model, is mentioned in Seber (1989, page 340).



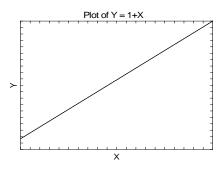


Normal: $Y = A + B(exp(-C(X - D)^2))$



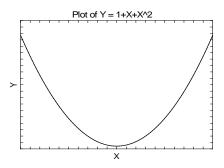
Polynomial (Linear): Y = A + BX

This common model is usually fit using standard linear regression techniques. We include it here to allow for various special forms made by transforming X and Y



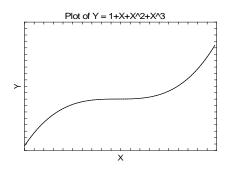
Polynomial (Quadratic): Y = A + BX + CX^2

The quadratic or second-order polynomial model results in the familiar parabola

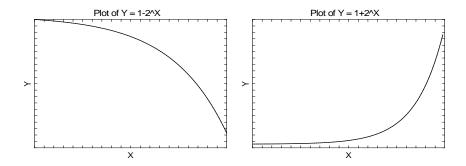


Polynomial (Cubic): $Y = A + BX + CX^2 + DX^3$

This is the cubic or third-order polynomial model.

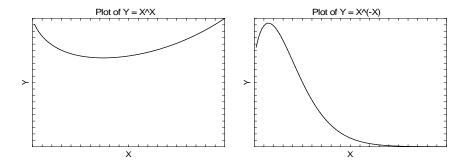


Power: $Y = A(1 - B^X)$



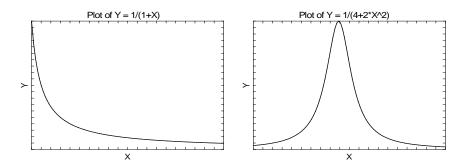
Power^Power: Y = AX^(BX^C)

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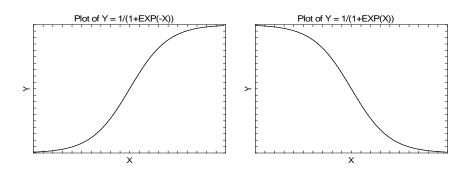
Reciprocal: Y = 1 / (A + BX)

This model, known as the reciprocal or Shinozaki and Kira model, is mentioned in Ratkowsky (1989, page 89) and Seber (1989, page 362).



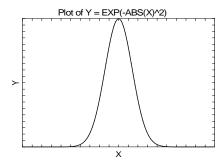
Richards: $Y = A(1 + (B - 1)exp(-C(X - D)))^{(1 / (1 - B))}$

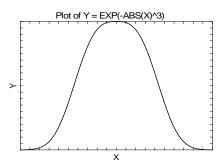
This model, known as the Richards model, is mentioned in Seber (1989, page 333).



Weibull: $Y = A - (A - B)exp(-(C|X|)^D)$

This model, known as the Weibull model, is mentioned in Seber (1989, page 338).





Custom Models

You are not limited to the preset models that are shown above. You can enter your own custom model using standard mathematical notation. The only difference between using a preset model and using your own model is that with a preset model the starting values of the search algorithm are chosen based on the model. When using a custom model, you will have to set your own starting values based on the data you are trying to fit. When you do not specify starting values, the program uses all zeros, which may or may not lead to a reasonable solution.

Using a Custom Model

The custom model is only used when the Preset Model option is set to 'Custom Model'. When used, it contains the regression model written in standard mathematical notation.

Use 'X' to represent the independent variable specified in the X Variable box, not its variable name. Hence, if your independent variable is HEAT, you would enter A+B*In(X), not A+B*In(HEAT).

Use the letters (case ignored) A,B,C, ... (except X and Y) to represent the parameters to be estimated from the data. The letters used must be specified in one of the Parameter boxes listed under the Search tab. Note that you do not include a 'Y=' in the expression. That is, you would enter A+B*X, not Y=A+B*X.

