Statistics Toolbox

For Use with MATLAB®

Computation

Visualization

Programming

The MATH WORKS Inc.

User's Guide

Version 2

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Statistics Toolbox User's Guide

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Preface

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Before You Begin

This introduction describes how to begin using the Statistics Toolbox. It explains how to use this guide, and points you to additional books for toolbox installation information.

What Is the Statistics Toolbox?

The Statistics Toolbox is a collection of tools built on the MATLAB® numeric computing environment. The toolbox supports a wide range of common statistical tasks, from random number generation, to curve fitting, to design of experiments and statistical process control. The toolbox provides two categories of tools:

- Building-block probability and statistics functions
- Graphical, interactive tools

The first category of tools is made up of functions that you can call from the command line or from your own applications. Many of these functions are MATLAB M-files, series of MATLAB statements that implement specialized Statistics algorithms. You can view the MATLAB code for these functions using the statement

```
type function_name
```

You can change the way any toolbox function works by copying and renaming the M-file, then modifying your copy. You can also extend the toolbox by adding your own M-files.

Secondly, the toolbox provides a number of interactive tools that let you access many of the functions through a graphical user interface (GUI). Together, the GUI-based tools provide an environment for polynomial fitting and prediction, as well as probability function exploration.

How to Use This Guide

If you are a new user begin with Chapter 1, *Tutorial*. This chapter introduces the MATLAB statistics environment through the toolbox functions. It describes the functions with regard to particular areas of interest, such as probability distributions, linear and nonlinear models, principal components analysis, design of experiments, statistical process control, and descriptive statistics.

All toolbox users should use Chapter 2, *Reference*, for information about specific tools. For functions, reference descriptions include a synopsis of the function's syntax, as well as a complete explanation of options and operation. Many reference descriptions also include examples, a description of the function's algorithm, and references to additional reading material.

Use this guide in conjunction with the software to learn about the powerful features that MATLAB provides. Each chapter provides numerous examples that apply the toolbox to representative statistical tasks.

The random number generation functions for various probability distributions are based on all the primitive functions, `randn` and `rand`. There are many examples that start by generating data using random numbers. To duplicate the results in these examples, first execute the commands below.

```
seed = 931316785;
rand('seed',seed);
randn('seed',seed);
```

You might want to save these commands in an M-file script called `init.m`. Then, instead of three separate commands, you need only type `init`.

Mathematical Notation

This manual and the Statistics Toolbox functions use the following mathematical notation conventions.

β	Parameters in a linear model.
$E(x)$	Expected value of x. $E(x) = \int tf(t)d$
$f(x\|a,b)$	Probability density function. x is the independent variable; a and b are fixed parameters.
$F(x\|a,b)$	Cumulative distribution function.
$I([a, b])$	Indicator function. In this example the function takes the value 1 on the closed interval from a to b and is 0 elsewhere.
p and q	p is the probability of some event. q is the probability of $\sim p$, so $q = 1 - p$.

Typographical Conventions

To Indicate	This Guide Uses	Example
Example code	`Monospace type` (Use **Code** tag.)	To assign the value 5 to `A`, enter `A = 5`
Function names/syntax	`Monospace type` (Use **Code** tag.) For syntax lines, use paragraph tag `Syntax`.	The `cos` function finds the cosine of each array element. Syntax line example is `MLGetVar ML_var_name`
Keys	**Boldface** with an initial capital letter (Use **Menu-Bodytext** tag.)	Press the **Return** key.
Mathematical expressions	Variables in *italics*. Functions, operators, and constants in standard type. (Use **EquationVariables** tag.)	This vector represents the polynomial $p = x^2 + 2x + 3$
MATLAB output	`Monospace type` (Use **Code** tag.)	MATLAB responds with `A =` `5`
Menu names, menu items, and controls	**Boldface** with an initial capital letter (Use **Menu-Bodytext** tag.)	Choose the **File** menu.
New terms	NCS *italics* (Use **Body text-ital** tag.)	An *array* is an ordered collection of information.

In addition, some words in our syntax lines are shown within single quotation marks (sometimes double). These marks are a MATLAB requirement and must be typed. For example,

```
dir dirname
f = hex2num('s')
```

or

```
f ="pressure"
```

Tutorial

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Introduction

The Statistics Toolbox, for use with MATLAB, supplies basic statistics capability on the level of a first course in engineering or scientific statistics. The statistics functions it provides are building blocks suitable for use inside other analytical tools.

Primary Topic Areas

The Statistics Toolbox has more than 200 M-files, supporting work in the topical areas below:

- Probability distributions
- Descriptive statistics
- Cluster Analysis
- Linear models
- Nonlinear models
- Hypothesis tests
- Multivariate statistics
- Statistical plots
- Statistical Process Control
- Design of Experiments

Probability Distributions

The Statistics Toolbox supports 20 probability distributions. For each distribution there are five associated functions. They are:

- Probability density function (pdf)
- Cumulative distribution function (cdf)
- Inverse of the cumulative distribution function
- Random number generator
- Mean and variance as a function of the parameters

For data driven distributions (beta, binomial, exponential, gamma, normal, Poisson, uniform and Weibull), the Statistics Toolbox has functions for computing parameter estimates and confidence intervals.

Descriptive Statistics

The Statistics Toolbox provides functions for describing the features of a data sample. These descriptive statistics include measures of location and spread, percentile estimates and functions for dealing with data having missing values.

Cluster Analysis

The Statistics Toolbox provides functions that allow you to divide a set of objects into subgroups, each having members that are as much alike as possible. This process is called *cluster analysis*.

Linear Models

In the area of linear models the Statistics Toolbox supports one-way and two-way analysis of variance (ANOVA), multiple linear regression, stepwise regression, response surface prediction, and ridge regression.

Nonlinear Models

For nonlinear models there are functions for parameter estimation, interactive prediction and visualization of multidimensional nonlinear fits, and confidence intervals for parameters and predicted values.

Hypothesis Tests

There are also functions that do the most common tests of hypothesis – t-tests and Z-tests.

Multivariate Statistics

The Statistics Toolbox supports methods in Multivariate Statistics, including Principal Components Analysis and Linear Discriminant Analysis.

Statistical Plots

The Statistics Toolbox adds box plots, normal probability plots, Weibull probability plots, control charts, and quantile-quantile plots to the arsenal of graphs in MATLAB. There is also extended support for polynomial curve fitting and prediction.

Statistical Process Control (SPC)

For SPC there are functions for plotting common control charts and performing process capability studies.

Design of Experiments (DOE)

The Statistics Toolbox supports both factorial and D-optimal design. There are functions for generating designs, augmenting designs and optimally assigning units with fixed covariates.

Probability Distributions

Probability distributions arise from experiments where the outcome is subject to chance. The nature of the experiment dictates which probability distributions may be appropriate for modeling the resulting random outcomes. There are two types of probability distributions – *continuous* and *discrete*.

Continuous (data)	Continuous (statistics)	Discrete
Beta	Chi-square	Binomial
Exponential	Noncentral Chi-square	Discrete Uniform
Gamma	F	Geometric
Lognormal	Noncentral F	Hypergeometric
Normal	t	Negative Binomial
Rayleigh	Noncentral t	Poisson
Uniform		
Weibull		

Suppose you are studying a machine that produces videotape. One measure of the quality of the tape is the number of visual defects per hundred feet of tape. The result of this experiment is an integer, since you cannot observe 1.5 defects. To model this experiment you should use a discrete probability distribution.

A measure affecting the cost and quality of videotape is its thickness. Thick tape is more expensive to produce, while variation in the thickness of the tape on the reel increases the likelihood of breakage. Suppose you measure the thickness of the tape every 1000 feet. The resulting numbers can take a continuum of possible values, which suggests using a continuous probability distribution to model the results.

Using a probability model does not allow you to predict the result of any individual experiment but you can determine the probability that a given outcome will fall inside a specific range of values.

Overview of the Functions

MATLAB provides five functions for each distribution:

- Probability density function (pdf)
- Cumulative distribution function (cdf)
- Inverse cumulative distribution function
- Random number generator
- Mean and variance

This section discusses each of these functions.

Probability Density Function (pdf)

The probability density function has a different meaning depending on whether the distribution is discrete or continuous.

For discrete distributions, the pdf is the probability of observing a particular outcome. In our videotape example, the probability that there is exactly one defect in a given hundred feet of tape is the value of the pdf at 1.

Unlike discrete distributions, the pdf of a continuous distribution at a value is not the probability of observing that value. For continuous distributions the probability of observing any particular value is zero. To get probabilities you must integrate the pdf over an interval of interest. For example the probability of the thickness of a videotape being between one and two millimeters is the integral of the appropriate pdf from one to two.

A pdf has two theoretical properties:

- The pdf is zero or positive for every possible outcome.
- The integral of a pdf over its entire range of values is one.

A pdf is not a single function. Rather a pdf is a family of functions characterized by one or more parameters. Once you choose (or estimate) the parameters of a pdf, you have uniquely specified the function.

The pdf function call has the same general format for every distribution in the Statistics Toolbox. The following commands illustrate how to call the pdf for the normal distribution.

```
x = [-3:0.1:3];
f = normpdf(x,0,1);
```

The variable `f` contains the density of the normal pdf with parameters 0 and 1 at the values in `x`. The first input argument of every pdf is the set of values for which you want to evaluate the density. Other arguments contain as many parameters as are necessary to define the distribution uniquely. The normal distribution requires two parameters, a location parameter (the mean, μ) and a scale parameter (the standard deviation, σ).

Cumulative Distribution Function (cdf)

If f is a probability density function, the associated cumulative distribution function F is

$$F(x) = P(X \le x) = \int_{-\infty}^{x} f(t)\,dt$$

The cdf of a value x, $F(x)$, is the probability of observing any outcome less than or equal to x.

A cdf has two theoretical properties:

- The cdf ranges from 0 to 1.
- If $y > x$, then the cdf of y is greater than or equal to the cdf of x.

The cdf function call has the same general format for every distribution in the Statistics Toolbox. The following commands illustrate how to call the cdf for the normal distribution:

```
x = [–3:0.1:3];
p = normcdf(x,0,1);
```

The variable `p` contains the probabilities associated with the normal cdf with parameters 0 and 1 at the values in `x`. The first input argument of every cdf is the set of values for which you want to evaluate the probability. Other arguments contain as many parameters as are necessary to define the distribution uniquely.

Inverse Cumulative Distribution Function

The inverse cumulative distribution function returns critical values for hypothesis testing given significance probabilities. To understand the relationship between a continuous cdf and its inverse function, try the following:

```
x = [–3:0.1:3];
xnew = norminv(normcdf(x,0,1),0,1);
```

How does xnew compare with x? Conversely, try this:

```
p = [0.1:0.1:0.9];
pnew = normcdf(norminv(p,0,1),0,1);
```

How does pnew compare with p?

Calculating the cdf of values in the domain of a continuous distribution returns probabilities between zero and one. Applying the inverse cdf to these probabilities yields the original values.

For discrete distributions, the relationship between a cdf and its inverse function is more complicated. It is likely that there is no x value such that the cdf of x yields p. In these cases the inverse function returns the first value x such that the cdf of x equals or exceeds p. Try this:

```
x = [0:10];
y = binoinv(binocdf(x,10,0.5),10,0.5);
```

How does x compare with y?

The commands below show the problem with going the other direction for discrete distributions.

```
p = [0.1:0.2:0.9];
pnew = binocdf(binoinv(p,10,0.5),10,0.5)

pnew =

    0.1719    0.3770    0.6230    0.8281    0.9453
```

The inverse function is useful in hypothesis testing and production of confidence intervals. Here is the way to get a 99% confidence interval for a normally distributed sample.

```
p = [0.005 0.995];
x = norminv(p,0,1)

x =

   -2.5758    2.5758
```

The variable `x` contains the values associated with the normal inverse function with parameters 0 and 1 at the probabilities in `p`. The difference `p(2) - p(1)` is 0.99. Thus, the values in `x` define an interval that contains 99% of the standard normal probability.

The inverse function call has the same general format for every distribution in the Statistics Toolbox. The first input argument of every inverse function is the set of probabilities for which you want to evaluate the critical values. Other arguments contain as many parameters as are necessary to define the distribution uniquely.

Random Numbers

The methods for generating random numbers from any distribution all start with uniform random numbers. Once you have a uniform random number generator, you can produce random numbers from other distributions either directly or by using inversion or rejection methods.

Direct. Direct methods flow from the definition of the distribution.

As an example, consider generating binomial random numbers. You can think of binomial random numbers as the number of heads in n tosses of a coin with probability p of a heads on any toss. If you generate n uniform random numbers and count the number that are greater than p, the result is binomial with parameters n and p.

Inversion. The inversion method works due to a fundamental theorem that relates the uniform distribution to other continuous distributions.

If F is a continuous distribution with inverse F^{-1}, and U is a uniform random number, then F -1(U) has distribution F.

So, you can generate a random number from a distribution by applying the inverse function for that distribution to a uniform random number. Unfortunately, this approach is usually not the most efficient.

Rejection. The functional form of some distributions makes it difficult or time consuming to generate random numbers using direct or inversion methods. Rejection methods can sometimes provide an elegant solution in these cases.

Suppose you want to generate random numbers from a distribution with pdf f. To use rejection methods you must first find another density, g, and a constant, c, so that the inequality below holds.

$$f(x) \le cg(x) \forall x$$

You then generate the random numbers you want using the following steps:

1 Generate a random number x from distribution G with density g.

2 Form the ratio $r = \frac{cg(x)}{f(x)}$

3 Generate a uniform random number u.

4 If the product of u and r is less than one, return x.

5 Otherwise repeat steps one to three.

For efficiency you need a cheap method for generating random numbers from G and the scalar, c, should be small. The expected number of iterations is c.

Syntax for Random Number Functions. You can generate random numbers from each distribution. This function provides a single random number or a matrix of random numbers, depending on the arguments you specify in the function call.

For example, here is the way to generate random numbers from the beta distribution. Four statements obtain random numbers: the first returns a single number, the second returns a 2-by-2 matrix of random numbers, and the third and fourth return 2-by-3 matrices of random numbers.

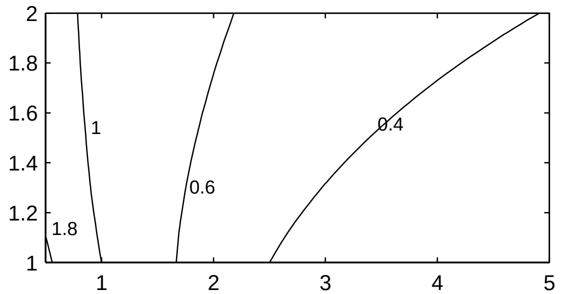
```
a = 1;
b = 2;
c = [.1 .5; 1 2];
d = [.25 .75; 5 10];
m = [2 3];
nrow = 2;
ncol = 3;
r1 = betarnd(a,b)
r1 =

    0.4469


r2 = betarnd(c,d)
r2 =

    0.8931    0.4832
    0.1316    0.2403

r3 = betarnd(a,b,m)
r3 =

    0.4196    0.6078    0.1392
    0.0410    0.0723    0.0782

r4 = betarnd(a,b,nrow,ncol)
r4 =

    0.0520    0.3975    0.1284
    0.3891    0.1848    0.5186
```

Mean and Variance

The mean and variance of a probability distribution are generally simple functions of the parameters of the distribution. The Statistics Toolbox functions ending in stat all produce the mean and variance of the desired distribution given the parameters.

The example shows a contour plot of the mean of the Weibull distribution as a function of the parameters.

```
x = (0.5:0.1:5);
y = (1:0.04:2);
[X,Y] = meshgrid(x,y);
Z = weibstat(X,Y);
[c,h] = contour(x,y,Z,[0.4 0.6 1.0 1.8]);
clabel(c);
```



Overview of the Distributions

The Statistics Toolbox supports 20 probability distributions. These are:

- Beta
- Binomial
- Chi-square
- Noncentral Chi-square
- Discrete Uniform
- Exponential
- F
- Noncentral F
- Gamma
- Geometric
- Hypergeometric

- Lognormal
- Negative Binomial
- Normal
- Poisson
- Rayleigh
- Student's t
- Noncentral t
- Uniform
- Weibull

This section gives a short introduction to each distribution.

Beta Distribution

Background. The beta distribution describes a family of curves that are unique in that they are nonzero only on the interval [0 1]. A more general version of the function assigns parameters to the end-points of the interval.

The beta cdf is the same as the incomplete beta function.

The beta distribution has a functional relationship with the t distribution. If Y is an observation from Student's t distribution with ν degrees of freedom then the following transformation generates X, which is beta distributed:

$$X = \frac{1}{2} + \frac{1}{2}\frac{Y}{\sqrt{\nu + Y^2}}$$

if: $Y \sim t(\nu)$ then $X \sim \beta\left(\frac{\nu}{2}, \frac{\nu}{2}\right)$

The Statistics Toolbox uses this relationship to compute values of the t cdf and inverse function as well as generating t distributed random numbers.

Mathematical Definition. The beta pdf is:

$$y = f(x|a, b) = \frac{1}{B(a, b)} x^{a-1}(1-x)^{b-1} I_{(0, 1)}(x)$$

Parameter Estimation. Suppose you are collecting data that has hard lower and upper bounds of zero and one respectively. Parameter estimation is the process of determining the parameters of the beta distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the beta pdf. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the xs) are already observed. So they are the fixed constants. The variables are the unknown parameters. Maximum likelihood estimation (MLE) involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `betafit` returns the MLEs and confidence intervals for the parameters of the beta distribution. Here is an example using random numbers from the beta distribution with $a = 5$ and $b = 0.2$.

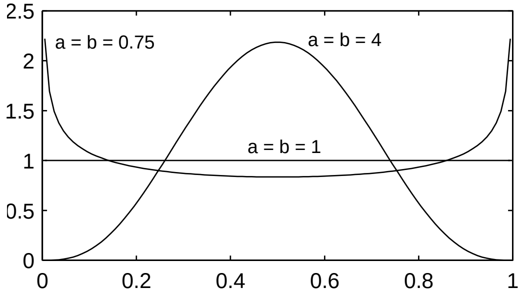
```
r = betarnd(5,0.2,100,1);
[phat, pci] = betafit(r)

phat =

    4.5330    0.2301


pci =

    2.8051    0.1771
    6.2610    0.2832
```

The MLE for the parameter, a is 4.5330 compared to the true value of 5. The 95% confidence interval for a goes from 2.8051 to 6.2610, which includes the true value.

Similarly the MLE for the parameter, b is 0.2301 compared to the true value of 0.2. The 95% confidence interval for b goes from 0.1771 to 0.2832, which also includes the true value.

Of course in this made-up example we know the “true value.” In experimentation we do not.

Example and Plot. The shape of the beta distribution is quite variable depending on the values of the parameters, as illustrated by this plot.



The constant pdf (the flat line) shows that the standard uniform distribution is a special case of the beta distribution.

Binomial Distribution

Background. The binomial distribution models the total number of successes in repeated trials from an infinite population under the following conditions:

- Only two outcomes are possible on each of n trials.
- The probability of success for each trial is constant.
- All trials are independent of each other.

James Bernoulli derived the binomial distribution in 1713 (*Ars Conjectandi*). Earlier, Blaise Pascal had considered the special case where p = 1/2.

Mathematical Definition. The binomial pdf is:

$$y = f(x|n, p) = \binom{n}{x} p^x q^{(1-x)} I_{(0, 1, \ldots, n)}(x)$$

where: $\binom{n}{x} = \frac{n!}{x!(n-x)!}$ and $q = 1 - p$.

The binomial distribution is discrete. For zero and for positive integers less than n, the pdf is nonzero.

Parameter Estimation. Suppose you are collecting data from a widget manufacturing process, and you record the number of widgets within specification in each batch of 100. You might be interested in the probability that an individual widget is within specification. Parameter estimation is the process of determining the parameter, *p*, of the binomial distribution that fits this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the binomial pdf above. But for the pdf, the parameters (*n* and *p*) are known constants and the variable is *x*. The likelihood function reverses the roles of the variables. Here, the sample values (the *x*s) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the value of *p* that give the highest likelihood given the particular set of data.

The function `binofit` returns the MLEs and confidence intervals for the parameters of the binomial distribution. Here is an example using random numbers from the binomial distribution with $n = 100$ and $p = 0.9$.

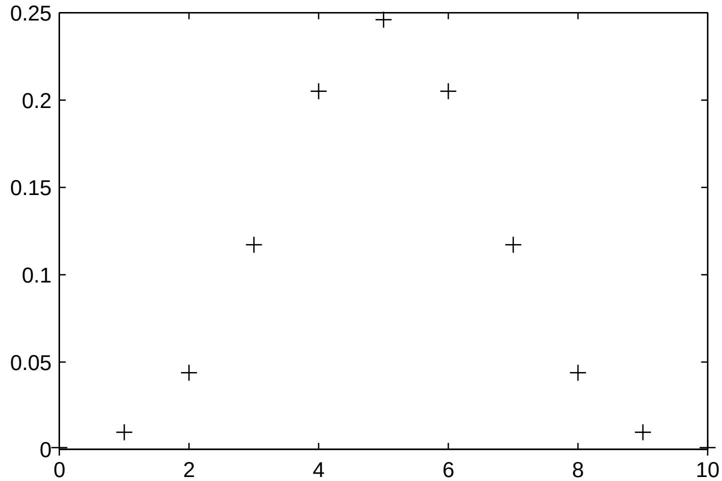
```
r = binornd(100,0.9)

r =

    88

[phat, pci] = binofit(r,100)

phat =

    0.8800


pci =

    0.7998
    0.9364
```

The MLE for the parameter, *p* is 0.8800 compared to the true value of 0.9. The 95% confidence interval for *p* goes from 0.7998 to 0.9364, which includes the true value.

Of course in this made-up example we know the “true value” of *p*.

Example and Plot. The following commands generate a plot of the binomial pdf for n = 10 and p = 1/2.

```
x = 0:10;
y = binopdf(x,10,0.5);
plot(x,y,'+')
```



Chi-Square (χ^2) Distribution

Background. The χ^2 distribution is a special case of the gamma distribution where $b = 2$, in the equation for gamma distribution below.

$$y = f(x|a, b) = \frac{1}{b^a\Gamma(a)} x^{a-1} e^{-\frac{x}{b}}$$

The χ^2 distribution gets special attention because of its importance in normal sampling theory. If a set of n observations are normally distributed with variance σ^2, and s^2 is the sample standard deviation, then:

$$\frac{(n-1)s^2}{\sigma^2} \sim \chi^2(n-1)$$

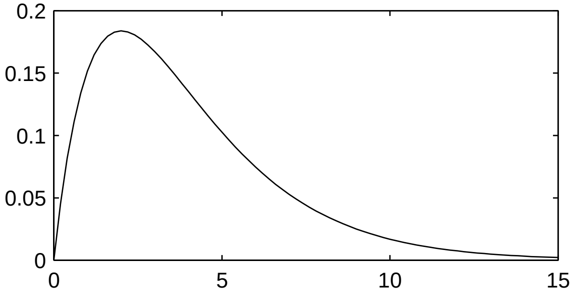
The Statistics Toolbox uses the above relationship to calculate confidence intervals for the estimate of the normal parameter σ^2 in the function `normfit`.

Mathematical Definition. The χ^2 pdf is:

$$y = f(x \mid \nu) = \frac{x^{(\nu-2)/2} e^{-x/2}}{2^{\frac{\nu}{2}} \Gamma(\nu/2)}$$

Example and Plot. The χ^2 distribution is skewed to the right especially for few degrees of freedom (ν). The plot shows the χ^2 distribution with four degrees of freedom.

```
x = 0:0.2:15;
y = chi2pdf(x,4);
plot(x,y)
```



Noncentral Chi-Square Distribution

Background. The χ^2 distribution is actually a simple special case of the noncentral chi-square distribution. One way to generate random numbers with a χ^2 distribution (with ν degrees of freedom) is to sum the squares of ν standard normal random numbers (mean equal to zero.)

What if we allow the normally distributed quantities to have a mean other than zero? The sum of squares of these numbers yields the noncentral chi-square distribution. The noncentral chi-square distribution requires two parameters: the degrees of freedom and the noncentrality. The noncentrality parameter is the sum of the squared means of the normally distributed quantities.

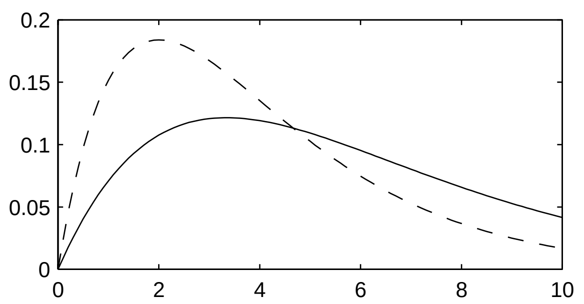
The noncentral chi-square has scientific application in thermodynamics and signal processing. The literature in these areas may refer to it as the Ricean or generalized Rayleigh distribution.

Mathematical Definition. There are many equivalent formulas for the noncentral chi-square distribution function. One formulation uses a modified Bessel function of the first kind. Another uses the generalized Laguerre polynomials. The Statistics Toolbox computes the cumulative distribution function values using a weighted sum of χ^2 probabilities with the weights equal to the probabilities of a Poisson distribution. The Poisson parameter is one-half of the noncentrality parameter of the noncentral chi-square.

$$F(x|\nu,\delta) = \sum_{j=0}^{\infty}\left(\frac{\left(\frac{1}{2}\delta\right)^{j}}{j!}e^{-\frac{\delta}{2}}\right)Pr[\chi^2_{\nu+2j} \le x]$$

Example and Plot. The following commands generate a plot of the noncentral chi-square pdf.

```
x = (0:0.1:10)';
p1 = ncx2pdf(x,4,2);
p = chi2pdf(x,4);
plot(x,p,'--',x,p1,'-')
```



Discrete Uniform Distribution

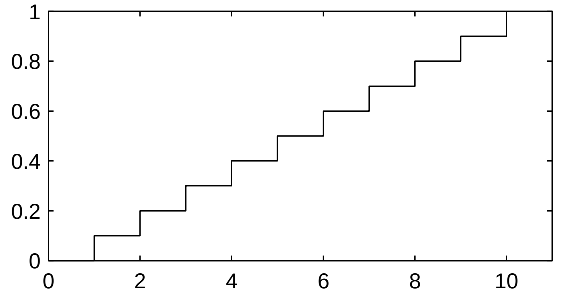
Background. The discrete uniform distribution is a simple distribution that puts equal weight on the integers from one to N.

Mathematical Definition. The discrete uniform pdf is:

$$y = f(x|N) = \frac{1}{N} I_{(1, \ldots, N)}(x)$$

Example and Plot. As for all discrete distributions, the cdf is a step function. The plot shows the discrete uniform cdf for $N = 10$.

```
x = 0:10;
y = unidcdf(x,10);
stairs(x,y)
set(gca,'Xlim',[0 11])
```



To pick a random sample of 10 from a list of 553 items:

```
numbers = unidrnd(553,1,10)

numbers =
   293   372     5   213    37   231   380   326   515   468
```

Exponential Distribution

Background. Like the chi-square, the exponential distribution is a special case of the gamma distribution (obtained by setting a = 1 in the equation below.)

$$y = f(x|a,b) = \frac{1}{b^a \Gamma(a)} x^{a-1} e^{-\frac{x}{b}}$$

The exponential distribution is special because of its utility in modeling events that occur randomly over time. The main application area is in studies of lifetimes.

Mathematical Definition. The exponential pdf is:

$$y = f(x|\mu) = \frac{1}{\mu} e^{-\frac{x}{\mu}}$$

Parameter Estimation. Suppose you are stress testing light bulbs and collecting data on their lifetimes. You assume that these lifetimes follow an exponential distribution. You want to know how long you can expect the average light bulb to last. Parameter estimation is the process of determining the parameters of the exponential distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the beta pdf on the previous page. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the xs) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `expfit` returns the MLEs and confidence intervals for the parameters of the exponential distribution. Here is an example using random numbers from the exponential distribution with $\mu = 700$.

```
lifetimes = exprnd(700,100,1);
[muhat, muci] = expfit(lifetimes)
muhat =
  672.8207

muci =

  547.4338
  810.9437
```

The MLE for the parameter, μ is 672 compared to the true value of 700. The 95% confidence interval for μ goes from 547 to 811, which includes the true value.

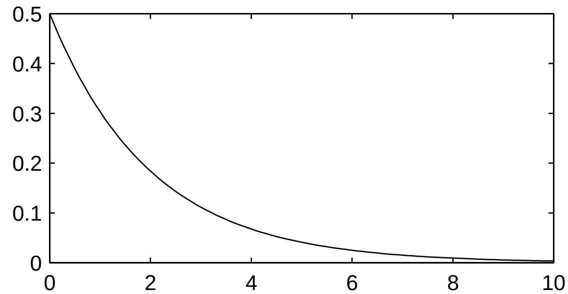
In our life tests we do not know the true value of μ so it is nice to have a confidence interval on the parameter to give a range of likely values.

Example and Plot. For exponentially distributed lifetimes, the probability that an item will survive an extra unit of time is independent of the current age of the item. The example shows a specific case of this special property.

```
l = 10:10:60;
lpd = l+0.1;
deltap = (expcdf(lpd,50)–expcdf(l,50))./(1–expcdf(l,50))

deltap =

    0.0020    0.0020    0.0020    0.0020    0.0020    0.0020
```

The plot shows the exponential pdf with its parameter (and mean), *lambda*, set to two.

```
x = 0:0.1:10;
y = exppdf(x,2);
plot(x,y)
```



F Distribution

Background. The F distribution has a natural relationship with the chi-square distribution. If χ_1 and χ_2 are both chi-square with ν_1 and ν_2 degrees of freedom respectively, then the statistic, F is F distributed.

$$F(\nu_1, \nu_2) = \frac{\frac{\chi_1}{\nu_1}}{\frac{\chi_2}{\nu_2}}$$

The two parameters, ν_1 and ν_2, are the numerator and denominator degrees of freedom. That is, ν_1 and ν_2 are the number of independent pieces information used to calculate χ_1 and χ_2 respectively.

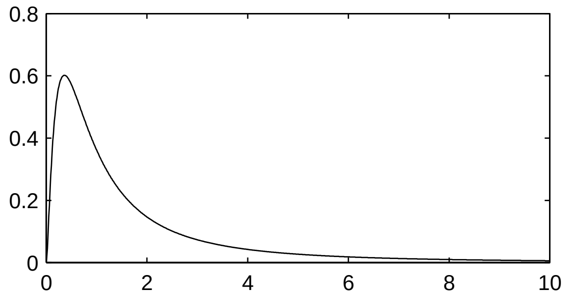
Mathematical Definition. The pdf for the F distribution is:

$$y = f(x|\nu_1,\nu_2) = \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}}\frac{x^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)x\right]^{\frac{\nu_1+\nu_2}{2}}}$$

Example and Plot. The most common application of the F distribution is in standard tests of hypotheses in analysis of variance and regression.

The plot shows that the F distribution exists on the positive real numbers and is skewed to the right.

```
x = 0:0.01:10;
y = fpdf(x,5,3);
plot(x,y)
```



Noncentral F Distribution

Background. As with the χ^2 the F distribution is a special case of the noncentral F distribution. The F distribution is the result of taking the ratio of two χ^2 random variables each divided by its degrees of freedom.

If the numerator of the ratio is a noncentral chi-square random variable divided by its degrees of freedom, the resulting distribution is the noncentral F.

The main application of the noncentral F distribution is to calculate the power of a hypothesis test relative to a particular alternative.

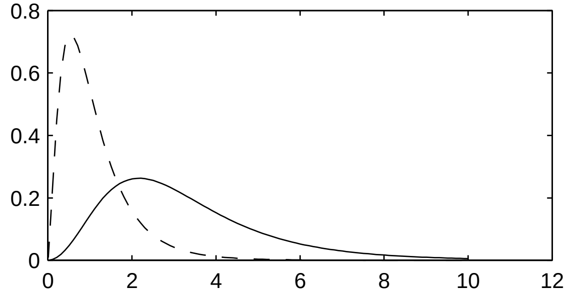
Mathematical Definition. Similarly to the noncentral chi-square, the Statistics Toolbox calculates noncentral F distribution probabilities as a weighted sum of incomplete beta function using Poisson probabilities as the weights.

$$F(x|\nu_1, \nu_2, \delta) = \sum_{j=0}^{\infty} \left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!} e^{-\frac{\delta}{2}} \right) I\left(\frac{\nu_1 \cdot x}{\nu_2 + \nu_1 \cdot x} \middle| \frac{\nu_1}{2} + j, \frac{\nu_2}{2} \right)$$

where *I(x | a,b)* is the incomplete beta function with parameters *a* and *b*.

Example and Plot. The following commands generate a plot of the noncentral F pdf.

```
x = (0.01:0.1:10.01)';
p1 = ncfpdf(x,5,20,10);
p  = fpdf(x,5,20);
plot(x,p,'--',x,p1,'-')
```



Gamma Distribution

Background. The gamma distribution is a family of curves based on two parameters. The chi-square and exponential distributions, which are children of the gamma distribution, are one-parameter distributions that fix one of the two gamma parameters.

The gamma distribution has the following relationship with the incomplete gamma function:

$$\Gamma(x|a,b) = \text{gammainc}\left(\frac{x}{b},a\right)$$

For $b = 1$ the functions are identical.

When a is large, the gamma distribution closely approximates a normal distribution with the advantage that the gamma distribution has density only for positive real numbers.

Mathematical Definition. The gamma pdf is:

$$y = f(x|a,b) = \frac{1}{b^a\Gamma(a)}x^{a-1}e^{-\frac{x}{b}}$$

Parameter Estimation. Suppose you are stress testing computer memory chips and collecting data on their lifetimes. You assume that these lifetimes follow a gamma distribution. You want to know how long you can expect the average computer memory chip to last. Parameter estimation is the process of determining the parameters of the gamma distribution that fit this data best in some sense.

One popular criterion of goodness is to maximize the likelihood function. The likelihood has the same form as the gamma pdf above. But for the pdf, the parameters are known constants and the variable is x. The likelihood function reverses the roles of the variables. Here, the sample values (the xs) are already observed. So they are the fixed constants. The variables are the unknown parameters. MLE involves calculating the values of the parameters that give the highest likelihood given the particular set of data.

The function `gamfit` returns the MLEs and confidence intervals for the parameters of the gamma distribution. Here is an example using random numbers from the gamma distribution with $a = 10$ and $b = 5$.

```
lifetimes = gamrnd(10,5,100,1);
[phat, pci] = gamfit(lifetimes)
phat =
   10.9821    4.7258

pci =

    7.4001    3.1543
   14.5640    6.2974
```

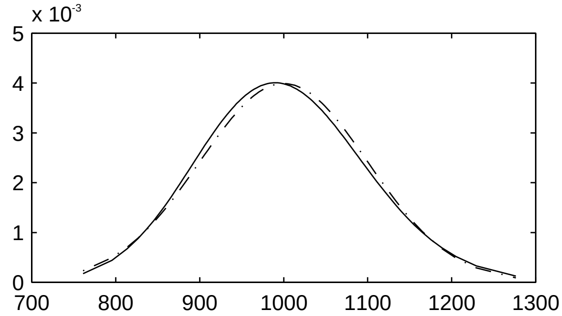
Note `phat(1)` = $\hat{a}$ and `phat(2)` = $\hat{b}$. The MLE for the parameter, a is 10.98 compared to the true value of 10. The 95% confidence interval for a goes from 7.4 to 14.6, which includes the true value.

Similarly the MLE for the parameter, b is 4.7 compared to the true value of 5. The 95% confidence interval for b goes from 3.2 to 6.3, which also includes the true value.

In our life tests we do not know the true value of a and b so it is nice to have a confidence interval on the parameters to give a range of likely values.

Example and Plot. In the example the gamma pdf is plotted with the solid line. The normal pdf has a dashed line type.

```
x = gaminv((0.005:0.01:0.995),100,10);
y = gampdf(x,100,10);
y1 = normpdf(x,1000,100);
plot(x,y,'-',x,y1,'-.')
```



Geometric Distribution

Background. The geometric distribution is discrete, existing only on the nonnegative integers. It is useful for modeling the runs of consecutive successes (or failures) in repeated independent trials of a system.

The geometric distribution models the number of successes before one failure in an independent succession of tests where each test results in success or failure.

Mathematical Definition. The geometric pdf is:

$$y = f(x|p) = pq^x I_{(0, 1, \mathrm{K})}(x)$$

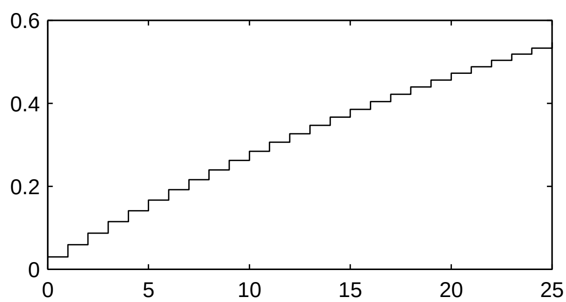
where $q = 1 - p$

Example and Plot. Suppose the probability of a five-year-old battery failing in cold weather is 0.03. What is the probability of starting 25 consecutive days during a long cold snap?

```
1 – geocdf(25,0.03)

ans =

    0.4530
```

The plot shows the cdf for this scenario.

```
x = 0:25;
y = geocdf(x,0.03);
stairs(x,y)
```



Hypergeometric Distribution

Background. The hypergeometric distribution models the total number of successes in a fixed size sample drawn without replacement from a finite population.

The distribution is discrete, existing only for nonnegative integers less than the number of samples or the number of possible successes, whichever is greater.

The hypergeometric distribution differs from the binomial only in that the population is finite and the sampling from the population is without replacement.

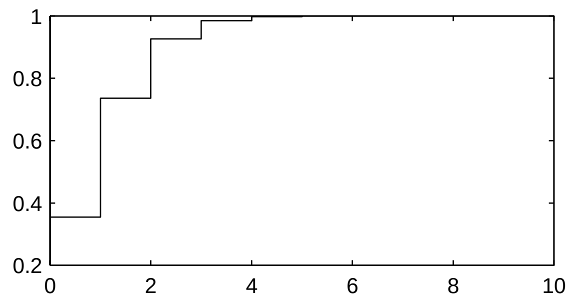
The hypergeometric distribution has three parameters that have direct physical interpretation. M is the size of the population. K is the number of items with the desired characteristic in the population. n is the number of samples drawn. Sampling “without replacement” means that once a particular sample is chosen, it is removed from the relevant population for drawing the next sample.

Mathematical Definition. The hypergeometric pdf is:

$$y = f(x|M,K,n) = \frac{\binom{K}{x}\binom{M-K}{n-x}}{\binom{M}{n}}$$

Example and Plot. The plot shows the cdf of an experiment taking 20 samples from a group of 1000 where there are 50 items of the desired type.

```
x = 0:10;
y = hygecdf(x,1000,50,20);
stairs(x,y)
```



Lognormal Distribution

Background. The normal and lognormal distributions are closely related. If X is distributed lognormal with parameters μ and σ^2, then lnX is distributed normal with parameters μ and σ^2.

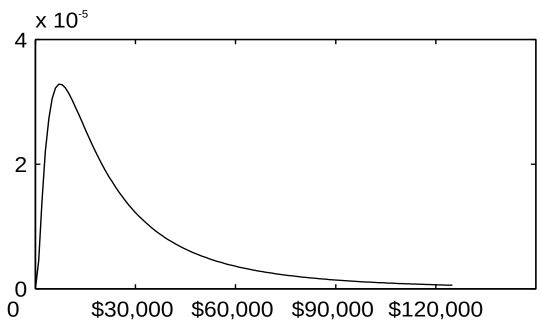
The lognormal distribution is applicable when the quantity of interest must be positive, since lnX exists only when the random variable X is positive. Economists often model the distribution of income using a lognormal distribution.

Mathematical Definition. The lognormal pdf is:

$$y = f(x|\mu, \sigma) = \frac{1}{x\sigma\sqrt{2\pi}} e^{\frac{-(\ln x - \mu)^2}{2\sigma^2}}$$

Example and Plot. Suppose the income of a family of four in the United States follows a lognormal distribution with $\mu = \log(20{,}000)$ and $\sigma^2 = 1.0$. Plot the income density.

```
x = (10:1000:125010)';
y=lognpdf(x,log(20000),1.0);
plot(x,y)
set(gca,'Xtick',[0 30000 60000 90000 120000 ])
set(gca,'xticklabel',str2mat('0','$30,000','$60,000',...
'$90,000','$120,000'))
```



Negative Binomial Distribution

Background. The geometric distribution is a special case of the negative binomial distribution (also called the Pascal distribution). The geometric distribution models the number of successes before one failure in an independent succession of tests where each test results in success or failure.

In the negative binomial distribution the number of failures is a parameter of the distribution. The parameters are the probability of success, p, and the number of failures, r.

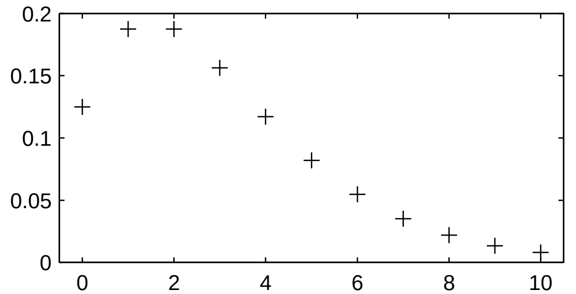
Mathematical Definition. The negative binomial pdf is

$$y = f(x|r, p) = \binom{r + x - 1}{x} p^r q^x I_{(0, 1, \ldots)}(x)$$

where $q = 1 - p$

Example and Plot. The following commands generate a plot of the negative binomial pdf.

```
x = (0:10);
y = nbinpdf(x,3,0.5);
plot(x,y,'+')
set(gca,'XLim',[-0.5,10.5])
```



Normal Distribution

Background. The normal distribution is a two parameter family of curves. The first parameter, μ, is the mean. The second, σ, is the standard deviation. The standard normal distribution (written $\Phi(x)$) sets μ to zero and σ to one.