Expression Syntax

Construct the expression using standard mathematical syntax. Possible symbols and functions are

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Symbols

- + add
- subtract
- * multiply
- / divide
- $^{\wedge}$ exponent ($X^2 = X^*X$)
- () parentheses
- < less than.
- > greater than
- = equals
- <= less than or equal
- >= greater than or equal
- <> not equal

Functions

(a logic b) Indicator function. If true, the result is 1; otherwise, result is 0. Logic values are <, >,

=, <>, <=, and >=. The symbols a and b are replaced by numbers or letters.

abs(X) Absolute value of X.

arcosh(X)Arc cosh of X.arsinh(X)Arc sinh of X.artanh(X)Arc tanh of X.asn(X)Arc sine of X.atn(X)Arc tangent of X.cos(X)Cosine of X.

cosh(X) Hyperbolic cosine of X. erf(X) The error function of X

exp(X) Exponential of X. Integer part of X. In(X) Log base e of X. log(X) Log base 10 of X.

loggamma(X) Log of the gamma function.

normden(X) Normal density.

normprob(X) Normal CDF (probability). normvalue(X) Inverse normal CDF.

sgn(X) Sign of X which is -1 if X<0, 0 if X=0, and 1 if X>0.

sin(X) Sine of X.

sinh(X) Hyperbolic sine of X. sqr(X) Square root of X. tan(X) Tangent of X.

tanh(X) Hyperbolic tangent of X. tnh(X) Hyperbolic tangent of X. trigamma(X) Trigamma function. NCSS.com

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Independent Variable

Use 'X' in your expression to represent the independent variable you have specified.

Parameters

The letters of the alphabet (except X and Y) may be used to represent the parameters. Parameters can be only one character long and case is ignored. Each parameter must be defined in the Parameter fields below.

Numbers

You can enter numbers in standard format such as 23.456 and 254.43, or you can use scientific notation such as 1E-5 (which is 0.00001) and 1E5 (which is 100000).

Examples

Standard mathematical syntax is used. This is discussed in detail in the Transformation section. Examples of valid expressions are:

A+B*X

C+D*X+E*X*X or G+H*X+B*X^2

A*exp(B*X)

 $(X \le 5)*A + (X \ge 5)*B + C$

Confidence Intervals

Two methods are used to calculate confidence intervals of the regression parameters and predicted values. The first method is based on the usual normality and constant variance of residuals assumption. When the data follow these assumptions, standard expressions for the confidence intervals are used based on the Student's t distribution. Unfortunately, nonlinear regression datasets rarely follow these assumptions.

The second method is called the bootstrap method. This is a modern, computer-intensive method that has only become available in recent years as extensive computer power has become available.

Bootstrap Confidence Intervals

Bootstrapping provides standard errors and confidence intervals for nonlinear-regression parameter, predicted means, and predicted values. The method is simple in concept, but it requires extensive computation time.

Bootstrap confidence intervals are based on the assumption that your sample is actually representative of the population. Beginning with this assumption, B samples are drawn (B is over 1000) of size N from your original sample with replacement. With replacement sampling means that each observation may be selected more than once. For each bootstrap sample, the nonlinear-regression results are computed and stored.

Suppose you want the standard error and a confidence interval of a regression parameter. The bootstrap sampling process provides B estimates of this parameter. The standard deviation of these B estimates is the bootstrap estimate of the standard error of the parameter. The bootstrap confidence interval is found by

General (Custom and Preset) Model Fit - Y vs One X

arranging the *B* values in sorted order and selecting the appropriate percentiles from the list. For example, a 90% bootstrap confidence interval for the parameter is given by fifth and ninety-fifth percentiles of the bootstrap parameter values.

The main assumption made when using the bootstrap is that your sample approximates the population. Because of this assumption, bootstrapping does not work well for small samples in which there is little likelihood that the sample is representative of the population. Bootstrapping should only be used in medium to large samples.

Bootstrap Prediction Intervals

Bootstrap confidence intervals for the mean of *Y* given *X* are generated from the bootstrap sample in the usual way. To calculate prediction intervals for the predicted value (not the mean) of *Y* given *X* requires a modification to the predicted value of *Y* to be made to account for the variation of *Y* about its mean. This modification of the predicted *Y* values in the bootstrap sample, suggested by Davison and Hinkley, is as follows.

$$\hat{y}_i = \hat{y}_i + e_r^*$$

where e_r^* is a randomly selected modified residual (see below). By adding the residual, we have added an appropriate amount of variation to represent the variance of individual Y's about their mean value.

Modified Residuals

Davison and Hinkley (1999) page 279 recommend the use of a special rescaling of the residuals when bootstrapping to keep results unbiased. Because of the high amount of computing involved in bootstrapping, these modified residuals are calculated using

$$e_j^* = \frac{e_j}{\sqrt{1 - \frac{1}{N}}} - \bar{e}$$

where

$$\bar{e} = \frac{\sum_{j=1}^{N} e_j}{N}$$

Note that there is a different rescaling than Davison and Hinkley recommended. We have used this rescaling because it is much quicker to calculate.

Hypothesis Testing

When curves are fit to two or more groups, it is often of interest to test whether certain regression parameters are equal and whether the fitted curves coincide. Although some approximate results have been obtained using indicator variables, these are asymptotic results, and little is known about their appropriateness in sample samples. We provide a test of the hypothesis that all group curves coincide using an *F*-test that compares the residual sum of squares obtained when the grouping is

ignored with the total of the residual sum of squares obtained for each group. This test is routinely used in the analysis of variance associated with linear models and its application to nonlinear models has occasionally been suggested. However, it is based on naive assumptions that seldom occur.

Because of the availability of fast computing speed in recent years, a second method of hypothesis testing, called the *randomization test*, is now available. This test will be discussed next.

Randomization Test

Randomization testing is discussed by Edgington (1987). The details of the randomization test are simple: all possible permutations of the group variable while leaving the dependent and independent variables in their original order are investigated. For each permutation, the difference between the estimated group parameters is calculated. The number of permutations with a magnitude greater than or equal to that of the actual sample is counted. Dividing this count by the number of permutations gives the significance level of the test.

The randomization test is suggested because an exact test is achieved without making unrealistic assumptions about the data such as constant variance, normality, or model accuracy. The test was not used in the past because the number of computations was prohibitive. In fact, the randomization test was originally proposed by Fisher and he chose his *F*-test because its distribution close approximated the randomization distribution.

The only assumption that a randomization test makes is that the data values are *exchangeable* under the null hypothesis.

For even moderate sample sizes, the total number of permutations is in the trillions, so a Monte Carlo approach is used in which the permutations are found by random selection rather than enumeration. Using this approach, a reasonable approximation to the test's probability level may be found by considering only a few thousand permutations rather than the trillions needed for complete enumeration. Edgington suggests that at least 1000 permutations be computed. We suggest that this be increased to 10000 for important results.

The program tests two types of hypotheses using randomization tests. The first is that each of the estimated model parameters is equal. The second is that the individual fitted curves coincide across all groups.

Randomization Statistics for Testing Parameter Equivalence

The test statistic for comparing a model parameter is formed by summing the difference between the group parameter estimates for each pair of groups. If there are *G* groups, the test statistic is computed using the formula

$$B_{RT} = \sum_{i=1}^{G-1} \sum_{j=i+1}^{G} |\hat{\beta}_i - \hat{\beta}_j|$$

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Randomization Statistics for Testing Curve Equivalence

The test statistic for comparing the whole curve is formed by summing the difference between the estimated predicted values for each pair of groups at several points along the curve. If there are *G* groups and *K* equally spaced test points, the test statistic is computed using the formula

$$C_{RT} = \sum_{k=1}^{K} \sum_{i=1}^{G-1} \sum_{j=i+1}^{G} |\hat{y}_{ki} - \hat{y}_{kj}|$$

Data Structure

The data are entered in two variables: one dependent variable and one independent variable. Additionally, you may specify a frequency variable containing the observation count for each row and a group variable that is used to partition the data into independent groups.

Missing Values

Rows with missing values in the variables being analyzed are ignored in the calculations. When only the value of the dependent variable is missing, predicted values are generated.

Example 1 - Curve Fitting

This section presents an example of how to fit and compare a Michaelis-Menten model in two groups of data. This example will use the data in the **FnReg5** dataset. In this example, the dependent variable is Response, and the independent variable is Temp. The groups are defined by the values of Type.

Setup

To run this example, complete the following steps:

1 Open the FnReg5 example dataset

- From the File menu of the NCSS Data window, select **Open Example Data**.
- Select FnReg5 and click OK.

2 Specify the Curve Fitting - General procedure options

- Find and open the **Curve Fitting General** procedure using the menus or the Procedure Navigator.
- The settings for this example are listed below and are stored in the **Example 1** settings file. To load these settings to the procedure window, click **Open Example Settings File** in the Help Center or File menu.

Y Variable	Response
X Variable	Temp
Group Variable	Туре
Model to Fit	Michaelis-Menten: Y = AX / (B + X)
Reports Tab	
Combined Summary	Checked
Group Difference F-Test	Checked
Model Estimation	Checked
Analysis of Variance	Checked
Parameter Correlations	Checked
Iterations	Checked
X Values for Prediction	5 10 15 20
Predict Y at the Above X Values	Checked
Prediction Intervals and Residuals	Checked
Random Seed	17448 (for reproducibility)
Randomization Tests	Checked
Samples	1000
Bootstrap Confidence Intervals	Checked
Samples (N)	3000

3 Run the procedure

• Click the **Run** button to perform the calculations and generate the output.