$\Phi(x)$ is functionally related to the error function, *erf*.

$$erf(x) = 2\Phi(x\sqrt{2}) - 1$$

The first use of the normal distribution was as a continuous approximation to the binomial.

The usual justification for using the normal distribution for modeling is the Central Limit Theorem which states (roughly) that the sum of independent samples from any distribution with finite mean and variance converges to the normal distribution as the sample size goes to infinity.

Mathematical Definition. The normal pdf is:

$$y = f(x|\mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}$$

Parameter Estimation. One of the first applications of the normal distribution in data analysis was modeling the height of school children. Suppose we want to estimate the mean, μ, and the variance, σ^2, of all the 4th graders in the United States.

We have already introduced MLEs. Another desirable criterion in a statistical estimator is unbiasedness. A statistic is unbiased if the expected value of the statistic is equal to the parameter being estimated. MLEs are not always unbiased. For any data sample, there may be more than one unbiased estimator of the parameters of the parent distribution of the sample. For instance, every sample value is an unbiased estimate of the parameter μ of a normal distribution. The Minimum Variance Unbiased Estimator (MVUE) is the statistic that has the minimum variance of all unbiased estimators of a parameter.

The MVUEs of the parameters, μ and σ^2 for the normal distribution are the sample average and variance. The sample average is also the MLE for μ. There are two common textbook formulas for the variance.

They are:

$$1)\quad s^2 = \frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2$$

$$2)\quad s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2$$

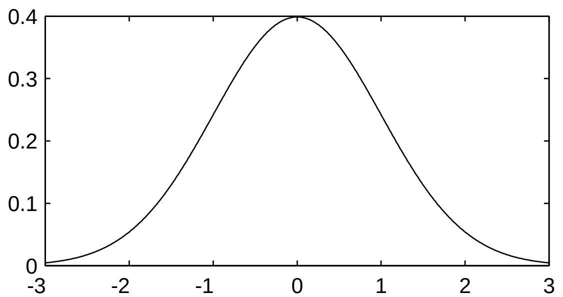
$$\text{where } \bar{x} = \sum^{n} \frac{x_i}{n}$$

Equation 1 is the maximum likelihood estimator for σ^2, and equation 2 is the MVUE.

The function `normfit` returns the MVUEs and confidence intervals for μ and σ^2. Here is a playful example modeling the "heights" (inches) of a randomly chosen 4th grade class.

```
height = normrnd(50,2,30,1); % Simulate heights.
[mu, s, muci, sci] = normfit(height)
mu =
   50.2025
s =
    1.7946
muci =
   49.5210
   50.8841
sci =
    1.4292
    2.4125
```

Example and Plot. The plot shows the "bell" curve of the standard normal pdf $\mu = 0, \sigma = 1$.



Poisson Distribution

Background. The Poisson distribution is appropriate for applications that involve counting the number of times a random event occurs in a given amount of time, distance, area, etc. Sample applications that involve Poisson distributions include the number of Geiger counter clicks per second, the number of people walking into a store in an hour, and the number of flaws per 1000 feet of video tape.

The Poisson distribution is a one parameter discrete distribution that takes nonnegative integer values. The parameter, λ, is both the mean and the variance of the distribution. Thus, as the size of the numbers in a particular sample of Poisson random numbers gets larger, so does the variability of the numbers.

As Poisson (1837) showed, the Poisson distribution is the limiting case of a binomial distribution where N approaches infinity and p goes to zero while $Np = \lambda$.

The Poisson and exponential distributions are related. If the number of counts follows the Poisson distribution, then the interval between individual counts follows the exponential distribution.

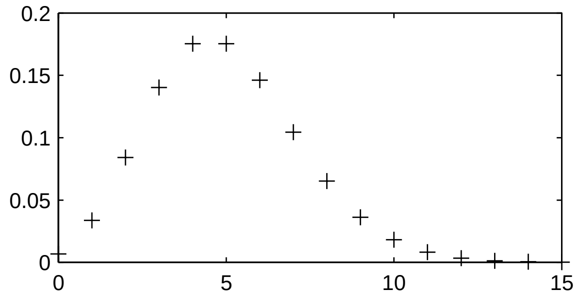
Mathematical Definition. The Poisson pdf is:

$$y = f(x|\lambda) = \frac{\lambda^x}{x!} e^{-\lambda} I_{(0, 1, K)}(x)$$

Parameter Estimation. The MLE and the MVUE of the Poisson parameter, λ, is the sample mean. The sum of independent Poisson random variables is also Poisson with parameter equal to the sum of the individual parameters. The Statistics Toolbox makes use of this fact to calculate confidence intervals on λ. As λ gets large the Poisson distribution can be approximated by a normal distribution with $\mu = \lambda$ and $\sigma^2 = \lambda$. The Statistics Toolbox uses this approximation for calculating confidence intervals for values of λ greater than 100.

Example and Plot. The plot shows the probability for each nonnegative integer when $\lambda = 5$.

```
x = 0:15;
y = poisspdf(x,5);
plot(x,y,'+')
```



Rayleigh Distribution

Background. The Rayleigh distribution is a special case of the Weibull distribution substituting 2 for the parameter p in the equation below:

$$y = f\left(x\middle|\frac{b^2}{2}, p\right) = \frac{b^2}{2} p^{p-1} e^{-\frac{b^2}{2}x^p} I_{(0,\infty)}(x)$$

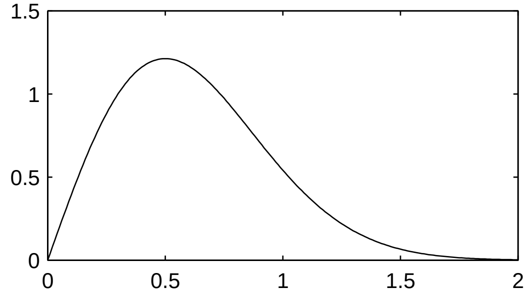
If the velocity of a particle in the x and y directions are two independent normal random variables with zero means and equal variances, then the distance the particle travels per unit time is distributed Rayleigh.

Mathematical Definition. The Rayleigh pdf is:

$$y = f(x|b) = \frac{x}{b^2} e^{\left(\frac{-x^2}{2b^2}\right)}$$

Example and Plot. The following commands generate a plot of the Rayleigh pdf.

```
x = [0:0.01:2];
p = raylpdf(x,0.5);
plot(x,p)
```



Parameter Estimation. The MLE of the Rayleigh parameter is:

$$b = \frac{\sum_{i=1}^{n} x_i^{2}}{2n}$$

Student's t Distribution

Background. The t distribution is a family of curves depending on a single parameter ν (the degrees of freedom). As ν goes to infinity the t distribution converges to the standard normal distribution.

W. S. Gossett (1908) discovered the distribution through his work at Guinness brewery. At that time, Guinness did not allow its staff to publish, so Gossett used the pseudonym Student.

If x and s are the mean and standard deviation of an independent random sample of size n from a normal distribution with mean μ, and $\sigma^2 = n$, then:

$$t(\nu) = \frac{x - \mu}{s}$$

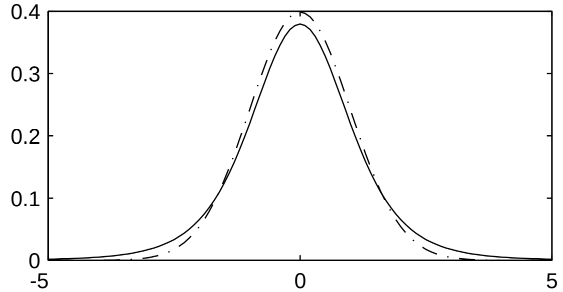
$$\nu = n - 1$$

Mathematical Definition. Student's t pdf is:

$$y = f(x|\nu) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{x^2}{\nu}\right)^{\frac{\nu+1}{2}}}$$

Example and Plot. The plot compares the t distribution with $\nu = 5$ (solid line) to the shorter tailed standard normal distribution (dashed line).

```
x = –5:0.1:5;
y = tpdf(x,5);
z = normpdf(x,0,1);
plot(x,y,'–',x,z,'–.')
```



Noncentral t Distribution

Background. The noncentral t distribution is a generalization of the familiar Student's t distribution.

If x and s are the mean and standard deviation of an independent random sample of size n from a normal distribution with mean μ, and $\sigma^2 = n$, then:

$$t(\nu) = \frac{x-\mu}{s}$$

$$\nu = n-1$$

Suppose that the mean of the normal distribution is not μ. Then the ratio has the noncentral t distribution. The noncentrality parameter is the difference between the sample mean and μ.

The noncentral t distribution allows us to determine the probability that we would detect a difference between x and μ in a t test. This probability is the *power* of the test. As x–μ increases, the power of a test also increases.

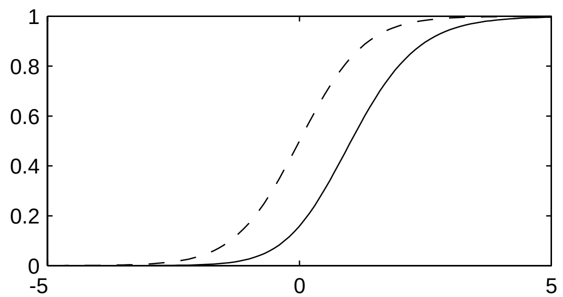
Mathematical Definition. The most general representation of the noncentral t distribution is quite complicated. Johnson and Kotz (1970) give a formula for the probability that a noncentral t variate falls in the range [–t, t].

$$Pr((-t) < x < t|(\nu, \delta)) = \sum_{j=0}^{\infty}\left(\frac{\left(\frac{1}{2}\delta^2\right)^j}{j!}e^{-\frac{\delta^2}{2}}\right)I\left(\frac{x^2}{\nu + x^2}\middle|\frac{1}{2}+j, \frac{\nu}{2}\right)$$

where $I(x \mid a,b)$ is the incomplete beta function with parameters a and b.

Example and Plot. The following commands generate a plot of the noncentral t pdf.

```
x = (–5:0.1:5)';
p1 = nctcdf(x,10,1);
p = tcdf(x,10);
plot(x,p,'––',x,p1,'–')
```



Uniform (Continuous) Distribution

Background. The uniform distribution (also called rectangular) has a constant pdf between its two parameters a, the minimum, and b, the maximum. The standard uniform distribution (a = 0 and b =1) is a special case of the beta distribution, setting both of its parameters to one.

The uniform distribution is appropriate for representing the distribution of round-off errors in values tabulated to a particular number of decimal places.

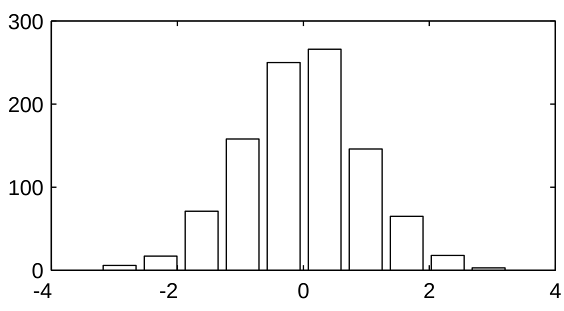
Mathematical Definition. The uniform cdf is:

$$p = F(x|a,b) = \frac{x-a}{b-a} I_{[a,b]}(x)$$

Parameter Estimation. The sample minimum and maximum are the MLEs of a and b respectively.

Example and Plot. The example illustrates the inversion method for generating normal random numbers using `rand` and `norminv`. Note that the MATLAB function, `randn`, does not use inversion since it is not efficient for this case.

```
u = rand(1000,1);
x = norminv(u,0,1);
hist(x)
```



Weibull Distribution

Background. Waloddi Weibull (1939) offered the distribution that bears his name as an appropriate analytical tool for modeling breaking strength of materials. Current usage also includes reliability and lifetime modeling. The Weibull distribution is more flexible than the exponential for these purposes.

To see why, consider the hazard rate function (instantaneous failure rate). If $f(t)$ and $F(t)$ are the pdf and cdf of a distribution, then the hazard rate is:

$$h(t) = \frac{f(t)}{1-F(t)}$$

Substituting the pdf and cdf of the exponential distribution for *f(t)* and *F(t)* above yields a constant. The example on the next page shows that the hazard rate for the Weibull distribution can vary.

Mathematical Definition. The Weibull pdf is:

$$y = f(x|a,b) = abx^{b-1}e^{-ax^b}I_{(0,\infty)}(x)$$

Parameter Estimation. Suppose we want to model the tensile strength of a thin filament using the Weibull distribution. The function `weibfit` give MLEs and confidence intervals for the Weibull parameters.

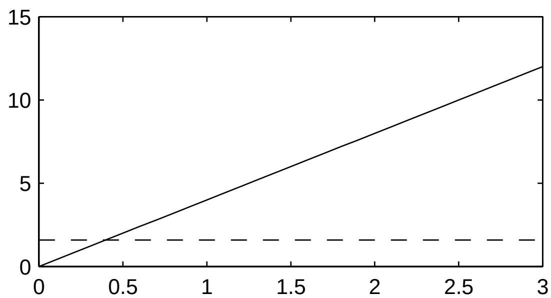
```
strength = weibrnd(0.5,2,100,1); % Simulated strengths.
[p, ci] = weibfit(strength)

p =

    0.4746    1.9582


ci =

    0.3851    1.6598
    0.5641    2.2565
```

The default 95% confidence interval for each parameter contains the “true” value.

Example and Plot. The exponential distribution has a constant hazard function, which is not generally the case for the Weibull distribution.

The plot shows the hazard functions for exponential (dashed line) and Weibull (solid line) distributions having the same mean life. The Weibull hazard rate here increases with age (a reasonable assumption).

```
t = 0:0.1:3;
h1 = exppdf(t,0.6267)./(1 - expcdf(t,0.6267));
h2 = weibpdf(t,2,2)./(1 - weibcdf(t,2,2));
plot(t,h1,'--',t,h2,'-')
```



Descriptive Statistics

Data samples can have thousands (even millions) of values. Descriptive statistics are a way to summarize this data into a few numbers that contain most of the relevant information.

Measures of Central Tendency (Location)

The purpose of measures of central tendency is to locate the data values on the number line. In fact, another term for these statistics is measures of location.

The table gives the function names and descriptions.

Measures of Location	
`geomean`	Geometric Mean.
`harmmean`	Harmonic Mean.
`mean`	Arithmetic average (in MATLAB).
`median`	50th percentile (in MATLAB).
`trimmean`	Trimmed Mean.

The average is a simple and popular estimate of location. If the data sample comes from a normal distribution, then the sample average is also optimal (MVUE of μ).

Unfortunately, outliers, data entry errors, or glitches exist in almost all real data. The sample average is sensitive to these problems. One bad data value can move the average away from the center of the rest of the data by an arbitrarily large distance.

The median and trimmed mean are two measures that are resistant (robust) to outliers. The median is the 50th percentile of the sample, which will only change slightly if you add a large perturbation to any value. The idea behind the trimmed mean is to ignore a small percentage of the highest and lowest values of a sample for determining the center of the sample.

The geometric mean and harmonic mean, like the average, are not robust to outliers. They are useful when the sample is distributed lognormal or heavily skewed.

The example shows the behavior of the measures of location for a sample with one outlier.

```
x = [ones(1,6) 100]

x =

1     1     1     1     1     1   100

locate = [geomean(x) harmmean(x) mean(x) median(x) ...
trimmean(x,25)]

locate =

    1.9307    1.1647   15.1429    1.0000    1.0000
```

You can see that the mean is far from any data value because of the influence of the outlier. The median and trimmed mean ignore the outlying value and describe the location of the rest of the data values.

Measures of Dispersion

The purpose of measures of dispersion is to find out how spread out the data values are on the number line. Another term for these statistics is measures of spread.

The table gives the function names and descriptions.

Measures of Dispersion	
`iqr`	Interquartile Range.
`mad`	Mean Absolute Deviation.
`range`	Range.

Measures of Dispersion	
`std`	Standard Deviation (in MATLAB).
`var`	Variance.

The range (the difference between the maximum and minimum values) is the simplest measure of spread. But if there is an outlier in the data, it will be the minimum or maximum value. Thus, the range is not robust to outliers.

The standard deviation and the variance are popular measures of spread that are optimal for normally distributed samples. The sample variance is the MVUE of the normal parameter σ^2. The standard deviation is the square root of the variance and has the desirable property of being in the same units as the data. That is, if the data is in meters the standard deviation is in meters as well. The variance is in meters^2, which is more difficult to interpret.

Neither the standard deviation nor the variance is robust to outliers. A data value that is separate from the body of the data can increase the value of the statistics by an arbitrarily large amount.

The Mean Absolute Deviation (MAD) is also sensitive to outliers. But the MAD does not move quite as much as the standard deviation or variance in response to bad data.

The Interquartile Range (IQR) is the difference between the 75th and 25th percentile of the data. Since only the middle 50% of the data affects this measure, it is robust to outliers.

The example below shows the behavior of the measures of dispersion for a sample with one outlier.

```
x = [ones(1,6) 100]

x =

     1     1     1     1     1     1   100

stats = [iqr(x) mad(x) range(x) std(x)]

stats =

         0   24.2449   99.0000   37.4185
```

Functions for Data with Missing Values (NaNs)

Most real-world datasets have one or more missing elements. It is convenient to code missing entries in a matrix as `NaN` (Not a Number.)

Here is a simple example:

```
m = magic(3);
m([1 5 9]) = [NaN NaN NaN]

m =

   NaN     1     6
     3   NaN     7
     4     9   NaN
```

Simply removing any row with a `NaN` in it would leave us with nothing, but any arithmetic operation involving `NaN` yields `NaN` as below.

```
sum(m)

ans =

   NaN   NaN   NaN
```

The `NaN` functions support the tabled arithmetic operations ignoring `NaN`.

```
nansum(m)

ans =

     7    10    13
```

NaN Functions	
`nanmax`	Maximum ignoring `NaN`s.
`nanmean`	Mean ignoring `NaN`s.
`nanmedian`	Median ignoring `NaN`s.
`nanmin`	Minimum ignoring `NaN`s.

NaN Functions	
nanstd	Standard deviation ignoring NaNs.
nansum	Sum ignoring NaNs.

Percentiles and Graphical Descriptions

Trying to describe a data sample with two numbers, a measure of location and a measure of spread, is frugal but may be misleading.

Another option is to compute a reasonable number of the sample percentiles. This provides information about the shape of the data as well as its location and spread.

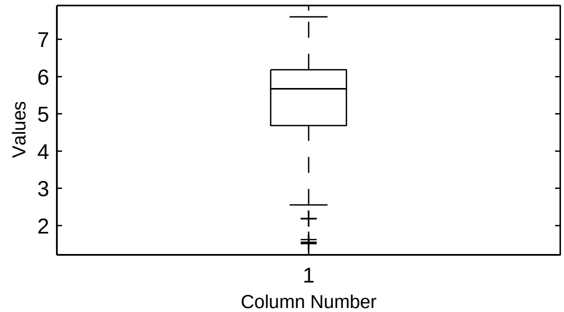
The example shows the result of looking at every quartile of a sample containing a mixture of two distributions.

```
x = [normrnd(4,1,1,100) normrnd(6,0.5,1,200)];
p = 100*(0:0.25:1);
y = prctile(x,p);
z = [p; y]

z =

         0   25.0000   50.0000   75.0000  100.0000
    1.5172    4.6842    5.6706    6.1804    7.6035
```

Compare the first two quantiles to the rest.

The box plot is a graph for descriptive statistics. The graph below is a box plot of the data above.

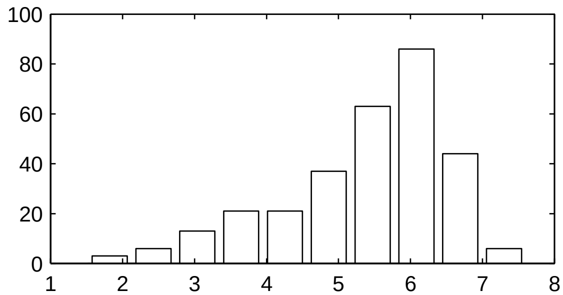
```
boxplot(x)
```



The long lower tail and plus signs show the lack of symmetry in the sample values. For more information on box plots see page 1-103.

The histogram is a complementary graph.

```
hist(x)
```



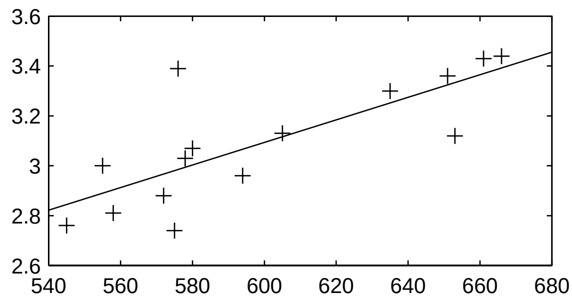
The Bootstrap

In the last decade the statistical literature has examined the properties of resampling as a means to acquire information about the uncertainty of statistical estimators.

The bootstrap is a procedure that involves choosing random samples *with replacement* from a data set and analyzing each sample the same way. Sampling *with replacement* means that every sample is returned to the data set after sampling. So a particular data point from the original data set could appear multiple times in a given bootstrap sample. The number of elements in each bootstrap sample equals the number of elements in the original data set. The range of sample estimates we obtain allows us to establish the uncertainty of the quantity we are estimating.

Here is an example taken from Efron and Tibshirani (1993) comparing LSAT scores and subsequent law school GPA for a sample of 15 law schools.

```
load lawdata
plot(lsat,gpa,'+')
lsline
```



The least squares fit line indicates that higher LSAT scores go with higher law school GPAs. But how sure are we of this conclusion? The plot gives us some intuition but nothing quantitative.

We can calculate the correlation coefficient of the variables using the corrcoef function.

```
rhohat = corrcoef(lsat,gpa)

rhohat =

    1.0000    0.7764
    0.7764    1.0000
```

Now we have a number, 0.7764, describing the positive connection between LSAT and GPA, but though 0.7764 may seem large, we still do not know if it is statistically significant.

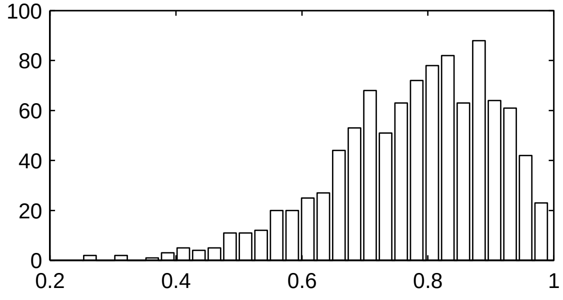
Using the `bootstrp` function we can resample the `lsat` and `gpa` vectors as many times as we like and consider the variation in the resulting correlation coefficients.

Here is an example:

```
rhos1000 = bootstrp(1000,'corrcoef',lsat,gpa);
```

This command resamples the `lsat` and `gpa` vectors 1000 times and computes the `corrcoef` function on each sample. Here is a histogram of the result.

```
hist(rhos1000(:,2),30)
```



Nearly all the estimates lie on the interval [0.4 1.0].

This is strong quantitative evidence that LSAT and subsequent GPA are positively correlated. Moreover, it does not require us to make any strong assumptions about the probability distribution of the correlation coefficient.

Cluster Analysis

Cluster analysis, also called segmentation analysis or taxonomy analysis, is a way to partition a set of objects into groups, or *clusters*, in such a way that the profiles of objects in the same cluster are very similar and the profiles of objects in different clusters are quite distinct.

Cluster analysis can be performed on many different types of datasets. For example, a dataset might contain a number of observations of subjects in a study where each observation contains a set of variables.

Many different fields of study, such as engineering, zoology, medicine, linguistics, anthropology, psychology, and marketing, have contributed to the development of clustering techniques and the application of such techniques. For example, cluster analysis can be used to find two similar groups for the experiment and control groups in a study. In this way, if statistical differences are found in the groups, they can be attributed to the experiment and not to any initial difference between the groups.

Terminology and Basic Procedure

To perform cluster analysis on a dataset using the Statistics Toolbox functions, follow this procedure:

1. **Find the similarity or dissimilarity between every pair of objects in the dataset**. In this step, you calculate the *distance* between objects using the `pdist` function. The `pdist` function supports many different ways to compute this measurement. See the section "Finding the Similarities Between Objects" for more information.

2. **Group the objects into a binary, hierarchical cluster tree.** In this step, you link together pairs of objects that are in close proximity using the `linkage` function. The `linkage` function uses the distance information generated in step 1 to determine the proximity of objects to each other. As objects are paired into binary clusters, the newly formed clusters are grouped into larger clusters until a hierarchical tree is formed. See the section "Defining the Links Between Objects" for more information.

3. **Determine where to divide the hierarchical tree into clusters**. In this step, you divide the objects in the hierarchical tree into clusters using the `cluster` function. The `cluster` function can create clusters by detecting

natural groupings in the hierarchical tree or by cutting off the hierarchical tree at an arbitrary point. See the section “Creating Clusters” for more information.

The following sections provide more information about each of these steps.

Note The Statistics Toolbox includes a convenience function, `clusterdata`, which performs all these steps for you. You do not need to execute the `pdist`, `linkage`, or `cluster` functions separately. However, the `clusterdata` function does not give you access to the options each of the individual routines offers. For example, if you use the `pdist` function, you can choose the distance calculation method.

Finding the Similarities Between Objects

You use the `pdist` function to calculate the distance between every pair of objects in a dataset. For a dataset made up of m objects, there are $m \cdot (m-1)/2$ pairs in the dataset. The result of this computation is commonly known as a similarity matrix (or dissimilarity matrix).

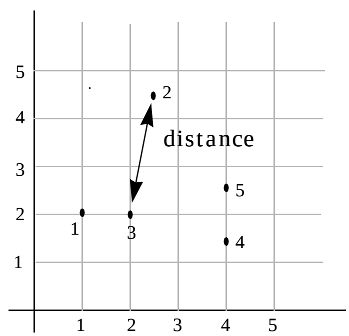
There are many ways to calculate this distance information. By default, the `pdist` function calculates the Euclidean distance between objects; however, you can specify one of several other options. See `pdist` for more information.

Note You can optionally normalize the values in the dataset before calculating the distance information. In a real world dataset, variables can be measured against different scales. For example, one variable can measure IQ test scores and another variable measure head circumference. These discrepancies can distort the proximity calculations. Using the `zscore` function, you can convert all the values in the dataset to use the same proportional scale. See the `zscore` function for more information.

For example, consider a data set, X, made up of five objects where each object is a set of *x*,*y* coordinates.

Object	Value	
1	1	2
2	2.5	4.5
3	2	2
4	4	1.5
5	4	2.5

You can define this dataset as a matrix, `X = [1 2;2.5 4.5;2 2;4 1.5;4 2.5]`, and pass it to `pdist`. The `pdist` function calculates the distance between object 1 and object 2, object 1 and object 3, and so on until the distances between all the pairs have been calculated. The following figure plots these objects in a graph. The distance between object 2 and object 3 is shown to illustrate one interpretation of distance.



Returning Distance Information

The `pdist` function returns this distance information in a vector, `Y`, where each element contains the distance between a pair of objects.

```
Y = pdist(X)
Y =
  Columns 1 through 7
   2.9155   1.0000   3.0414   3.0414   2.5495   3.3541   2.5000
  Columns 8 through 10
    2.0616    2.0616    1.0000
```

To make it easier to see the relationship between the distance information generated by `pdist` and the objects in the original dataset, you can reformat the distance vector into a matrix using the `squareform` function. In this matrix, element *i*,*j* corresponds to the distance between object *i* and object *j* in the original dataset. In the following example, element 1,1 represents the distance between object 1 and itself (which is zero). Element 1,2 represents the distance between object 1 and object 2, and so on.

```
squareform(Y)
ans =
         0    2.9155    1.0000    3.0414    3.0414
    2.9155         0    2.5495    3.3541    2.5000
    1.0000    2.5495         0    2.0616    2.0616
    3.0414    3.3541    2.0616         0    1.0000
    3.0414    2.5000    2.0616    1.0000         0
```

Defining the Links Between Objects

Once the proximity between objects in the dataset has been computed, you can determine which objects in the data set should be grouped together into clusters, using the `linkage` function. The `linkage` function takes the distance information generated by `pdist` and links pairs of objects that are close together into binary clusters (clusters made up of two objects). The `linkage` function then links these newly formed clusters to other objects to create bigger clusters until all the objects in the original data set are linked together in a hierarchical tree.

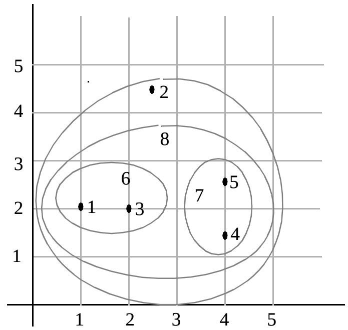
For example, given the distance vector, Y, generated by `pdist` from the sample dataset of *x* and *y* coordinates, the `linkage` function generates a hierarchical cluster tree, returning the linkage information in a matrix, Z.

```
Z = linkage(Y)
Z =
     1.0000    3.0000    1.0000
     4.0000    5.0000    1.0000
     6.0000    7.0000    2.0616
     8.0000    2.0000    2.5000
```

In this output, each row identifies a link. The first two columns identify the objects that have been linked, that is, object 1, object 2, and so on. The third column contains the distance between these objects. For the sample dataset of *x* and *y* coordinates, the `linkage` function begins by grouping together objects 1 and 3, which have the closest proximity (distance value = 1.0000). The `linkage` function continues by grouping objects 4 and 5, which also have a distance value of 1.0000.

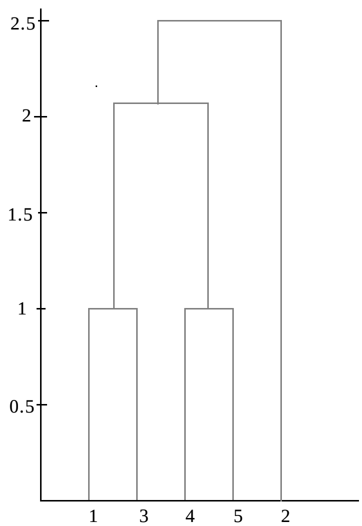
The third row indicates that the `linkage` function grouped together objects 6 and 7. If our original sample dataset contained only 5 objects, what are objects 6 and 7? Object 6 is the newly formed binary cluster created by the grouping of objects 1 and 3. When the `linkage` function groups two objects together into a new cluster, it must assign the cluster a unique index value, starting with the value $m+1$, where m is the number of objects in the original dataset. (Values 1 through m are already used by the original dataset.) Object 7 is the index for the cluster formed by objects 4 and 5.

As the final cluster, the `linkage` function grouped object 8, the newly formed cluster made up of objects 6 and 7, with object 2 from the original dataset. The following figure graphically illustrates the way `linkage` groups the objects into a hierarchy of clusters.



The hierarchical, binary cluster tree created by the `linkage` function is most easily understood when viewed graphically. The Statistics Toolbox includes the `dendrogram` function that plots this hierarchical tree information as a graph, as in the following example.

```
dendrogram(Z)
```



In the figure, the numbers along the horizontal axis represent the indices of the objects in the original dataset. The links between objects are represented as upside down U-shaped lines. The height of the U indicates the distance between the objects. For example, the link representing the cluster containing objects 1 and 3 has a height of 1. For more information about creating a dendrogram diagram, see the `dendrogram` function reference page.

Evaluating Cluster Formation

After linking the objects in a dataset into a hierarchical cluster tree, you may want to verify that the tree represents significant similarity groupings. In addition, you may want more information about the links between the objects. The Statistics Toolbox provides functions to perform both these tasks.

Verifying the Cluster Tree

One way to measure the validity of the cluster information generated by the `linkage` function is to compare it with the original proximity data generated by the `pdist` function. If the clustering is valid, the linking of objects in the cluster tree should have a strong correlation with the distances between objects in the distance vector. The `cophenet` function compares these two sets of values and computes their correlation, returning a value called the *cophenetic correlation coefficient*. The closer the value of the cophenetic correlation coefficient is to 1, the better the clustering solution.

You can use the cophenetic correlation coefficient to compare the results of clustering the same dataset using different distance calculation methods or clustering algorithms.

For example, you can use the `cophenet` function to evaluate the clusters created for the sample dataset

```
c = cophenet(Z,Y)
c =
    0.8573
```

where `Z` is the matrix output by the `linkage` function and `Y` is the distance vector output by the `pdist` function.

Execute `pdist` again on the same dataset, this time specifying the City Block metric. After running the `linkage` function on this new `pdist` output, use the `cophenet` function to evaluate the clustering using a different distance metric.

```
c = cophenet(Z,Y)

c =
    0.9289
```

The cophenetic correlation coefficient shows a stronger correlation when the City Block metric is used.

Getting More Information about Cluster Links

One way to determine the natural cluster divisions in a dataset is to compare the length of each link in a cluster tree with the lengths of neighboring links below it in the tree.

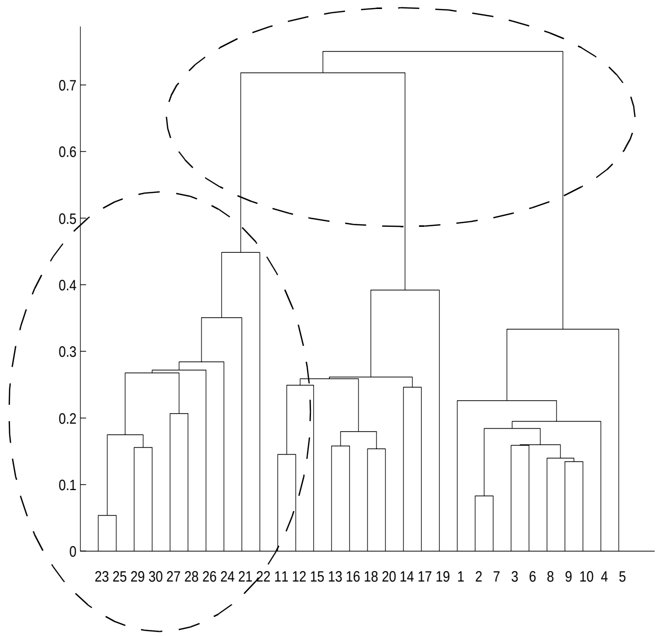
If a link is approximately the same length as neighboring links, it indicates that there are similarities between the objects joined at this level of the hierarchy. These links are said to exhibit a high level of consistency.

If the length of a link differs from neighboring links, it indicates that there are dissimilarities between the objects at this level in the cluster tree. This link is said to be inconsistent with the links around it. In cluster analysis, inconsistent links can indicate the border of a natural division in a dataset. The `cluster` function uses a measure of inconsistency to determine where to divide a dataset into clusters. (See "Creating Clusters" for more information.)

To illustrate, the following example creates a dataset of random numbers with three deliberate natural groupings. In the dendrogram, note how the objects tend to collect into three groups. These three groups are then connected by three longer links. These longer links are inconsistent when compared with the links below them in the hierarchy.

```
rand('seed',3)
X = [rand(10,2)+1;rand(10,2)+2;rand(10,2)+3];
Y = pdist(X);
Z = linkage(Y);
dendrogram(Z);
```

These links show inconsistency, when compared to links below them.



These links show consistency

The relative consistency of each link in a hierarchical cluster tree can be quantified and expressed as the *inconsistency coefficient*. This value compares the length of a link in a cluster hierarchy with the average length of neighboring links. If the object is consistent with those around it, it will have a low inconsistency coefficient. If the object is inconsistent with those around it, it will have a higher inconsistency coefficient.

To generate a listing of the inconsistency coefficient for each link the cluster tree, use the `inconsistent` function. The `inconsistent` function compares each link in the cluster hierarchy with adjacent links two levels below it in the cluster hierarchy. This is called the *depth* of the comparison. Using the `inconsistent` function, you can specify other depths. The objects at the bottom of the cluster tree, called leaf nodes, that have no further objects below them, have an inconsistency coefficient of zero.

For example, returning to the sample dataset of *x* and *y* coordinates, let's use the `inconsistent` function to calculate the inconsistency values for the links created by the `linkage` function, described in "Defining the Links Between Objects" on page 1-53.

```
I = inconsistent(Z)
I =
    1.0000         0    1.0000         0
    1.0000         0    1.0000         0
    1.3539    0.8668    3.0000    0.8165
    2.2808    0.3100    2.0000    0.7071
```

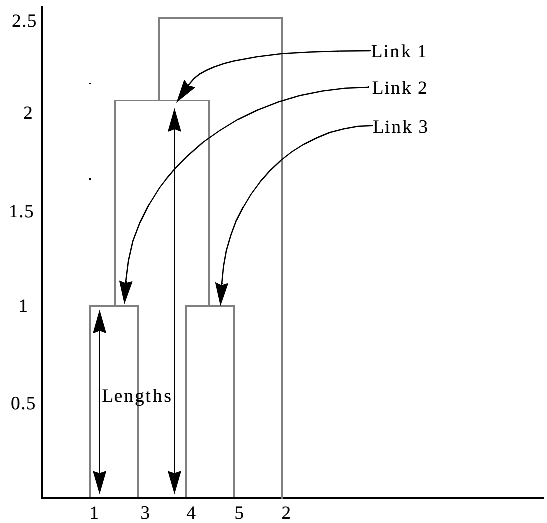
The `inconsistent` function returns data about the links in an *m*-1 by 4 matrix where each column provides data about the links.

Column	Description
1	Mean of the lengths of all the links included in the calculation.
2	Standard deviation of all the links included in the calculation.
3	Number of links included in the calculation.
4	Inconsistency coefficient.

In the sample output, the first row represents the link between objects 1 and 3. (This cluster is assigned the index 6 by the linkage function.) Because this a leaf node, the inconsistency coefficient is zero. The second row represents the link between objects 4 and 5, also a leaf node. (This cluster is assigned the index 7 by the linkage function.)

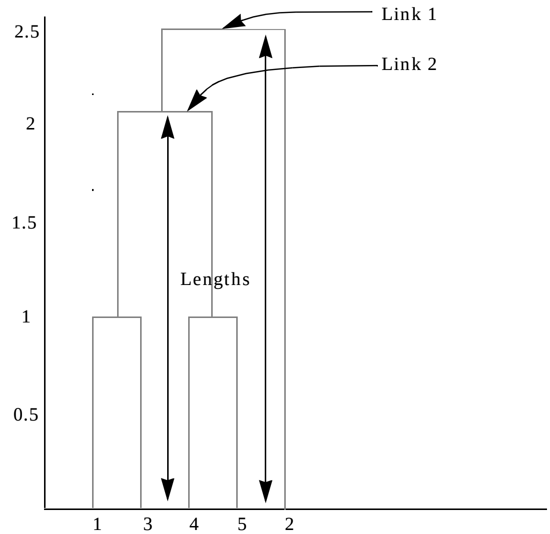
The third row evaluates the link that connects these two leaf nodes, objects 6 and 7. (This cluster is called object 8 in the linkage output). Column three indicates that three links are considered in the calculation: the link itself and the two links directly below it in the hierarchy. Column one represents the mean of the lengths of these links. The `inconsistent` function uses the length information output by the `linkage` function to calculate the mean. Column two represents the standard deviation between the links. The last column contains the inconsistency value for these links, 0.8165.

The following figure illustrates the links and lengths included in this calculation.



Row four in the output matrix describes the link between object 8 and object 2. Column three indicates that two links are included in this calculation: the link itself and the link directly below it in the hierarchy. The inconsistency coefficient for this link is 0.7071.

The following figure illustrates the links and lengths included in this calculation.



Creating Clusters

After you create the hierarchical tree of binary clusters, you can divide the hierarchy into larger clusters using the `cluster` function. The `cluster` function lets you create clusters in two ways:

- By finding the natural divisions in the original data set
- By specifying an arbitrary number of clusters

Finding the Natural Divisions in the Dataset

In the hierarchical cluster tree, the dataset may naturally align itself into clusters. This can be particularly evident in a dendrogram diagram where groups of objects are densely packed in certain areas and not in others. The inconsistency coefficient of the links in the cluster tree can identify these points where the similarities between objects change. (See "Evaluating Cluster Formation" for more information about the inconsistency coefficient.) You can use this value to determine where the `cluster` function draws cluster boundaries.

For example, if you use the `cluster` function to group the sample dataset into clusters, specifying an inconsistency coefficient threshold of 0.9 as the value of the `cutoff` argument, the `cluster` function groups all the objects in the sample dataset into one cluster. In this case, none of the links in the cluster hierarchy had an inconsistency coefficient greater than 0.9.

```
T = cluster(Z,0.9)
T =
      1
      1
      1
      1
      1
```

The `cluster` function outputs a vector, `T`, that is the same size as the original dataset. Each element in this vector contains the number of the cluster into which the corresponding object from the original data set was placed.

If you lower the inconsistency coefficient threshold to 0.8, the `cluster` function divides the sample dataset into three separate clusters.

```
T = cluster(Z,0.8)
T =
     1
     3
     1
     2
     2
```

This output indicates that objects 1 and 3 were placed in cluster 1, objects 4 and 5 were placed in cluster 2, and object 2 was placed in cluster 3.

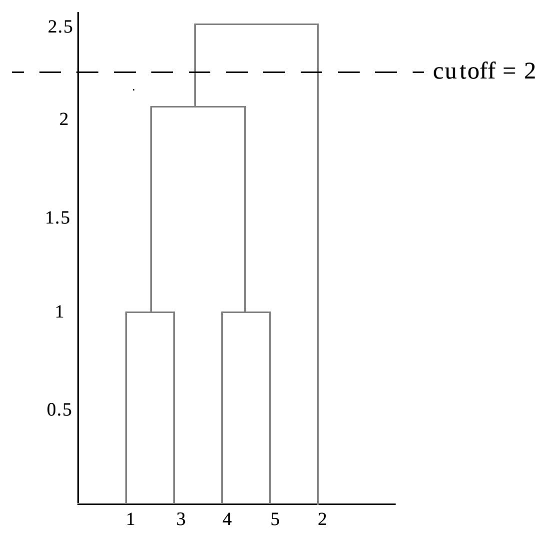
Specifying Arbitrary Clusters

Instead of letting the `cluster` function create clusters determined by the natural divisions in the data set, you can specify the number of clusters you want created. In this case, the value of the `cutoff` argument specifies the point in the cluster hierarchy at which to create the clusters.