Parameter Estimates for All Groups

Parameter Estimates for All Groups Count **Iterations** Pseudo-R² В **Type** 21 4 0.98356 10.72798 4.95941 6 21 0.97645 10.31200 1.42325 Combined 42 4 0.81153 10.20315 2.54358

This report displays a summary of the results for each group and then for the case in which all groups are combined into one group.

Group Name (Type)

This column, headed by the name of the Group Variable, lists the group value that is displayed on this line. Note that the Value Labels option may be used to give more meaningful names to these values.

Count

This is the number of observations used by the nonlinear regression algorithm.

Iterations

This is the number of iterations used by the nonlinear regression algorithm to find the estimates. You should note whether the maximum number of iterations has been reached (in which case the algorithm did not converge).

Pseudo-R²

This is the value of the pseudo R-squared. A value near one indicates that the model fits the data well. A value near zero indicates that the model does not fit the data well. When the value is negative, it is reset to zero.

A_B

The final values of the estimated parameters are displayed so that you may compare them across groups.

Goodness-of-Fit Statistics

Group Goodness-of-Fit Statistics

Group	Count	Iterations	Pseudo-R ²	Error DF	Sum of Squares Error	Mean Square Error
Type = 1	21	4	0.98356	19	1.73157	0.09114
Type = 3 Group Ignore	21 ed	6	0.97645	19	2.16427	0.11391
, ,	42	4	0.81153	40	43.74009	1.09350
Combined	42	0.98321	38	3.89585	0.10252	

This report displays goodness of fit results for each group and then for the case in which all groups are combined into one dataset. The final row of the report, labeled 'Ignored', gives the goodness of fit statistics for the model in which a separate curve is fit for each group.

Group Name (Type)

This column, headed by the name of the Group Variable, lists the group value that is displayed on this line.

Count

This is the number of observations used by the nonlinear regression algorithm.

Iterations

This is the number of iterations used by the nonlinear regression algorithm to find the estimates. You should note whether the maximum number of iterations has been reached (in which case the algorithm did not converge).

Pseudo-R²

This is the value of the pseudo R-squared value. A value near one indicates that the model fits the data well. A value near zero indicates that the model does not fit the data well. Note

Error DF

The degrees of freedom are the number of observations minus the number of parameters fit.

Sum of Squares Error

This is the sum of the squared residuals for this group.

Mean Square Error

This is a rough estimate of the variance of the residuals for this group.

Group Equality F-Test

Group Equality F-Test

Term	DF	Mean Square	F-Ratio	P-Value
Groups Error	2 38	19.92212 0.10252	194.3200	0.00000

This report displays an F-Test of whether all of the group curves are equal. This test compares the residual sum of squares obtained when the grouping is ignored with the total of the residual sum of squares obtained for each group. This test is routinely used in analysis linear models and its application to nonlinear models has occasionally been suggested. However, it is based on normality assumptions which seldom occur. When testing curve coincidence is important, we suggest you use a randomization test.

Term

This column indicates the term presented on this row.

DF

The degrees of freedom of this term.

Mean Square

The mean square associated with this term.

F-Ratio

The F-ratio for testing the hypothesis that all curves coincide.

P-Value

This is the probability level of the F-ratio. When this value is less than 0.05 (a common value for alpha), the test is 'significant' meaning that the hypothesis of equal curves is rejected. If this value is larger than the nominal level (0.05), the null hypothesis cannot be rejected. We do not have enough evidence to reject.

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Group Equality Randomization Test

Group Equality Randomization Test

Comparison	Randomization P-Value	Monte Carlo Samples	Number of Points Compared Along the Curve
1 vs. 3	0.00000	1000	10

User-Entered Random Seed: 17448

This report displays the results of a randomization test whose null hypothesis is that the all the group curves coincide. When more than two groups are present, a separate test is provided for each pair of groups, plus a combined test of the equality of all groups.

Comparison

This column indicates the groups whose equality is being tested on this row.

Randomization P-Value

This is the two-sided probability level of the randomization test. When this value is less than 0.05, the test is 'significant' meaning that the null hypothesis of equal curves is rejected. If this value is larger than the nominal level (0.05), there is not enough evidence in the data to reject the null hypothesis of equality.

(Note: because this is a Monte Carlo test, your results may vary from those displayed here.)

Monte Carlo Samples

The number of Monte Carlo samples.

Number of Points Compared Along the Curve

The number of values along the X axis at which a comparison between curves is made. Of course, the more X values used, the more accurate (and time consuming) will be the test.