For example, you can specify that you want the `cluster` function to divide the sample dataset into two clusters. In this case, the `cluster` function creates one cluster containing objects 1, 3, 4, and 5 and another cluster containing object 2.

```
T = cluster(Z,2)
T =
    1
    2
    1
    1
    1
```

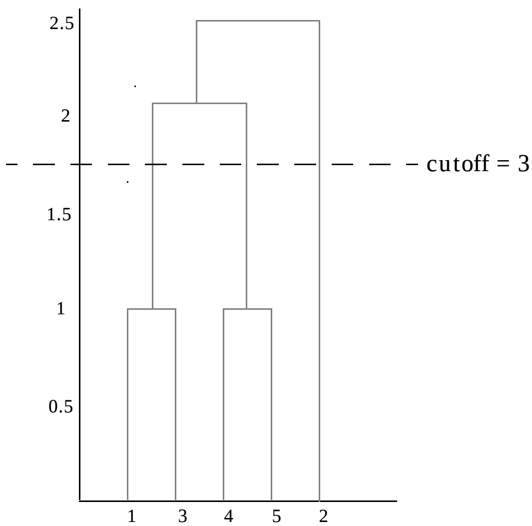
To help you visualize how the `cluster` function determines how to create these clusters, the following figure shows the dendrogram of the hierarchical cluster tree. When you specify a value of 2, the cluster function draws an imaginary horizontal line across the dendrogram that bisects two vertical lines. All the objects below the line belong to one of these two clusters.



If you specify a `cutoff` value of 3, the `cluster` function cuts off the hierarchy at a lower point, bisecting three lines.

```
T = cluster(Z,3)
T =
     1
     3
     1
     2
     2
```

This time, objects 1 and 3 are grouped in a cluster, objects 4 and 5 are grouped in a cluster and object 2 is placed into a cluster, as seen in the following figure.



Linear Models

Linear models are problems that take the form

$$y = X\beta + \varepsilon$$

where:

- y is an n by 1 vector of observations.
- X is the n by p design matrix for the model.
- β is a p by 1 vector of parameters.
- ε is an n by 1 vector of random disturbances.

One-way analysis of variance (ANOVA), two-way ANOVA, polynomial regression, and multiple linear regression are specific cases of the linear model.

One-Way Analysis of Variance (ANOVA)

The purpose of a one-way ANOVA is to find out whether data from several groups have a common mean. That is, to determine whether the groups are actually different in the measured characteristic.

One-way ANOVA is a simple special case of the linear model. The one-way ANOVA form of the model is

$$y_{ij} = \alpha_{.j} + \varepsilon_{ij}$$

where:

- y_{ij} is a matrix of observations.
- $\alpha_{.j}$ is a matrix whose columns are the group means. (The “dot j” notation means that α applies to all rows of the jth column.)
- ε_{ij} is a matrix of random disturbances.

The model posits that the columns of y are a constant plus a random disturbance. You want to know if the constants are all the same.

The data below comes from a study by Hogg and Ledolter (1987) of bacteria counts in shipments of milk. The columns of the matrix `hogg` represent different shipments. The rows are bacteria counts from cartons of milk chosen randomly from each shipment. Do some shipments have higher counts than others?

```
load hogg
p = anova1(hogg)

p =

   1.1971e-04

hogg

hogg =

    24    14    11     7    19
    15     7     9     7    24
    21    12     7     4    19
    27    17    13     7    15
    33    14    12    12    10
    23    16    18    18    20
```

The standard ANOVA table has columns for the sums of squares, degrees of freedom, mean squares (SS/df), and F statistic.

ANOVA Table

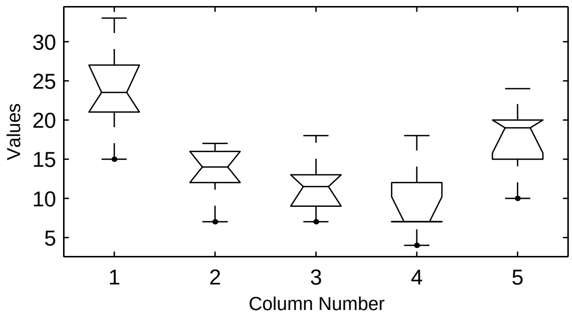
Source	SS	df	MS	F
Columns	803	4	200.7	9.008
Error	557.2	25	22.29	
Total	1360	29		

You can use the F statistic to do a hypothesis test to find out if the bacteria counts are the same. anova1 returns the p-value from this hypothesis test.

In this case the p-value is about 0.0001, a very small value. This is a strong indication that the bacteria counts from the different tankers are not the same. An F statistic as extreme as the observed F would occur by chance only once in 10,000 times if the counts were truly equal.

The p-value returned by anova1 depends on assumptions about the random disturbances in the model equation. For the p-value to be correct, these disturbances need to be independent, normally distributed and have constant variance.

You can get some graphic assurance that the means are different by looking at the box plots in the second figure window displayed by anova1.



Since the notches in the box plots do not all overlap, this is strong confirming evidence that the column means are not equal.

Two-Way Analysis of Variance (ANOVA)

The purpose of two-way ANOVA is to find out whether data from several groups have a common mean. One-way ANOVA and two-way ANOVA differ in that the groups in two-way ANOVA have two categories of defining characteristics instead of one.

Suppose an automobile company has two factories that both make three models of car. It is reasonable to ask if the gas mileage in the cars varies from factory to factory as well as model to model.

There could be an overall difference in mileage due to a difference in the production methods between factories. There is probably a difference in the mileage of the different models (irrespective of the factory) due to differences in design specifications. These effects are called *additive*.

Finally, a factory might make high mileage cars in one model (perhaps because of a superior production line), but not be different from the other factory for other models. This effect is called an *interaction*. It is impossible to detect an interaction unless there are duplicate observations for some combination of factory and car model.

Two-way ANOVA is a special case of the linear model. The two-way ANOVA form of the model is

$$y_{ijk} = \mu + \alpha_{.j} + \beta_{i.} + \gamma_{ij} + \varepsilon_{ijk}$$

where:

- y_{ijk} is a matrix of observations.
- μ is a constant matrix of the overall mean.
- $\alpha_{.j}$ is a matrix whose columns are the group means (the rows of α sum to 0).
- $\beta_{i.}$ is a matrix whose rows are the group means (the columns of β sum to 0).
- γ_{ij} is a matrix of interactions (the rows and columns of γ sum to zero).
- ε_{ijk} is a matrix of random disturbances.

The purpose of the example is to determine the effect of car model and factory on the mileage rating of cars.

```
load mileage
mileage

mileage =

   33.3000   34.5000   37.4000
   33.4000   34.8000   36.8000
   32.9000   33.8000   37.6000
   32.6000   33.4000   36.6000
   32.5000   33.7000   37.0000
   33.0000   33.9000   36.7000

cars = 3;
p = anova2(mileage,cars)

p =

    0.0000    0.0039    0.8411
```

There are three models of cars (columns) and two factories (rows). The reason there are six rows instead of two is that each factory provides three cars of each model for the study. The data from the first factory is in the first three rows, and the data from the second factory is in the last three rows.

The standard ANOVA table has columns for the sums of squares, degrees of freedom, mean squares (SS/df), and F statistics.

ANOVA Table

Source	SS	df	MS	F
Columns	53.35	2	26.68	234.2
Rows	1.445	1	1.445	12.69
Interaction	0.04	2	0.02	0.1756
Error	1.367	12	0.1139	
Total	56.2	17		

You can use the F statistics to do hypotheses tests to find out if the mileage is the same across models, factories, and model-factory pairs (after adjusting for the additive effects). anova2 returns the p-value from these tests.

The p-value for the model effect is zero to four decimal places. This is a strong indication that the mileage varies from one model to another. An F statistic as extreme as the observed F would occur by chance less than once in 10,000 times if the gas mileage were truly equal from model to model.

The p-value for the factory effect is 0.0039, which is also highly significant. This indicates that one factory is out-performing the other in the gas mileage of the cars it produces. The observed p-value indicates that an F statistic as extreme as the observed F would occur by chance about four out of 1000 times if the gas mileage were truly equal from factory to factory.

There does not appear to be any interaction between factories and models. The p-value, 0.8411, means that the observed result is quite likely (84 out 100 times) given that there is no interaction.

The p-values returned by anova2 depend on assumptions about the random disturbances in the model equation. For the p-values to be correct these disturbances need to be independent, normally distributed and have constant variance.

Multiple Linear Regression

The purpose of multiple linear regression is to establish a quantitative relationship between a group of predictor variables (the columns of X) and a response, y. This relationship is useful for:

- Understanding which predictors have the most effect.
- Knowing the direction of the effect (i.e., increasing x increases/decreases y).
- Using the model to predict future values of the response when only the predictors are currently known.

The linear model takes its common form

$$y = X\beta + \varepsilon$$

where:

- y is an n by 1 vector of observations.
- X is an n by p matrix of regressors.
- β is a p by 1 vector of parameters.
- ε is an n by 1 vector of random disturbances.

The solution to the problem is a vector, b, which estimates the unknown vector of parameters, β. The least-squares solution is:

$$b = \beta = (X'X)^{-1}X'y$$

This equation is useful for developing later statistical formulas, but has poor numeric properties. `regress` uses QR decomposition of X followed by the backslash operator to compute b. The QR decomposition is not necessary for computing b, but the matrix, R, is useful for computing confidence intervals.

You can plug b back into the model formula to get the predicted y values at the data points.

$$\hat{y} = Xb = Hy$$

$$H = X(X'X)^{-1}X'$$

Statisticians use a hat (circumflex) over a letter to denote an estimate of a parameter or a prediction from a model. The projection matrix H, is called the hat matrix, because it puts the “hat” on y.

The residuals are the difference between the observed and predicted y values.

$$r = y - \hat{y} = (I - H)y$$

The residuals are useful for detecting failures in the model assumptions, since they correspond to the errors, ε, in the model equation. By assumption, these errors each have independent normal distributions with mean zero and a constant variance.

The residuals, however, are correlated and have variances that depend on the locations of the data points. It is a common practice to scale ("Studentize") the residuals so they all have the same variance.

In the equation below, the scaled residual, t_i, has a Student's t distribution with *(n–p)* degrees of freedom.

$$t_i = \frac{r_i}{\hat{\sigma}_{(i)}\sqrt{1-h_i}}$$

where:

$$\hat{\sigma}^2_{(i)} = \frac{\|r\|^2}{n-p-1} - \frac{r_i^2}{(n-p-1)(1-h_i)}$$

- t_i is the scaled residual for the ith data point.
- r_i is the raw residual for the ith data point.
- n is the sample size.
- p is the number of parameters in the model.
- h_i is the ith diagonal element of H.

The left-hand side of the second equation is the estimate of the variance of the errors excluding the ith data point from the calculation.

A hypothesis test for outliers involves comparing t_i with the critical values of the t distribution. If t_i is large, this casts doubt on the assumption that this residual has the same variance as the others.

A confidence interval for the mean of each error is:

$$c_i = r_i \pm t_{\left(1-\frac{\alpha}{2},\nu\right)}\hat{\sigma}_{(i)}\sqrt{1-h_i}$$

Confidence intervals that do not include zero are equivalent to rejecting the hypothesis (at a significance probability of α) that the residual mean is zero. Such confidence intervals are good evidence that the observation is an outlier for the given model.

Example

The example comes from Chatterjee and Hadi (1986) in a paper on regression diagnostics. The dataset (originally from Moore (1975)) has five predictor variables and one response.

```
load moore
X = [ones(size(moore,1),1) moore(:,1:5)];
```

The matrix, `X`, has a column of ones, then one column of values for each of the five predictor variables. The column of ones is necessary for estimating the *y*-intercept of the linear model.

```
y = moore(:,6);
[b,bint,r,rint,stats] = regress(y,X);
```

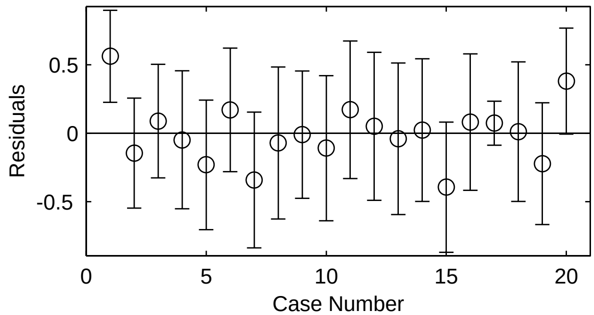
The *y*-intercept is `b(1)`, which corresponds to the column index of the column of ones.

```
stats

stats =

    0.8107   11.9886    0.0001
```

The elements of the vector `stats` are the regression R^2 statistic, the F statistic (for the hypothesis test that all the regression coefficients are zero), and the p-value associated with this F statistic.

R^2 is 0.8107 indicating the model accounts for over 80% of the variability in the observations. The F statistic of about 12 and its p-value of 0.0001 indicate that it is highly unlikely that all of the regression coefficients are zero.

```
rcoplot(r,rint)
```



The plot shows the residuals plotted in case order (by row). The 95% confidence intervals about these residuals are plotted as error bars. The first observation is an outlier since its error bar does not cross the zero reference line.

Quadratic Response Surface Models

Response Surface Methodology (RSM) is a tool for understanding the quantitative relationship between multiple input variables and one output variable.

Consider one output, z, as a polynomial function of two inputs, x and y..$z = f(x,y)$ describes a two dimensional surface in the space (x,y,z). Of course, you can have as many input variables as you want and the resulting surface becomes a hyper-surface.

For three inputs (x_1, x_2, x_3) the equation of a quadratic response surface is:

$$y = b_0 + b_1x_1 + b_2x_2 + b_3x_3 + \ldots \quad \text{(linear terms)}$$

$$b_{12}x_1x_2 + b_{13}x_1x_3 + b_{23}x_2x_3 + \ldots \quad \text{(interaction terms)}$$

$$b_{11}x_1^2 + b_{22}x_2^2 + b_{33}x_3^2 \quad \text{(quadratic terms)}$$

It is difficult to visualize a k-dimensional surface in k+1 dimensional space when k>2. The function `rstool` is a GUI designed to make this visualization more intuitive.

Exploring Graphs of Multidimensional Polynomials

The function `rstool` is useful for fitting response surface models. The purpose of `rstool` is larger than just fitting and prediction for polynomial models. This GUI provides an environment for exploration of the graph of a multidimensional polynomial.

You can learn about `rstool` by trying the commands below. The chemistry behind the data in `reaction.mat` deals with reaction kinetics as a function of the partial pressure of three chemical reactants: hydrogen, n-pentane, and isopentane.

```
load reaction
rstool(reactants,rate,'quadratic',0.01,xn,yn)
```

You will see a “vector” of three plots. The dependent variable of all three plots is the reaction rate. The first plot has hydrogen as the independent variable. The second and third plots have n-pentane and isopentane respectively.

Each plot shows the fitted relationship of the reaction rate to the independent variable at a fixed value of the other two independent variables. The fixed value of each independent variable is in an editable text box below each axis. You can change the fixed value of any independent variable by either typing a new value in the box or by dragging any of the 3 vertical lines to a new position.

When you change the value of an independent variable, all the plots update to show the current picture at the new point in the space of the independent variables.

Note that while this example only uses three reactants, `rstool` can accommodate an arbitrary number of independent variables. Interpretability may be limited by the size of the monitor for large numbers of inputs.

The GUI also has two pop-up menus. The **Export** menu facilitates saving various important variables in the GUI to the base workspace. Below the Export menu there is another menu that allows you to change the order of the polynomial model from within the GUI. If you used the commands above, this menu will have the string **Full Quadratic**. Other choices are:

- Linear – has the constant and first order terms only.
- Pure Quadratic – includes constant, linear and squared terms.
- Interactions – includes constant, linear, and cross product terms.

Stepwise Regression

Stepwise regression is a technique for choosing the variables to include in a multiple regression model. Forward stepwise regression starts with no model terms. At each step it adds the most statistically significant term (the one with the highest F statistic or lowest p-value) until there are none left. Backward stepwise regression starts with all the terms in the model and removes the least significant terms until all the remaining terms are statistically significant. It is also possible to start with a subset of all the terms and then add significant terms or remove insignificant terms.

An important assumption behind the method is that some input variables in a multiple regression do not have an important explanatory effect on the response. If this assumption is true, then it is a convenient simplification to keep only the statistically significant terms in the model.

One common problem in multiple regression analysis is multicollinearity of the input variables. The input variables may be as correlated with each other as they are with the response. If this is the case, the presence of one input variable in the model may mask the effect of another input. Stepwise regression used as a canned procedure is a dangerous tool because the resulting model may include different variables depending on the choice of starting model and inclusion strategy.

The Statistics Toolbox uses an interactive graphical user interface (GUI) to provide a more understandable comparison of competing models. You can explore the GUI using the Hald (1960) data set. Here are the commands to get started.

```
load hald
stepwise(ingredients,heat)
```

The Hald data come from a study of the heat of reaction of various cement mixtures. There are 4 components in each mixture, and the amount of heat produced depends on the amount of each ingredient in the mixture.

Stepwise Regression Interactive GUI

The interface consists of three interactively linked figure windows:

- The Stepwise Regression Plot
- The Stepwise Regression Diagnostics Table
- The Stepwise History Plot

All three windows have *hot* regions. When your mouse is above one of these regions, the pointer changes from an arrow to a circle. Clicking on this point initiates some activity in the interface.

Stepwise Regression Plot

This plot shows the regression coefficient and confidence interval for every term (in or out of the model). The green lines represent terms in the model while red lines indicate that the term is not currently in the model.

Statistically significant terms are solid lines. Dotted lines show that the fitted coefficient is not significantly different from zero.

Clicking on a line in this plot toggles its state. That is, a term in the model (green line) gets removed (turns red), and terms out of the model (red line) enter the model (turn green).

The coefficient for a term out of the model is the coefficient resulting from adding that term to the current model.

Scale Inputs. Pressing this button centers and normalizes the columns of the input matrix to have a standard deviation of one.

Export. This pop-up menu allows you to export variables from the stepwise function to the base workspace.

Close. The **Close** button removes all the figure windows.

Stepwise Regression Diagnostics Figure

This table is a quantitative view of the information in the Stepwise Regression Plot. The table shows the Hald model with the second and third terms removed.

		Confidence Intervals	
Column #	Parameter	Lower	Upper
1	1.44	1.02	1.86
2	0.4161	-0.1602	0.9924
3	-0.41	-1.029	0.2086
4	-0.614	-0.7615	-0.4664

RMSE	R-square	F	P
2.734	0.9725	176.6	1.581e-08

Coefficients and Confidence Intervals. The table at the top of the figure shows the regression coefficient and confidence interval for every term (in or out of the model.) The green rows in the table (on your monitor) represent terms in the model while red rows indicate terms not currently in the model.

Clicking on a row in this table toggles the state of the corresponding term. That is, a term in the model (green row) gets removed (turns red), and terms out of the model (red rows) enter the model (turn green).

The coefficient for a term out of the model is the coefficient resulting from adding that term to the current model.

Additional Diagnostic Statistics. There are also several diagnostic statistics at the bottom of the table:

- RMSE - the root mean squared error of the current model.
- R-square - the amount of response variability explained by the model.
- F - the overall F statistic for the regression.
- P - the associated significance probability.

Close Button. Shuts down all windows.

Help Button. Activates online help.

Stepwise History. This plot shows the RMSE and a confidence interval for every model generated in the course of the interactive use of the other windows.

Recreating a Previous Model. Clicking on one of these lines re-creates the current model at that point in the analysis using a *new* set of windows. You can thus compare the two candidate models directly.

Nonlinear Regression Models

Response Surface Methodology (RSM) is an empirical modeling approach using polynomials as local approximations to the true input/output relationship. This empirical approach is often adequate for process improvement in an industrial setting.

In scientific applications there is usually relevant theory that allows us to make a mechanistic model. Often such models are nonlinear in the unknown parameters. Nonlinear models are more difficult to fit, requiring iterative methods that start with an initial guess of the unknown parameters. Each iteration alters the current guess until the algorithm converges.

Mathematical Form

The Statistics Toolbox has functions for fitting nonlinear models of the form

$$y = f(X, \beta) + \varepsilon$$

where:

- y is an n by 1 vector of observations.
- f is any function of X and β.
- X is an n by p matrix of input variables.
- β is a p by 1 vector of unknown parameters to be estimated.
- ε is an n by 1 vector of random disturbances.

Nonlinear Modeling Example

The Hougen-Watson model (Bates and Watts 1988) for reaction kinetics is one specific example of this type. The form of the model is:

$$rate = \frac{\beta_1 \cdot x_2 - x_3/\beta_5}{1 + \beta_2 \cdot x_1 + \beta_3 \cdot x_2 + \beta_4 \cdot x_3}$$

where β_1, β_2,...,β_5 are the unknown parameters, and x_1, x_2, and x_3 are the three input variables. The three inputs are hydrogen, n-pentane, and isopentane. It is easy to see that the parameters do not enter the model linearly.

The file reaction.mat contains simulated data from this reaction.

```
load reaction
who
Your variables are:

beta        rate        xn
model       reactants   yn
```

where:

- rate is a vector of observed reaction rates 13 by 1.
- reactants is a three column matrix of reactants 13 by 3.
- beta is vector of initial parameter estimates 5 by 1.
- '*model*' is a string containing the nonlinear function name.
- '*xn*' is a string matrix of the names of the reactants.
- '*yn*' is a string containing the name of the response.

Fitting the Hougen-Watson Model

The Statistics Toolbox provides the function nlinfit for finding parameter estimates in nonlinear modeling. nlinfit returns the least-squares parameter estimates. That is, it finds the parameters that minimize the sum of the squared differences between the observed responses and their fitted values. It uses the Gauss-Newton algorithm with Levenberg-Marquardt modifications for global convergence.

nlinfit requires the input data, the responses, and an initial guess of the unknown parameters. You must also supply a function that takes the input data and the current parameter estimate and returns the predicted responses. In MATLAB this is called a “function” function.

Here is the hougen function:

```
function yhat = hougen(beta,x)
%HOUGEN Hougen-Watson model for reaction kinetics.
%   YHAT = HOUGEN(BETA,X) gives the predicted values of the
%   reaction rate, YHAT, as a function of the vector of
%   parameters, BETA, and the matrix of data, X.
%   BETA must have 5 elements and X must have three
%   columns.
%
%   The model form is:
%   y = (b1*x2 - x3/b5)./(1+b2*x1+b3*x2+b4*x3)
%
%   Reference:
%      [1]  Bates, Douglas, and Watts, Donald, "Nonlinear
%      Regression Analysis and Its Applications", Wiley
%      1988 p. 271-272.

%   Copyright (c) 1993-97 by The MathWorks, Inc.
%   B.A. Jones 1-06-95.

b1 = beta(1);
b2 = beta(2);
b3 = beta(3);
b4 = beta(4);
b5 = beta(5);

x1 = x(:,1);
x2 = x(:,2);
x3 = x(:,3);


yhat = (b1*x2 - x3/b5)./(1+b2*x1+b3*x2+b4*x3);
```

To fit the `reaction` data, call the function `nlinfit`:

```
load reaction
betahat = nlinfit(reactants,rate,'hougen',beta)

betahat =

    1.2526
    0.0628
    0.0400
    0.1124
    1.1914
```

`nlinfit` has two optional outputs. They are the residuals and Jacobian matrix at the solution. The residuals are the differences between the observed and fitted responses. The Jacobian matrix is the direct analog of the matrix, X, in the standard linear regression model.

These outputs are useful for obtaining confidence intervals on the parameter estimates and predicted responses.

Confidence Intervals on the Parameter Estimates

Using `nlparci`, form 95% confidence intervals on the parameter estimates, `betahat`, from the reaction kinetics example.

```
[betahat,f,J] = nlinfit(reactants,rate,'hougen',beta);
betaci = nlparci(betahat,f,J)

betaci =

   –0.7467    3.2519
   –0.0377    0.1632
   –0.0312    0.1113
   –0.0609    0.2857
   –0.7381    3.1208
```

Confidence Intervals on the Predicted Responses

Using `nlpredci`, form 95% confidence intervals on the predicted responses from the reaction kinetics example.

```
[yhat, delta] = nlpredci('hougen',reactants,betahat,f,J);
opd = [rate yhat delta]

opd =

    8.5500    8.2937    0.9178
    3.7900    3.8584    0.7244
    4.8200    4.7950    0.8267
    0.0200   -0.0725    0.4775
    2.7500    2.5687    0.4987
   14.3900   14.2227    0.9666
    2.5400    2.4393    0.9247
    4.3500    3.9360    0.7327
   13.0000   12.9440    0.7210
    8.5000    8.2670    0.9459
    0.0500   -0.1437    0.9537
   11.3200   11.3484    0.9228
    3.1300    3.3145    0.8418
```

The matrix, `opd`, has the observed rates in column 1 and the predictions in column 2. The 95% confidence interval is column 2 ± column 3. Note that the confidence interval contains the observations in each case.

An Interactive GUI for Nonlinear Fitting and Prediction

The function `nlintool` for nonlinear models is a direct analog of `rstool` for polynomial models. `nlintool` requires the same inputs as `nlinfit`. `nlintool` calls `nlinfit`.

The purpose of `nlintool` is larger than just fitting and prediction for nonlinear models. This GUI provides an environment for exploration of the graph of a multidimensional nonlinear function.

If you have already loaded `reaction.mat`, you can start `nlintool`:

```
nlintool(reactants,rate,'hougen',beta,0.01,xn,yn)
```

You will see a “vector” of three plots. The dependent variable of all three plots is the reaction rate. The first plot has hydrogen as the independent variable. The second and third plots have n-pentane and isopentane respectively.

Each plot shows the fitted relationship of the reaction rate to the independent variable at a fixed value of the other two independent variables. The fixed value of each independent variable is in an editable text box below each axis. You can change the fixed value of any independent variable by either typing a new value in the box or by dragging any of the 3 vertical lines to a new position.

When you change the value of an independent variable, all the plots update to show the current picture at the new point in the space of the independent variables.

Note that while this example only uses three reactants, `nlintool`, can accommodate an arbitrary number of independent variables. Interpretability may be limited by the size of the monitor for large numbers of inputs.

Hypothesis Tests

A hypothesis test is a procedure for determining if an assertion about a characteristic of a population is reasonable.

For example, suppose that someone says that the average price of a gallon of regular unleaded gas in Massachusetts is $1.15. How would you decide whether this statement is true? You could try to find out what every gas station in the state was charging and how many gallons they were selling at that price. That approach might be definitive, but it could end up costing more than the information is worth.

A simpler approach is to find out the price of gas at a small number of randomly chosen stations around the state and compare the average price to $1.15.

Of course, the average price you get will probably not be exactly $1.15 due to variability in price from one station to the next. Suppose your average price was $1.18. Is this three cent difference a result of chance variability, or is the original assertion incorrect? A hypothesis test can provide an answer.

Terminology

To get started, there are some terms to define and assumptions to make.

- The *null hypothesis* is the original assertion. In this case the null hypothesis is that the average price of a gallon of gas is $1.15. The notation is H_0: $\mu = 1.15$.
- There are three possibilities for the *alternative hypothesis*. You might only be interested in the result if gas prices were actually higher. In this case, the alternative hypothesis is H_1: $\mu > 1.15$. The other possibilities are H_1: $\mu < 1.15$ and H_1: $\mu \neq 1.15$.
- The *significance level* is related to the degree of certainty you require in order to reject the null hypothesis in favor of the alternative. By taking a small sample you cannot be certain about your conclusion. So you decide in advance to reject the null hypothesis if the probability of observing your sampled result is less than the significance level. For a typical significance level of 5% the notation is $\alpha = 0.05$. For this significance level, the probability of incorrectly rejecting the null hypothesis when it is actually true is 5%. If you need more protection from this error, then choose a lower value of α.

- The *p-value* is the probability of observing the given sample result under the assumption that the null hypothesis is true. If the p-value is less than α, then you reject the null hypothesis. For example, if $\alpha = 0.05$ and the p-value is 0.03, then you reject the null hypothesis.

  The converse is not true. If the p-value is greater than α, you do not accept the null hypothesis. You just have insufficient evidence to reject the null hypothesis (which is the same for practical purposes).
- The outputs for the hypothesis test functions also include *confidence intervals*. Loosely speaking, a confidence interval is a range of values that have a chosen probability of containing the true hypothesized quantity. Suppose, in our example, 1.15 is inside a 95% confidence interval for the mean, μ. That is equivalent to being unable to reject the null hypothesis at a significance level of 0.05. Conversely if the $100(1-\alpha)$ confidence interval does not contain 1.15, then you reject the null hypothesis at the α level of significance.

Assumptions

The difference between hypothesis test procedures often arises from differences in the assumptions that the researcher is willing to make about the data sample. The Z-test assumes that the data represents independent samples from the same normal distribution and that you know the standard deviation, σ. The t-test has the same assumptions except that you estimate the standard deviation using the data instead of specifying it as a known quantity.

Both tests have an associated signal-to-noise ratio:

$$z = \frac{\bar{x} - \mu}{\sigma} \quad or \quad T = \frac{\bar{x} - \mu}{s}$$

$$\text{where } \bar{x} = \sum_{i=1}^{n} \frac{x_i}{n}$$

The signal is the difference between the average and the hypothesized mean. The noise is the standard deviation posited or estimated.

If the null hypothesis is true, then Z has a standard normal distribution, N(0,1). T has a Student's t distribution with the degrees of freedom, ν, equal to one less than the number of data values.

Given the observed result for Z or T, and knowing their distribution assuming the null hypothesis is true, it is possible to compute the probability (p-value) of observing this result. If the p-value is very small, then that casts doubt on the truth of the null hypothesis. For example, suppose that the p-value was 0.001, meaning that the probability of observing the given Z (or T) was one in a thousand. That should make you skeptical enough about the null hypothesis that you reject it rather than believe that your result was just a lucky 999 to 1 shot.

Example

This example uses the gasoline price data in `gas.mat`. There are two samples of 20 observed gas prices for the months of January and February 1993.

```
load gas
prices = [price1 price2]

prices =

   119   118
   117   115
   115   115
   116   122
   112   118
   121   121
   115   120
   122   122
   116   120
   118   113
   109   120
   112   123
   119   121
   112   109
   117   117
   113   117
   114   120
   109   116
   109   118
   118   125
```

Suppose it is historically true that the standard deviation of gas prices at gas stations around Massachusetts is four cents a gallon. The Z-test is a procedure for testing the null hypothesis that the average price of a gallon of gas in January (`price1`) is $1.15.

```
[h,pvalue,ci] = ztest(price1/100,1.15,0.04)

h =

     0

pvalue =

    0.8668

ci =

    1.1340    1.1690
```

The result of the hypothesis test is the boolean variable, `h`. When `h` = 0, you do not reject the null hypothesis.

The result suggests that $1.15 is reasonable. The 95% confidence interval `[1.1340 1.1690]` neatly brackets $1.15.

What about February? Try a t-test with `price2`. Now you are not assuming that you know the standard deviation in price.

```
[h,pvalue,ci] = ttest(price2/100,1.15)

h =

     1

pvalue =

   4.9517e-04

ci =

    1.1675    1.2025
```

With the boolean result, `h` = 1, you can reject the null hypothesis at the default significance level, 0.05.

It looks like $1.15 is not a reasonable estimate of the gasoline price in February. The low end of the 95% confidence interval is greater than 1.15.

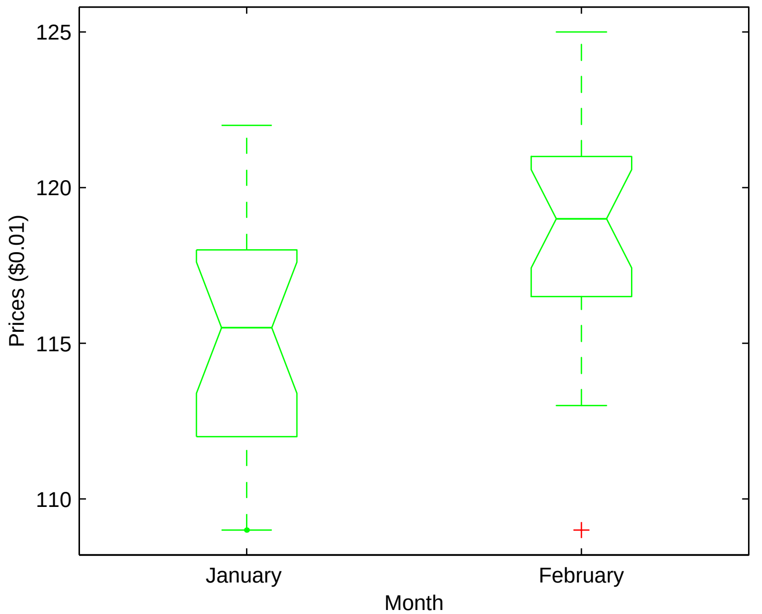
The function `ttest2` allows you to compare the means of the two data samples.

```
[h,sig,ci] = ttest2(price1,price2)

h =

     1


sig =

    0.0083


ci =

   -5.7845   -0.9155
```

The confidence interval (`ci` above) indicates that gasoline prices were between one and six cents lower in January than February.

The box plot gives the same conclusion graphically. Note that the notches have little, if any, overlap. Refer to "Statistical Plots" for more information about box plots.

```
boxplot(prices,1)
set(gca,'XtickLabel',str2mat('January','February'))
xlabel('Month')
ylabel('Prices ($0.01)')
```



Multivariate Statistics

Multivariate statistics is an omnibus term for a number of different statistical methods. The defining characteristic of these methods is that they all aim to understand a data set by considering a group of variables together rather than focusing on only one variable at a time.

Principal Components Analysis

One of the difficulties inherent in multivariate statistics is the problem of visualizing multi-dimensionality. In MATLAB, the `plot` command displays a graph of the relationship between two variables. The `plot3` and `surf` commands display different three-dimensional views. When there are more than three variables, it stretches the imagination to visualize their relationships.

Fortunately in data sets with many variables, groups of variables often move together. One reason for this is that more than one variable may be measuring the same driving principle governing the behavior of the system. In many systems there are only a few such driving forces. But an abundance of instrumentation allows us to measure dozens of system variables. When this happens, we can take advantage of this redundancy of information. We can simplify our problem by replacing a group of variables with a single new variable.

Principal Components Analysis is a quantitatively rigorous method for achieving this simplification. The method generates a new set of variables, called principal components. Each principal component is a linear combination of the original variables. All the principal components are orthogonal to each other so there is no redundant information. The principal components as a whole form an orthogonal basis for the space of the data.

There are an infinite number of ways to construct an orthogonal basis for several columns of data. What is so special about the principal component basis?

The first principal component is a single axis in space. When you project each observation on that axis, the resulting values form a new variable. And the variance of this variable is the maximum among all possible choices of the first axis.

The second principal component is another axis in space, perpendicular to the first. Projecting the observations on this axis generates another new variable. The variance of this variable is the maximum among all possible choices of this second axis.

The full set of principal components is as large as the original set of variables. But, it is commonplace for the sum of the variances of the first few principal components to exceed 80% of the total variance of the original data. By examining plots of these few new variables, researchers often develop a deeper understanding of the driving forces that generated the original data.

Example

Let us look at a sample application that uses nine different indices of the quality of life in 329 U.S. cities. These are climate, housing, health, crime, transportation, education, arts, recreation, and economics. For each index, higher is better; so, for example, a higher index for crime means a lower crime rate.

We start by loading the data in `cities.mat`.

```
load cities
whos
  Name              Size          Bytes  Class

  categories         9x14           252  char array
  names            329x43         28294  char array
  ratings          329x9          23688  double array

Grand total is 17234 elements using 52234 bytes
```

The `whos` command generates a table of information about all the variables in the workspace. The cities data set contains three variables:

- `categories`, a string matrix containing the names of the indices.
- `names`, a string matrix containing the 329 city names.
- `ratings`, the data matrix with 329 rows and 9 columns.

Let's look at the value of the categories variable:

```
categories

categories =

climate
housing
health
crime
transportation
education
arts
recreation
economics
```

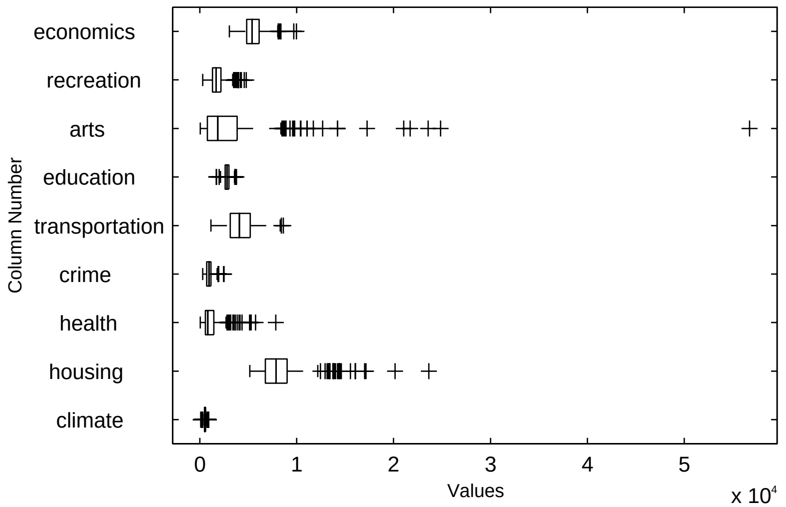
Now, let's look at the first several rows of names variable, too.

```
first5 = names(1:5,:)

first5 =

Abilene, TX
Akron, OH
Albany, GA
Albany-Troy, NY
Albuquerque, NM
```

To get a quick impression of the ratings data, make a box plot.

```
boxplot(ratings,0,'+',0)
set(gca,'YTicklabel',categories)
```

These commands generate the plot below. Note that there is substantially more variability in the ratings of the arts and housing than in the ratings of crime and climate.



Ordinarily you might also graph pairs of the original variables, but there are 36 two-variable plots. Maybe principal components analysis can reduce the number of variables we need to consider.

Sometimes it makes sense to compute principal components for raw data. This is appropriate when all the variables are in the same units. Standardizing the data is reasonable when the variables are in different units or when the variance of the different columns is substantial (as in this case).

You can standardize the data by dividing each column by its standard deviation.

```
stdr = std(ratings);
sr = ratings./stdr(ones(329,1),:);
```

Now we are ready to find the principal components.

```
[pcs, newdata, variances, t2] = princomp(sr);
```

The Principal Components (First Output)

The first output of the `princomp` function, `pcs`, contains the nine principal components. These are the linear combinations of the original variables that generate the new variables.

Let's look at the first three principal component vectors.

```
p3 = pcs(:,1:3)

p3 =

    0.2064   –0.2178    0.6900
    0.3565   –0.2506    0.2082
    0.4602    0.2995    0.0073
    0.2813   –0.3553   –0.1851
    0.3512    0.1796   –0.1464
    0.2753    0.4834   –0.2297
    0.4631    0.1948    0.0265
    0.3279   –0.3845    0.0509
    0.1354   –0.4713   –0.6073
```

The largest weights in the first column (first principal component) are the third and seventh elements corresponding to the variables, `arts` and `health`. All the elements of the first principal component are the same sign, making it a weighted average of all the variables.

To show the orthogonality of the principal components note that premultiplying them by their transpose yields the identity matrix.

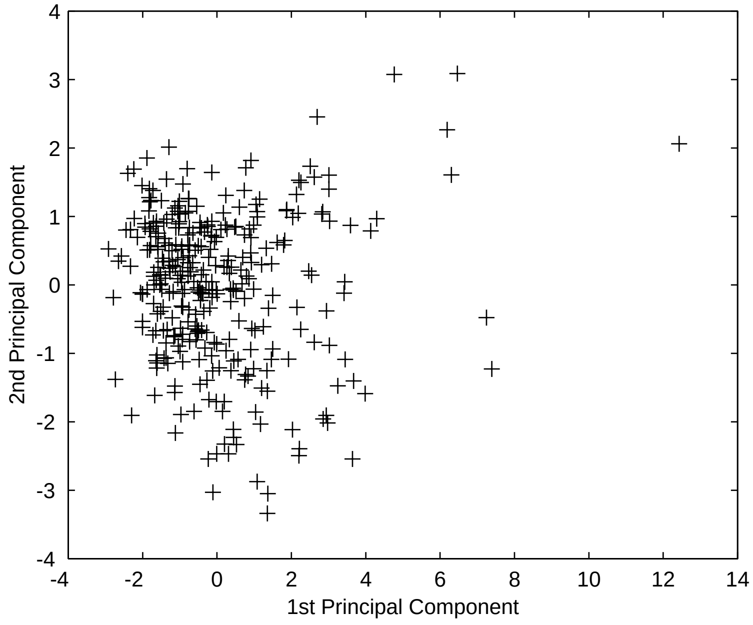
```
I = p3'*p3

I =

    1.0000    0.0000   –0.0000
    0.0000    1.0000   –0.0000
   –0.0000   –0.0000    1.0000
```

The Component Scores (Second Output)

The second output, `newdata`, is the data in the new coordinate system defined by the principal components. This output is the same size as the input data matrix.

A plot of the first two columns of newdata shows the ratings data projected onto the first two principal components.

```
plot(newdata(:,1),newdata(:,2),'+')
xlabel('1st Principal Component');
ylabel('2nd Principal Component');
```

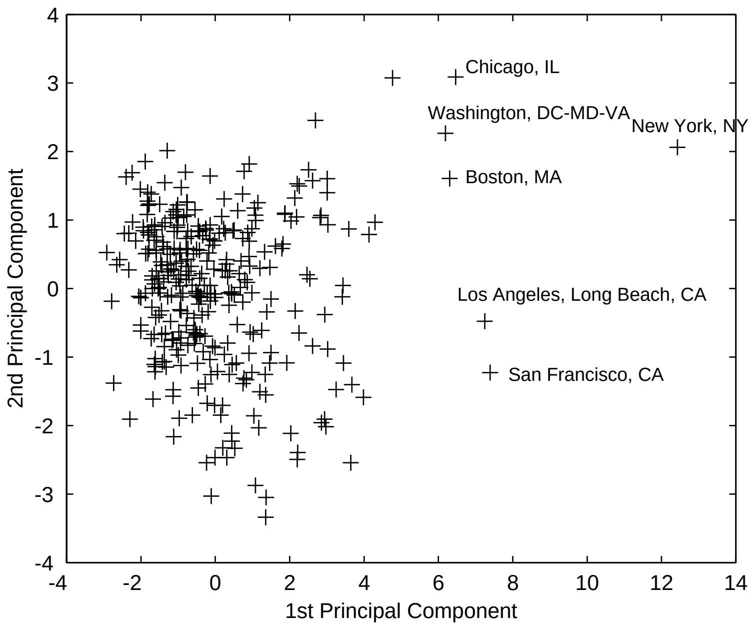


Note the outlying points in the upper right corner.