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Parameter Inequality Randomization Tests

Parameter Equality Across Groups Randomization Tests

Comparison	Parameter Tested	Randomization P-Value	Monte Carlo Iterations
1 vs. 3	Α	0.70700	1000
1 vs. 3	В	0.00900	1000

User-Entered Random Seed: 17448

This report displays the results of randomization tests about the equality of each parameter across groups. When more than two groups are present, a separate test is provided for each pair of groups, plus a combined test of parameter equality of all groups.

Comparison

This column indicates the groups being tested on this row.

Parameter Tested

This column indicates model parameter whose equality is being tested.

Randomization P-Value

This is the two-sided probability level of the randomization test. When this value is less than 0.05, the test is 'significant' meaning that the null hypothesis of equal parameter values across groups is rejected. If this value is larger than the nominal level (0.05), there is not enough evidence in the data to reject the null hypothesis of equality.

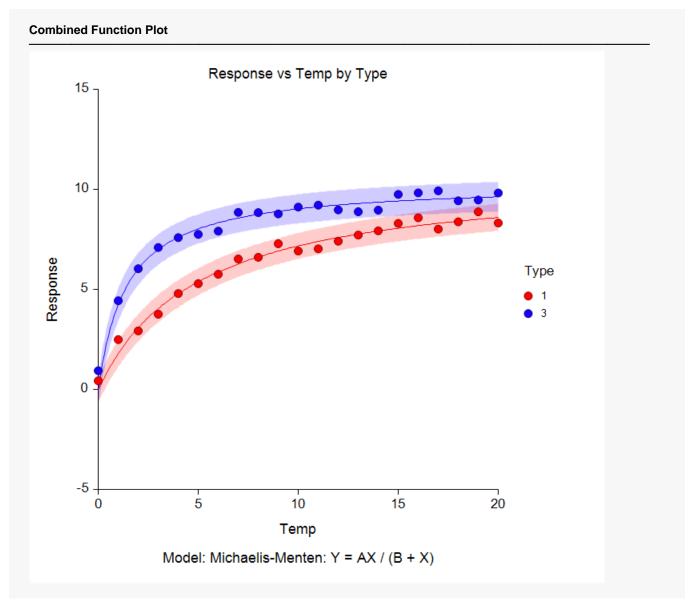
(Note: because this is a Monte Carlo test, your results may vary from those displayed here.)

Monte Carlo Iterations

The number of Monte Carlo samples.

Combined Function Plot

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This plot displays all of the data and fitted curves, allowing you to quickly assess the quality of the results.

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Iterations

Iteration	Sum of Squares	_	_
Number	Error	Α	В
1	1.81547	10.51692	4.58046
2	1.73188	10.71254	4.93394
3	1.73157	10.72751	4.95871
4	1.73157	10.72798	4.95941

This report displays the progress of the search algorithm in its search for a solution. It allows you to assess whether the algorithm had indeed converged or whether the program should be re-run with the Maximum Iterations increased or the model changed.

Note that if over ten iterations were needed, the program does not display every iteration.

Model Estimation

Model Estimation for Type = 1

Rows Used: 21 of 21 lterations: 4
Pseudo-R²: 0.983564
Random Seed: 17448

Para	ameter	Asymptotic	95% Confide Limits for th	
Name	Estimate	Standard Error	Lower	Upper
A B	10.72798 4.95941	0.30895 0.44270	10.08135 4.03282	11.37461 5.88599

Estimated Model (Double Precision)

Response =

(10.7279796046503)*(Temp)/((4.95940560324547)+(Temp))

This report displays the details of the estimation of the model parameters.

Rows Used

The number of rows used in the calculations followed by the number of rows processed.

Iterations

The number of iterations that were completed before the nonlinear algorithm terminated. If the number of iterations is equal to the Maximum Iterations that you set, the algorithm did not converge, but was aborted.

General (Custom and Preset) Model Fit – Y vs One X

Pseudo-R²

There is no direct R-squared defined for nonlinear regression. This is a pseudo R-squared constructed to approximate the usual R-squared value used in multiple regression. We use the following generalization of the usual R-squared formula:

R-Squared = (ModelSS - MeanSS)/(TotalSS-MeanSS)

where *MeanSS* is the sum of squares due to the mean, *ModelSS* is the sum of squares due to the model, and *TotalSS* is the total (uncorrected) sum of squares of Y (the dependent variable).

This version of R-squared tells you how well the model performs after removing the influence of the mean of Y. Since many nonlinear models do not explicitly include a parameter for the mean of Y, this R-squared may be negative (in which case we set it to zero) or difficult to interpret. However, if you think of it as a direct extension of the R-squared that you use in multiple regression, it will serve well for comparative purposes.