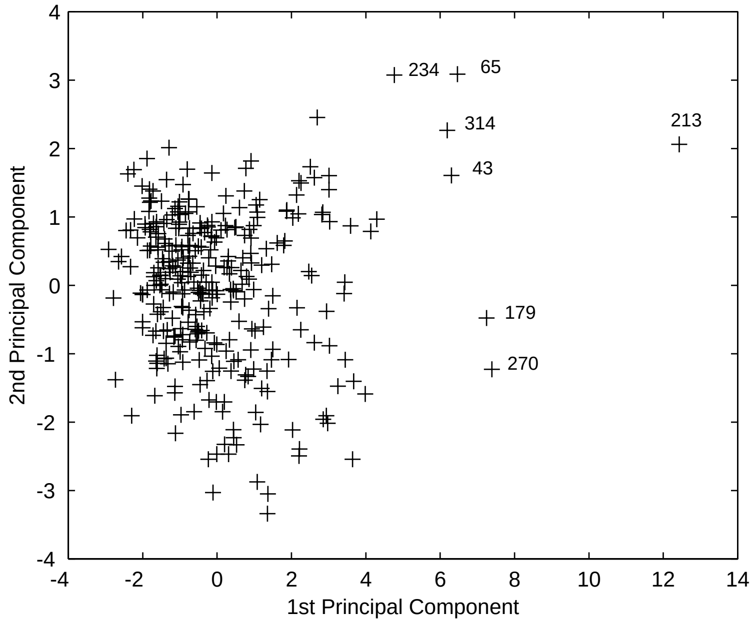
The function gname is useful for graphically identifying a few points in a plot like this. You can call gname with a string matrix containing as many case labels as points in the plot. The string matrix names works for labeling points with the city names.

```
gname(names)
```

Move your cursor over the plot and click once near each point at the top right. When you finish press the return key. Here is the resulting plot.



The labeled cities are the biggest population centers in the United States. Perhaps we should consider them as a completely separate group. If we call `gname` without arguments, it labels each point with its row number.



We can create an index variable containing the row numbers of all the metropolitan areas we chose.

```
metro = [43 65 179 213 234 270 314];
names(metro,:)
ans =

Boston, MA
Chicago, IL
Los Angeles, Long Beach, CA
New York, NY
Philadelphia, PA-NJ
San Francisco, CA
Washington, DC-MD-VA
```

To remove these rows from the ratings matrix:

```
rsubset = ratings;
nsubset = names;
nsubset(metro,:) = [];
rsubset(metro,:) = [];
size(rsubset)

ans =

   322     9
```

To practice, repeat the analysis using the variable `rsubset` as the new data matrix and `nsubset` as the string matrix of labels.

The Component Variances (Third Output)

The third output, `variances`, is a vector containing the variance explained by the corresponding column of `newdata`.

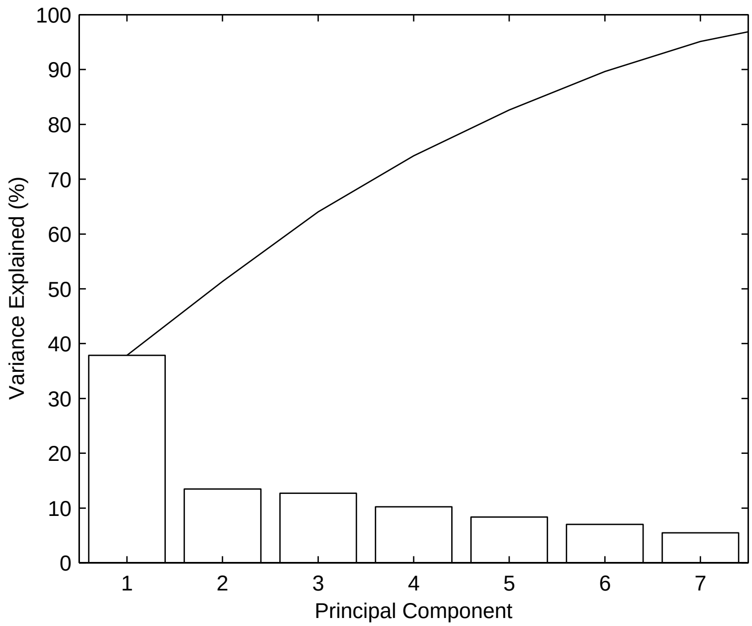
```
variances

variances =

     3.4083
     1.2140
     1.1415
     0.9209
     0.7533
     0.6306
     0.4930
     0.3180
     0.1204
```

You can easily calculate the percent of the total variability explained by each principal component.

```
percent_explained = 100*variances/sum(variances)
percent_explained =

   37.8699
   13.4886
   12.6831
   10.2324
    8.3698
    7.0062
    5.4783
    3.5338
    1.3378
```

A “Scree” plot is a pareto plot of the percent variability explained by each principal component.

```
pareto(percent_explained)
xlabel('Principal Component')
ylabel('Variance Explained (%)')
```



We can see that the first three principal components explain roughly two thirds of the total variability in the standardized ratings.

Hotelling's T^2 (Fourth Output)

The last output of the princomp function, t2, is Hotelling's T^2, a statistical measure of the multivariate distance of each observation from the center of the data set. This is an analytical way to find the most extreme points in the data.

```
[st2, index] = sort(t2); % Sort in ascending order.
st2 = flipud(st2); % Values in descending order.
index = flipud(index); % Indices in descending order.
extreme = index(1)

extreme =

   213
names(extreme,:)

ans =

New York, NY
```

It is not surprising that the ratings for New York are the furthest from the average U.S. town.

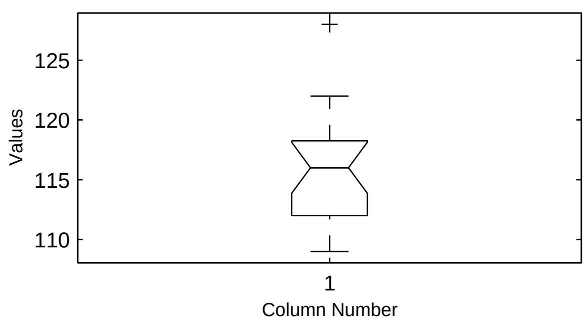
Statistical Plots

The Statistics Toolbox adds specialized plots to the extensive graphics capabilities of MATLAB.

- *Box plots* are graphs for data sample description. They are also useful for graphic comparisons of the means of many samples (see the discussion of one-way ANOVA on page 1-65).
- *Normal probability plots* are graphs for determining whether a data sample has normal distribution.
- *Quantile-quantile plots* graphically compare the distributions of two samples.
- *Weibull probability plots* are graphs for assessing whether data comes from a Weibull distribution.

Box Plots

The graph shows an example of a notched box plot.



This plot has several graphic elements:

- The lower and upper lines of the "box" are the 25th and 75th percentiles of the sample. The distance between the top and bottom of the box is the interquartile range.
- The line in the middle of the box is the sample median. If the median is not centered in the box, that is an indication of skewness.
- The "whiskers" are lines extending above and below the box. They show the extent of the rest of the sample (unless there are outliers). Assuming no

outliers, the maximum of the sample is the top of the upper whisker. The minimum of the sample is the bottom of the lower whisker. By default, an outlier is a value that is more than 1.5 times the interquartile range away from the top or bottom of the box.

- The plus sign at the top of the plot is an indication of an outlier in the data. This point may be the result of a data entry error, a poor measurement or a change in the system that generated the data.
- The “notches” in the box are a graphic confidence interval about the median of a sample. Box plots do not have notches by default.

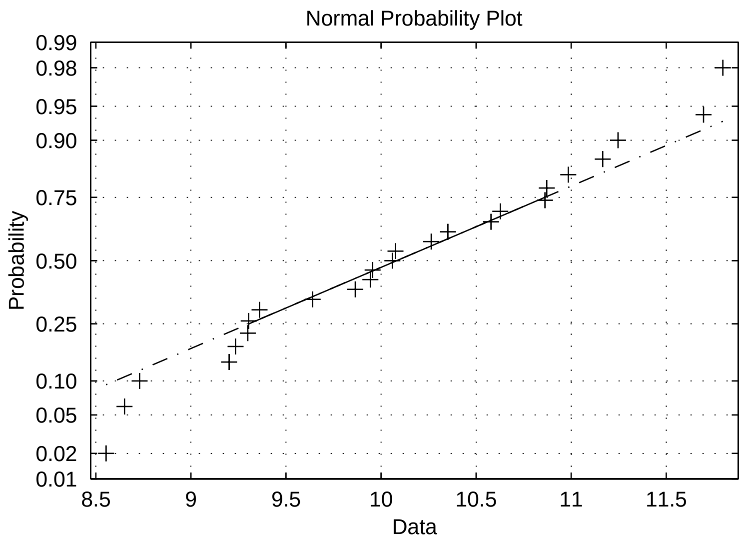
A side-by-side comparison of two notched box plots is the graphical equivalent of a t-test. See the section “Hypothesis Tests” on page 1-85.

Normal Probability Plots

A normal probability plot is a useful graph for assessing whether data comes from a normal distribution. Many statistical procedures make the assumption that the underlying distribution of the data is normal, so this plot can provide some assurance that the assumption of normality is not being violated or provide an early warning of a problem with your assumptions.

This example shows a typical normal probability plot.

```
x = normrnd(10,1,25,1);
normplot(x)
```

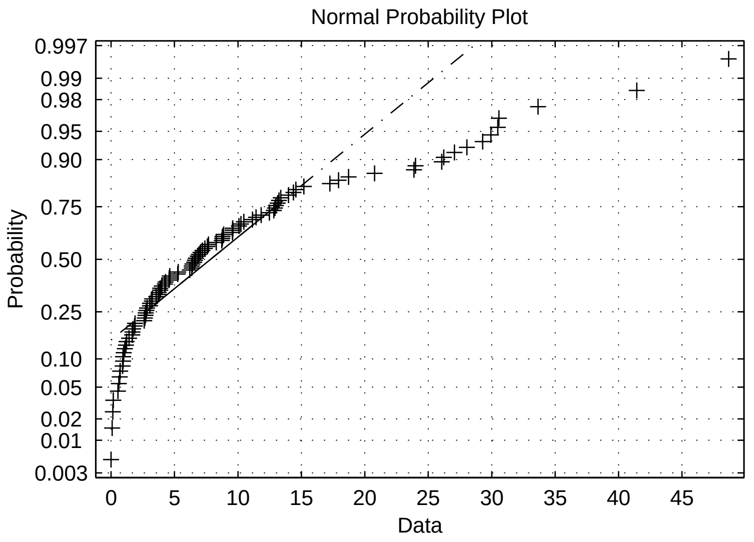


The plot has three graphic elements. The plus signs show the empirical probability versus the data value for each point in the sample. The solid line connects the 25th and 75th percentiles of the data and represents a robust linear fit (i.e., insensitive to the extremes of the sample). The dashed line extends the solid line to the ends of the sample.

The scale of the *y*-axis is not uniform. The *y*-axis values are probabilities and, as such, go from zero to one. The distance between the tick marks on the *y*-axis matches the distance between the quantiles of a normal distribution. The quantiles are close together near the median (probability = 0.5) and stretch out symmetrically moving away from the median. Compare the vertical distance from the bottom of the plot to the probability 0.25 with the distance from 0.25 to 0.50. Similarly, compare the distance from the top of the plot to the probability 0.75 with the distance from 0.75 to 0.50.

If all the data points fall near the line, the assumption of normality is reasonable. But, if the data is nonnormal, the plus signs may follow a curve, as in the example using exponential data below.

```
x = exprnd(10,100,1);
normplot(x)
```



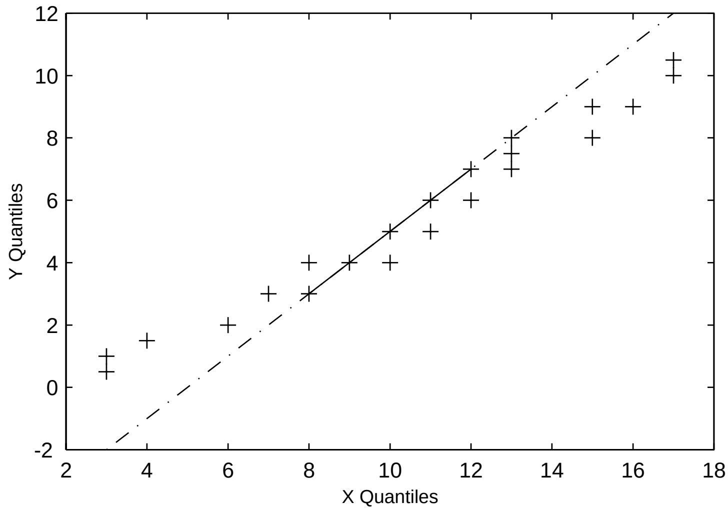
This plot is clear evidence that the underlying distribution is not normal.

Quantile-Quantile Plots

A quantile-quantile plot is useful for determining whether two samples come from the same distribution (whether normally distributed or not).

The example shows a quantile-quantile plot of two samples from a Poisson distribution.

```
x = poissrnd(10,50,1);
y = poissrnd(5,100,1);
qqplot(x,y);
```

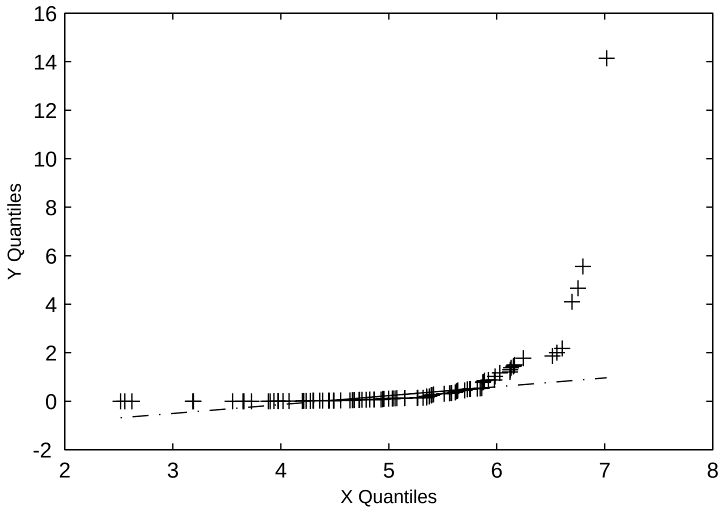


Even though the parameters and sample sizes are different, the straight line relationship shows that the two samples come from the same distribution.

Like the normal probability plot, the quantile-quantile plot has three graphic elements. The pluses are the quantiles of each sample. By default the number of pluses is the number of data values in the smaller sample. The solid line joins the 25th and 75th percentiles of the samples. The dashed line extends the solid line to the extent of the sample.

The example below shows what happens when the underlying distributions are not the same.

```
x = normrnd(5,1,100,1);
y = weibrnd(2,0.5,100,1);
qqplot(x,y);
```



These samples clearly are not from the same distribution.

It is incorrect to interpret a linear plot as a guarantee that the two samples come from the same distribution. But, for assessing the validity of a statistical procedure that depends on the two samples coming from the same distribution, a linear quantile-quantile plot should be sufficient.

Weibull Probability Plots

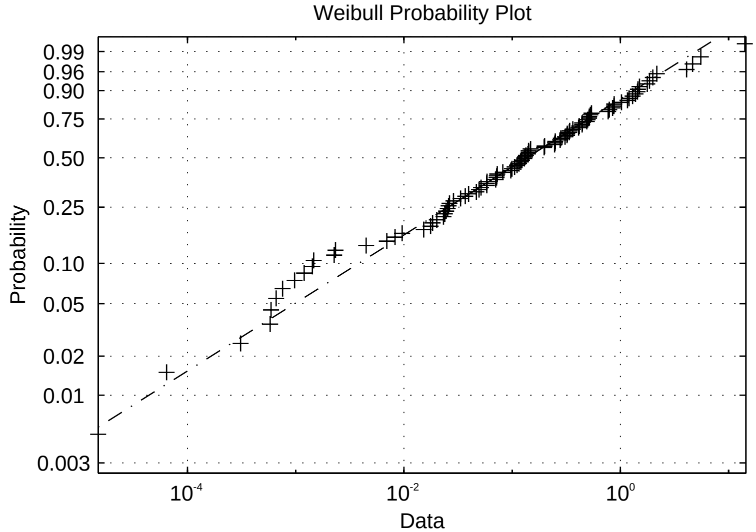
A Weibull probability plot is a useful graph for assessing whether data comes from a Weibull distribution. Many reliability analyses make the assumption that the underlying distribution of the life times is Weibull, so this plot can provide some assurance that this assumption is not being violated or provide an early warning of a problem with your assumptions.

The scale of the *y*-axis is not uniform. The *y*-axis values are probabilities and, as such, go from zero to one. The distance between the tick marks on the *y*-axis matches the distance between the quantiles of a Weibull distribution.

If the data points (pluses) fall near the line, the assumption that the data come from a Weibull distribution is reasonable.

This example shows a typical Weibull probability plot.

```
y = weibrnd(2,0.5,100,1);
weibplot(y)
```



Statistical Process Control (SPC)

SPC is an omnibus term for a number of methods for assessing and monitoring the quality of manufactured goods. These methods are simple which makes them easy to implement even in a production environment.

Control Charts

These graphs were popularized by Walter Shewhart in his work in the 1920s at Western Electric. A control chart is a plot of a measurements over time with statistical limits applied. Actually *control* chart is a slight misnomer. The chart itself is actually a monitoring tool. The control activity may occur if the chart indicates that the process is changing in an undesirable systematic direction.

The Statistics Toolbox supports three common control charts:

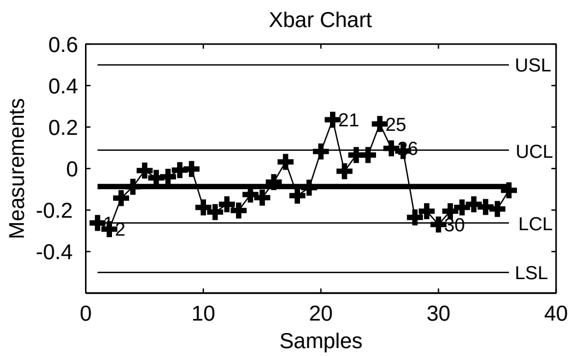
- Xbar charts
- S charts
- Exponentially weighted moving average (EWMA) charts.

Xbar Charts

Xbar charts are a plot of the average of a sample of a process taken at regular intervals. Suppose we are manufacturing pistons to a tolerance of 0.5

thousandths of an inch. We measure the runout (deviation from circularity in thousandths of an inch) at four points on each piston.

```
load parts
conf = 0.99;
spec = [−0.5 0.5];
xbarplot(runout,conf,spec)
```

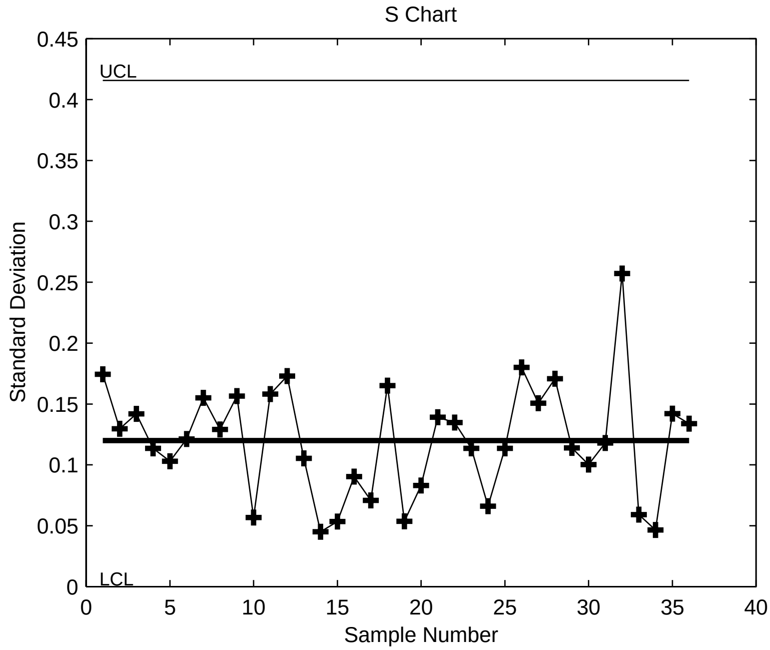


The lines at the bottom and the top of the plot show the process specifications. The central line is the average runout over all the pistons. The two lines flanking the center line are the 99% statistical control limits. By chance only one measurement in 100 should fall outside these lines. We can see that even in this small run of 36 parts, there are several points outside the boundaries (labeled by their observation numbers). This is an indication that the process mean is not in statistical control. This might not be of much concern in practice, since all the parts are well within specification.

S Charts

The S chart is a plot of the standard deviation of a process taken at regular intervals. The standard deviation is a measure of the variability of a process. So, the plot indicates whether there is any systematic change in the process variability. Continuing with the piston manufacturing example, we can look at the standard deviation of each set of 4 measurements of runout.

```
schart(runout)
```



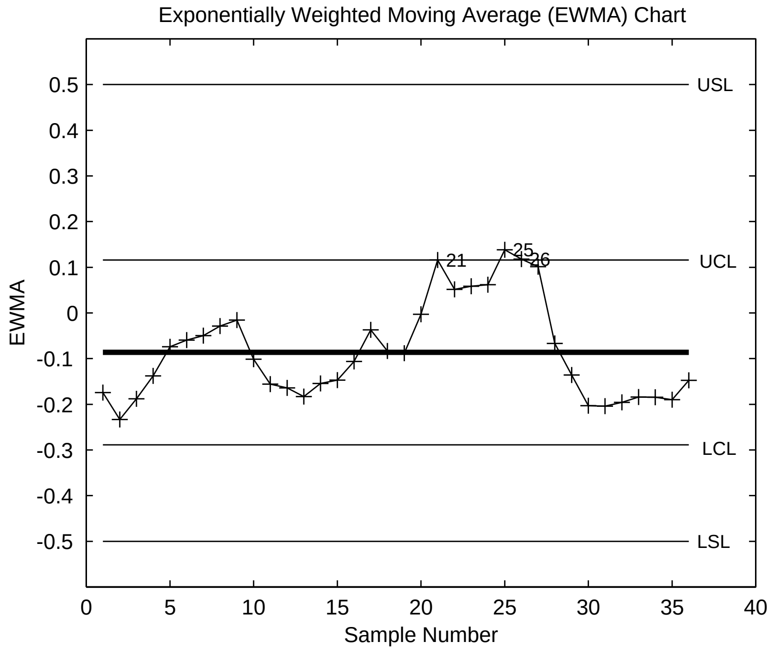
The average runout is about one ten-thousandth of an inch. There is no indication of nonrandom variability.

EWMA Charts

The EWMA chart is another chart for monitoring the process average. It operates on slightly different assumptions than the Xbar chart. The mathematical model behind the Xbar chart posits that the process mean is actually constant over time and any variation in individual measurements is due entirely to chance.

The EWMA model is a little looser. Here we assume that the mean may be varying in time. Here is an EWMA chart of our runout example. Compare this with the plot on page 1-111.

```
ewmaplot(runout,0.5,0.01,spec)
```



Capability Studies

Before going into full-scale production, many manufacturers run a pilot study to determine whether their process can actually build parts to the specifications demanded by the engineering drawing.

Using the data from these capability studies with a statistical model allows us to get a preliminary estimate of the percentage of parts that will fall outside the specifications.

```
[p, Cp, Cpk] = capable(mean(runout),spec)

p =

   1.3940e–09

Cp =

    2.3950

Cpk =

    1.9812
```

The result above shows that the probability (p = 1.3940e–09) of observing an unacceptable runout is extremely low. `Cp` and `Cpk` are two popular capability indices.

Cp is the ratio of the range of the specifications to six times the estimate of the process standard deviation.

$$C_p = \frac{USL - LSL}{6\sigma}$$

For a process that has its average value on target, a *Cp* of one translates to a little more than one defect per thousand. Recently many industries have set a quality goal of one part per million. This would correspond to a $Cp = 1.6$. The higher the value of *Cp* the more capable the process.

Cpk is the ratio of difference between the process mean and the closer specification limit to three times the estimate of the process standard deviation.

$$C_{pk} = min\left(\frac{USL - \mu}{3\sigma}, \frac{\mu - LSL}{3\sigma}\right)$$

where the process mean is μ. For processes that do not maintain their average on target, *Cpk*, is a more descriptive index of process capability.

Design of Experiments (DOE)

There is a world of difference between data and information. To extract information from data you have to make assumptions about the system that generated the data. Using these assumptions and physical theory you may be able to develop a mathematical model of the system.

Generally, even rigorously formulated models have some unknown constants. The goal of experimentation is to acquire data that allow us to estimate these constants.

But why do we need to experiment at all? We could instrument the system we want to study and just let it run. Sooner or later we would have all the data we could use.

In fact, this is a fairly common approach. There are three characteristics of historical data that pose problems for statistical modeling:

- Suppose we observe a change in the operating variables of a system followed by a change in the outputs of the system. That does *not* necessarily mean that the change in the system *caused* the change in the outputs.
- A common assumption in statistical modeling is that the observations are independent of each other. This is not the way a system in normal operation works.
- Controlling a system in operation often means changing system variables in tandem. But if two variables change together, it is impossible to separate their effects mathematically.

Designed experiments directly address these problems. The overwhelming advantage of a designed experiment is that you actively manipulate the system you are studying.

With DOE you may generate fewer data points than by using passive instrumentation, but the quality of the information you get will be higher.

The Statistics Toolbox provides several functions for generating experimental designs appropriate to various situations.

Full Factorial Designs

Suppose you want to determine whether the variability of a machining process is due to the difference in the lathes that cut the parts or the operators who run the lathes.

If the same operator always runs a given lathe then you cannot tell whether the machine or the operator is the cause of the variation in the output. By allowing every operator to run every lathe you can separate their effects.

This is a factorial approach. `fullfact` is the function that generates the design. Suppose we have four operators and three machines. What is the factorial design?

```
d = fullfact([4 3])

d =

     1     1
     2     1
     3     1
     4     1
     1     2
     2     2
     3     2
     4     2
     1     3
     2     3
     3     3
     4     3
```

Each row of `d` represents one operator/machine combination. Note that there are 4*3 = 12 rows.

One special subclass of factorial designs is when all the variables take only two values. Suppose you want to quickly determine the sensitivity of a process to high and low values of three variables.

```
d2 = ff2n(3)

d2 =
     0     0     0
     0     0     1
     0     1     0
     0     1     1
     1     0     0
     1     0     1
     1     1     0
     1     1     1
```

There are $2^3 = 8$ combinations to check.

Fractional Factorial Designs

One difficulty with factorial designs is that the number of combinations increases exponentially with the number of variables you want to manipulate.

For example the sensitivity study discussed above might be impractical if there were seven variables to study instead of just three. A full factorial design would require $2^7 = 128$ runs!

If we assume that the variables do not act synergistically in the system, we can assess the sensitivity with far fewer runs. The theoretical minimum number is eight. To see the design (X) matrix we use the `hadamard` function.

```
X = hadamard(8)

X =

     1     1     1     1     1     1     1     1
     1    –1     1    –1     1    –1     1    –1
     1     1    –1    –1     1     1    –1    –1
     1    –1    –1     1     1    –1    –1     1
     1     1     1     1    –1    –1    –1    –1
     1    –1     1    –1    –1     1    –1     1
     1     1    –1    –1    –1    –1     1     1
     1    –1    –1     1    –1     1     1    –1
```

The last seven columns are the actual variable settings (–1 for low, 1 for high.) The first column (all ones) allows us to measure the mean effect in the linear equation, $y = X\beta + \varepsilon$.

D-Optimal Designs

All the designs above were in use by early in the 20th century. In the 1970s statisticians started to use the computer in experimental design by recasting DOE in terms of optimization. A D-optimal design is one that maximizes the determinant of Fisher's information matrix, $X'X$. This matrix is proportional to the inverse of the covariance matrix of the parameters. So maximizing $det(X'X)$ is equivalent to minimizing the determinant of the covariance of the parameters.

A D-optimal design minimizes the volume of the confidence ellipsoid of the regression estimates of the linear model parameters, β.

There are several functions in the Statistics Toolbox that generate D-optimal designs. These are `cordexch`, `daugment`, `dcovary`, and `rowexch`.

Generating D-Optimal Designs

`cordexch` and `rowexch` are two competing optimization algorithms for computing a D-optimal design given a model specification.

Both `cordexch` and `rowexch` are iterative algorithms. They operate by improving a starting design by making incremental changes to its elements. In the coordinate exchange algorithm, the increments are the individual elements of the design matrix. In row exchange, the elements are the rows of the design matrix. Atkinson and Donev (1992) is a reference.

To generate a D-optimal design you must specify the number of inputs, the number of runs, and the order of the model you want to fit.

Both `cordexch` and `rowexch` take the following strings to specify the model:

- `'linear'` (`'l'`) – the default model with constant and first order terms.
- `'interaction'` (`'i'`) – includes constant, linear, and cross product terms.
- `'quadratic'` (`'q'`) – interactions plus squared terms.
- `'purequadratic'` (`'p'`) – includes constant, linear and squared terms.

Alternatively, you can use a matrix of integers to specify the terms. Details are in the help for the utility function `x2fx`.

For a simple example using the coordinate-exchange algorithm consider the problem of quadratic modeling with two inputs. The model form is:

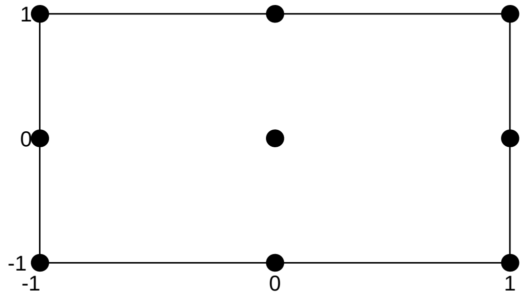
$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 x_2 + \beta_{11} x_1^2 + \beta_{22} x_2^2 + \varepsilon$$

Suppose we want the D-optimal design for fitting this model with nine runs.

```
settings = cordexch(2,9,'q')

settings =

    –1     1
     1     1
     0     1
     1    –1
    –1    –1
     0    –1
     1     0
     0     0
    –1     0
```

We can plot the columns of settings against each other to get a better picture of the design.

```
h = plot(settings(:,1),settings(:,2),'.');
set(gca,'Xtick',[-1 0 1])
set(gca,'Ytick',[-1 0 1])
set(h,'Markersize',20)
```



For a simple example using the row-exchange algorithm, consider the interaction model with two inputs. The model form is:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 x_2 + \varepsilon$$

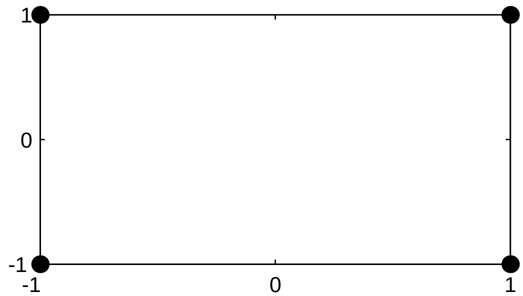
Suppose we want the D-optimal design for fitting this model with four runs.

```
[settings, X] = rowexch(2,4,'i')

settings =

    –1     1
    –1    –1
     1    –1
     1     1

X =

     1    –1     1    –1
     1    –1    –1     1
     1     1    –1    –1
     1     1     1     1
```

The settings matrix shows how to vary the inputs from run to run. The X matrix is the design matrix for fitting the above regression model. The first column of X is for fitting the constant term. The last column is the element-wise product of the second and third columns.

The associated plot is simple but elegant.

```
h = plot(settings(:,1),settings(:,2),'.');
set(gca,'Xtick',[-1 0 1])
set(gca,'Ytick',[-1 0 1])
set(h,'Markersize',20)
```



Augmenting D-Optimal Designs

In practice, experimentation is an iterative process. We often want to add runs to a completed experiment to learn more about our system. The function daugment allows you choose these extra runs optimally.

Suppose we have executed the eight-run design below for fitting a linear model to four input variables.

```
settings = cordexch(4,8)

settings =

     1    -1     1     1
    -1    -1     1    -1
    -1     1     1     1
     1     1     1    -1
    -1     1    -1     1
     1    -1    -1     1
    -1    -1    -1    -1
     1     1    -1    -1
```

This design is adequate to fit the linear model for four inputs, but cannot fit the six cross-product (interaction) terms. Suppose we are willing to do eight more runs to fit these extra terms. Here's how.

```
[augmented, X] = daugment(settings,8,'i');
augmented

augmented =

     1    -1     1     1
    -1    -1     1    -1
    -1     1     1     1
     1     1     1    -1
    -1     1    -1     1
     1    -1    -1     1
    -1    -1    -1    -1
     1     1    -1    -1
    -1    -1    -1     1
     1     1     1     1
    -1    -1     1     1
    -1     1     1    -1
     1    -1     1    -1
     1    -1    -1    -1
    -1     1    -1    -1
     1     1    -1     1
info = X'*X

info =

    16     0     0     0     0     0     0     0     0     0     0
     0    16     0     0     0     0     0     0     0     0     0
     0     0    16     0     0     0     0     0     0     0     0
     0     0     0    16     0     0     0     0     0     0     0
     0     0     0     0    16     0     0     0     0     0     0
     0     0     0     0     0    16     0     0     0     0     0
     0     0     0     0     0     0    16     0     0     0     0
     0     0     0     0     0     0     0    16     0     0     0
     0     0     0     0     0     0     0     0    16     0     0
     0     0     0     0     0     0     0     0     0    16     0
     0     0     0     0     0     0     0     0     0     0    16
```

The augmented design is orthogonal, since `X'*X` is a multiple of the identity matrix. In fact, this design is the same as a 2^4 factorial design.

Designing Experiments with Uncontrolled Inputs

Sometimes it is impossible to control every experimental input. But you may know the values of some inputs in advance. An example is the time each run takes place. If a process is experiencing linear drift, you may want to include the time of each test run as a variable in the model.

The function `dcovary` allows you to choose the settings for each run in order to maximize your information despite a linear drift in the process.

Suppose we want to execute an eight-run experiment with three factors that is optimal with respect to a linear drift in the response over time. First we create our `drift` input variable. Note, that `drift` is normalized to have mean zero. Its minimum is –1 and its maximum is +1.

```
drift = (linspace(–1,1,8))'
drift =

   –1.0000
   –0.7143
   –0.4286
   –0.1429
    0.1429
    0.4286
    0.7143
    1.0000

settings = dcovary(3,drift,'linear')
settings =

    1.0000    1.0000   –1.0000   –1.0000
   –1.0000   –1.0000   –1.0000   –0.7143
   –1.0000    1.0000    1.0000   –0.4286
    1.0000   –1.0000    1.0000   –0.1429
   –1.0000    1.0000   –1.0000    0.1429
    1.0000    1.0000    1.0000    0.4286
   –1.0000   –1.0000    1.0000    0.7143
    1.0000   –1.0000   –1.0000    1.0000
```

Demos

The Statistics Toolbox has demonstration programs that create an interactive environment for exploring the probability distribution, random number generation, curve fitting, and design of experiments functions.

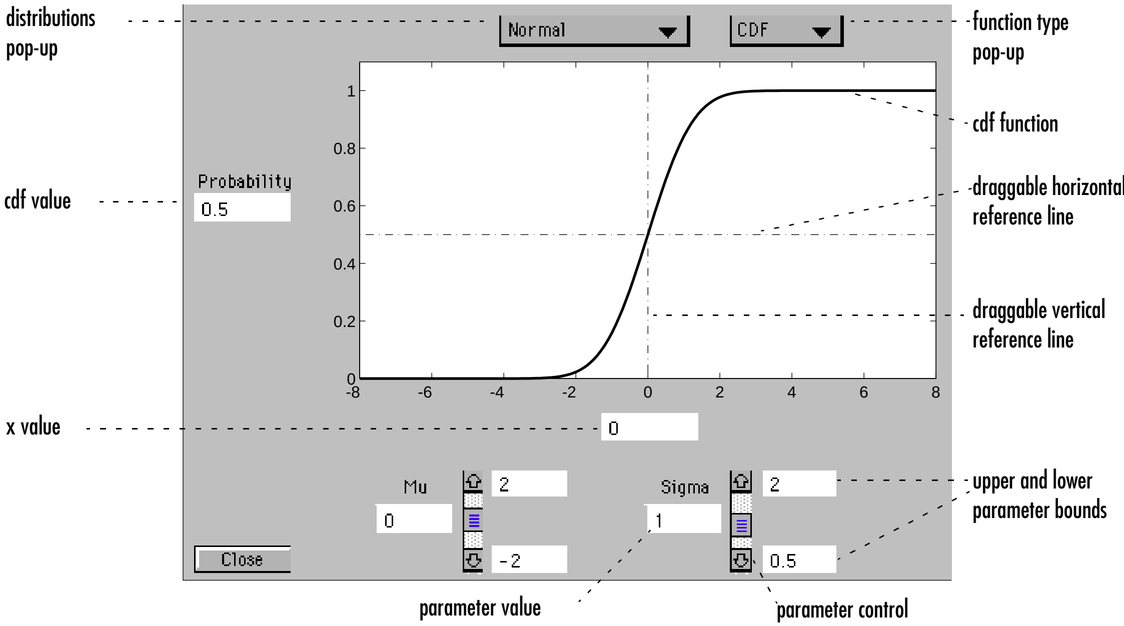
Demo	Purpose
`disttool`	Graphic interaction with probability distributions.
`polytool`	Interactive graphic prediction of polynomial fits.
`randtool`	Interactive control of random number generation.
`rsmdemo`	Design of Experiments and regression modeling.

The disttool Demo

`disttool` is a graphic environment for developing an intuitive understanding of probability distributions.

The `disttool` demo has the following features:

- A graph of the cdf (pdf) for the given parameters of a distribution.
- A pop-up menu for changing the distribution function.
- A pop-up menu for changing the function type (cdf <–> pdf).
- Sliders to change the parameter settings.
- Data entry boxes to choose specific parameter values.
- Data entry boxes to change the limits of the parameter sliders.
- Draggable horizontal and vertical reference lines to do interactive evaluation of the function at varying values.
- A data entry box to evaluate the function at a specific *x*-value.
- For cdf plots, a data entry box on the probability axis (*y*-axis) to find critical values corresponding to a specific probability.
- A **Close** button to end the demonstration.



The polytool Demo

The `polytool` demo is an interactive graphic environment for polynomial curve fitting and prediction.

The `polytool` demo has the following features:

- A graph of the data, the fitted polynomial, and global confidence bounds on a new predicted value.
- *y*-axis text to display the predicted *y*-value and its uncertainty at the current *x*-value.
- A data entry box to change the degree of the polynomial fit.
- A data entry box to evaluate the polynomial at a specific *x*-value.
- A draggable vertical reference line to do interactive evaluation of the polynomial at varying *x*-values.
- A **Close** button to end the demonstration.

You can use polytool to do curve fitting and prediction for any set of *x*-*y* data, but, for the sake of demonstration, the Statistics Toolbox provides a dataset (polydata.mat) to teach some basic concepts.

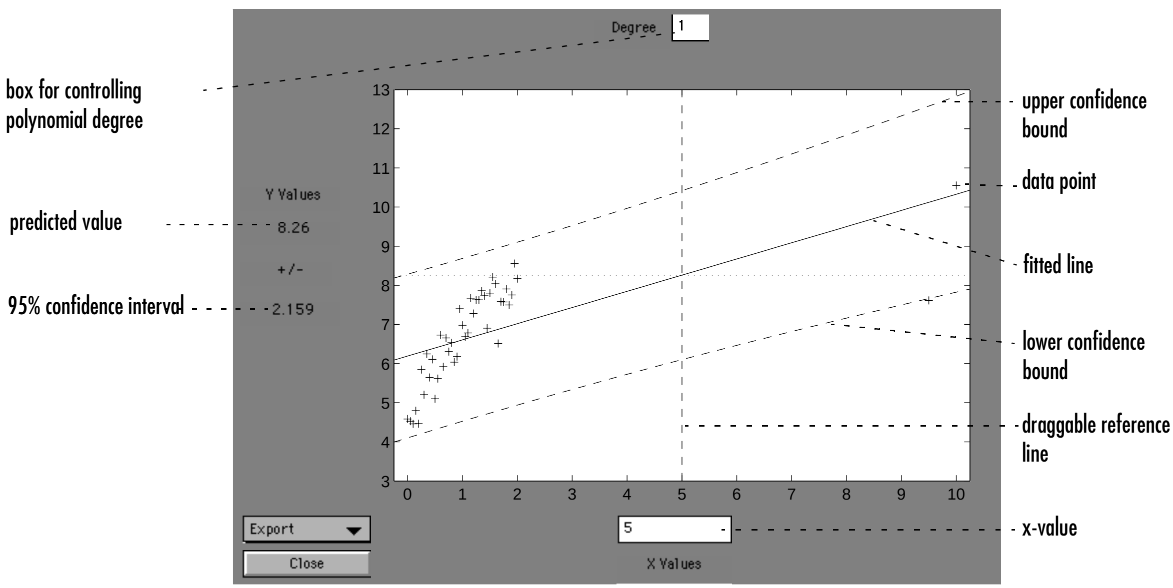
To start the demonstration you must first load the dataset.

```
load polydata
who
Your variables are:

x          x1          y          y1
```

The variables x and y are observations made with error from a cubic polynomial. The variables x1 and y1 are data points from the “true” function without error.