Random Seed

This is the value of the random seed that was used when running the bootstrap confidence intervals and randomization tests. If you want to duplicate your results exactly, enter this random seed into the Random Seed box under the Simulation tab.

Parameter Name

The name of the parameter whose results are shown on this line.

Parameter Estimate

The estimated value of this parameter.

Asymptotic Standard Error

An estimate of the standard error of the parameter based on asymptotic (large sample) results.

Lower and Upper 95% Confidence Interval Limits for the Parameter

The lower and upper values of the 95% confidence limits for this parameter. This is a large sample (at least 25 observations for each parameter) confidence limit. In most cases, the bootstrap confidence interval will be more accurate.

Estimated Model

This is the model that was estimated with the parameters replaced with their estimated values. This expression may be copied and pasted as a variable transformation in the spreadsheet. This will allow you to predict for additional values of X. Note that to ensure accuracy, the parameter estimates are always given to double-precision accuracy.

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Analysis of Variance Table

Analysis of Varian	Analysis of Variance for Type = 1						
Source	DF	Sum of Squares	Mean Square				
Mean	1	847.88494	847.88494				
Model	2	951.50296	475.75148				
Model (Adjusted)	1	103.61802	103.61802				
Error	19	1.73157	0.09114				
Total (Adjusted)	20	105.34959					
Total	21	953.23453					

Source

The labels of the various sources of variation.

DF

The degrees of freedom.

Sum of Squares

The sum of squares associated with this term. Note that these sums of squares are based on Y, the dependent variable. Individual terms are defined as follows:

Mean

The sum of squares associated with the mean of Y. This may or may not be a part of the model. It is presented since it is the amount used to adjust the other sums of squares.

Model

The sum of squares associated with the model.

Model (Adjusted)

The model sum of squares minus the mean sum of squares.

Error The sum of the squared residuals. This is often called the sum of squares error or

just "SSE."

Total The sum of the squared Y values.

Total (Adjusted) The sum of the squared Y values minus the mean sum of squares.

Mean Square

The sum of squares divided by the degrees of freedom. The Mean Square for Error is an estimate of the underlying variation in the data.

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Bootstrap Section

Bootstrap	Section	when	Type	= 1
-----------	---------	------	------	-----

Estimation Res	ults		Bootstrap Con	fidence Interva	I Limits
Parameter	Estimate	1	Confidence Level	Lower	Upper
A					
Original Value	10.72798	1	90%	10.244700	11.296540
Bootstrap Mean	10.72736	ł	95%	10.135710	11.385970
Bias (BM - OV)	-0.01872	-	99%	9.988630	11.599560
Bias Corrected Value	10.74670	ı	3370	3.300000	11.000000
Standard Error	0.31672				
В					
Original Value	4.95941	1	90%	4.286410	5.775430
Bootstrap Mean	4.93387	İ	95%	4.175890	5.916290
Bias (BM - OV)	-0.02554	Ĺ	99%	3.938430	6.267310
Bias Corrected Value	4.98494				
Standard Error	0.45076				
Predicted Mean and C	onfidence Li	mits	of Response When T	Temp = 5	
Original Value	5.385853		90%	5.181854	5.525915
Bootstrap Mean	5.394537		95%	5.135468	5.549533
Bias (BM - OV)	0.00868		99%	5.025221	5.599965
Bias Corrected Value	5.37717				
Standard Error	0.10463				
Predicted Mean and C	onfidence Li	mits	of Response When T	Temp = 10	
Original Value	7.171394		90%	7.065913	7.266379
Bootstrap Mean	7.171529		95%	7.044761	7.287542
Bias (BM - OV)	0.00013		99%	6.996003	7.324547
Bias Corrected Value	7.171259				
Standard Error	0.06140				
Predicted Mean and C	onfidence Li	mits	of Response When T	Temp = 15	
Original Value	8.062349		90%	7.936631	8.201722
Bootstrap Mean	8.05754		95%	7.907758	8.233053
Bias (BM - OV)	-0.00481		99%	7.851605	8.287663
Bias Corrected Value	8.067158				
Standard Error	0.08168				
Predicted Mean and C		mits	-	Temp = 20	
Original Value	8.596342		90%	8.423151	8.794850
Bootstrap Mean	8.588529		95%	8.384797	8.832062
Bias (BM - OV)	-0.00781		99%	8.320841	8.921685
Bias Corrected Value	8.604156				
Standard Error	0.11400				
Predicted Value and C	onfidence Li	mits		Гетр = 5	
Original Value	5.385853		90%	4.806019	5.800971
Bootstrap Mean	5.391974		95%	4.700211	5.841319
Bias (BM - OV)	0.00612		99%	4.569519	5.908210
Bias Corrected Value	5.379733				
Standard Error	0.30743				