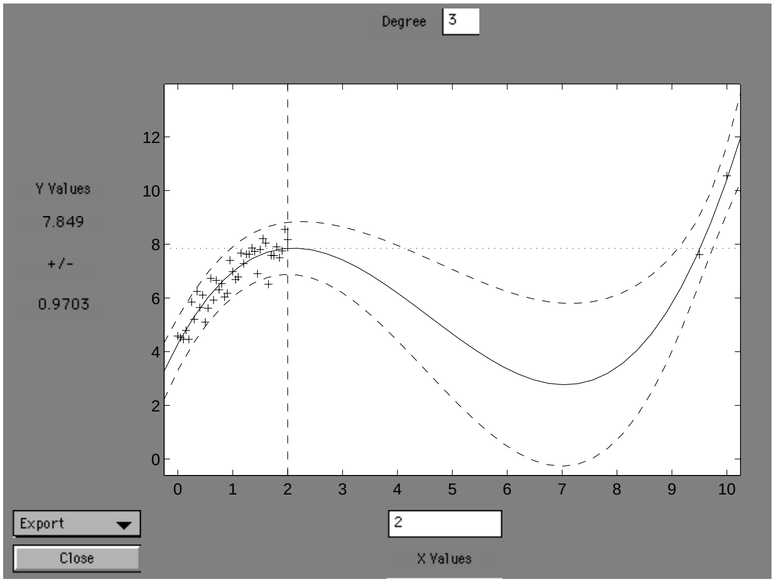
If you do not specify the degree of the polynomial, polytool does a linear fit to the data.

```
polytool(x,y)
```



The linear fit is not very good. The bulk of the data with *x*-values between zero and two has a steeper slope than the fitted line. The two points to the right are dragging down the estimate of the slope.

Go to the data entry box at the top and type 3 for a cubic model. Then, drag the vertical reference line to the *x*-value of two (or type 2 in the *x*-axis data entry box).



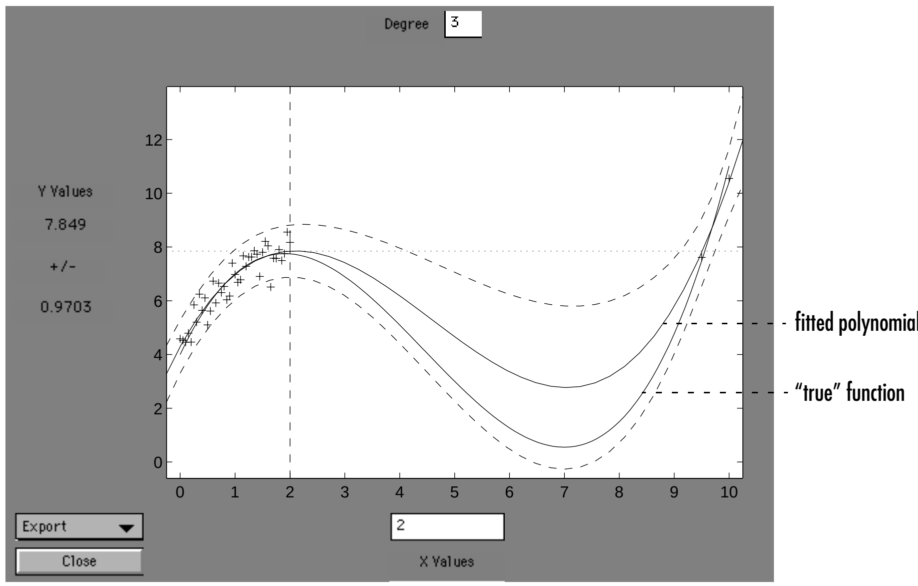
This graph shows a much better fit to the data. The confidence bounds are closer together indicating that there is less uncertainty in prediction. The data at both ends of the plot tracks the fitted curve.

The true function in this case is cubic.

$$y = 4 + 4.3444x - 1.4533x^2 + 0.1089x^3 + \varepsilon$$
$$\varepsilon \sim N(0, 0.1I)$$

To superimpose the "true" function on the plot use the command:

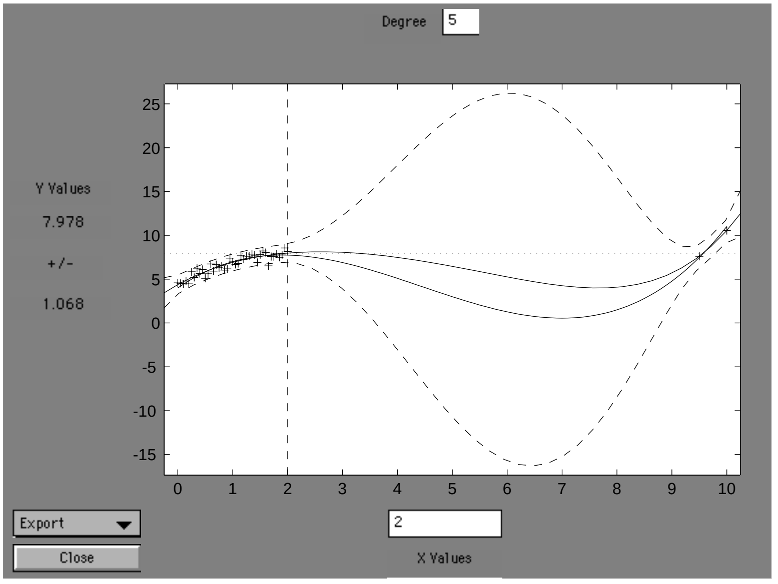
```
plot(x1,y1)
```



The true function is quite close to the fitted polynomial in the region of the data. Between the two groups of data points the two functions separate, but both fall inside the 95% confidence bounds.

If the cubic polynomial is a good fit, it is tempting to try a higher order polynomial to see if even more precise predictions are possible.

Since the true function is cubic, this amounts to overfitting the data. Use the data entry box for degree and type `5` for a quintic model.



The resulting fit again does well predicting the function near the data points. But, in the region between the data groups, the uncertainty of prediction rises dramatically.

This bulge in the confidence bounds happens because the data really do not contain enough information to estimate the higher order polynomial terms precisely, so even interpolation using polynomials can be risky in some cases.

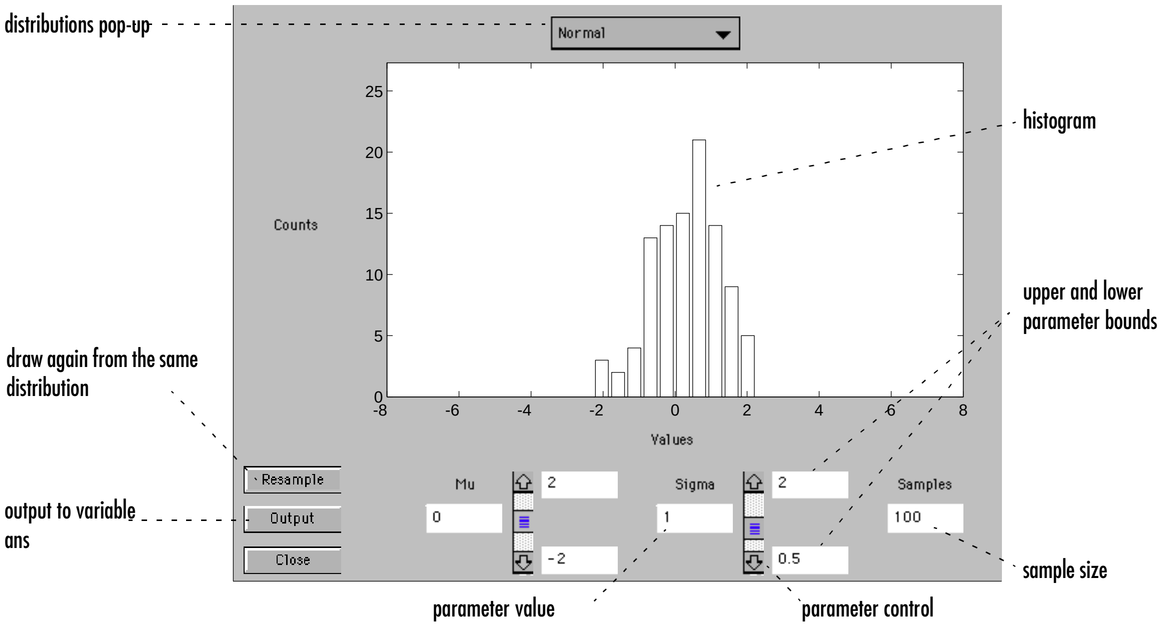
The randtool Demo

`randtool` is a graphic environment for generating random samples from various probability distributions and displaying the sample histogram.

The `randtool` demo has the following features:

- A histogram of the sample.
- A pop-up menu for changing the distribution function.
- Sliders to change the parameter settings.

- A data entry box to choose the sample size.
- Data entry boxes to choose specific parameter values.
- Data entry boxes to change the limits of the parameter sliders.
- An **Output** button to output the current sample to the variable ans.
- A **Resample** button to allow repetitive sampling with constant sample size and fixed parameters.
- A **Close** button to end the demonstration



The rsmdemo Demo

`rsmdemo` is an interactive graphic environment that demonstrates design of experiments and surface fitting through the simulation of a chemical reaction. The goal of the demo is to find the levels of the reactants needed to maximize the reaction rate.

There are two parts to the demo:

1 Compare data gathered through trial and error with data from a designed experiment.

2 Compare response surface (polynomial) modeling with nonlinear modeling.

Part 1

Begin the demo by using the sliders in the Reaction Simulator to control the partial pressures of three reactants: Hydrogen, n-Pentane, and Isopentane. Each time you click the **Run** button, the levels for the reactants and results of the run are entered in the Trial and Error Data window.

Based on the results of previous runs, you can change the levels of the reactants to increase the reaction rate. (The results are determined using an underlying model that takes into account the noise in the process, so even if you keep all of the levels the same, the results will vary from run to run.) You are allotted a budget of 13 runs. When you have completed the runs, you can use the **Plot** menu on the Trial and Error Data window to plot the relationships between the reactants and the reaction rate, or click the **Analyze** button. When you click **Analyze**, `rsmdemo` calls the `rstool` function, which you can then use to try to optimize the results.)

Next, perform another set of 13 runs, this time from a designed experiment. In the Experimental Design Data window, click the **Do Experiment** button. `rsmdemo` calls the `cordexch` function to generate a D-optimal design, and then, for each run, computes the reaction rate.

Now use the **Plot** menu on the Experimental Design Data window to plot the relationships between the levels of the reactants and the reaction rate, or click the **Response Surface** button to call `rstool` to find the optimal levels of the reactants.

Compare the analysis results for the two sets of data. It is likely (though not certain) that you'll find some or all of these differences:

- You can fit a full quadratic model with the data from the designed experiment, but the trial and error data may be insufficient for fitting a quadratic model or interactions model.
- Using the data from the designed experiment, you are more likely to be able to find levels for the reactants that result in the maximum reaction rate.

Even if you find the best settings using the trial and error data, the confidence bounds are likely to be wider than those from the designed experiment.

Part 2

Now analyze the experimental design data with a polynomial model and a nonlinear model, and comparing the results. The true model for the process, which is used to generate the data, is actually a nonlinear model. However, within the range of the data, a quadratic model approximates the true model quite well.

To see the polynomial model, click the **Response Surface** button on the Experimental Design Data window. `rsmdemo` calls `rstool`, which fits a full quadratic model to the data. Drag the reference lines to change the levels of the reactants, and find the optimal reaction rate. Observe the width of the confidence intervals.

Now click the **Nonlinear Model** button on the Experimental Design Data window. `rsmdemo` calls `nlintool`, which fits a Hougen-Watson model to the data. As with the quadratic model, you can drag the reference lines to change the reactant levels. Observe the reaction rate and the confidence intervals.

Compare the analysis results for the two models. Even though the true model is nonlinear, you may find that the polynomial model provides a good fit. Because polynomial models are much easier to fit and work with than nonlinear models, a polynomial model is often preferable even when modeling a nonlinear process. Keep in mind, however, that such models are unlikely to be reliable for extrapolating outside the range of the data.

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2

Reference

The Statistics Toolbox provides several categories of functions. These categories appear in the table below.

The Statistics Toolbox's Main Categories of Functions	
Probability	Probability distribution functions.
Descriptive	Descriptive statistics for data samples.
Plots	Statistical plots.
SPC	Statistical Process Control.
Cluster Analysis	Grouping items with similar characteristics into clusters.
Linear	Fitting linear models to data.
Nonlinear	Fitting nonlinear regression models.
DOE	Design of Experiments.
PCA	Principal Components Analysis.
Hypotheses	Statistical tests of hypotheses.
File I/O	Reading data from and writing data to operating-system files.
Demos	Demonstrations.
Data	Data for examples.

The following pages contain tables of functions from each of these specific areas. The first seven tables contain probability distribution functions. The remaining tables describe the other categories of functions.

	Parameter Estimation
betafit	Parameter estimation for the beta distribution.
betalike	Beta log-likelihood function.
binofit	Parameter estimation for the binomial distribution.
expfit	Parameter estimation for the exponential distribution.
gamfit	Parameter estimation for the gamma distribution.
gamlike	Gamma log-likelihood function.
mle	Maximum likelihood estimation.
normlike	Normal log-likelihood function.
normfit	Parameter estimation for the normal distribution.
poissfit	Parameter estimation for the Poisson distribution.
unifit	Parameter estimation for the uniform distribution.

	Cumulative Distribution Functions (cdf)
betacdf	Beta cdf.
binocdf	Binomial cdf.
cdf	Parameterized cdf routine.
chi2cdf	Chi-square cdf.
expcdf	Exponential cdf.
fcdf	F cdf.
gamcdf	Gamma cdf.
geocdf	Geometric cdf.
hygecdf	Hypergeometric cdf.

	Cumulative Distribution Functions (cdf) (Continued)
logncdf	Lognormal cdf.
nbincdf	Negative binomial cdf.
ncfcdf	Noncentral F cdf.
nctcdf	Noncentral t cdf.
ncx2cdf	Noncentral Chi-square cdf.
normcdf	Normal (Gaussian) cdf.
poisscdf	Poisson cdf.
raylcdf	Rayleigh cdf.
tcdf	Student's t cdf.
unidcdf	Discrete uniform cdf.
unifcdf	Continuous uniform cdf.
weibcdf	Weibull cdf.

	Probability Density Functions (pdf)
betapdf	Beta pdf.
binopdf	Binomial pdf.
chi2pdf	Chi-square pdf.
exppdf	Exponential pdf.
fpdf	F pdf.
gampdf	Gamma pdf.
geopdf	Geometric pdf.
hygepdf	Hypergeometric pdf.

	Probability Density Functions (pdf) (Continued)
`normpdf`	Normal (Gaussian) pdf.
`lognpdf`	Lognormal pdf.
`nbinpdf`	Negative binomial pdf.
`ncfpdf`	Noncentral F pdf.
`nctpdf`	Noncentral t pdf.
`ncx2pdf`	Noncentral Chi-square pdf.
`pdf`	Parameterized pdf routine.
`poisspdf`	Poisson pdf.
`raylpdf`	Rayleigh pdf.
`tpdf`	Student's t pdf.
`unidpdf`	Discrete uniform pdf.
`unifpdf`	Continuous uniform pdf.
`weibpdf`	Weibull pdf.

	Inverse Cumulative Distribution Functions
`betainv`	Beta critical values.
`binoinv`	Binomial critical values.
`chi2inv`	Chi-square critical values.
`expinv`	Exponential critical values.
`finv`	F critical values.
`gaminv`	Gamma critical values.
`geoinv`	Geometric critical values.

	Inverse Cumulative Distribution Functions (Continued)
`hygeinv`	Hypergeometric critical values.
`logninv`	Lognormal critical values.
`nbininv`	Negative binomial critical values
`ncfinv`	Noncentral F critical values.
`nctinv`	Noncentral t critical values.
`ncx2inv`	Noncentral Chi-square critical values.
`icdf`	Parameterized inverse distribution routine.
`norminv`	Normal (Gaussian) critical values.
`poissinv`	Poisson critical values.
`raylinv`	Rayleigh critical values.
`tinv`	Student's t critical values.
`unidinv`	Discrete uniform critical values.
`unifinv`	Continuous uniform critical values.
`weibinv`	Weibull critical values.

	Random Number Generators
`betarnd`	Beta random numbers.
`binornd`	Binomial random numbers.
`chi2rnd`	Chi-square random numbers.
`exprnd`	Exponential random numbers.
`frnd`	F random numbers.
`gamrnd`	Gamma random numbers.

	Random Number Generators (Continued)
georndd	Geometric random numbers.
hygernd	Hypergeometric random numbers.
lognrnd	Lognormal random numbers.
nbinrnd	Negative binomial random numbers.
ncfrnd	Noncentral F random numbers.
nctrnd	Noncentral t random numbers.
ncx2rnd	Noncentral Chi-square random numbers.
normrnd	Normal (Gaussian) random numbers.
poissrnd	Poisson random numbers.
raylrnd	Rayleigh random numbers.
random	Parameterized random number routine.
trnd	Student's t random numbers.
unidrnd	Discrete uniform random numbers.
unifrnd	Continuous uniform random numbers.
weibrnd	Weibull random numbers.

	Moments of Distribution Functions
`betastat`	Beta mean and variance.
`binostat`	Binomial mean and variance.
`chi2stat`	Chi-square mean and variance.
`expstat`	Exponential mean and variance.
`fstat`	F mean and variance.
`gamstat`	Gamma mean and variance.
`geostat`	Geometric mean and variance.
`hygestat`	Hypergeometric mean and variance.
`lognstat`	Lognormal mean and variance.
`nbinstat`	Negative binomial mean and variance.
`ncfstat`	Noncentral F mean and variance.
`nctstat`	Noncentral t mean and variance.
`ncx2stat`	Noncentral Chi-square mean and variance.
`normstat`	Normal (Gaussian) mean and variance.
`poisstat`	Poisson mean and variance.
`raylstat`	Rayleigh mean and variance.
`tstat`	Student's t mean and variance.
`unidstat`	Discrete uniform mean and variance.
`unifstat`	Continuous uniform mean and variance.
`weibstat`	Weibull mean and variance.

Descriptive Statistics	
`corrcoef`	Correlation coefficients (in MATLAB).
`cov`	Covariance matrix (in MATLAB).
`geomean`	Geometric mean.
`harmmean`	Harmonic mean.
`iqr`	Interquartile range.
`kurtosis`	Sample kurtosis.
`mad`	Mean absolute deviation.
`mean`	Arithmetic average (in MATLAB).
`median`	50th percentile (in MATLAB).
`moment`	Central moments of all orders.
`nanmax`	Maximum ignoring missing data.
`nanmean`	Average ignoring missing data.
`nanmedian`	Median ignoring missing data.
`nanmin`	Minimum ignoring missing data.
`nanstd`	Standard deviation ignoring missing data.
`nansum`	Sum ignoring missing data.
`prctile`	Empirical percentiles of a sample.
`range`	Sample range.
`skewness`	Sample skewness.
`std`	Standard deviation (in MATLAB).
`trimmean`	Trimmed mean.
`var`	Variance.

	Statistical Plotting
`boxplot`	Box plots.
`errorbar`	Error bar plot.
`fsurfht`	Interactive contour plot of a function.
`gline`	Interactive line drawing.
`gname`	Interactive point labeling.
`lsline`	Add least-squares fit line to plotted data.
`normplot`	Normal probability plots.
`pareto`	Pareto charts.
`qqplot`	Quantile-Quantile plots.
`rcoplot`	Regression case order plot.
`refcurve`	Reference polynomial.
`refline`	Reference line.
`surfht`	Interactive interpolating contour plot.
`weibplot`	Weibull plotting.

Statistical Process Control	
capable	Quality capability indices.
capaplot	Plot of process capability.
ewmaplot	Exponentially weighted moving average plot.
histfit	Histogram and normal density curve.
normspec	Plot normal density between limits.
schart	Time plot of standard deviation.
xbarplot	Time plot of means.

Cluster Analysis	
cluster	Create clusters from linkage output.
clusterdata	Create clusters from a dataset.
cophenet	Calculate the cophenetic correlation coefficient.
dendrogram	Plot a hierarchical tree in a dendrogram graph.
inconsistent	Calculate the inconsistency values of objects in a cluster hierarchy tree.
linkage	Link objects in a dataset into a hierarchical tree of binary clusters.
pdist	Calculate the pairwise distance between objects in a dataset.
squareform	Reformat output of pdist function from vector to square matrix.
zscore	Normalize a dataset before calculating the distance.

	Linear Models
`anova1`	One-way Analysis of Variance (ANOVA).
`anova2`	Two-way Analysis of Variance.
`lscov`	Regression given a covariance matrix (in MATLAB).
`polyconf`	Polynomial prediction with confidence intervals.
`polyfit`	Polynomial fitting (in MATLAB).
`polyval`	Polynomial prediction (in MATLAB).
`regress`	Multiple linear regression.
`ridge`	Ridge regression.
`rstool`	Response surface tool.
`stepwise`	Stepwise regression GUI.

	Nonlinear Regression
`nlinfit`	Nonlinear least-squares fitting.
`nlintool`	Prediction graph for nonlinear fits.
`nlparci`	Confidence intervals on parameters.
`nlpredci`	Confidence intervals for prediction.
`nnls`	Nonnegative least squares (in MATLAB).

	Design of Experiments
cordexch	D-optimal design using coordinate exchange.
daugment	D-optimal augmentation of designs.
dcovary	D-optimal design with fixed covariates.
ff2n	Two-level full factorial designs.
fullfact	Mixed level full factorial designs.
hadamard	Hadamard designs (in MATLAB).
rowexch	D-optimal design using row exchange.

	Principal Components Analysis
barttest	Bartlett's test.
pcacov	PCA from covariance matrix.
pcares	Residuals from PCA.
princomp	PCA from raw data matrix.

	Hypothesis Tests
ranksum	Wilcoxon rank sum test.
signrank	Wilcoxon signed rank test.
signtest	Sign test for paired samples.
ttest	One sample t-test.
ttest2	Two sample t-test.
ztest	Z-test.

	File I/O
caseread	Read casenames from a file.
casewrite	Write casenames from a string matrix to a file.
tblread	Retrieve tabular data from the file system.
tblwrite	Write data in tabular form to the file system.

	Demonstrations
disttool	Interactive exploration of distribution functions.
randtool	Interactive random number generation.
polytool	Interactive fitting of polynomial models.
rsmdemo	Interactive process experimentation and analysis.
statdemo	Demonstrates capabilities of the Statistics Toolbox.

	Data
census.mat	U. S. Population 1790 to 1980.
cities.mat	Names of U.S. metropolitan areas.
discrim.mat	Classification data.
gas.mat	Gasoline prices.
hald.mat	Hald data.
hogg.mat	Bacteria counts from milk shipments.
lawdata.mat	GPA versus LSAT for 15 law schools.
mileage.mat	Mileage data for three car models from two factories.

	Data (Continued)
moore.mat	Five factor – one response regression data.
parts.mat	Dimensional runout on 36 circular parts.
popcorn.mat	Data for popcorn example.
polydata.mat	Data for polytool demo.
reaction.mat	Reaction kinetics data.
sat.dat	ASCII data for tblread example.

Purpose

One-way Analysis of Variance (ANOVA).

Syntax

```
p = anova1(X)
p = anova1(x,group)
```

Description

`anova1(X)` performs a balanced one-way ANOVA for comparing the means of two or more columns of data on the sample in `X`. It returns the p-value for the null hypothesis that the means of the columns of `X` are equal. If the p-value is near zero, this casts doubt on the null hypothesis and suggests that the means of the columns are, in fact, different.

`anova1(x,group)` performs a one-way ANOVA for comparing the means of two or more samples of data in `x` indexed by the vector, `group`. The input, `group`, identifies the group of the corresponding element of the vector `x`.

The values of `group` are integers with minimum equal to one and maximum equal to the number of different groups to compare. There must be at least one element in each group. This two-input form of `anova1` does not require equal numbers of elements in each group, so it is appropriate for unbalanced data.

The choice of a limit for the p-value to determine whether the result is “statistically significant” is left to the researcher. It is common to declare a result significant if the p-value is less than 0.05 or 0.01.

`anova1` also displays two figures.

The first figure is the standard ANOVA table, which divides the variability of the data in `X` into two parts:

- The variability due to the differences among the column means.
- The variability due to the differences between the data in each column and the column mean.

The ANOVA table has five columns:

- The first shows the source of the variability.
- The second shows the Sum of Squares (SS) due to each source.
- The third shows the degrees of freedom (df) associated with each source.
- The fourth shows the Mean Squares (MS), which is the ratio SS/df.
- The fifth shows the *F* statistic, which is the ratio of the MS’s.

The p-value is a function (fcdf) of F. As F increases the p-value decreases.

The second figure displays box plots of each column of X. Large differences in the center lines of the box plots correspond to large values of F and correspondingly small p-values.

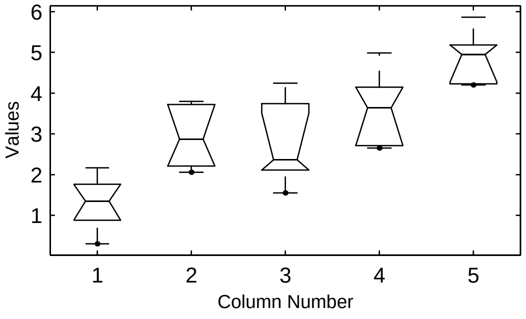
Examples

The five columns of x are the constants one through five plus a random normal disturbance with mean zero and standard deviation one. The ANOVA procedure detects the difference in the column means with great assurance. The probability (p) of observing the sample x by chance given that there is no difference in the column means is less than 6 in 100,000.

```
x = meshgrid(1:5)

x =

1      2      3      4      5
1      2      3      4      5
1      2      3      4      5
1      2      3      4      5

x = x + normrnd(0,1,5,5)

x =

2.1650    3.6961    1.5538    3.6400    4.9551
1.6268    2.0591    2.2988    3.8644    4.2011
1.0751    3.7971    4.2460    2.6507    4.2348
1.3516    2.2641    2.3610    2.7296    5.8617
0.3035    2.8717    3.5774    4.9846    4.9438

p = anova1(x)

p =

   5.9952e–05
```

ANOVA Table

Source	SS	df	MS	F
Columns	32.93	4	8.232	11.26
Error	14.62	20	0.7312	
Total	47.55	24		



The following example comes from a study of material strength in structural beams Hogg (1987). The vector, `strength`, measures the deflection of a beam in thousandths of an inch under 3,000 pounds of force. Stronger beams deflect less. The civil engineer performing the study wanted to determine whether the strength of steel beams was equal to the strength of two more expensive alloys. Steel is coded 1 in the vector, `alloy`. The other materials are coded 2 and 3.

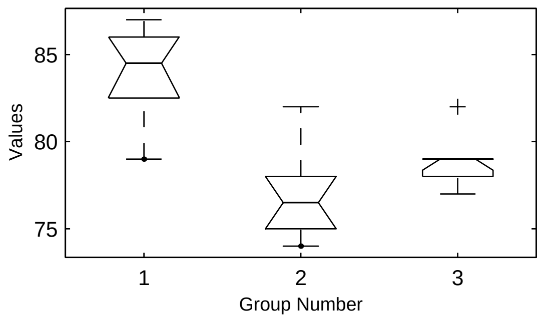
```
strength = [82 86 79 83 84 85 86 87 74 82 78 75 76 77 79 ...
79 77 78 82 79];
alloy =[1 1 1 1 1 1 1 1 2 2 2 2 2 2 3 3 3 3 3 3];
```

Though `alloy` is sorted in this example, you do not need to sort the grouping variable.

```
p = anova1(strength,alloy)
p =

1.5264e–04
```

ANOVA Table

Source	SS	df	MS	F
Columns	184.8	2	92.4	15.4
Error	102	17	6	
Total	286.8	19		



The p-value indicates that the three alloys are significantly different. The box plot confirms this graphically and shows that the steel beams deflect more than the more expensive alloys.

References

Hogg, R. V., and J. Ledolter. *Engineering Statistics*. MacMillan Publishing Company, 1987.

Purpose Two-way Analysis of Variance (ANOVA).

Syntax

```
p = anova2(X,reps)
```

Description

`anova2(X,reps)` performs a balanced two-way ANOVA for comparing the means of two or more columns and two or more rows of the sample in `X`. The data in different columns represent changes in one factor. The data in different rows represent changes in the other factor. If there is more than one observation per row-column pair, then the argument, `reps`, indicates the number of observations per "cell."

The matrix below shows the format for a set-up where the column factor has two levels, the row factor has three levels, and there are two replications. The subscripts indicate row, column and replicate, respectively.

$$\begin{bmatrix} x_{111} & x_{121} \\ x_{112} & x_{122} \\ x_{211} & x_{221} \\ x_{212} & x_{222} \\ x_{311} & x_{321} \\ x_{312} & x_{322} \end{bmatrix}$$

`anova2` returns the p-values for the null hypotheses that the means of the columns and the means of the rows of `X` are equal. If any p-value is near zero, this casts doubt on the null hypothesis and suggests that the means of the source of variability associated with that p-value are, in fact, different.

The choice of a limit for the p-value to determine whether the result is "statistically significant" is left to the researcher. It is common to declare a result significant if the p-value is less than 0.05 or 0.01.

`anova2` also displays a figure showing the standard ANOVA table, which divides the variability of the data in `X` into three or four parts depending on the value of `reps`:

- The variability due to the differences among the column means.
- The variability due to the differences among the row means.

- The variability due to the interaction between rows and columns (if `reps` is greater than its default value of one.)
- The remaining variability not explained by any systematic source.

The ANOVA table has five columns:

- The first shows the source of the variability.
- The second shows the Sum of Squares (SS) due to each source.
- The third shows the degrees of freedom (df) associated with each source.
- The fourth shows the Mean Squares (MS), which is the ratio SS/df.
- The fifth shows the F statistics, which is the ratio of the mean squares.

The p-value is a function (fcdf) of F. As F increases the p-value decreases.

Examples

The data below comes from a study of popcorn brands and popper type (Hogg 1987). The columns of the matrix `popcorn` are brands (Gourmet, National, and Generic). The rows are popper type (Oil and Air.) The study popped a batch of each brand three times with each popper. The values are the yield in cups of popped popcorn.

```
load popcorn
popcorn

popcorn =

    5.5000    4.5000    3.5000
    5.5000    4.5000    4.0000
    6.0000    4.0000    3.0000
    6.5000    5.0000    4.0000
    7.0000    5.5000    5.0000
    7.0000    5.0000    4.5000

p = anova2(popcorn,3)

p =

   0.0000    0.0001    0.7462
```

ANOVA Table

Source	SS	df	MS	F
Columns	15.75	2	7.875	56.7
Rows	4.5	1	4.5	32.4
Interaction	0.08333	2	0.04167	0.3
Error	1.667	12	0.1389	
Total	22	17		

The vector, `p`, shows the p-values for the three brands of popcorn `0.0000`, the two popper types `0.0001`, and the interaction between brand and popper type `0.7462`. These values indicate that both popcorn brand and popper type affect the yield of popcorn, but there is no evidence of a synergistic (interaction) effect of the two.

The conclusion is that you can get the greatest yield using the Gourmet brand and an Air popper (the three values located in `popcorn(4:6,1)`).

Reference

Hogg, R. V. and J. Ledolter. *Engineering Statistics*. MacMillan Publishing Company, 1987.

Purpose

Bartlett's test for dimensionality.

Syntax

```
ndim = barttest(x,alpha)
[ndim,prob,chisquare] = barttest(x,alpha)
```

Description

`ndim = barttest(x,alpha)` returns the number of dimensions necessary to explain the nonrandom variation in the the data matrix `x`, using the significance probability `alpha`. The dimension is determined by a series of hypothesis tests. The test for `ndim = 1` tests the hypothesis that the variances of the data values along each principal component are equal; the test for `ndim = 2` tests the hypothesis that the variances along the second through last components are equal; and so on.

`[ndim,prob,chisquare] = barttest(x,alpha)` returns the number of dimensions, the significance values for the hypothesis tests, and the χ^2 values associated with the tests.

Example

```
x = mvnrnd([0 0], [1 0.99; 0.99 1],20);
x(:,3:4) = mvnrnd([0 0], [1 0.99; 0.99 1],20);
x(:,5:6) = mvnrnd([0 0], [1 0.99; 0.99 1],20);
[ndim, prob] = barttest(x,0.05)

ndim =

     3

prob =

          0
          0
          0
     0.5081
     0.6618
     1.0000
```

See Also

`princomp`, `pcacov`, `pcares`

betacdf

Purpose Beta cumulative distribution function (cdf).

Syntax `P = betacdf(X,A,B)`

Description `betacdf(X,A,B)` computes the beta cdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A`, and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `A` and `B` must both be positive and `x` must lie on the interval [0 1].

The beta cdf is:

$$p = F(x|a,b) = \frac{1}{B(a,b)}\int_0^x t^{a-1}(1-t)^{b-1}dt$$

The result, p, is the probability that a single observation from a beta distribution with parameters a and b will fall in the interval [0 x].

Examples

```
x = 0.1:0.2:0.9;
a = 2;
b = 2;
p = betacdf(x,a,b)

p =

    0.0280    0.2160    0.5000    0.7840    0.9720

a = [1 2 3];
p = betacdf(0.5,a,a)

p =

    0.5000    0.5000    0.5000
```

Purpose Parameter estimates and confidence intervals for beta distributed data.

Syntax

```
phat = betafit(x)
[phat,pci] = betafit(x,alpha)
```

Description `betafit` computes the maximum likelihood estimates of the parameters of the beta distribution from the data in the vector, `x`. With two output parameters, `betafit` also returns confidence intervals on the parameters, in the form of a 2-by-2 matrix. The first column of the matrix contains the lower and upper confidence bounds for parameter `A`, and the second column contains the confidence bounds for parameter `B`.

The optional input argument, `alpha`, controls the width of the confidence interval. By default, `alpha` is 0.05 which corresponds to 95% confidence intervals.

Example This example generates 100 beta distributed observations. The “true” parameters are 4 and 3 respectively. Compare these to the values in `p`. Note that the columns of `ci` both bracket the true parameters.

```
r = betarnd(4,3,100,1);
[p,ci] = betafit(r,0.01)

p =

    3.9010    2.6193

ci =

    2.5244    1.7488
    5.2777    3.4899
```

Reference Hahn, Gerald J., & Shapiro, Samuel, S."*Statistical Models in Engineering*", Wiley Classics Library John Wiley & Sons, New York. 1994. p. 95.

See Also `betalike`, `mle`

betainv

Purpose Inverse of the beta cumulative distribution function.

Syntax

```
X = betainv(P,A,B)
```

Description `betainv(P,A,B)` computes the inverse of the beta cdf with parameters `A` and `B` for the probabilities in `P`. The arguments `P`, `A`, and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `A` and `B` must both be positive and `P` must lie on the interval [0 1].

The beta inverse function in terms of the beta cdf is:

$$x = F^{-1}(p|a,b) = \{x:F(x|a,b) = p\}$$

where

$$p = F(x|a,b) = \frac{1}{B(a,b)}\int_0^x t^{a-1}(1-t)^{b-1}dt$$

The result, x, is the solution of the integral equation of the beta cdf with parameters a and b where you supply the desired probability p.

Algorithm We use Newton's Method with modifications to constrain steps to the allowable range for x, i.e., [0 1].

Examples

```
p = [0.01 0.5 0.99];
x = betainv(p,10,5)

x =

    0.3726    0.6742    0.8981
```

Purpose Negative beta log-likelihood function.

Syntax

```
logL = betalike(params,data)
[logL,info] = betalike(params,data)
```

Description `logL = betalike(params,data)` returns the negative of the beta log-likelihood function for the two beta parameters, `params`, given the column vector, `data`. The length of `logL` is the length of `data`.

`[logL,info] = betalike(params,data)` also returns Fisher's information matrix, `info`. The diagonal elements of `info` are the asymptotic variances of their respective parameters.

`betalike` is a utility function for maximum likelihood estimation of the beta distribution. The likelihood assumes that all the elements in the data sample are mutually independent. Since `betalike` returns the negative gamma log-likelihood function, minimizing `betalike` using `fmins` is the same as maximizing the likelihood.

Example This continues the example for `betafit` where we calculated estimates of the beta parameters for some randomly generated beta distributed data.

```
r = betarnd(4,3,100,1);
[logl,info] = betalike([3.9010 2.6193],r)

logl =

  –33.0514


info =

    0.2856    0.1528
    0.1528    0.1142
```

See Also `betafit`, `fmins`, `gamlike`, `mle`, `weiblike`

betapdf

Purpose Beta probability density function (pdf).

Syntax

```
Y = betapdf(X,A,B)
```

Description `betapdf(X,A,B)` computes the beta pdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A`, and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `A` and `B` must both be positive and `X` must lie on the interval [0 1].

The probability density function for the beta distribution is:

$$y = f(x|a,b) = \frac{1}{B(a,b)}x^{a-1}(1-x)^{b-1}I_{(0,1)}(x)$$

A *likelihood function* is the pdf viewed as a function of the parameters. Maximum likelihood estimators (MLEs) are the values of the parameters that maximize the likelihood function for a fixed value of x.

The uniform distribution on [0 1] is a degenerate case of the beta where $a = 1$ and $b = 1$.

Examples

```
a = [0.5 1; 2 4]

a =

    0.5000    1.0000
    2.0000    4.0000

y = betapdf(0.5,a,a)

y =
    0.6366    1.0000
    1.5000    2.1875
```

Purpose

Random numbers from the beta distribution.

Syntax

```
R = betarnd(A,B)
R = betarnd(A,B,m)
R = betarnd(A,B,m,n)
```

Description

`R = betarnd(A,B)` generates beta random numbers with parameters `A` and `B`. The size of `R` is the common size of `A` and `B` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other.

`R = betarnd(A,B,m)` generates beta random numbers with parameters `A` and `B`. `m` is a 1-by-2 vector that contains the row and column dimensions of `r`.

`R = betarnd(A,B,m,n)` generates an `m` by `n` matrix of beta random numbers with parameters `A` and `B`.

Examples

```
a = [1 1; 2 2];
b = [1 2; 1 2];
r = betarnd(a,b)

r =

    0.6987    0.6139
    0.9102    0.8067

r = betarnd(10,10,[1 5])

r =

    0.5974    0.4777    0.5538    0.5465    0.6327

r = betarnd(4,2,2,3)

r =

    0.3943    0.6101    0.5768
    0.5990    0.2760    0.5474
```

betastat

Purpose Mean and variance for the beta distribution.

Syntax

```
[M,V] = betastat(A,B)
```

Description For the beta distribution:

- The mean is $\frac{a}{a+b}$
- The variance is $\frac{ab}{(a+b+1)(a+b)^2}$

Examples If the parameters are equal, the mean is 1/2.

```
a = 1:6;
[m,v] = betastat(a,a)

m =

    0.5000    0.5000    0.5000    0.5000    0.5000    0.5000

v =

    0.0833    0.0500    0.0357    0.0278    0.0227    0.0192
```

Purpose Binomial cumulative distribution function (cdf).

Syntax

```
Y = binocdf(X,N,P)
```

Description `binocdf(X,N,P)` computes the binomial cdf with parameters `N` and `P` at the values in `X`. The arguments `X`, `N`, and `P` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameter `N` must be a positive integer and `P` must lie on the interval [0 1].

The binomial cdf is:

$$y = F(x|n,p) = \sum_{i=0}^{x} \binom{n}{i} p^i q^{(1-i)} I_{(0,1,\ldots,n)}(i)$$

The result, y, is the probability of observing up to x successes in n independent trials of where the probability of success in any given trial is p.

Examples If a baseball team plays 162 games in a season and has a 50-50 chance of winning any game, then the probability of that team winning more than 100 games in a season is:

```
1 – binocdf(100,162,0.5)
```

The result is 0.001 (i.e., 1 – 0.999). If a team wins 100 or more games in a season, this result suggests that it is likely that the team's true probability of winning any game is greater than 0.5.

binofit

Purpose

Parameter estimates and confidence intervals for binomial data.

Syntax

```
phat = binofit(x,n)
[phat,pci] = binofit(x,n)
[phat,pci] = binofit(x,n,alpha)
```

Description

`binofit(x,n)` returns the estimate of the probability of success for the binomial distribution given the data in the vector, `x`.

`[phat,pci] = binofit(x,n)` gives maximum likelihood estimate, `phat`, and 95% confidence intervals, `pci`.

`[phat,pci] = binofit(x,n,alpha)` gives 100(1–`alpha`) percent confidence intervals. For example, `alpha` = 0.01 yields 99% confidence intervals.

Example

First we generate one binomial sample of 100 elements with a probability of success of 0.6. Then, we estimate this probability given the results from the sample. The 95% confidence interval, `pci`, contains the true value, 0.6.

```
r = binornd(100,0.6);
[phat,pci] = binofit(r,100)

phat =

    0.5800

pci =

    0.4771    0.6780
```

Reference

Johnson, N. L., S. Kotz, and A.W. Kemp, *"Univariate Discrete Distributions, Second Edition,"* Wiley 1992. pp. 124–130.

See Also

`mle`

Purpose

Inverse of the binomial cumulative distribution function (cdf).

Syntax

```
X = binoinv(Y,N,P)
```

Description

`binoinv(Y,N,P)` returns the smallest integer `X` such that the binomial cdf evaluated at `X` is equal to or exceeds `Y`. You can think of `Y` as the probability of observing `X` successes in `N` independent trials where `P` is the probability of success in each trial.

The parameter `n` must be a positive integer and both `P` and `Y` must lie on the interval [0 1]. Each `X` is a positive integer less than or equal to `N`.

Examples

If a baseball team has a 50-50 chance of winning any game, what is a reasonable range of games this team might win over a season of 162 games? We assume that a surprising result is one that occurs by chance once in a decade.

```
binoinv([0.05 0.95],162,0.5)

ans =

    71    91
```

This result means that in 90% of baseball seasons, a .500 team should win between 71 and 91 games.

binopdf

Purpose Binomial probability density function (pdf).