General (Custom and Preset) Model Fit – Y vs One X

Original Value	7.171394	!	90%	6.651251	7.565130	
Bootstrap Mean	7.168966	- !	95%	6.493280	7.598008	
Bias (BM - OV)	-0.00243	- 1	99%	6.393167	7.650403	
Bias Corrected Value						
Standard Error	0.29582					
Predicted Value and C	onfidence Li	mits	of Response When	Temp = 15		
Original Value	8.062349		90%	7.527347	8.469990	
Bootstrap Mean	8.054977	İ	95%	7.385470	8.513791	
Bias (BM - OV)	-0.00737	Ĺ	99%	7.285653	8.591002	
Bias Corrected Value	8.069721					
Standard Error	0.30082					
Predicted Value and C	onfidence Li	mits	of Response When	Temp = 20		
Original Value	8.596342	1	90%	8.040409	9.028446	
Bootstrap Mean	8.585965	i	95%	7.913822	9.089715	
Bias (BM - OV)	-0.01038	Ĺ	99%	7.784964	9.197958	
Bias Corrected Value	8.606719	•				
Standard Error	0.31122					

This report provides bootstrap estimates and confidence intervals for the parameters, predicted means, and predicted values. Note that bootstrap confidence intervals and prediction intervals are provided for each of the *X* (Temp) value requested. Details of the bootstrap method were presented earlier in this chapter.

Original Value

This is the parameter estimate obtained from the complete sample without bootstrapping.

Bootstrap Mean

This is the average of the parameter estimates of the bootstrap samples.

Bias (BM - OV)

This is an estimate of the bias in the original estimate. It is computed by subtracting the original value from the bootstrap mean.

Bias Corrected Value

This is an estimated of the parameter that has been corrected for its bias. The correction is made by subtracting the estimated bias from the original parameter estimate.

Standard Error

This is the bootstrap method's estimate of the standard error of the parameter estimate. It is simply the standard deviation of the parameter estimate computed from the bootstrap estimates.

Confidence Level

This is the confidence coefficient of the bootstrap confidence interval given to the right.

General (Custom and Preset) Model Fit - Y vs One X

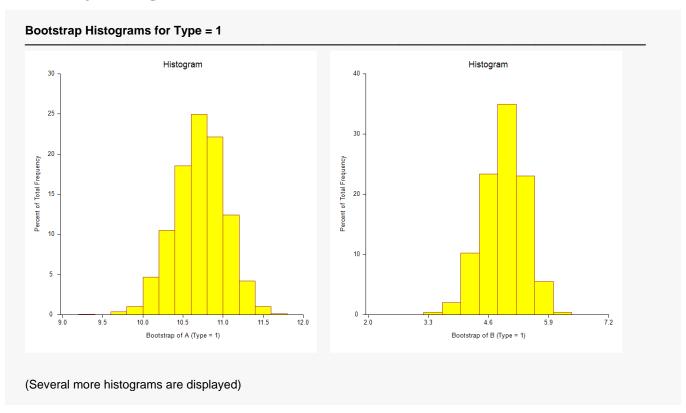
Bootstrap Confidence Interval Limits - Lower and Upper

These are the limits of the bootstrap confidence interval with the confidence coefficient given to the left. These limits are computed using the confidence interval method (percentile or reflection) designated on the Bootstrap panel.

Note that to be accurate, these intervals must be based on over a thousand bootstrap samples and the original sample must be representative of the population.

Bootstrap Histograms

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Each histogram shows the distribution of the corresponding estimate.

Asymptotic Correlation Matrix of Parameter Estimates

	Α	В
1.0	.000000	0.940484
	.940484	1.000000

This report displays the asymptotic correlations of the parameter estimates. When these correlations are high (absolute value greater than 0.98), the precision of the parameter estimates is suspect.

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Predicted Values for Specified X Values

Predicted Values for Specified X Values for Type = 1

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Temp	Predicted Value for Response	95% Prediction Interval Limits for the Predicted Value		
		Lower	Upper	
5	5.38585	4.71548	6.05623	
10	7.17139	6.52162	7.82116	
15	8.06235	7.40400	8.72069	
20	8.59634	7.91914	9.27355	

This section shows the predicted mean values and asymptotic (large sample) prediction intervals for the X values that were specified. Note that these are prediction limits for a new value, not confidence limits for the mean of the values.

Predicted Values and Residuals

Predicted Values and Residuals for Type = 1

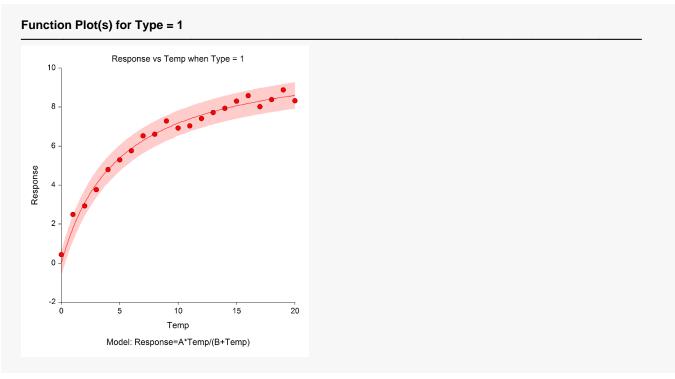
Row	Temp	Response	Predicted Value	95% Prediction Interval Limits for Predicted Value		
				Lower	Upper	Residual
1	0	0.4384633	0.00000	-0.63186	0.63186	0.43846
2	1	2.497315	1.80018	1.14295	2.45740	0.69714
3	2	2.932073	3.08302	2.40603	3.76000	-0.15094
4	3	3.767072	4.04351	3.36238	4.72464	-0.27644
5	4	4.797627	4.78959	4.11244	5.46675	0.00803
6	5	5.294741	5.38585	4.71548	6.05623	-0.09111
7	6	5.762443	5.87330	5.20980	6.53680	-0.11086
8	7	6.525773	6.27923	5.62147	6.93699	0.24654
9	8	6.608124	6.62251	5.96895	7.27607	-0.01439
10	9	7.288437	6.91661	6.26567	7.56756	0.37182

This section shows the values of the predicted values, prediction limits, and residuals. If you have observations in which the independent variable is given, but the dependent (Y) variable is blank, a predicted value and prediction limits will be generated and displayed in this report.

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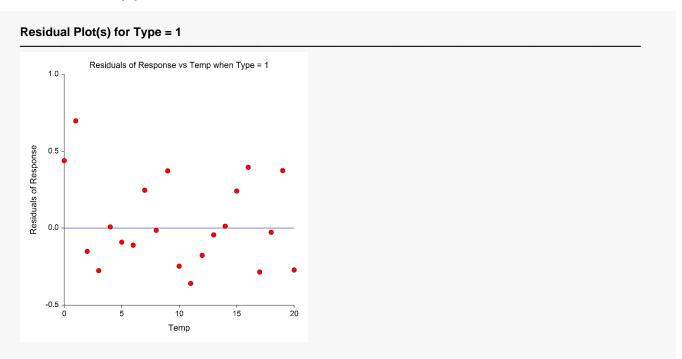
Function Plot(s)

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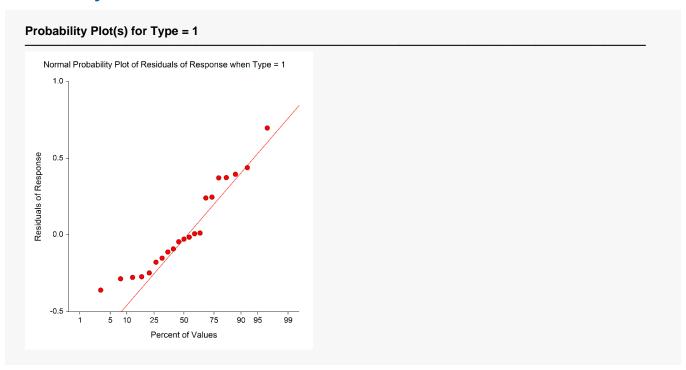
This plot displays the data along with the estimated function. It is useful in deciding if the fit is adequate and the prediction limits are appropriate.

Residual Plot(s)



This is a scatter plot of the residuals versus the independent variable, X. The preferred pattern is a rectangular shape or point cloud. Any nonrandom pattern may require a redefinition of the model.

Probability Plot(s)



If the residuals are normally distributed, the data points of the normal probability plot will fall along a straight line. Major deviations from this ideal picture reflect departures from normality. Stragglers at either end of the normal probability plot indicate outliers, curvature at both ends of the plot indicates long or short distributional tails, convex or concave curvature indicates a lack of symmetry, and gaps or plateaus or segmentation in the normal probability plot may require a closer examination of the data or model. We do not recommend that you use this diagnostic with small sample sizes.