Syntax

```
Y = binopdf(X,N,P)
```

Description `binopdf(X,N,P)` computes the binomial pdf with parameters `N` and `P` at the values in `X`. The arguments `X`, `N` and `P` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

`N` must be a positive integer and `P` must lie on the interval [0 1].

The binomial pdf is

$$y = f(x|n, p) = \binom{n}{x} p^x q^{(1-x)} I_{(0, 1, \ldots, n)}(x)$$

The result, y, is the probability of observing x successes in n independent trials of where the probability of success in any given trial is p.

Examples A Quality Assurance inspector tests 200 circuit boards a day. If 2% of the boards have defects, what is the probability that the inspector will find no defective boards on any given day?

```
binopdf(0,200,0.02)
ans =

    0.0176
```

What is the most likely number of defective boards the inspector will find?

```
y = binopdf([0:200],200,0.02);
[x,i] = max(y);
i

i =

     5
```

Purpose

Random numbers from the binomial distribution.

Syntax

```
R = binornd(N,P)
R = binornd(N,P,mm)
R = binornd(N,P,mm,nn)
```

Description

`R = binornd(N,P)` generates binomial random numbers with parameters `N` and `P`. The size of `R` is the common size of `N` and `P` if both are matrices . If either parameter is a scalar, the size of `R` is the size of the other.

`R = binornd(N,P,mm)` generates binomial random numbers with parameters `N` and `P`. `mm` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = binornd(N,p,mm,nn)` generates binomial random numbers with parameters `N` and `P`. The scalars `mm` and `nn` are the row and column dimensions of `R`.

Algorithm

The `binornd` function uses the direct method using the definition of the binomial distribution as a sum of Bernoulli random variables.

Examples

```
n = 10:10:60;
r1 = binornd(n,1./n)

r1 =

     2     1     0     1     1     2

r2 = binornd(n,1./n,[1 6])

r2 =

     0     1     2     1     3     1

r3 = binornd(n,1./n,1,6)

r3 =

     0     1     1     1     0     3
```

binostat

Purpose Mean and variance for the binomial distribution.

Syntax

```
[M,V] = binostat(N,P)
```

Description For the binomial distribution:

- The mean is *np*.
- The variance is *npq*.

Examples

```
n = logspace(1,5,5)

n =

          10         100        1000       10000      100000

[m,v] = binostat(n,1./n)

m =

     1     1     1     1     1

v =

    0.9000    0.9900    0.9990    0.9999    1.0000

[m,v] = binostat(n,1/2)

m =

           5          50         500        5000       50000

v =

   1.0e+04 *

    0.0003    0.0025    0.0250    0.2500    2.5000
```

Purpose Bootstrap statistics through resampling of data.

Syntax

```
bootstat = bootstrp(nboot,'bootfun',d1,...)
[bootstat,bootsam] = bootstrp(...)
```

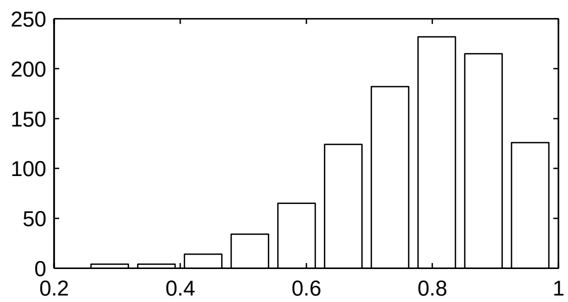
Description `bootstrp(nboot,'bootfun',d1,...)` draws `nboot` bootstrap data samples and analyzes them using the function `bootfun`. `nboot` must be a positive integer. `bootstrp` passes the data `d1`, `d2`, etc., to `bootfun`.

`[bootstat,bootsam] = bootstrap(...)` returns the bootstrap statistics in `bootstat`. Each row of `bootstat` contains the results of applying `'bootfun'` to one bootstrap sample. If `'bootfun'` returns a matrix, then this output is converted to a long vector for storage in `bootstat`. `bootsam` is a matrix of indices into the rows of the data matrix.

Example Correlate the LSAT scores and and law-school GPA for 15 students. These 15 data points are resampled to create 1000 different datasets, and the correlation between the two variables is computed for each dataset.

```
load lawdata
[bootstat,bootsam] = bootstrp(1000,'corrcoef',lsat,gpa);
bootstat(1:5,:)

ans =

    1.0000    0.3021    0.3021    1.0000
    1.0000    0.6869    0.6869    1.0000
    1.0000    0.8346    0.8346    1.0000
    1.0000    0.8711    0.8711    1.0000
    1.0000    0.8043    0.8043    1.0000
```

```
bootsam(:,1:5)

ans =

     4     7     5    12     8
     1    11    10     8     4
    11     9    12     4     2
    11    14    15     5    15
    15    13     6     6     2
     6     8     4     3     8
     8     2    15     8     6
    13    10    11    14     5
     1     7    12    14    14
     1    11    10     1     8
     8    14     2    14     7
    11    12    10     8    15
     1     4    14     8     1
     6     1     5     5    12
     2    12     7    15    12

hist(bootstat(:,2))
```



The histogram shows the variation of the correlation coefficient across all the bootstrap samples. The sample minimum is positive indicating that the relationship between LSAT and GPA is not accidental.

Purpose Box plots of a data sample.

Syntax

```
boxplot(X)
boxplot(X,notch)
boxplot(X,notch,'sym')
boxplot(X,notch,'sym',vert)
boxplot(X,notch,'sym',vert,whis)
```

Description

`boxplot(X)` produces a box and whisker plot for each column of `X`. The box has lines at the lower quartile, median, and upper quartile values. The whiskers are lines extending from each end of the box to show the extent of the rest of the data. Outliers are data with values beyond the ends of the whiskers. If there is no data outside the whisker, there is a dot at the bottom whisker. The dot color is the same as the whisker color.

`boxplot(X,notch)` with `notch` = 1 produces a notched-box plot. Notches graph a robust estimate of the uncertainty about the means for box to box comparison. The default, `notch` = 0 produces a rectangular box plot.

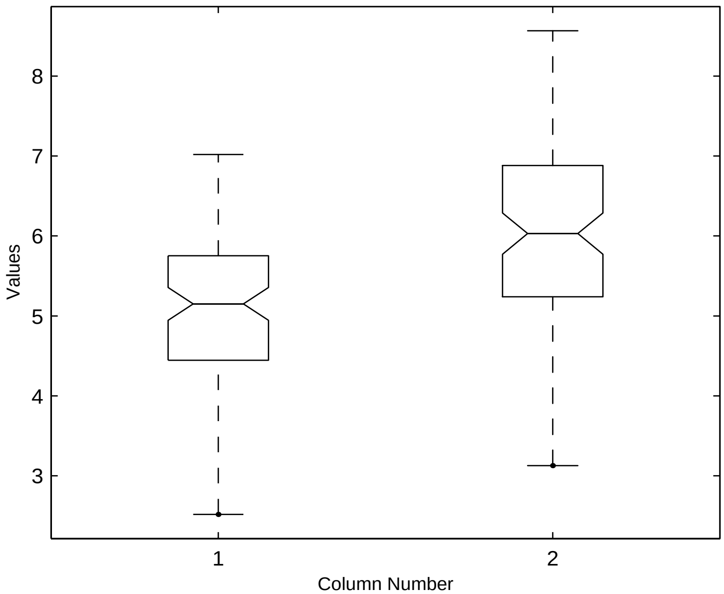
`boxplot(X,notch,'sym')` where `'sym'` is a plotting symbol allows control of the symbol for outliers if any (default = '+').

`boxplot(X,notch,'sym',vert)` with `vert` = 0 makes the boxes horizontal (default: `vert` = 1, for vertical)

`boxplot(X,notch,'sym',vert,whis)` enables you to specify the length of the "whiskers". `whis` defines the length of the whiskers as a function of the inter-quartile range (default = 1.5 * IQR.) If `whis` = 0, then `boxplot` displays all data values outside the box using the plotting symbol, `'sym'`.

Examples

```
x1 = normrnd(5,1,100,1);
x2 = normrnd(6,1,100,1);
x = [x1 x2];
boxplot(x,1)
```



The difference between the means of the two columns of x is 1. We can detect this difference graphically since the notches do not overlap.

Purpose

Process capability indices.

Syntax

```
p = capable(data,lower,upper)
[p,Cp,Cpk] = capable(data,lower,upper)
```

Description

`capable(data,lower,upper)` computes the probability that a sample, `data`, from some process falls outside the bounds specified in `lower` and `upper`.

The assumptions are that the measured values in the vector, `data`, are normally distributed with constant mean and variance and the the measurements are statistically independent.

`[p,Cp,Cpk] = capable(data,lower,upper)` also returns the capability indices `Cp` and `Cpk`.

Cp is the ratio of the range of the specifications to six times the estimate of the process standard deviation

$$C_p = \frac{USL - LSL}{6\sigma}$$

For a process that has its average value on target, a *Cp* of one translates to a little more than one defect per thousand. Recently many industries have set a quality goal of one part per million. This would correspond to a *Cp* = 1.6. The higher the value of *Cp* the more capable the process.

Cpk is the ratio of difference between the process mean and the closer specification limit to three times the estimate of the process standard deviation

$$C_{pk} = min\left(\frac{USL - \mu}{3\sigma}, \frac{\mu - LSL}{3\sigma}\right)$$

where the process mean is μ. For processes that do not maintain their average on target, *Cpk* is a more descriptive index of process capability.

Example

Imagine a machined part with specifications requiring a dimension to be within three thousandths of an inch of nominal. Suppose that the machining process cuts too thick by one thousandth of an inch on average and also has a standard deviation of one thousandth of an inch. What are the capability indices of this process?

```
data = normrnd(1,1,30,1);
[p,Cp,Cpk] = capable(data,[–3 3]);
indices = [p Cp Cpk]

indices =

    0.0172    1.1144    0.7053
```

We expect 17 parts out of a thousand to be out-of-specification. `Cpk` is less than `Cp` because the process is not centered.

Reference

Montgomery, D., "*Introduction to Statistical Quality Control,*" John Wiley & Sons 1991. pp. 369–374.

See Also

`capaplot`, `histfit`

Purpose

Process capability plot.

Syntax

```
p = capaplot(data,specs)
[p,h] = capaplot(data,specs)
```

Description

`capaplot(data,specs)` fits the observations in the vector `data` assuming a normal distribution with unknown mean and variance and plots the distribution of a new observation (T distribution.) The part of the distribution between the lower and upper bounds contained in the two element vector, `specs`, is shaded in the plot.

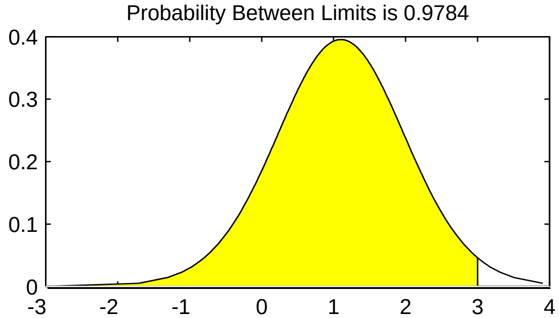
`[p,h] = capaplot(data,specs)` returns the probability of the new observation being within specification in `p` and handles to the plot elements in `h`.

Example

Imagine a machined part with specifications requiring a dimension to be within 3 thousandths of an inch of nominal. Suppose that the machining process cuts too thick by one thousandth of an inch on average and also has a standard deviation of one thousandth of an inch.

```
data = normrnd(1,1,30,1);
p = capaplot(data,[–3 3])
p =

    0.9784
```

The probability of a new observation being within specs is 97.84%.



See Also

`capable`, `histfit`

caseread

Purpose Read casenames from a file.

Syntax

```
names = caseread(filename)
names = caseread
```

Description `names = caseread(filename)` reads the contents of `filename` and returns a string matrix of `names`. `filename` is the name of a file in the current directory, or the complete pathname of any file elsewhere. `caseread` treats each line as a separate case.

`names = caseread` displays the **File Open** dialog box for interactive selection of the input file.

Example Use the file `months.dat` created using the function `casewrite` on the next page.

```
type months.dat

January
February
March
April
May

names = caseread('months.dat')

names =

January
February
March
April
May
```

See Also `tblread`, `gname`, `casewrite`

Purpose Write casenames from a string matrix to a file.

Syntax

```
casewrite(strmat,filename)
casewrite(strmat)
```

Description `casewrite (strmat,filename)` writes the contents of `strmat` to `filename`. Each row of `strmat` represents one casename. `filename` is the name of a file in the current directory, or the complete pathname of any file elsewhere. `casewrite` writes each name to a separate line in `filename`.

`casewrite(strmat)` displays the **File Open** dialog box for interactive specification of the output file.

Example

```
strmat = str2mat('January','February','March','April','May')

strmat =

January
February
March
April
May


casewrite(strmat,'months.dat')
type months.dat

January
February
March
April
May
```

See Also `gname`, `caseread`, `tblwrite`

Purpose Computes a chosen cumulative distribution function (cdf).

Syntax

```
P = cdf('name',X,A1,A2,A3)
```

Description `cdf` is a utility routine allowing you to access all the cdfs in the Statistics Toolbox using the name of the distribution as a parameter.

`P = cdf('name',X,A1,A2,A3)` returns a matrix of probabilities. `name` is a string containing the name of the distribution. `X` is a matrix of values, and `A`, `A2`, and `A3` are matrices of distribution parameters. Depending on the distribution, some of the parameters may not be necessary.

The arguments `X`, `A1`, `A2`, and `A3` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

Examples

```
p = cdf('Normal',–2:2,0,1)

p =

    0.0228    0.1587    0.5000    0.8413    0.9772

p = cdf('Poisson',0:5,1:6)

p =

    0.3679    0.4060    0.4232    0.4335    0.4405    0.4457
```

See Also `icdf`, `mle`, `pdf`, `random`

Purpose Chi-square (χ^2) cumulative distribution function (cdf).

Syntax

```
P = chi2cdf(X,V)
```

Description `chi2cdf(X,V)` computes the χ^2 cdf with parameter `V` at the values in `X`. The arguments `X` and `V` must be the same size except that a scalar argument functions as a constant matrix of the same size as the other argument.

The degrees of freedom,`V`, must be a positive integer.

The χ^2 cdf is:

$$p = F(x|\nu) = \int_0^x \frac{t^{(\nu-2)/2}e^{-t/2}}{2^{\frac{\nu}{2}}\Gamma(\nu/2)}dt$$

The result, p, is the probability that a single observation from the χ^2 distribution with degrees of freedom, ν, will fall in the interval [0 x].

The χ^2 density function with n degrees of freedom is the same as the gamma density function with parameters n/2 and 2.

Examples

```
probability = chi2cdf(5,1:5)

probability =

    0.9747    0.9179    0.8282    0.7127    0.5841

probability = chi2cdf(1:5,1:5)

probability =

    0.6827    0.6321    0.6084    0.5940    0.5841
```

Purpose

Inverse of the chi-square (χ^2) cumulative distribution function (cdf).

Syntax

```
X = chi2inv(P,V)
```

Description

`chi2inv(P,V)` computes the inverse of the χ^2 cdf with parameter `V` for the probabilities in `P`. The arguments `P` and `V` must be the same size except that a scalar argument functions as a constant matrix of the size of the other argument.

The degrees of freedom,`V`, must be a positive integer and `P` must lie in the interval [0 1].

We define the χ^2 inverse function in terms of the χ^2 cdf.

$$x = F^{-1}(p|\nu) = \{x:F(x|\nu) = p\}$$

$$where \quad p = F(x|\nu) = \int_0^x \frac{t^{(\nu-2)/2}e^{-t/2}}{2^{\frac{\nu}{2}}\Gamma(\nu/2)}dt$$

The result, x, is the solution of the integral equation of the χ^2 cdf with parameter ν where you supply the desired probability p.

Examples

Find a value that exceeds 95% of the samples from a χ^2 distribution with 10 degrees of freedom.

```
x = chi2inv(0.95,10)

x =

    18.3070
```

You would observe values greater than 18.3 only 5% of the time by chance.

Purpose Chi-square (χ^2) probability density function (pdf).

Syntax

```
Y = chi2pdf(X,V)
```

Description `chi2pdf(X,V)` computes the χ^2 pdf with parameter `V` at the values in `X`. The arguments `X` and `V` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument.

The degrees of freedom, `V`, must be a positive integer.

The chi-square pdf is:

$$y = f(x|\nu) = \frac{x^{(\nu-2)/2}e^{-x/2}}{2^{\frac{\nu}{2}}\Gamma(\nu/2)}$$

The χ^2 density function with n degrees of freedom is the same as the gamma density function with parameters $n/2$ and 2.

If x is standard normal , then x^2 is distributed χ^2 with one degree of freedom. If x_1, x_2, ..., x_n are n independent standard normal observations, then the sum of the squares of the x's is distributed χ^2 with n degrees of freedom.

Examples

```
nu = 1:6;
x = nu;
y = chi2pdf(x,nu)

y =

    0.2420    0.1839    0.1542    0.1353    0.1220    0.1120
```

The mean of the χ^2 distribution is the value of the parameter, `nu`. The above example shows that the probability density of the mean falls as `nu` increases.

chi2rnd

Purpose Random numbers from the chi-square (χ^2) distribution.

Syntax

```
R = chi2rnd(V)
R = chi2rnd(V,m)
R = chi2rnd(V,m,n)
```

Description `R = chi2rnd(V)` generates χ^2 random numbers with `V` degrees of freedom. The size of `R` is the size of `V`.

`R = chi2rnd(V,m)` generates χ^2 random numbers with `V` degrees of freedom. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = chi2rnd(V,m,n)` generates χ^2 random numbers with `V` degrees of freedom. The scalars `m` and `n` are the row and column dimensions of `R`.

Examples Note that the first and third commands are the same but are different from the second command.

```
r = chi2rnd(1:6)

r =

    0.0037    3.0377    7.8142    0.9021    3.2019    9.0729

r = chi2rnd(6,[1 6])

r =

    6.5249    2.6226   12.2497    3.0388    6.3133    5.0388

r = chi2rnd(1:6,1,6)

r =

    0.7638    6.0955    0.8273    3.2506    1.5469   10.9197
```

Purpose Mean and variance for the chi-square (χ^2) distribution.

Syntax

```
[M,V] = chi2stat(NU)
```

Description For the χ^2 distribution:

- The mean is n
- The variance is $2n$.

Example

```
nu = 1:10;
nu = nu'*nu;
[m,v] = chi2stat(nu)

m =

     1     2     3     4     5     6     7     8     9    10
     2     4     6     8    10    12    14    16    18    20
     3     6     9    12    15    18    21    24    27    30
     4     8    12    16    20    24    28    32    36    40
     5    10    15    20    25    30    35    40    45    50
     6    12    18    24    30    36    42    48    54    60
     7    14    21    28    35    42    49    56    63    70
     8    16    24    32    40    48    56    64    72    80
     9    18    27    36    45    54    63    72    81    90
    10    20    30    40    50    60    70    80    90   100

v =

     2     4     6     8    10    12    14    16    18    20
     4     8    12    16    20    24    28    32    36    40
     6    12    18    24    30    36    42    48    54    60
     8    16    24    32    40    48    56    64    72    80
    10    20    30    40    50    60    70    80    90   100
    12    24    36    48    60    72    84    96   108   120
    14    28    42    56    70    84    98   112   126   140
    16    32    48    64    80    96   112   128   144   160
    18    36    54    72    90   108   126   144   162   180
    20    40    60    80   100   120   140   160   180   200
```

classify

Purpose Linear discriminant analysis.

Syntax `class = classify(sample,training,group)`

Description `class = classify(sample,training,group)` assigns each row of the data in `sample` into one of the groups that the training set, `training`, is already divided into. `sample` and `training` must have the same number of columns.

The vector `group` contains integers, from one to the number of groups, that identify which group each row of the training set belongs. `group` and `training` must have the same number of rows.

The function returns `class`, a vector with the same number of rows as `sample`. Each element of `class` identifies the group to which the corresponding element of `sample` has been assigned. The `classify` function determines into which group each row in `sample` belongs by computing the Mahalanobis distance of each row in `sample` to each row in `training`.

Example

```
load discrim
sample = ratings(idx,:);
training = ratings(1:200,:);
g = group(1:200);
class = classify(sample,training,g);
first5 = class(1:5)

first5 =

     2
     2
     2
     2
     2
```

See Also `mahal`

Purpose

Construct clusters from `linkage` output.

Syntax

```
T = cluster(Z,cutoff)
T = cluster(Z,cutoff,depth)
```

Description

`cluster(Z,cutoff)` constructs clusters from hierarchical cluster tree, `Z`, generated by the `linkage` function. `Z` is a matrix of size *m*-1 by 3, where *m* is the number of observations in the original data.

`cutoff` is a threshold value that determines how the `cluster` function creates clusters. The value of `cutoff` determines how `cluster` interprets it.

Value	Meaning
`0 < cutoff < 1`	`cutoff` is interpreted as the threshold for the inconsistency coefficient. The inconsistency coefficient quantifies the degree of difference between objects in the hierarchical cluster tree. If inconsistency coefficient of a link is greater than the threshold, the `cluster` function uses the link as a boundary for a cluster grouping. For more information about the inconsistency coefficient, see the `inconsistent` function.
`cutoff >= 1`	`cutoff` is interpreted as the maximum number of clusters to keep in the hierarchical tree.

`cluster(Z,cutoff,depth)`constructs clusters from cluster tree `Z`. The `depth` argument specifies the number of levels in the hierarchical cluster tree to include in the inconsistency coefficient computation. (The inconsistency coefficient compares a link between two objects in the cluster tree with neighboring links up to a specified depth. See the `inconsistent` function for more information.) When the `depth` argument is specified, `cutoff` is always interpreted as the inconsistency coefficient threshold.

The output, `T`, is a vector of size *m* that identifies, by number, the cluster in which each object was grouped. To find out which object from the original dataset are contained in cluster *i*, use `find(T==i)`.

Example

The example uses the `pdist` function to calculate the distance between items in a matrix of random numbers and then uses the `linkage` function to compute the hierarchical cluster tree based on the matrix. The output of the linkage function is passed to the `cluster` function. The `cutoff` value `3` indicates that you want to group the items into three clusters. The example uses the `find` function to list all the items grouped into cluster 2.

```
rand('seed', 0);
X = [rand(10,3); rand(10,3)+1; rand(10,3)+2];
Y = pdist(X);
Z = linkage(Y);
T = cluster(Z,3);
find(T == 3)

ans =

    11
    12
    13
    14
    15
    16
    17
    18
    19
    20
```

See Also

`clusterdata`, `cophenet`, `dendrogram`, `inconsistent`, `linkage`, `pdist`, `squareform`

Purpose

Construct clusters from data.

Syntax

```
T = clusterdata(X,cutoff)
```

Description

`T = clusterdata(X,cutoff)` constructs clusters from the data matrix `X`. `X` is a matrix of size *m* by *n*, interpreted as *m* observations of *n* variables.

`cutoff` is a threshold value that determines how the `cluster` function creates clusters. The value of `cutoff` determines how `clusterdata` interprets it.

Value	Meaning
`0 < cutoff < 1`	`cutoff` is interpreted as the threshold for the inconsistency coefficient. The inconsistency coefficient quantifies the degree of difference between objects in the hierarchical cluster tree. If inconsistency coefficient of a link is greater than the threshold, the `cluster` function uses the link as a boundary for a cluster grouping. For more information about the inconsistency coefficient, see the `inconsistent` function.
`cutoff >= 1`	`cutoff` is interpreted as the maximum number of clusters to keep in the hierarchical tree.

The output, `T`, is a vector of size *m* that identifies, by number, the cluster in which each object was grouped.

`T = clusterdata(X,cutoff)` is the same as

```
Y = pdist(X,'euclid');
Z = linkage(Y,'single');
T = cluster(Z,cutoff);
```

Follow this sequence to use nondefault parameters for `pdist` and `linkage`.

Example

The example first creates a sample dataset of random numbers. The example then uses the `clusterdata` function to compute the distances between items in the dataset and create a hierarchical cluster tree from the dataset. Finally, the clusterdata function groups the items in the dataset into three clusters. The example uses the find function to list all the items in cluster 2.

```
rand('seed', 12);
X = [rand(10,3); rand(10,3)+1.2; rand(10,3)+2.5;
T = clusterdata(X,3);
find(T == 2)

ans =


    21
    22
    23
    24
    25
    26
    27
    28
    29
    30
```

See Also

cluster, cophenet, dendrogram, inconsistent, linkage, pdist, squareform

Purpose Enumeration of all combinations of *n* objects *k* at a time.

Syntax

```
C = combnk(v,k)
```

Description

`C = combnk(v,k)` returns all combinations of the *n* elements in `v` taken `k` at a time.

`C = combnk(v,k)` produces a matrix, with `k` columns. Each row of `C` has `k` of the elements in the vector `v`. `C` has $n!/k!(n-k)!$ rows.

It is not feasible to use this function if `v` has more than about 10 elements.

Example

Combinations of characters from a string.

```
C = combnk('tendril',4);
last5 = C(31:35,:)

last5 =

tedr
tenl
teni
tenr
tend
```

Combinations of elements from a numeric vector.

```
c = combnk(1:4,2)

c =

     3     4
     2     4
     2     3
     1     4
     1     3
     1     2
```

cophenet

Purpose

Cophenetic correlation coefficient.

Syntax

```
c = cophenet(Z,Y)
```

Description

`c = cophenet(Z,Y)` computes the cophenetic correlation coefficient which compares the distance information in `Z`, generated by `linkage`, and the distance information in `Y`, generated by `pdist`. `Z` is a matrix of size m-1 by 3, with distance information in the third column. `Y` is a vector of size $m \cdot (m-1)/2$.

For example, given a group of objects $\{1,2,....m\}$ with distances `Y`, the function `linkage` produces a hierarchical cluster tree. The `cophenet` function measures the distortion of this classification, indicating how readily the data fits into the structure suggested by the classification.

The output value, `c`, is the cophenetic correlation coefficient. The magnitude of this value should be very close to 1 for a high-quality solution. This measure can be used to compare alternative cluster solutions obtained using different algorithms.

The cophenetic correlation between `Z(:,3)` and `Y` is defined as

$$c = \frac{\Sigma_{i<j}(Y_{ij}-y)(Z_{ij}-z)}{\sqrt{\Sigma_{i<j}(Y_{ij}-y)^2\Sigma_{i<j}(Z_{ij}-z)^2}}$$

where:

- Y_{ij} is the distance between objects i and j in `Y`.
- Z_{ij} is the distance between objects i and j in `Z(:,3)`.
- y and z are the average of `Y` and `Z(:,3)`, respectively.

Example

```
rand('seed',12);
X = [rand(10,3);rand(10,3)+1;rand(10,3)+2];
Y = pdist(X);
Z = linkage(Y,'centroid');
c = cophenet(Z,Y)
c =
    0.6985
```

See Also

`cluster`, `dendrogram`, `inconsistent`, `linkage`, `pdist`, `squareform`

Purpose

D-optimal design of experiments – coordinate exchange algorithm.

Syntax

```
settings = cordexch(nfactors,nruns)
[settings,X] = cordexch(nfactors,nruns)
[settings,X] = cordexch(nfactors,nruns,'model')
```

Description

`settings = cordexch(nfactors,nruns)` generates the factor settings matrix, `settings`, for a D-optimal design using a linear additive model with a constant term. `settings` has `nruns` rows and `nfactors` columns.

`[settings,X] = cordexch(nfactors,nruns)` also generates the associated design matrix, `X`.

`[settings,X] = cordexch(nfactors,nruns,'model')` produces a design for fitting a specified regression model. The input, `'model'`, can be one of these strings:

- `'interaction'` – includes constant, linear, and cross product terms.
- `'quadratic'` – interactions plus squared terms.
- `'purequadratic'` – includes constant, linear and squared terms.

Example

The D-optimal design for two factors in nine run using a quadratic model is the 3^2 factorial as shown below:

```
settings = cordexch(2,9,'quadratic')

settings =

   –1     1
    1     1
    0     1
    1    –1
   –1    –1
    0    –1
    1     0
    0     0
   –1     0
```

See Also

`rowexch`, `daugment`, `dcovary`, `hadamard`, `fullfact`, `ff2n`

Purpose Correlation coefficients.

Syntax

```
R = corrcoef(X)
```

Description

`R = corrcoef(X)` returns a matrix of correlation coefficients calculated from an input matrix whose rows are observations and whose columns are variables. The element `(i,j)` of the matrix `R` is related to the corresponding element of the covariance matrix `C = cov(X)` by

$$rR(i,j) = \frac{C(i,j))}{\sqrt{C(i,i)C(j,j)}}$$

See Also

`cov`, `mean`, `std`, `var`

`corrcoef` is a function in MATLAB.

Purpose Covariance matrix.

Syntax

```
C = cov(X)
C = cov(x,y)
```

Description

`cov` computes the covariance matrix. For a single vector, `cov(x)` returns a scalar containing the variance. For matrices, where each row is an observation, and each column a variable, `cov(X)` is the covariance matrix.

The variance function, `var(X)` is the same as `diag(cov(X))`.

The standard deviation function, `std(X)` is equivalent to `sqrt(diag(cov(X)))`.

`cov(x,y)`, where `x` and `y` are column vectors of equal length, gives the same result as `cov([x y])`.

Algorithm

The algorithm for `cov` is

```
[n,p] = size(X);
X = X – ones(n,1) * mean(X);
Y = X'*X/(n–1);
```

See Also

`corrcoef`, `mean`, `std`, `var`
`xcov`, `xcorr` in the Signal Processing Toolbox

`cov` is a function in MATLAB.

crosstab

Purpose

Cross-tabulation of two vectors.

Syntax

```
table = crosstab(col1,col2)
[table,chi2,p] = crosstab(col1,col2)
```

Description

`table = crosstab(col1,col2)` takes two vectors of positive integers and returns a matrix, `table`, of cross-tabulations. The *ij*th element of `table` contains the count of all instances where `col1` = *i* and `col2` = *j*.

`[table,chi2,p] = crosstab(col1,col2)` also returns the chisquare statistic, `chi2`, for testing the independence of the rows and columns `table`. The scalar, `p`, is the significance level of the test. Values of `p` near zero cast doubt on the assumption of independence of the rows and columns of `table`.

Example

We generate 2 columns of 50 discrete uniform random numbers. The first column has numbers from one to three. The second has only ones and twos. The two columns are independent so we would be surprised if `p` were near zero.

```
r1 = unidrnd(3,50,1);r2 = unidrnd(2,50,1);
[table,chi2,p] = crosstab(r1,r2)

table =

    10     5
     8     8
     6    13

chi2 =

    4.1723

p =

    0.1242
```

The result, 0.1242, is not a surprise. A very small value of `p` would make us suspect the “randomness” of the random number generator.

See Also

`tabulate`

Purpose D-optimal augmentation of an experimental design.

Syntax

```
settings = daugment(startdes,nruns)
[settings,X] = daugment(startdes,nruns,'model')
```

Description `settings = daugment(startdes,nruns)` augments an initial experimental design, `startdes`, with `nruns` new tests.

`[settings,X] = daugment(startdes,nruns,'model')` also supplies the design matrix, `X`. The input, `'model'`, controls the order of the regression model. By default, `daugment` assumes a linear additive model. Alternatively, `'model'` can be any of these:

- `'interaction'` – includes constant, linear, and cross product terms.
- `'quadratic'` – interactions plus squared terms.
- `'purequadratic'` – includes constant, linear and squared terms.

`daugment` uses the coordinate exchange algorithm.

Example We add 5 runs to a 2^2 factorial design to allow us to fit a quadratic model.

```
startdes = [–1 –1; 1 –1; –1 1; 1 1];
settings = daugment(startdes,5,'quadratic')

settings =

    –1    –1
     1    –1
    –1     1
     1     1
     1     0
    –1     0
     0     1
     0     0
     0    –1
```

The result is a 3^2 factorial design.

See Also `cordexch`, `dcovary`, `rowexch`

dcovary

Purpose D-optimal design with specified fixed covariates.

Syntax

```
settings = dcovary(factors,covariates)
[settings,X] = dcovary(factors,covariates,'model')
```

Description

`settings = dcovary(factors,covariates,'model')` creates a D-optimal design subject to the constraint of fixed `covariates` for each run. `factors` is the number of experimental variables you want to control.

`[settings,X] = dcovary(factors,covariates,'model')` also creates the associated design matrix, `X`. The input, `'model'`, controls the order of the regression model. By default, `dcovary` assumes a linear additive model. Alternatively, `'model'` can be any of these:

- `'interaction'` – includes constant, linear, and cross product terms.
- `'quadratic'` – interactions plus squared terms.
- `'purequadratic'` – includes constant, linear and squared terms.

Example

Suppose we want to block an eight run experiment into 4 blocks of size 2 to fit a linear model on two factors.

```
covariates = dummyvar([1 1 2 2 3 3 4 4]);
settings = dcovary(2,covariates(:,1:3),'linear')
settings =

     1     1     1     0     0
    –1    –1     1     0     0
    –1     1     0     1     0
     1    –1     0     1     0
     1     1     0     0     1
    –1    –1     0     0     1
    –1     1     0     0     0
     1    –1     0     0     0
```

The first two columns of the output matrix contain the settings for the two factors. The last three columns are *dummy variable* codings for the four blocks.

See Also

`daugment`, `cordexch`

Purpose Plot dendrogram graphs.

Syntax

```
H = dendrogram(Z)
H = dendrogram(Z,p)
[H,T] = dendrogram(...)
```

Description

`H = dendrogram(Z)` generates a dendrogram plot of the hierarchical, binary cluster tree, `Z`. `Z` is an *m*-1 by 3 matrix, generated by the `linkage` function, where *m* is the number of objects in the original dataset.

A dendrogram consists of many upside-down, U-shaped lines connecting objects in a hierarchical tree. Except for the Ward linkage (see `linkage`), the height of each U represents the distance between the two objects being connected. The output, `H`, is a vector of line handles.

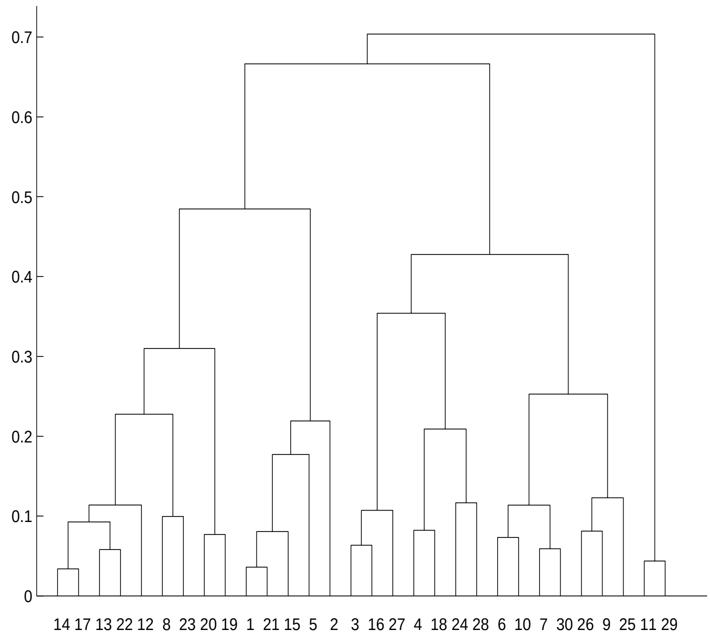
`H = dendrogram(Z,p)` generates a dendrogram with only the top *p* nodes. By default, `dendrogram` uses 30 as the value of *p*. When there are more than 30 initial nodes, a dendrogram may look crowded. To display every node, set `p = 0`.

`[H,T] = dendrogram(...)` generates a dendrogram, returning `T`, a vector of size *m* that contains the cluster number for each object in the original dataset. `T` provides access to the nodes of a cluster hierarchy that are not displayed in the dendrogram because they fall below the cutoff value *p*. For example, to find out which objects are contained in leaf node `k` of the dendrogram, use `find(T==k)`. Leaf nodes are the nodes at the bottom of the dendrogram that have no other nodes below them.

When there are fewer than *p* objects in the original data, all objects are displayed in the dendrogram. In this case, `T` is the identical map, i.e., `T = (1:m)'`, where each node contains only itself.

Example

```
rand('seed',12);
X= rand(100,2);
Y= pdist(X,'citiblock');
Z= linkage(Y,'average');
[H, T] = dendrogram(Z);
```




```
find(T==20)

ans =

    20
    49
    62
    65
    73
    96
```

This output indicates that leaf node 20 in the dendrogram contains the original data points 20, 49, 62, 65, 73, and 96.

See Also

`cluster`, `clusterdata`, `cophenet`, `inconsistent`, `linkage`, `pdist`, `squareform`

disttool

Purpose Interactive graph of cdf (or pdf) for many probability distributions.

Syntax

```
disttool
```

Description The `disttool` command sets up a graphic user interface for exploring the effects of changing parameters on the plot of a cdf or pdf. Clicking and dragging a vertical line on the plot allows you to evaluate the function over its entire domain interactively.

Evaluate the plotted function by typing a value in the x-axis edit box or dragging the vertical reference line on the plot. For cdfs, you can evaluate the inverse function by typing a value in the y-axis edit box or dragging the horizontal reference line on the plot. The shape of the pointer changes from an arrow to a crosshair when you are over the vertical or horizontal line to indicate that the reference line is draggable.

To change the distribution function choose from the pop-up menu of functions at the top left of the figure. To change from cdfs to pdfs, choose from the pop-up menu at the top right of the figure.

To change the parameter settings move the sliders or type a value in the edit box under the name of the parameter. To change the limits of a parameter, type a value in the edit box at the top or bottom of the parameter slider.

When you are done, press the **Close** button.

See Also `randtool`

Purpose Matrix of 0-1 “dummy” variables.

Syntax

```
D = dummyvar(group)
```

Description

`D = dummyvar(group)` generates a matrix, `D`, of 0-1 columns. `D` has one column for each unique value in each column of the matrix `group`. Each column of `group` contains positive integers that indicate the group membership of an individual row.

Example

Suppose we are studying the effects of two machines and three operators on a process. The first column of `group` would have the values one or two depending on which machine was used. The second column of `group` would have the values one, two, or three depending on which operator ran the machine.

```
group = [1 1;1 2;1 3;2 1;2 2;2 3];
D = dummyvar(group)

D =

     1     0     1     0     0
     1     0     0     1     0
     1     0     0     0     1
     0     1     1     0     0
     0     1     0     1     0
     0     1     0     0     1
```

See Also

`pinv`, `regress`

errorbar

Purpose

Plot error bars along a curve.

Syntax

```
errorbar(X,Y,L,U,symbol)
errorbar(X,Y,L)
errorbar(Y,L)
```

Description

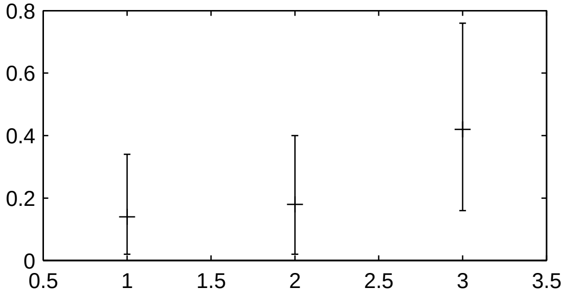
`errorbar(X,Y,L,U,symbol)` plots `X` versus `Y` with error bars specified by `L` and `U`. `X`, `Y`, `L`, and `U` must be the same length. If `X`, `Y`, `L`, and `U` are matrices, then each column produces a separate line. The error bars are each drawn a distance of `U(i)` above and `L(i)` below the points in `(X,Y)`. `symbol` is a string that controls the line type, plotting symbol, and color of the error bars.

`errorbar(X,Y,L)` plots `X` versus `Y` with symmetric error bars about `Y`.

`errorbar(Y,L)` plots `Y` with error bars `[Y–L Y+L]`.

Example

```
lambda = (0.1:0.2:0.5);
r = poissrnd(lambda(ones(50,1),:));
[p,pci] = poissfit(r,0.001);
L = p – pci(1,:)
U = pci(2,:) – p
errorbar(1:3,p,L,U,'+')

L =
    0.1200    0.1600    0.2600

U =
    0.2000    0.2200    0.3400
```



See Also

`errorbar` is a function in MATLAB.

Purpose

Exponentially Weighted Moving Average (EWMA) chart for Statistical Process Control (SPC).

Syntax

```
ewmaplot(data)
ewmaplot(data,lambda)
ewmaplot(data,lambda,alpha)
ewmaplot(data,lambda,alpha,specs)
h = ewmaplot(...)
```

Description

`ewmaplot(data)` produces an EWMA chart of the grouped responses in `data`. The rows of `data` contain replicate observations taken at a given time. The rows should be in time order.

`ewmaplot(data,lambda)` produces an EWMA chart of the grouped responses in `data`, and specifes how much the current prediction is influenced by past observations. Higher values of `lambda` give more weight to past observations. By default, `lambda` = 0.4; `lambda` must be between 0 and 1.

`ewmaplot(data,lambda,alpha)` produces an EWMA chart of the grouped responses in `data`, and specifies the significance level of the upper and lower plotted confidence limits. `alpha` is 0.01 by default. This means that roughly 99% of the plotted points should fall between the control limits.

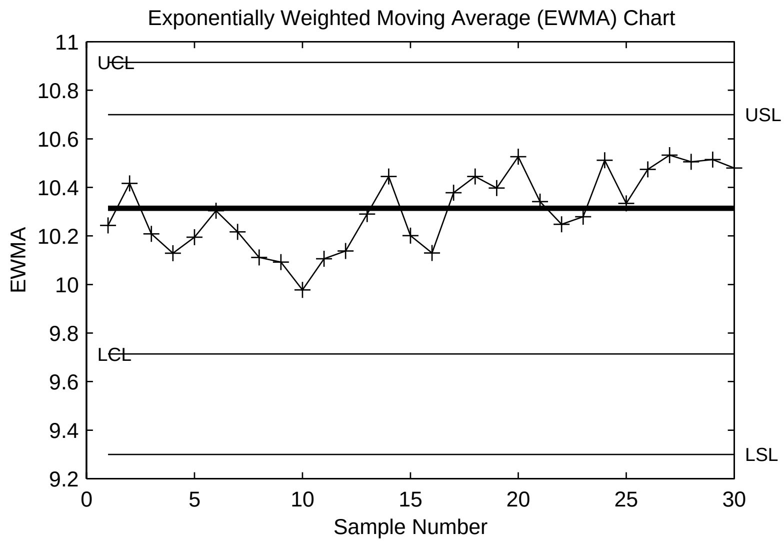
`ewmaplot(data,lambda,alpha,specs)` produces an EWMA chart of the grouped responses in `data`, and specifies a two element vector, `specs`, for the lower and upper specification limits of the response. Note

`h = ewmaplot(...)` returns a vector of handles to the plotted lines.

Example

Consider a process with a slowly drifting mean over time. An EWMA chart is preferable to an x-bar chart for monitoring this kind of process. This simulation demonstrates an EWMA chart for a slow linear drift.

```
t = (1:30)';
r = normrnd(10+0.02*t(:,ones(4,1)),0.5);
ewmaplot(r,0.4,0.01,[9.3 10.7])
```



Reference Montgomery, D., *Introduction to Statistical Quality Control*, John Wiley & Sons 1991. p. 299.

See Also `xbarplot`, `schart`

Purpose

Exponential cumulative distribution function (cdf).

Syntax

```
P = expcdf(X,MU)
```

Description

`expcdf(X,MU)` computes the exponential cdf with parameter settings `MU` at the values in `X`. The arguments `X` and `MU` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument.

The parameter `MU` must be positive.

The exponential cdf is:

$$p = F(x|\mu) = \int_0^x \frac{1}{\mu} e^{-\frac{t}{\mu}} dt = 1 - e^{-\frac{x}{\mu}}$$

The result, p, is the probability that a single observation from an exponential distribution will fall in the interval [0 x].

Examples

The median of the exponential distribution is $\mu*\log(2)$. Demonstrate this fact.

```
mu = 10:10:60;
p = expcdf(log(2)*mu,mu)

p =

    0.5000    0.5000    0.5000    0.5000    0.5000    0.5000
```

What is the probability that an exponential random variable will be less than or equal to the mean, μ?

```
mu = 1:6;
x = mu;
p = expcdf(x,mu)

p =

    0.6321    0.6321    0.6321    0.6321    0.6321    0.6321
```

Purpose Parameter estimates and confidence intervals for exponential data.

Syntax

```
muhat = expfit(x)
[muhat,muci] = expfit(x)
[muhat,muci] = expfit(x,alpha)
```

Description `muhat = expfit(x)` returns the estimate of the parameter, μ, of the exponential distribution given the data, `x`.

`[muhat,muci] = expfit(x)` also returns the 95% confidence interval in `muci`.

`[muhat,muci] = expfit(x,alpha)` gives `100(1—alpha)` percent confidence intervals. For example, `alpha` = 0.01 yields 99% confidence intervals.

Example We generate 100 independent samples of exponential data with $\mu = 3$. `muhat` is an estimate of `true_mu` and `muci` is a 99% confidence interval around `muhat`. Notice that `muci` contains `true_mu`.

```
true_mu = 3;
[muhat,muci] = expfit(r,0.01)

muhat =

    2.8835

muci =

    2.1949
    3.6803
```

See Also `betafit`, `binofit`, `gamfit`, `normfit`, `poissfit`, `unifit`, `weibfit`

Purpose

Inverse of the exponential cumulative distribution function (cdf).

Syntax

```
X = expinv(P,MU)
```

Description

`expinv(P,MU)` computes the inverse of the exponential cdf with parameter `MU` for the probabilities in `P`. The arguments `P` and `MU` must be the same size except that a scalar argument functions as a constant matrix of the size of the other argument.

The parameter `MU` must be positive and `P` must lie on the interval [0 1].

The inverse of the exponential cdf is:

$$x = F(p|\mu) = -\mu \ln(1-p)$$

The result, x, is the value such that the probability is p that an observation from an exponential distribution with parameter μ will fall in the range $[0\ x]$.

Examples

Let the lifetime of light bulbs be exponentially distributed with `mu` equal to 700 hours. What is the median lifetime of a bulb?

```
expinv(0.50,700)

ans =

  485.2030
```

So, suppose you buy a box of “700 hour” light bulbs. If 700 hours is mean life of the bulbs, then half them will burn out in less than 500 hours.

exppdf

Purpose Exponential probability density function (pdf).

Syntax

```
Y = exppdf(X,MU)
```

Description `exppdf(X,MU)` computes the exponential pdf with parameter settings `MU` at the values in `X`. The arguments `X` and `MU` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument.

The parameter `MU` must be positive.

The exponential pdf is:

$$y = f(x|\mu) = \frac{1}{\mu}e^{-\frac{x}{\mu}}$$

The exponential pdf is the gamma pdf with its first parameter (a) equal to 1.

The exponential distribution is appropriate for modeling waiting times when you think the probability of waiting an additional period of time is independent of how long you've already waited. For example, the probability that a light bulb will burn out in its next minute of use is relatively independent of how many minutes it has already burned.

Examples

```
y = exppdf(5,1:5)

y =

    0.0067    0.0410    0.0630    0.0716    0.0736

y = exppdf(1:5,1:5)

y =

    0.3679    0.1839    0.1226    0.0920    0.0736
```

Purpose

Random numbers from the exponential distribution.

Syntax

```
R = exprnd(MU)
R = exprnd(MU,m)
R = exprnd(MU,m,n)
```

Description

`R = exprnd(MU)` generates exponential random numbers with mean `MU`. The size of `R` is the size of `MU`.

`R = exprnd(MU,m)` generates exponential random numbers with mean `MU`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = exprnd(MU,m,n)` generates exponential random numbers with mean `MU`. The scalars `m` and `n` are the row and column dimensions of `R`.

Examples

```
n1 = exprnd(5:10)

n1 =

    7.5943   18.3400    2.7113    3.0936    0.6078    9.5841

n2 = exprnd(5:10,[1 6])

n2 =

    3.2752    1.1110   23.5530   23.4303    5.7190    3.9876

n3 = exprnd(5,2,3)

n3 =

   24.3339   13.5271    1.8788
    4.7932    4.3675    2.6468
```

expstat

Purpose Mean and variance for the exponential distribution.

Syntax

```
[M,V] = expstat(MU)
```

Description For the exponential distribution:

- The mean is μ.
- The variance is μ^2.

Examples

```
[m,v] = expstat([1 10 100 1000])

m =

           1          10         100        1000

v =

           1         100       10000     1000000
```

Purpose

F cumulative distribution function (cdf).

Syntax

```
P = fcdf(X,V1,V2)
```

Description

`fcdf(X,V1,V2)` computes the F cdf with parameters `V1` and `V2` at the values in `X`. The arguments `X`, `V1` and `V2` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

Parameters `V1` and `V2` must contain positive integers.

The F cdf is:

$$F(x|\nu_1,\nu_2) = \int_0^x \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{t^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)t\right]^{\frac{\nu_1+\nu_2}{2}}}\,dt$$

The result, p, is the probability that a single observation from an F distribution with parameters $\nu 1$ and $\nu 2$ will fall in the interval $[0\ x]$.

Examples

This example illustrates an important and useful mathematical identity for the F distribution.

```
nu1 = 1:5;
nu2 = 6:10;
x = 2:6;
F1 = fcdf(x,nu1,nu2)

F1 =

    0.7930    0.8854    0.9481    0.9788    0.9919

F2 = 1 – fcdf(1./x,nu2,nu1)

F2 =

    0.7930    0.8854    0.9481    0.9788    0.9919
```

ff2n

Purpose Two-level full-factorial designs.

Syntax `X = ff2n(n)`

Description `X = ff2n(n)` creates a two-level full-factorial design, `X`. `n` is the number of columns of `X`. The number of rows is 2^n.

Example

```
X = ff2n(3)

X =

     0     0     0
     0     0     1
     0     1     0
     0     1     1
     1     0     0
     1     0     1
     1     1     0
     1     1     1
```

`X` is the binary representation of the numbers from 0 to 2^n-1.

See Also `fullfact`

Purpose Inverse of the F cumulative distribution function (cdf).

Syntax

```
X = finv(P,V1,V2)
```

Description `finv(P,V1,V2)` computes the inverse of the F cdf with numerator degrees of freedom,`V1`, and denominator degrees of freedom, `V2`, for the probabilities in `P`. The arguments `P`, `V1` and `V2` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `V1` and `V2` must both be positive integers and `P` must lie on the interval [0 1].

The F inverse function is defined in terms of the F cdf:

$$x = F^{-1}(p|\nu_1,\nu_2) = \{x{:}F(x|\nu_1,\nu_2) = p\}$$

$$where \quad p = F(x|\nu_1,\nu_2) = \int_0^x \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}} \frac{t^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)t\right]^{\frac{\nu_1+\nu_2}{2}}}dt$$

Examples Find a value that should exceed 95% of the samples from an F distribution with 5 degrees of freedom in the numerator and 10 degrees of freedom in the denominator.

```
x = finv(0.95,5,10)

x =

    3.3258
```

You would observe values greater than 3.3258 only 5% of the time by chance.

fpdf

Purpose

F probability density function (pdf).

Syntax

```
Y = fpdf(X,V1,V2)
```

Description

`fpdf(X,V1,V2)` computes the F pdf with parameters `V1` and `V2` at the values in `X`. The arguments `X`, `V1` and `V2` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `V1` and `V2` must both be positive integers and `X` must lie on the interval $[0\ \infty)$.

The probability density function for the F distribution is:

$$y = f(x|\nu_1,\nu_2) = \frac{\Gamma\left[\frac{(\nu_1+\nu_2)}{2}\right]}{\Gamma\left(\frac{\nu_1}{2}\right)\Gamma\left(\frac{\nu_2}{2}\right)}\left(\frac{\nu_1}{\nu_2}\right)^{\frac{\nu_1}{2}}\frac{x^{\frac{\nu_1-2}{2}}}{\left[1+\left(\frac{\nu_1}{\nu_2}\right)x\right]^{\frac{\nu_1+\nu_2}{2}}}$$

Examples

```
y = fpdf(1:6,2,2)

y =

    0.2500    0.1111    0.0625    0.0400    0.0278    0.0204

z = fpdf(3,5:10,5:10)

z =

      0.0689    0.0659    0.0620    0.0577    0.0532    0.0487
```

Purpose Random numbers from the F distribution.

Syntax

```
R = frnd(V1,V2)
R = frnd(V1,V2,m)
R = frnd(V1,V2,m,n)
```

Description `R = frnd(V1,V2)` generates random numbers from the F distribution with numerator degrees of freedom, `V1`, and denominator degrees of freedom, `V2`. The size of `R` is the common size of `V1` and `V2` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other parameter.

`R = frnd(V1,V2,m)` generates random numbers from the F distribution with parameters `V1` and `V2`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = frnd(V1,V2,m,n)` generates random numbers from the F distribution with parameters `V1` and `V2`. The scalars `m` and `n` are the row and column dimensions of `R`.

Examples

```
n1 = frnd(1:6,1:6)

n1 =

    0.0022    0.3121    3.0528    0.3189    0.2715    0.9539

n2 = frnd(2,2,[2 3])

n2 =

    0.3186    0.9727    3.0268
    0.2052  148.5816    0.2191

n3 = frnd([1 2 3;4 5 6],1,2,3)

n3 =

    0.6233    0.2322   31.5458
    2.5848    0.2121    4.4955
```

fstat

Purpose Mean and variance for the F distribution.

Syntax

```
[M,V] = fstat(V1,V2)
```

Description For the F distribution:

- The mean, for values of n_2 greater than 2, is:

$$\frac{\nu_2}{\nu_2 - 2}$$

- The variance, for values of n greater than 4, is:

$$\frac{2\nu_2^{\ 2}(\nu_1 + \nu_2 - 2)}{\nu_1(\nu_2 - 2)^2(\nu_2 - 4)}$$

The mean of the F distribution is undefined if $\nu 2$ is less than 3. The variance is undefined for $\nu 2$ less than 5.

Examples `fstat` returns `NaN` when the mean and variance are undefined.

```
[m,v] = fstat(1:5,1:5)

m =

    NaN       NaN    3.0000    2.0000    1.6667

v =

    NaN       NaN       NaN       NaN    8.8889
```

Purpose Interactive contour plot of a function.

Syntax

```
fsurfht('fun',xlims,ylims)
fsurfht('fun',xlims,ylims,p1,p2,p3,p4,p5)
```

Description `fsurfht('fun',xlims,ylims)` is an interactive contour plot of the function specified by the text variable `fun`. The *x*-axis limits are specified by `xlims` = `[xmin xmax]` and the *y*-axis limits specified by `ylims`.

`fsurfht('fun',xlims,ylims,p1,p2,p3,p4,p5)` allows for five optional parameters that you can supply to the function `'fun'`. The first two arguments of `fun` are the *x*-axis variable and *y*-axis variable, respectively.

There are vertical and horizontal reference lines on the plot whose intersection defines the current *x*-value and *y*-value. You can drag these dotted white reference lines and watch the calculated *z*-values (at the top of the plot) update simultaneously. Alternatively, you can get a specific *z*-value by typing the *x*-value and *y*-value into editable text fields on the *x*-axis and *y*-axis respectively.

Example Plot the Gaussian likelihood function for the `gas.mat` data.

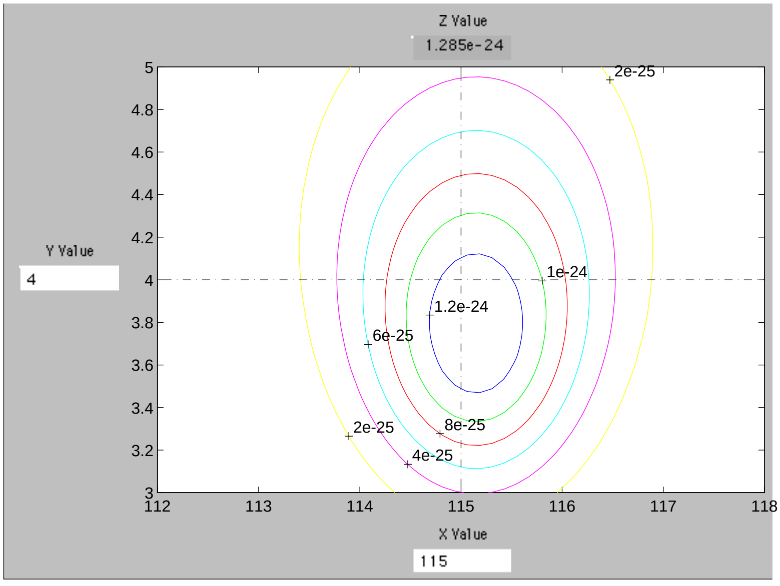
```
load gas
```

Write the M-file, `gauslike.m`.

```
function z = gauslike(mu,sigma,p1)
n = length(p1);
z = ones(size(mu));
for i = 1:n
z = z .* (normpdf(p1(i),mu,sigma));
end
```

gauslike calls normpdf treating the data sample as fixed and the parameters µ and σ as variables. Assume that the gas prices are normally distributed and plot the likelihood surface of the sample.

```
fsurfht('gauslike',[112 118],[3 5],price1)
```



The sample mean is the *x*-value at the maximum, but the sample standard deviation is not the *y*-value at the maximum.

```
mumax = mean(price1)

mumax =

  115.1500

sigmamax = std(price1)*sqrt(19/20)

sigmamax =

    3.7719
```

Purpose Full-factorial experimental design.

Syntax

```
design = fullfact(levels)
```

Description

`design = fullfact(levels)` give the factor settings for a full factorial design. Each element in the vector `levels` specifies the number of unique values in the corresponding column of `design`.

For example, if the first element of `levels` is 3, then the first column of `design` contains only integers from 1 to 3.

Example

If `levels = [2 4]`, `fullfact` generates an eight run design with two levels in the first column and four in the second column.

```
d = fullfact([2 4])

d =

     1     1
     2     1
     1     2
     2     2
     1     3
     2     3
     1     4
     2     4
```

See Also

`ff2n`, `dcovary`, `daugment`, `cordexch`

gamcdf

Purpose Gamma cumulative distribution function (cdf).

Syntax

```
P = gamcdf(X,A,B)
```

Description `gamcdf(X,A,B)` computes the gamma cdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A`, and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

Parameters `A` and `B` are positive.

The gamma cdf is:

$$p = F(x|a, b) = \frac{1}{b^a \Gamma(a)} \int_0^x t^{a-1} e^{-\frac{t}{b}} dt$$

The result, *p*, is the probability that a single observation from a gamma distribution with parameters *a* and *b* will fall in the interval [0 *x*].

`gammainc` is the gamma distribution with a single parameter, `a`, with `b` at its default value of 1.

Examples

```
a = 1:6;
b = 5:10;
prob = gamcdf(a.*b,a,b)

prob =

    0.6321    0.5940    0.5768    0.5665    0.5595    0.5543
```

The mean of the gamma distribution is the product of the parameters, *a*b*. In this example as the mean increases, it approaches the median (i.e., the distribution gets more symmetric).

Purpose Parameter estimates and confidence intervals for gamma distributed data.

Syntax

```
phat = gamfit(x)
[phat,pci] = gamfit(x)
[phat,pci] = gamfit(x,alpha)
```

Description `phat = gamfit(x)` returns the maximum likelihood estimates of the parameters of the gamma distribution given the data in the vector, `x`.

`[phat,pci] = gamfit(x)` gives MLEs and `95%` percent confidence intervals. The first row of `pci` is the lower bound of the confidence intervals; the last row is the upper bound.

`[phat,pci] = gamfit(x,alpha)` returns `100(1–alpha)` percent confidence intervals. For example, `alpha` = 0.01 yields 99% confidence intervals.

Example Note the 95% confidence intervals in the example bracket the "true" parameter values, 2 and 4, respectively.

```
a = 2; b = 4;
r = gamrnd(a,b,100,1);
[p,ci] = gamfit(r)

p =

    2.1990    3.7426

ci =

    1.6840    2.8298
    2.7141    4.6554
```

Reference Hahn, G. J., and S.S. Shapiro, *Statistical Models in Engineering*, Wiley Classics Library John Wiley & Sons, New York. 1994. p. 88.

See Also `betafit`, `binofit`, `expfit`, `normfit`, `poissfit`, `unifit`, `weibfit`

gaminv

Purpose Inverse of the gamma cumulative distribution function (cdf).

Syntax

```
X = gaminv(P,A,B)
```

Description `gaminv(P,A,B)` computes the inverse of the gamma cdf with parameters `A` and `B` for the probabilities in `P`. The arguments `P`, `A` and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `A` and `B` must both be positive and `P` must lie on the interval [0 1].

The gamma inverse function in terms of the gamma cdf is:

$$x = F^{-1}(p|a,b) = \{x:F(x|a,b) = p\}$$

$$where \quad p = F(x|a,b) = \frac{1}{b^a\Gamma(a)}\int_0^x t^{a-1}e^{-\frac{t}{b}}dt$$

Algorithm There is no known analytic solution to the integral equation above. `gaminv` uses an iterative approach (Newton's method) to converge to the solution.

Examples This example shows the relationship between the gamma cdf and its inverse function.

```
a = 1:5;
b = 6:10;
x = gaminv(gamcdf(1:5,a,b),a,b)

x =

    1.0000    2.0000    3.0000    4.0000    5.0000
```

Purpose Negative gamma log-likelihood function.

Syntax

```
logL = gamlike(params,data)
[logL,info] = gamlike(params,data)
```

Description `logL = gamlike(params,data)` returns the negative of the gamma log-likelihood function for the parameters, `params`, given `data`. The length of the vector, `logL`, is the length of the vector, `data`.

`[logL,info] = gamlike(params,data)` adds Fisher's information matrix, `info`. The diagonal elements of `info` are the asymptotic variances of their respective parameters.

`gamlike` is a utility function for maximum likelihood estimation of the gamma distribution. Since `gamlike` returns the negative gamma log-likelihood function, minimizing `gamlike` using `fmins` is the same as maximizing the likelihood.

Example Continuing the example for `gamfit`:

```
a = 2; b = 3;
r = gamrnd(a,b,100,1);
[logL,info] = gamlike([2.1990 2.8069],r)

logL =

  267.5585


info =

    0.0690   –0.0790
   –0.0790    0.1220
```

See Also `betalike`, `gamfit`, `mle`, `weiblike`

gampdf

Purpose

Gamma probability density function (pdf).

Syntax

```
Y = gampdf(X,A,B)
```

Description

`gampdf(X,A,B)` computes the gamma pdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A` and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `A` and `B` must both be positive and `X` must lie on the interval $[0\ \infty)$.

The gamma pdf is:

$$y = f(x|a,b) = \frac{1}{b^a\Gamma(a)}x^{a-1}e^{-\frac{x}{b}}$$

Gamma probability density function is useful in reliability models of lifetimes. The gamma distribution is more flexible than the exponential in that the probability of surviving an additional period may depend on age. Special cases of the gamma function are the exponential and χ^2 functions.

Examples

The exponential distribution is a special case of the gamma distribution.

```
mu = 1:5;
y = gampdf(1,1,mu)

y =

    0.3679    0.3033    0.2388    0.1947    0.1637

y1 = exppdf(1,mu)

y1 =

    0.3679    0.3033    0.2388    0.1947    0.1637
```

Purpose

Random numbers from the gamma distribution.

Syntax

```
R = gamrnd(A,B)
R = gamrnd(A,B,m)
R = gamrnd(A,B,m,n)
```

Description

`R = gamrnd(A,B)` generates gamma random numbers with parameters `A` and `B`. The size of `R` is the common size of `A` and `B` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other parameter.

`R = gamrnd(A,B,m)` generates gamma random numbers with parameters `A` and `B`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = gamrnd(A,B,m,n)` generates gamma random numbers with parameters `A` and `B`. The scalars `m` and `n` are the row and column dimensions of `R`.

Examples

```
n1 = gamrnd(1:5,6:10)

n1 =

    9.1132   12.8431   24.8025   38.5960  106.4164

n2 = gamrnd(5,10,[1 5])

n2 =

   30.9486   33.5667   33.6837   55.2014   46.8265

n3 = gamrnd(2:6,3,1,5)

n3 =

   12.8715   11.3068    3.0982   15.6012   21.6739
```

gamstat

Purpose Mean and variance for the gamma distribution.

Syntax

```
[M,V] = gamstat(A,B)
```

Description For the gamma distribution:

- The mean is ab.
- The variance is ab^2.

Examples

```
[m,v] = gamstat(1:5,1:5)

m =

     1     4     9    16    25

v =

     1     8    27    64   125

[m,v] = gamstat(1:5,1./(1:5))

m =

     1     1     1     1     1

v =

    1.0000    0.5000    0.3333    0.2500    0.2000
```

Purpose Geometric cumulative distribution function (cdf).

Syntax

```
Y = geocdf(X,P)
```

Description `geocdf(X,P)` computes the geometric cdf with probabilities, `P`, at the values in `X`. The arguments `X` and `P` must be the same size except that a scalar argument functions as a constant matrix of the same size as the other argument.

The parameter, `P`, is on the interval [0 1].

The geometric cdf is:

$$y = F(x|p) = \sum_{i=0}^{floorx} pq^{i}$$

where: $q = 1 - p$

The result, y, is the probability of observing up to x trials before a success when the probability of success in any given trial is p.

Examples Suppose you toss a fair coin repeatedly. If the coin lands face up (heads), that is a success. What is the probability of observing three or fewer tails before getting a heads?

```
p = geocdf(3,0.5)

p =

    0.9375
```

geoinv

Purpose Inverse of the geometric cumulative distribution function (cdf).

Syntax

```
X = geoinv(Y,P)
```

Description `geoinv(Y,P)` returns the smallest integer `X` such that the geometric cdf evaluated at `X` is equal to or exceeds `Y`. You can think of `Y` as the probability of observing `X` successes in a row in independent trials where `P` is the probability of success in each trial.

The arguments `P` and `Y` must lie on the interval [0 1]. Each `X` is a positive integer.

Examples The probability of correctly guessing the result of 10 coin tosses in a row is less than 0.001 (unless the coin is not fair.)

```
psychic = geoinv(0.999,0.5)

psychic =

     9
```

The example below shows the inverse method for generating random numbers from the geometric distribution.

```
rndgeo = geoinv(rand(2,5),0.5)

rndgeo =

     0     1     3     1     0
     0     1     0     2     0
```

Purpose Geometric mean of a sample.

Syntax

```
m = geomean(X)
```

Description `geomean` calculates the geometric mean of a sample. For vectors, `geomean(x)` is the geometric mean of the elements in `x`. For matrices, `geomean(X)` is a row vector containing the geometric means of each column.

The geometric mean is:

$$m = \left[\prod_{i=1}^{n} x_i\right]^{\frac{1}{n}}$$

Examples The sample average is greater than or equal to the geometric mean.

```
x = exprnd(1,10,6);
geometric = geomean(x)

geometric =

    0.7466    0.6061    0.6038    0.2569    0.7539    0.3478

average = mean(x)

average =

    1.3509    1.1583    0.9741    0.5319    1.0088    0.8122
```

See Also `mean`, `median`, `harmmean`, `trimmean`

Purpose Geometric probability density function (pdf).

Syntax

```
Y = geopdf(X,P)
```

Description `geocdf(X,P)` computes the geometric pdf with probabilities, `P`, at the values in `X`. The arguments `X` and `P` must be the same size except that a scalar argument functions as a constant matrix of the same size as the other argument.

The parameter, `P`, is on the interval [0 1].

The geometric pdf is:

$$y = f(x|p) = pq^x I_{(0,\,1,\,K)}(x)$$

where: $q = 1 - p$

Examples Suppose you toss a fair coin repeatedly. If the coin lands face up (heads), that is a success. What is the probability of observing exactly three tails before getting a heads?

```
p = geopdf(3,0.5)

p =

    0.0625
```

Purpose Random numbers from the geometric distribution.

Syntax

```
R = geornd(P)
R = geornd(P,m)
R = geornd(P,m,n)
```

Description The geometric distribution is useful when you want to model the number of failed trials in a row before a success where the probability of success in any given trial is the constant `P`.

`R = geornd(P)` generates geometric random numbers with probability parameter, `P` . The size of `R` is the size of `P`.

`R = geornd(P,m)` generates geometric random numbers with probability parameter, `P`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = geornd(P,m,n)` generates geometric random numbers with probability parameter, `P`. The scalars `m` and `n` are the row and column dimensions of `R`.

The parameter `P` must lie on the interval [0 1].

Examples

```
r1 = geornd(1 ./ 2.^(1:6))
r1 =

     2    10     2     5     2    60

r2 = geornd(0.01,[1 5])

r2 =

    65    18   334   291    63

r3 = geornd(0.5,1,6)

r3 =

     0     7     1     3     1     0
```

geostat

Purpose Mean and variance for the geometric distribution.

Syntax

```
[M,V] = geostat(P)
```

Description For the geometric distribution:

- The mean is $\frac{q}{p}$.
- The variance is $\frac{q}{p^2}$.

where $q = 1 - p$.

Examples

```
[m,v] = geostat(1./(1:6))

m =

     0    1.0000    2.0000    3.0000    4.0000    5.0000

v =

     0    2.0000    6.0000   12.0000   20.0000   30.0000
```

Purpose Interactively draw a line in a figure.

Syntax

```
gline(fig)
h = gline(fig)
gline
```

Description `gline(fig)` draws a line segment by clicking the mouse at the two end-points of the line segment in the figure, `fig`. A rubber band line tracks the mouse movement.

`h = gline(fig)` returns the handle to the line in `h`.

`gline` with no input arguments draws in the current figure.

See Also `refline`, `gname`

gname

Purpose Label plotted points with their case names or case number.

Syntax

```
gname('cases')
gname
h = gname('cases',line_handle)
```

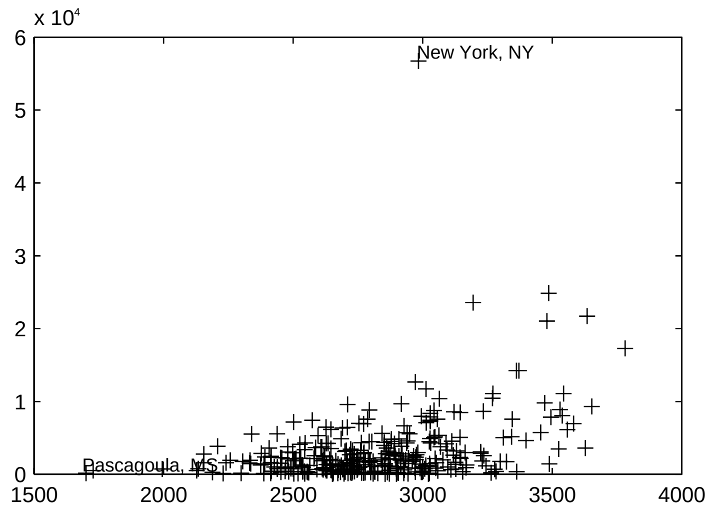
Description `gname('cases')` displays the graph window, puts up a cross-hair, and waits for a mouse button or keyboard key to be pressed. Position the cross-hair with the mouse and click once near each point that you want to label. When you are done, press the **Return** or **Enter** key and the labels will appear at each point that you clicked. `'cases'` is a string matrix. Each row is the case name of a data point.

`gname` with no arguments labels each case with its case number.

`h = gname(cases,line_handle)` returns a vector of handles to the text objects on the plot. Use the scalar, `line_handle`, to identify the correct line if there is more than one line object on the plot.

Example Let's use the city ratings datasets to find out which cities are the best and worst for education and the arts.

```
load cities
education = ratings(:,6); arts = ratings(:,7);
plot(education,arts,'+')
gname(names)
```



See Also `gtext`

grpstats

Purpose Summary statistics by group.

Syntax

```
means = grpstats(X,group)
[means,sem,counts] = grpstats(X,group)
grpstats(x,group)
grpstats(x,group,alpha)
```

Description `means = grpstats(X,group)` returns the `means` of each column of `X` by `group`. `X` is a matrix of observations. `group` is a column of positive integers that indicates the group membership of each row in `X`.

`[means,sem,counts] = grpstats(x,group,alpha)` supplies the standard error of the mean in `sem`. `counts` is the same size as the other outputs. The *i-th* row of `counts` contains the number of elements in the *i-th* `group`.

`grpstats(x,group)` displays a plot of the means versus index with 95% confidence intervals about the mean value of for each value of index.

`grpstats(x,group,alpha)` plots 100(1 – `alpha`)% confidence intervals around each mean.

Example We assign 100 observations to one of four groups. For each observation we measure five quantities with *true means* from 1 to 5. `grpstats` allows us to compute the means for each group.

```
group = unidrnd(4,100,1);
true_mean = 1:5;
true_mean = true_mean(ones(100,1),:);
x = normrnd(true_mean,1);
means = grpstats(x,group)

means =

    0.7947    2.0908    2.8969    3.6749    4.6555
    0.9377    1.7600    3.0285    3.9484    4.8169
    1.0549    2.0255    2.8793    4.0799    5.3740
    0.7107    1.9264    2.8232    3.8815    4.9689
```

See Also `tabulate`, `crosstab`

Purpose Harmonic mean of a sample of data.

Syntax

```
m = harmmean(X)
```

Description `harmmean` calculates the harmonic mean of a sample. For vectors, `harmmean(x)` is the harmonic mean of the elements in `x`. For matrices, `harmmean(X)` is a row vector containing the harmonic means of each column.

The harmonic mean is:

$$m = \frac{n}{\sum_{i=1}^{n} \frac{1}{x_i}}$$

Examples The sample average is greater than or equal to the harmonic mean.

```
x = exprnd(1,10,6);
harmonic = harmmean(x)

harmonic =

    0.3382    0.3200    0.3710    0.0540    0.4936    0.0907

average = mean(x)

average =

    1.3509    1.1583    0.9741    0.5319    1.0088    0.8122
```

See Also `mean`, `median`, `geomean`, `trimmean`

Purpose Plot histograms.

Syntax

```
hist(y)
hist(y,nb)
hist(y,x)
[n,x] = hist(y,...)
```

Description `hist` calculates or plots histograms.

`hist(y)` draws a 10-bin histogram for the data in vector `y`. The bins are equally spaced between the minimum and maximum values in `y`.

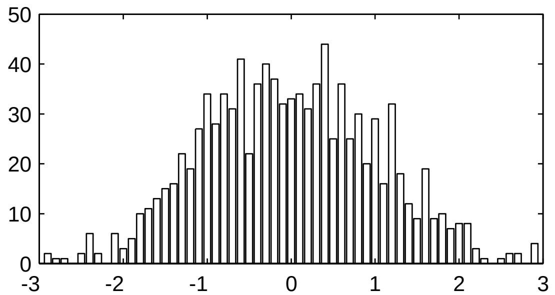
`hist(y,nb)` draws a histogram with `nb` bins.

`hist(y,x)` draws a histogram using the bins in the vector, `x`.

`[n,x] = hist(y)`, `[n,x] = hist(y,nb)`, and `[n,x] = hist(y,x)` do not draw graphs, but return vectors `n` and `x` containing the frequency counts and the bin locations such that `bar(x,n)` plots the histogram. This is useful in situations where more control is needed over the appearance of a graph, for example, to combine a histogram into a more elaborate plot statement.

Examples Generate bell-curve histograms from Gaussian data.

```
x = –2.9:0.1:2.9;
y = normrnd(0,1,1000,1);
hist(y,x)
```



See Also `hist` is a function in MATLAB.

Purpose Histogram with superimposed normal density.

Syntax

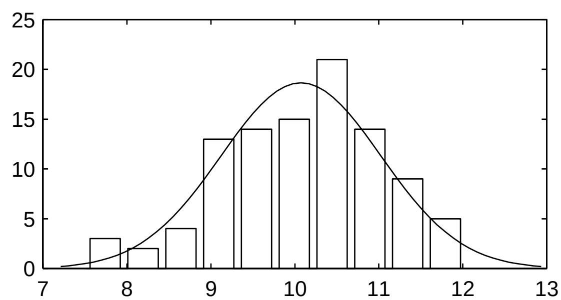
```
histfit(data)
histfit(data,nbins)
h = histfit(data,nbins)
```

Description `histfit(data,nbins)` plots a histogram of the values in the vector `data` using `nbins` bars in the histogram. With one input argument, `nbins` is set to the square root of the number of elements in `data`.

`h = histfit(data,nbins)` returns a vector of handles to the plotted lines. `h(1)` is the handle to the histogram, `h(2)` is the handle to the density curve.

Example

```
r = normrnd(10,1,100,1);
histfit(r)
```



See Also `hist`, `normfit`

hougen

Purpose

Hougen-Watson model for reaction kinetics.

Syntax

```
yhat = hougen(beta,X)
```

Description

`yhat = hougen(beta,x)` gives the predicted values of the reaction rate, `yhat`, as a function of the vector of parameters, `beta`, and the matrix of data, `X`. `beta` must have 5 elements and `X` must have three columns.

`hougen` is a utility function for `rsmdemo`.

The model form is:

$$\hat{y} = \frac{\beta_1 x_2 - x_3/\beta_5}{1 + \beta_2 x_1 + \beta_3 x_2 + \beta_4 x_3}$$

Reference

Bates, D., and D. Watts, *Nonlinear Regression Analysis and Its Applications*, Wiley 1988. p. 271–272.

See Also

`rsmdemo`

Purpose

Hypergeometric cumulative distribution function (cdf).

Syntax

```
P = hygecdf(X,M,K,N)
```

Description

`hygecdf(X,M,K,N)` computes the hypergeometric cdf with parameters `M`, `K`, and `N` at the values in `X`. The arguments `X`, `M`, `K`, and `N` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The hypergeometric cdf is:

$$p = F(x|M, K, N) = \sum_{i=0}^{x} \frac{\binom{K}{i}\binom{M-K}{N-i}}{\binom{M}{N}}$$

The result, p, is the probability of drawing up to x items of a possible K in N drawings without replacement from a group of M objects.

Examples

Suppose you have a lot of 100 floppy disks and you know that 20 of them are defective. What is the probability of drawing zero to two defective floppies if you select 10 at random?

```
p = hygecdf(2,100,20,10)

p =

    0.6812
```

Purpose Inverse of the hypergeometric cumulative distribution function (cdf).

Syntax

```
X = hygeinv(P,M,K,N)
```

Description `hygeinv(P,M,K,N)` returns the smallest integer `X` such that the hypergeometric cdf evaluated at `X` equals or exceeds `P`. You can think of `P` as the probability of observing `X` defective items in `N` drawings without replacement from a group of `M` items where `K` are defective.

Examples Suppose you are the Quality Assurance manager of a floppy disk manufacturer. The production line turns out floppy disks in batches of 1,000. You want to sample 50 disks from each batch to see if they have defects. You want to accept 99% of the batches if there are no more than 10 defective disks in the batch. What is the maximum number of defective disks should you allow in your sample of 50?

```
x = hygeinv(0.99,1000,10,50)

x =

     3
```

What is the median number of defective floppy disks in samples of 50 disks from batches with 10 defective disks?

```
x = hygeinv(0.50,1000,10,50)

x =

     0
```

Purpose Hypergeometric probability density function (pdf).

Syntax

```
Y = hygepdf(X,M,K,N)
```

Description `hygecdf(X,M,K,N)` computes the hypergeometric pdf with parameters `M`, `K`, and `N` at the values in `X`. The arguments `X`, `M`, `K`, and `N` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `M`, `K`, and `N` must be positive integers. Also `X` must be less than or equal to all the parameters and `N` must be less than or equal to `M`.

The hypergeometric pdf is:

$$y = f(x|M, K, N) = \frac{\binom{K}{x}\binom{M-K}{N-x}}{\binom{M}{N}}$$

The result, y, is the probability of drawing exactly x items of a possible K in n drawings without replacement from group of M objects.

Examples Suppose you have a lot of 100 floppy disks and you know that 20 of them are defective. What is the probability of drawing 0 through 5 defective floppy disks if you select 10 at random?

```
p = hygepdf(0:5,100,20,10)

p =

    0.0951    0.2679    0.3182    0.2092    0.0841    0.0215
```

hygernd

Purpose Random numbers from the hypergeometric distribution.

Syntax

```
R = hygernd(M,K,N)
R = hygernd(M,K,N,mm)
R = hygernd(M,K,N,mm,nn)
```

Description `R = hygernd(M,K,N)` generates hypergeometric random numbers with parameters `M`,`K` and `N`. The size of `R` is the common size of `M`, `K`, and `N` if all are matrices. If any parameter is a scalar, the size of `R` is the common size of the nonscalar parameters.

`R = hygernd(M,K,N,mm)` generates hypergeometric random numbers with parameters `M`, `K`, and `N`. `mm` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = hygernd(M,K,N,mm,nn)` generates hypergeometric random numbers with parameters `M`, `K`, and `N`. The scalars `mm` and `nn` are the row and column dimensions of `R`.

Examples

```
numbers = hygernd(1000,40,50)

numbers =

     1
```

Purpose

Mean and variance for the hypergeometric distribution.

Syntax

```
[MN,V] = hygestat(M,K,N)
```

Description

For the hypergeometric distribution:

- The mean is $N\frac{K}{M}$.
- The variance is $N\frac{K}{M}\frac{M-K}{M}\frac{M-N}{M-1}$.

Examples

The hypergeometric distribution approaches the binomial where $p = K/M$ as M goes to infinity.

```
[m,v] = hygestat(10.^(1:4),10.^(0:3),9)

m =

    0.9000    0.9000    0.9000    0.9000

v =

    0.0900    0.7445    0.8035    0.8094

[m,v] = binostat(9,0.1)

m =

    0.9000

v =

    0.8100
```

Purpose

Inverse of a specified cumulative distribution function (icdf).

Syntax

```
X = icdf('name',P,A1,A2,A3)
```

Description

`icdf` is a utility routine allowing you to access all the inverse cdfs in the Statistics Toolbox using the name of the distribution as a parameter.

`icdf('`*`name`*`',P,A1,A2,A3)` returns a matrix of critical values, `X`. `'`*`name`*`'` is a string containing the name of the distribution. `P` is a matrix of probabilities, and `A`, `B`, and `C` are matrices of distribution parameters. Depending on the distribution some of the parameters may not be necessary.

The arguments `P`, `A1`, `A2`, and `A3` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

Examples

```
x = icdf('Normal',0.1:0.2:0.9,0,1)

x =

   –1.2816   –0.5244         0    0.5244    1.2816

x = icdf('Poisson',0.1:0.2:0.9,1:5)

x =

     1     1     3     5     8
```

Purpose Calculate the inconsistency coefficient of a cluster tree.

Syntax

```
Y = inconsistent(Z)
Y = inconsistent(Z,d)
```

Description `Y = inconsistent(Z)` computes the inconsistency coefficient for each link of the hierarchical cluster tree, `Z`. `Z` is an m-1 by 3 matrix generated by the `linkage` function. The inconsistency coefficient characterizes each link in a cluster tree by comparing its length with the average length of other links at the same level of the hierarchy. The higher the value of this coefficient, the less similar the objects connected by the link.

`Y = inconsistent(Z,d)` computes the inconsistency coefficient for each link in the hierarchical cluster tree, `Z`, to depth `d`. `d` is an integer denoting the number of levels of the cluster tree that are included in the calculation. By default, `d=2`.

The output, `Y`, is an m-1 by 4 matrix formatted as follows.

Column	Description
1	Mean of the lengths of all the links included in the calculation.
2	Standard deviation of all the links included in the calculation.
3	Number of links included in the calculation.
4	Inconsistency coefficient.

For each link, k, the inconsistency coefficient is calculated as:

$$Y(k,4) = (z(k,3) - Y(k,1)) / Y(k,2)$$

For leaf nodes, nodes that have no further nodes under them, the inconsistency coefficient is set to 0.

Example

```
rand('seed',12);
X = rand(10,2);
Y = pdist(X);
Z = linkage(Y,'centroid');
W = inconsistent(Z,3)

W =

    0.0423         0    1.0000         0
    0.1406         0    1.0000         0
    0.1163    0.1047    2.0000    0.7071
    0.2101         0    1.0000         0
    0.2054    0.0886    3.0000    0.6792
    0.1742    0.1762    3.0000    0.6568
    0.2336    0.1317    4.0000    0.6408
    0.3081    0.2109    5.0000    0.7989
    0.4610    0.3728    4.0000    0.8004
```

See Also

`cluster`, `cophenet`, `clusterdata`, `dendrogram`, `linkage`, `pdist`, `squareform`

Purpose Interquartile range (IQR) of a sample.

Syntax

```
y = iqr(X)
```

Description `iqr(X)` computes the difference between the 75th and the 25th percentiles of the sample in `X`. The IQR is a robust estimate of the spread of the data, since changes in the upper and lower 25% of the data do not affect it.

If there are outliers in the data, then the IQR is more representative than the standard deviation as an estimate of the spread of the body of the data. The IQR is less efficient than the standard deviation as an estimate of the spread, when the data is all from the normal distribution.

Multiply the IQR by 0.7413 to estimate σ (the second parameter of the normal distribution.)

Examples This Monte Carlo simulation shows the relative efficiency of the IQR to the sample standard deviation for normal data.

```
x = normrnd(0,1,100,100);
s = std(x);
s_IQR = 0.7413 * iqr(x);
efficiency = (norm(s - 1)./norm(s_IQR - 1)).^2

efficiency =

    0.3297
```

See Also `std`, `mad`, `range`

kurtosis

Purpose Sample kurtosis.

Syntax `k = kurtosis(X)`

Description `k = kurtosis(X)` returns the sample kurtosis of `X`. For vectors, `kurtosis(x)` is the kurtosis of the elements in the vector, `x`. For matrices `kurtosis(X)` returns the sample kurtosis for each column of `X`.

Kurtosis is a measure of how outlier-prone a distribution is. The kurtosis of the normal distribution is 3. Distributions that are more outlier-prone than the normal distribution have kurtosis greater than 3; distributions that are less outlier-prone have kurtosis less than 3.

The kurtosis of a distribution is defined as

$$k = \frac{E(x-\mu)^4}{\sigma^4}$$

where $E(x)$ is the expected value of x.

Note: Some definitions of kurtosis subtract 3 from the computed value, so that the normal distribution has kurtosis of 0. The `kurtosis` function does not use this convention.

Example

```
X = randn([5 4])

X =

    1.1650    1.6961   –1.4462   –0.3600
    0.6268    0.0591   –0.7012   –0.1356
    0.0751    1.7971    1.2460   –1.3493
    0.3516    0.2641   –0.6390   –1.2704
   –0.6965    0.8717    0.5774    0.9846

k = kurtosis(X)

k =

    2.1658    1.2967    1.6378    1.9589
```

See Also `mean`, `moment`, `skewness`, `std`, `var`

Purpose

Leverage values for a regression.

Syntax

```
h = leverage(DATA)
h = leverage(DATA,'model')
```

Description

`h = leverage(DATA)` finds the leverage of each row (point) in the matrix, `DATA` for a linear additive regression model.

`h = leverage(DATA,'model')` finds the leverage on a regression, using a specified model type. `'model'` can be one of these strings:

- `'interaction'` – includes constant, linear, and cross product terms.
- `'quadratic'` – interactions plus squared terms.
- `'purequadratic'` – includes constant, linear and squared terms.

Leverage is a measure of the influence of a given observation on a regression due to its location in the space of the inputs.

Example

One rule of thumb is to compare the leverage to $2p/n$ where n is the number of observations and p is the number of parameters in the model. For the Hald dataset this value is 0.7692.

```
load hald
h = max(leverage(ingredients,'linear'))

h =

    0.7004
```

Since 0.7004 < 0.7692, there are no high leverage points using this rule.

Algorithm

```
[Q,R] = qr(x2fx(DATA,'model'));
leverage = (sum(Q'.*Q'))'
```

Reference

Goodall, C. R. (1993). *Computation using the QR decomposition*. Handbook in Statistics, Volume 9. Statistical Computing (C. R. Rao, ed.). Amsterdam, NL Elsevier/North-Holland.

See Also

`regstats`

linkage

Purpose

Create hierachical cluster tree.

Syntax

```
Z = linkage(Y)
Z = linkage(Y,'method')
```

Description

`Z = linkage(Y)` creates a hierarchical cluster tree, using the Single Linkage algorithm. The input matrix, `Y`, is the distance vector output by the `pdist` function, a vector of length $(m-1) \cdot m/2$ by 1, where m is the number of objects in the original dataset.

`Z = linkage(Y,'method')` computes a hierarchical cluster tree using the algorithm specified by *'method'*. `method` can be any of the following character strings that identify ways to create the cluster hierarchy. Their definitions are explained in the section, "Mathematical Definitions."

String	Meaning
`'single'`	Shortest distance (default)
`'complete'`	Largest distance
`'average'`	Average distance
`'centroid'`	Centroid distance
`'ward'`	Incremental sum of squares

The output, `Z`, is an m-1 by 3 matrix containing cluster tree information. The leaf nodes in the cluster hierarchy are the objects in the original dataset, numbered from 1 to m. They are the singleton clusters from which all higher clusters are built. Each newly formed cluster, corresponding to row i in `Z`, is assigned the index $m+i$, where m is the total number of initial leaves.

Columns 1 and 2, `Z(i,1:2)`, contain the indices of the objects that were linked in pairs to form a new cluster. This new cluster is assigned the index value $m+i$. There are m-1 higher clusters that correspond to the interior nodes of the hierarchical cluster tree.

Column 3, `Z(i,3)`, contains the corresponding linkage distances between the objects paired in the clusters at each row i.

For example, consider a case with 30 initial nodes. If the tenth cluster formed by the `linkage` function combines object 5 and object 7 and their distance is 1.5, then row 10 of `Z` will contain the values (5,7,1.5). This newly formed cluster will have the index 10+30=40. If cluster 40 shows up in a later row, that means this newly formed cluster is being combined again into some bigger cluster.

Mathematical Definitions. The *'method'* argument is a character string that specifies the algorithm used to generate the hierachical cluster tree information. These linkage algorithms are based on various measurements of proximity between two groups of objects. If n_r is the number of objects in cluster r and n_s is the number of objects in cluster s, and x_{ri} is the ith object in cluster r, the definitions of these various measurements are as follows:

- *Single linkage*, also called *nearest neighbor*, uses the smallest distance between objects in the two groups.

  $$d(r, s) = min(dist(x_{ri}, x_{sj})), i \in (i, \ldots, n_r), j \in (1, \ldots, n_s)$$

- *Complete linkage*, also called *furthest neighbor*, uses the largest distance between objects in the two groups.

  $$d(r, s) = max(dist(x_{ri}, x_{sj})), i \in (1, \ldots, n_r), j \in (1, \ldots, n_s)$$

- *Average linkage* uses the average distance between all pairs of objects in cluster r and cluster s.

  $$d(r, s) = \frac{1}{n_r n_s} \sum_{i=1}^{n_r} \sum_{j=1}^{n_s} dist(x_{ri}, x_{sj})$$

- *Centroid linkage* uses the distance between the centroids of the two groups

  $$d(r, s) = d(\bar{x}_r, \bar{x}_s)$$

  where:

  $$\bar{x}_r = \frac{1}{n_r} \sum_{i=1}^{n_r} x_{ri}$$

and $\bar{x}_s$ is defined similarly.

- *Ward linkage* uses the incremental sum of squares; that is, the increase in the total within-group sum of squares as a result of joining groups r and s. It is given by

  $$d(r, s) = n_r n_s d_{rs}^2 / (n_r + n_s)$$

  where d_{rs}^2 is the distance between cluster r and cluster s defined in the Centroid linkage. The within-group sum of squares of a cluster is defined as the sum of the squares of the distance between all objects in the cluster and the centroid of the cluster.

Example

```
X = [3 1.7; 1 1; 2 3; 2 2.5; 1.2 1; 1.1 1.5; 3 1];
Y = pdist(x);
Z = linkage(y)

Z =

    2.0000    5.0000    0.2000
    3.0000    4.0000    0.5000
    8.0000    6.0000    0.5099
    1.0000    7.0000    0.7000
   11.0000    9.0000    1.2806
   12.0000   10.0000    1.3454
```

See Also

`cluster`, `clusterdata`, `cophenet`, `dendrogram`, `inconsistent`, `pdist`, `squareform`

Purpose

Lognormal cumulative distribution function.

Syntax

```
P = logncdf(X,MU,SIGMA)
```

Description

`P = logncdf(X,MU,SIGMA)` computes the lognormal cdf with mean `MU` and standard deviation `SIGMA` at the values in `X`.

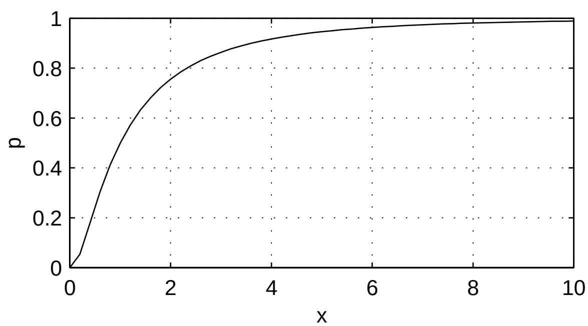
The size of `P` is the common size of `X`, `MU` and `SIGMA`. A scalar input functions as a constant matrix of the same size as the other inputs.

The lognormal cdf is:

$$p = F(x|\mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}}\int_0^x \frac{e^{\frac{-(\ln(t)-\mu)^2}{2\sigma^2}}}{t}dt$$

Example

```
x = (0:0.2:10);
y = logncdf(x,0,1);
plot(x,y);grid;xlabel('x');ylabel('p')
```



Reference

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition*, John Wiley and Sons, 1993. p. 102–105.

See Also

`cdf`, `logninv`, `lognpdf`, `lognrnd`, `lognstat`

logninv

Purpose

Inverse of the lognormal cumulative distribution function (cdf).

Syntax

```
X = logninv(P,MU,SIGMA)
```

Description

`X = logninv(P,MU,SIGMA)` computes the inverse lognormal cdf with mean `MU` and standard deviation `SIGMA`, at the probabilities in `P`.

The size of `X` is the common size of `P`, `MU` and `SIGMA`.

We define the lognormal inverse function in terms of the lognormal cdf.

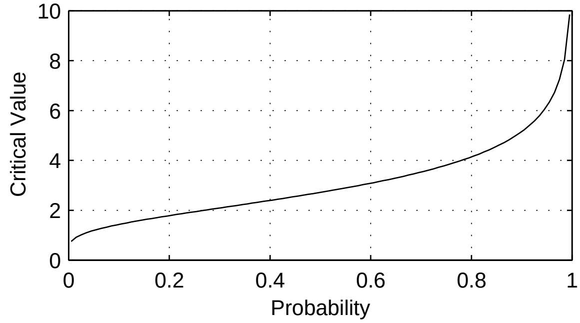
$$x = F^{-1}(p|\mu, \sigma) = \{x : F(x|\mu, \sigma) = p\}$$

where

$$p = F(x|\mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} \int_0^x \frac{e^{\frac{-(\ln(t) - \mu)^2}{2\sigma^2}}}{t} dt$$

Example

```
p = (0.005:0.01:0.995);
crit = logninv(p,1,0.5);
plot(p,crit)
xlabel('Probability');ylabel('Critical Value');grid
```



Reference

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition*, John Wiley and Sons, 1993. p. 102–105.

See Also

`icdf`, `logncdf`, `lognpdf`, `lognrnd`, `lognstat`

Purpose Lognormal probability density function (pdf).

Syntax

```
Y = lognpdf(X,MU,SIGMA)
```

Description `Y = logncdf(X,MU,SIGMA)` computes the lognormal cdf with mean `MU` and standard deviation `SIGMA` at the values in `X`.

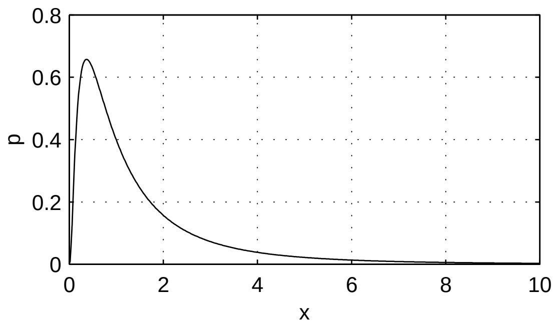
The size of `Y` is the common size of `X`, `MU` and `SIGMA`. A scalar input functions as a constant matrix of the same size as the other inputs.

The lognormal pdf is:

$$y = f(x|\mu, \sigma) = \frac{1}{x\sigma\sqrt{2\pi}} e^{\frac{-(\ln(x) - \mu)^2}{2\sigma^2}}$$

Example

```
x = (0:0.02:10);
y = lognpdf(x,0,1);
plot(x,y);grid;xlabel('x');ylabel('p')
```



Reference Mood, A. M., F.A. Graybill, and D.C. Boes, *Introduction to the Theory of Statistics, Third Edition*, McGraw Hill 1974 p. 540–541.

See Also `logncdf`, `logninv`, `lognrnd`, `lognstat`

lognrnd

Purpose Random matrices from the lognormal distribution.

Syntax

```
R = lognrnd(MU,SIGMA)
R = lognrnd(MU,SIGMA,m)
R = lognrnd(MU,SIGMA,m,n)
```

Description `R = lognrnd(MU,SIGMA)` generates lognormal random numbers with parameters, `MU` and `SIGMA`. The size of `R` is the common size of `MU` and `SIGMA` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other parameter.

`R = lognrnd(MU,SIGMA,m)` generates lognormal random numbers with parameters `MU` and `SIGMA`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = lognrnd(MU,SIGMA,m,n)` generates lognormal random numbers with parameters `MU` and `SIGMA`. The scalars `m` and `n` are the row and column dimensions of `R`.

Example

```
r = lognrnd(0,1,4,3)

r =

    3.2058    0.4983    1.3022
    1.8717    5.4529    2.3909
    1.0780    1.0608    0.2355
    1.4213    6.0320    0.4960
```

Reference Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition,* John Wiley and Sons, 1993. p. 102–105.

See Also `random`, `logncdf`, `logninv`, `lognpdf`, `lognstat`

Purpose

Mean and variance for the lognormal distribution.

Syntax

```
[M,V] = lognstat(MU,SIGMA)
```

Description

`[M,V] = lognstat(MU,SIGMA)` returns the mean and variance of the lognormal distribution with parameters `MU` and `SIGMA`. The size of `M` and `V` is the common size of `MU` and `SIGMA` if both are matrices. If either parameter is a scalar, the size of `M` and `V` is the size of the other parameter.

For the lognormal distribution, the mean is:

$$e^{\left(\mu + \frac{\sigma^2}{2}\right)}$$

The variance is:

$$e^{(2\mu + 2\sigma^2)} - e^{(2\mu + \sigma^2)}$$

Example

```
[m,v]= lognstat(0,1)

m =

    1.6487

v =

    7.0212
```

Reference

Mood, A. M., F.A. Graybill, and D.C. Boes, *Introduction to the Theory of Statistics, Third Edition*, McGraw Hill 1974 p. 540–541.

See Also

`logncdf`, `logninv`, `lognrnd`, `lognrnd`

lsline

Purpose

Least squares fit line(s).

Syntax

```
lsline
h = lsline
```

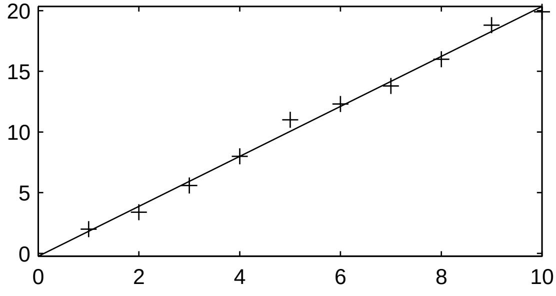
Description

`lsline` superimposes the least squares line on each line object in the current axes (except `LineStyles` `'-','--','.-'`).

`h = lsline` returns the handles to the line objects.

Example

```
y = [2 3.4 5.6 8 11 12.3 13.8 16 18.8 19.9]';
plot(y,'+');
lsline;
```



See Also

`polyfit`, `polyval`

Purpose

Mean absolute deviation (MAD) of a sample of data.

Syntax

```
y = mad(X)
```

Description

`mad(X)` computes the average of the absolute differences between a set of data and the sample mean of that data. For vectors, `mad(x)` returns the mean absolute deviation of the elements of x. For matrices, `mad(X)` returns the MAD of each column of `X`.

The MAD is less efficient than the standard deviation as an estimate of the spread, when the data is all from the normal distribution.

Multiply the MAD by 1.3 to estimate σ (the second parameter of the normal distribution).

Examples

This example shows a Monte Carlo simulation of the relative efficiency of the MAD to the sample standard deviation for normal data.

```
x = normrnd(0,1,100,100);
s = std(x);
s_MAD = 1.3 * mad(x);
efficiency = (norm(s - 1)./norm(s_MAD - 1)).^2

efficiency =

    0.5972
```

See Also

`std`, `range`

Purpose

Mahalanobis distance.

Syntax

```
d = mahal(Y,X)
```

Description

`mahal(Y,X)` computes the Mahalanobis distance of each point (row) of the matrix, `Y`, from the sample in the matrix, `X`.

The number of columns of `Y` must equal the number of columns in `X`, but the number of rows may differ. The number of rows in `X` must exceed the number of columns.

The Mahalanobis distance is a multivariate measure of the separation of a data set from a point in space. It is the criterion minimized in linear discriminant analysis.

Example

The Mahalanobis distance of a matrix, `r`, when applied to itself is a way to find outliers.

```
r = mvnrnd([0 0],[1 0.9;0.9 1],100);
r = [r;10 10];
d = mahal(r,r);
last6 = d(96:101)

last6 =

    1.1036
    2.2353
    2.0219
    0.3876
    1.5571
   52.7381
```

The last element is clearly an outlier.

See Also

`classify`

Purpose Average or mean value of vectors and matrices.

Syntax

```
m = mean(X)
```

Description `mean` calculates the sample average.

$$\bar{x}_j = \frac{1}{n}\sum_{i=1}^{n} x_{ij}$$

For vectors, `mean(x)` is the mean value of the elements in vector `x`. For matrices, `mean(X)` is a row vector containing the mean value of each column.

Example These commands generate five samples of 100 normal random numbers with mean, zero, and standard deviation, one. The sample averages in `xbar` are much less variable (0.00 ± 0.10).

```
x = normrnd(0,1,100,5);
xbar = mean(x)

xbar =

    0.0727    0.0264    0.0351    0.0424    0.0752
```

See Also `median`, `std`, `cov`, `corrcoef`, `var`

`mean` is a function in the MATLAB Toolbox.

median

Purpose Median value of vectors and matrices.

Syntax

```
m = median(X)
```

Description

`median(X)` calculates the median value, which is the 50th percentile of a sample. The median is a robust estimate of the center of a sample of data, since outliers have little effect on it.

For vectors, `median(x)` is the median value of the elements in vector `x`. For matrices, `median(X)` is a row vector containing the median value of each column. Since `median` is implemented using `sort`, it can be costly for large matrices.

Examples

```
xodd = 1:5;
modd = median(xodd)

modd =

     3

meven = median(xeven)

meven =

    2.5000
```

This example shows robustness of the median to outliers.

```
xoutlier = [x 10000];
moutlier = median(xoutlier)

moutlier =

     3
```

See Also

`mean`, `std`, `cov`, `corrcoef`

`median` is a function in MATLAB.

Purpose Maximum likelihood estimation.

Syntax

```
phat = mle('dist',data)
[phat,pci] = mle('dist',data)
[phat,pci] = mle('dist',data,alpha)
[phat,pci] = mle('dist',data,alpha,p1)
```

Description `phat = mle('dist',data)` returns the maximum likelihood estimates (MLEs) for the distribution specified in `'dist'` using the sample in the vector, `data`.

`[phat,pci] = mle('dist',data)` returns the MLEs and 95% percent confidence intervals.

`[phat,pci] = mle('dist',data,alpha)` returns the MLEs and 100(1–alpha) percent confidence intervals given the data and the specified `alpha`.

`[phat,pci] = mle('dist',data,alpha,p1)` is used for the binomial distribution only. `p1` is the number of trials.

Example

```
rv = binornd(20,0.75)
rv =

    16

[p,pci] = mle('binomial',rv,0.05,20)

p =

    0.8000

pci =

    0.5634
    0.9427
```

See Also `betafit`, `binofit`, `expfit`, `gamfit`, `normfit`, `poissfit`, `weibfit`

moment

Purpose Central moment of all orders.

Syntax

```
m = moment(X,order)
```

Description `m = moment(X,order)` returns the central moment of `X` specified by the positive integer, `order`. For vectors, `moment(X,order)` returns the central moment of the specified order for the elements of x. For matrices, `moment(X,order)` returns central moment of the specified order for each column.

Note that the central first moment is zero, and the second central moment is the variance computed using a divisor of n rather than n–1, where n is the length of the vector, `x` or the number of rows in the matrix, `X`.

The central moment of order k of a distribution is defined as:

$$m_n = E(x-\mu)^k$$

where $E(x)$ is the expected value of x.

Example

```
X = randn([6 5])

X =

    1.1650    0.0591    1.2460   –1.2704   –0.0562
    0.6268    1.7971   –0.6390    0.9846    0.5135
    0.0751    0.2641    0.5774   –0.0449    0.3967
    0.3516    0.8717   –0.3600   –0.7989    0.7562
   –0.6965   –1.4462   –0.1356   –0.7652    0.4005
    1.6961   –0.7012   –1.3493    0.8617   –1.3414

m = moment(X,3)

m =

   –0.0282    0.0571    0.1253    0.1460   –0.4486
```

See Also `kurtosis`, `mean`, `skewness`, `std`, `var`

Purpose Random matrices from the multivariate normal distribution.

Syntax

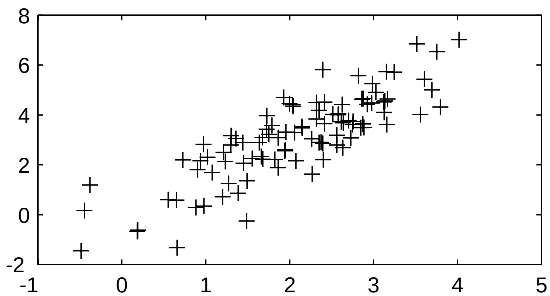
```
r = mvnrnd(mu,SIGMA,cases)
```

Description `r = mvnrnd(mu,SIGMA,cases)` returns a matrix of random numbers chosen from the multivariate normal distribution with mean vector, `mu`, and covariance matrix, `SIGMA`. `cases` is the number of rows in `r`.

`SIGMA` is a symmetric positive definite matrix with size equal to the length of `mu`.

Example

```
mu = [2 3];
sigma = [1 1.5; 1.5 3];
r = mvnrnd(mu,sigma,100);
plot(r(:,1),r(:,2),'+')
```



See Also `normrnd`

nanmax

Purpose Maximum ignoring NaNs.

Syntax

```
m = nanmax(a)
[m,ndx] = nanmax(a)
m = nanmax(a,b)
```

Description `m = nanmax(a)` returns the maximum with NaNs treated as missing. For vectors, `nanmax(a)` is the largest non-NaN element in `a`. For matrices, `nanmax(A)` is a row vector containing the maximum non-NaN element from each column.

`[m,ndx] = nanmax(a)` also returns the indices of the maximum values in vector `ndx`.

`m = nanmax(a,b)` returns the larger of `a` or `b`, which must match in size.

Example

```
m = magic(3);
m([1 6 8]) = [NaN NaN NaN]

m =

   NaN     1     6
     3     5   NaN
     4   NaN     2

[nmax,maxidx] = nanmax(m)

nmax =

     4     5     6

maxidx =

     3     2     1
```

See Also `nanmin`, `nanmean`, `nanmedian`, `nanstd`, `nansum`

Purpose Mean ignoring NaNs

Syntax `y = nanmean(X)`

Description `nanmean(X)` the average treating NaNs as missing values.

For vectors, `nanmean(x)` is the mean of the non-NaN elements of `x`. For matrices, `nanmean(X)` is a row vector containing the mean of the non-NaN elements in each column.

Example

```
m = magic(3);
m([1 6 8]) = [NaN NaN NaN]

m =

   NaN     1     6
     3     5   NaN
     4   NaN     2

nmean = nanmean(m)

nmean =

    3.5000    3.0000    4.0000
```

See Also `nanmin`, `nanmax`, `nanmedian`, `nanstd`, `nansum`

nanmedian

Purpose Median ignoring NaNs

Syntax `y = nanmedian(X)`

Description `nanmedian(X)` the median treating `NaN`s as missing values.

For vectors, `nanmedian(x)` is the median of the non-`NaN` elements of `x`. For matrices, `nanmedian(X)` is a row vector containing the median of the non-`NaN` elements in each column of `X`.

Example

```
m = magic(4);
m([1 6 9 11]) = [NaN NaN NaN NaN]

m =

   NaN     2   NaN    13
     5   NaN    10     8
     9     7   NaN    12
     4    14    15     1

nmedian = nanmedian(m)

nmedian =

    5.0000    7.0000   12.5000   10.0000
```

See Also `nanmin`, `nanmax`, `nanmean`, `nanstd`, `nansum`

Purpose

Minimum ignoring NaNs

Syntax

```
m = nanmin(a)
[m,ndx] = nanmin(a)
m = nanmin(a,b)
```

Description

`m = nanmin(a)` returns the minimum with NaNs treated as missing. For vectors, `nanmin(a)` is the smallest non-NaN element in a. For matrices, `nanmin(A)` is a row vector containing the minimum non-NaN element from each column.

`[m,ndx] = nanmin(a)` also returns the indices of the minimum values in vector ndx.

`m = nanmin(a,b)` returns the smaller of a or b, which must match in size.

Example

```
m = magic(3);
m([1 6 8]) = [NaN NaN NaN]

m =

   NaN     1     6
     3     5   NaN
     4   NaN     2

[nmin,minidx] = nanmin(m)

nmin =

     3     1     2

minidx =

     2     1     3
```

See Also

nanmax, nanmean, nanmedian, nanstd, nansum

nanstd

Purpose Standard deviation ignoring NaNs.

Syntax `y = nanstd(X)`

Description `nanstd(X)` the standard deviation treating NaNs as missing values.

For vectors, `nanstd(x)` is the standard deviation of the non-NaN elements of x. For matrices, `nanstd(X)` is a row vector containing the standard deviations of the non-NaN elements in each column of X.

Example

```
m = magic(3);
m([1 6 8]) = [NaN NaN NaN]

m =

   NaN     1     6
     3     5   NaN
     4   NaN     2


nstd = nanstd(m)

nstd =

    0.7071    2.8284    2.8284
```

See Also nanmax, nanmin, nanmean, nanmedian, nansum

Purpose Sum ignoring NaNs.

Syntax

```
y = nansum(X)
```

Description nansum(X) the sum treating NaNs as missing values.

For vectors, nansum(x) is the sum of the non-NaN elements of x. For matrices, nansum(X) is a row vector containing the sum of the non-NaN elements in each column of X.

Example

```
m = magic(3);
m([1 6 8]) = [NaN NaN NaN]

m =

   NaN     1     6
     3     5   NaN
     4   NaN     2


nsum = nansum(m)

nsum =

     7     6     8
```

See Also nanmax, nanmin, nanmean, nanmedian, nanstd

nbincdf

Purpose

Negative binomial cumulative distribution function.

Syntax

```
Y = nbincdf(X,R,P)
```

Description

`Y = nbincdf(X,R,P)` returns the negative binomial cumulative distributionfunction with parameters `R` and `P` at the values in `X`.

The size of `Y` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

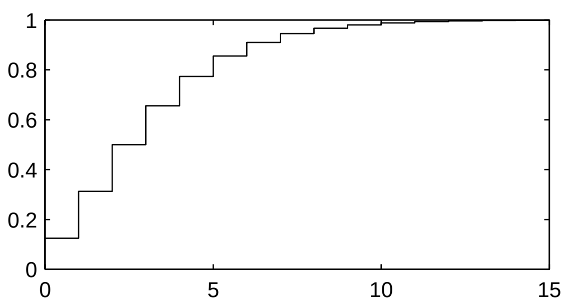
The negative binomial cdf is:

$$y = F(x|r,p) = \sum_{i=0}^{x} \binom{r+i-1}{i} p^r q^i I_{(0,1,\ldots)}(i)$$

The motivation for the negative binomial is performing successive trials each having a constant probability, `P`, of success. What you want to find out is how many *extra* trials you must do to observe a given number, `R`, of successes.

Example

```
x = (0:15);
p = nbincdf(x,3,0.5);
stairs(x,p)
```



See Also

`nbininv`, `nbinpdf`, `nbinrnd`, `nbinstat`

Purpose

Inverse of the negative binomial cumulative distribution function (cdf).

Syntax

```
X = nbininv(Y,R,P)
```

Description

`nbininv(Y,R,P)` returns the inverse of the negative binomial cdf with parameters `R` and `P`. Since the binomial distribution is discrete, `nbininv` returns the least integer `X` such that the negative binomial cdf evaluated at `X`, equals or exceeds `Y`.

The size of `X` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

The negative binomial models consecutive trials each having a constant probability, `P`, of success. The parameter, `R`, is the number of successes required before stopping.

Example

How many times would you need to flip a fair coin to have a 99% probability of having observed 10 heads?

```
flips = nbininv(0.99,10,0.5) + 10

flips =

    33
```

Note that you have to flip at least 10 times to get 10 heads. That is why the second term on the right side of the equals sign is a 10.

See Also

`nbincdf`, `nbinpdf`, `nbinrnd`, `nbinstat`

nbinpdf

Purpose Negative binomial probability density function.

Syntax

```
Y = nbinpdf(X,R,P)
```

Description `nbinpdf(X,R,P)` returns the negative binomial probability density function with parameters `R` and `P` at the values in `X`.

Note that the density function is zero unless `X` is an integer.

The size of `Y` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

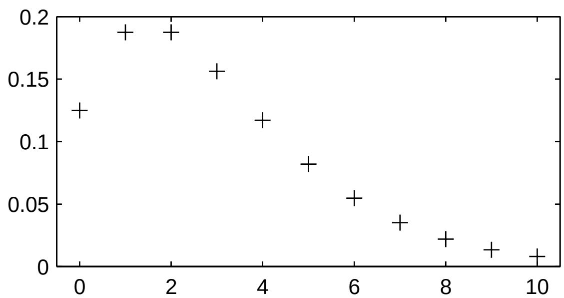
The negative binomial pdf is:

$$y = f(x|r, p) = \binom{r+x-1}{x} p^r q^x I_{(0,1,\ldots)}(x)$$

The negative binomial models consecutive trials each having a constant probability, `P`, of success. The parameter, `R`, is the number of successes required before stopping.

Example

```
x = (0:10);
y = nbinpdf(x,3,0.5);
plot(x,y,'+')
set(gca,'Xlim',[-0.5,10.5])
```



See Also `nbincdf`, `nbininv`, `nbinrnd`, `nbinstat`, `pdf`

Purpose Random matrices from a negative binomial distribution.

Syntax

```
RND = nbinrnd(R,P)
RND = nbinrnd(R,P,m)
RND = nbinrnd(R,P,m,n)
```

Description `RND = nbinrnd(R,P)` is a matrix of random numbers chosen from a negative binomial distribution with parameters `R` and `P`. The size of `RND` is the common size of `R` and `P` if both are matrices. If either parameter is a scalar, the size of `RND` is the size of the other parameter.

`RND = nbinrnd(R,P,m)` generates random numbers with parameters `R` and `P`. `m` is a 1-by-2 vector that contains the row and column dimensions of `RND`.

`RND = nbinrnd(R,P,m,n)` generates random numbers with parameters `R` and `P`. The scalars `m` and `n` are the row and column dimensions of `RND`.

The negative binomial models consecutive trials each having a constant probability, `P`, of success. The parameter, `R`, is the number of successes required before stopping.

Example Suppose you want to simulate a process that has a defect probability of 0.01. How many units might Quality Assurance inspect before finding three defective items?

```
r = nbinrnd(3,0.01,1,6) + 3

r =

   496   142   420   396   851   178
```

See Also `nbincdf`, `nbininv`, `nbinpdf`, `nbinstat`

nbinstat

Purpose Mean and variance of the negative binomial distribution.

Syntax `[M,V] = nbinstat(R,P)`

Description `[M,V] = nbinstat(R,P)` returns the mean and variance of the negative binomial distibution with parameters `R` and `P`.

For the negative binomial distribution:

- The mean is $\frac{rq}{p}$
- The variance is $\frac{rq}{p^2}$

where $q = 1 - p$.

Example

```
p = 0.1:0.2:0.9;
r = 1:5;
[R,P] = meshgrid(r,p);
[M,V] = nbinstat(R,P)

M =

    9.0000   18.0000   27.0000   36.0000   45.0000
    2.3333    4.6667    7.0000    9.3333   11.6667
    1.0000    2.0000    3.0000    4.0000    5.0000
    0.4286    0.8571    1.2857    1.7143    2.1429
    0.1111    0.2222    0.3333    0.4444    0.5556

V =

   90.0000  180.0000  270.0000  360.0000  450.0000
    7.7778   15.5556   23.3333   31.1111   38.8889
    2.0000    4.0000    6.0000    8.0000   10.0000
    0.6122    1.2245    1.8367    2.4490    3.0612
    0.1235    0.2469    0.3704    0.4938    0.6173
```

See Also `nbincdf`, `nbininv`, `nbinpdf`, `nbinrnd`

Purpose

Noncentral F cumulative distribution function (cdf).

Syntax

```
P = ncfcdf(X,NU1,NU2,DELTA)
```

Description

`P = ncfcdf(X,NU1,NU2,DELTA)` returns the noncentral F cdf with numerator degrees of freedom (df), `NU1`, denominator df, `NU2`, and positive noncentrality parameter, `DELTA`, at the values in `X`.

The size of `P` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

The noncentral F cdf is:

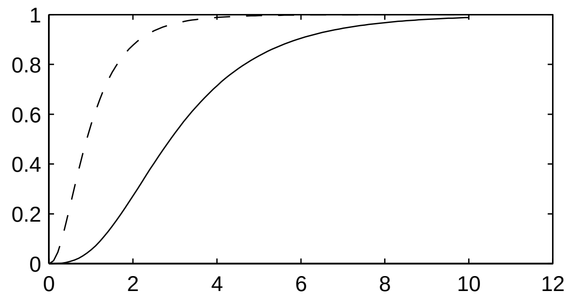
$$F(x|\nu_1,\nu_2,\delta) = \sum_{j=0}^{\infty}\left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!}e^{-\frac{\delta}{2}}\right)I\left(\frac{\nu_1 \cdot x}{\nu_2+\nu_1 \cdot x}\middle|\frac{\nu_1}{2}+j,\frac{\nu_2}{2}\right)$$

where $I(x\,|\,a,b)$ is the incomplete beta function with parameters a and b.

Example

Compare the noncentral F cdf with $\delta = 10$ to the F cdf with the same number of numerator and denominator degrees of freedom (5 and 20 respectively).

```
x = (0.01:0.1:10.01)';
p1 = ncfcdf(x,5,20,10);
p  = fcdf(x,5,20);
plot(x,p,'--',x,p1,'-')
```



References

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 189–200.

ncfinv

Purpose Inverse of the noncentral F cumulative distribution function (cdf).

Syntax

```
X = ncfinv(P,NU1,NU2,DELTA)
```

Description `X = ncfinv(P,NU1,NU2,DELTA)` returns the inverse of the noncentral F cdf with numerator degrees of freedom (df), `NU1`, denominator df, `NU2`, and positive noncentrality parameter, `DELTA`, for the probabilities, `P`.

The size of `X` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Example One hypothesis test for comparing two sample variances is to take their ratio and compare it to an F distribution. If the numerator and denominator degrees of freedom are 5 and 20 respectively then you reject the hypothesis that the first variance is equal to the second variance if their ratio is less than below:

```
critical = finv(0.95,5,20)

critical =

    2.7109
```

Suppose the truth is that the first variance is twice as big as the second variance. How likely is it that you would detect this difference?

```
prob = 1 - ncfcdf(critical,5,20,2)

prob =

    0.1297
```

References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition,* John Wiley and Sons, 1993. p. 102–105.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 189–200.

See Also `icdf`, `ncfcdf`, `ncfpdf`, `ncfrnd`, `ncfstat`

Purpose Noncentral F probability density function.

Syntax `Y = ncfpdf(X,NU1,NU2,DELTA)`

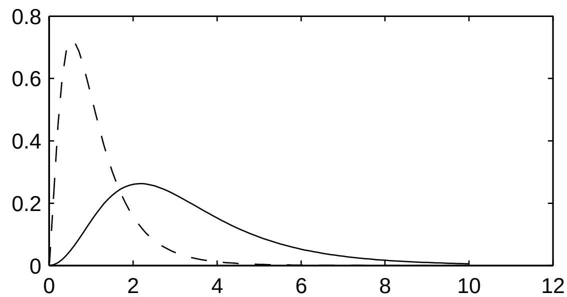
Description `Y = ncfpdf(X,NU1,NU2,DELTA)` returns the noncentral F pdf with with numerator degrees of freedom (df), `NU1`, denominator df, `NU2`, and positive noncentrality parameter, `DELTA`, at the values in `X`.

The size of `Y` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

The F distribution is a special case of the noncentral F where $\delta = 0$. As δ increases, the distribution flattens like the plot in the example.

Example Compare the noncentral F pdf with $\delta = 10$ to the F pdf with the same number of numerator and denominator degrees of freedom (5 and 20 respectively).

```
x = (0.01:0.1:10.01)';
p1 = ncfpdf(x,5,20,10);
p  = fpdf(x,5,20);
plot(x,p,'--',x,p1,'-')
```



References Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 189–200.

See Also `ncfcdf`, `ncfinv`, `ncfrnd`, `ncfstat`

ncfrnd

Purpose Random matrices from the noncentral F distribution.

Syntax

```
R = ncfrnd(NU1,NU2,DELTA)
R = ncfrnd(NU1,NU2,DELTA,m)
R = ncfrnd(NU1,NU2,DELTA,m,n)
```

Description `R = ncfrnd(NU1,NU2,DELTA)` returns a matrix of random numbers chosen from the noncentral F distribution with parameters `NU1`, `NU2` and `DELTA`. The size of `R` is the common size of `NU1`, `NU2` and `DELTA` if all are matrices. If any parameter is a scalar, the size of `R` is the size of the other parameters.

`R = ncfrnd(NU1,NU2,DELTA,m)` returns a matrix of random numbers with parameters `NU1`, `NU2` and `DELTA`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = ncfrnd(NU1,NU2,DELTA,m,n)` generates random numbers with parameters `NU1`, `NU2` and `DELTA`. The scalars `m` and `n` are the row and column dimensions of `R`.

Example Compute 6 random numbers from a noncentral F distribution with 10 numerator degrees of freedom, 100 denominator degrees of freedom and a noncentrality parameter, δ, of 4.0. Compare this to the F distribution with the same degrees of freedom.

```
r = ncfrnd(10,100,4,1,6)
r =

    2.5995    0.8824    0.8220    1.4485    1.4415    1.4864

r1 = frnd(10,100,1,6)
r1 =

    0.9826    0.5911    1.0967    0.9681    2.0096    0.6598
```

References

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2*, John Wiley and Sons, 1970. pp. 189–200.

See Also `ncfcdf`, `ncfinv`, `ncfpdf`, `ncfstat`

Purpose Mean and variance of the noncentral F distribution.

Syntax

```
[M,V] = ncfstat(NU1,NU2,DELTA)
```

Description `[M,V] = ncfstat(NU1,NU2,DELTA)` returns the mean and variance of the noncentral F pdf with `NU1` and `NU2` degrees of freedom and noncentrality parameter, `DELTA`.

- The mean is

$$\frac{\nu_2(\delta+\nu_1)}{\nu_1(\nu_2-2)}$$

where $\nu_2 > 2$.

- The variance is

$$2\left(\frac{\nu_2}{\nu_1}\right)^2\left[\frac{(\delta+\nu_1)^2+(2\delta+\nu_1)(\nu_2-2)}{(\nu_2-2)^2(\nu_2-4)}\right]$$

where $\nu_2 > 4$.

Example

```
[m,v]= ncfstat(10,100,4)

m =

    1.4286

v =

    3.9200
```

References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition*, John Wiley and Sons, 1993. p. 73–74.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2*, John Wiley and Sons, 1970. pp. 189–200.

See Also `ncfcdf`, `ncfinv`, `ncfpdf`, `ncfrnd`

Purpose Noncentral T cumulative distribution function.

Syntax

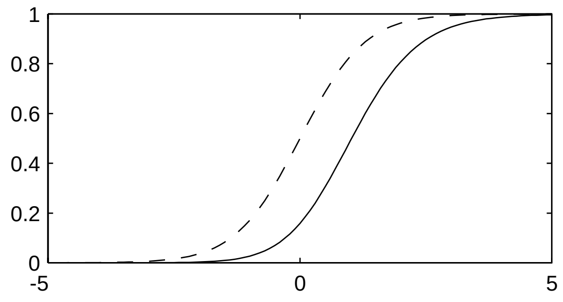
```
P = nctcdf(X,NU,DELTA)
```

Description `P = nctcdf(X,NU,DELTA)` returns the noncentral T cdf with `NU` degrees of freedom and noncentrality parameter, `DELTA`, at the values in `X`.

The size of `P` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Example Compare the noncentral T cdf with `DELTA` = 1 to the T cdf with the same number of degrees of freedom (10).

```
x = (–5:0.1:5)';
p1 = nctcdf(x,10,1);
p = tcdf(x,10);
plot(x,p,'––',x,p1,'–')
```



References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition*, John Wiley and Sons, 1993. p. 147–148.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2*, John Wiley and Sons, 1970. pp. 201–219.

See Also `cdf`, `nctcdf`, `nctinv`, `nctpdf`, `nctrnd`, `nctstat`

Purpose Inverse of the noncentral T cumulative distribution.

Syntax `X = nctinv(P,NU,DELTA)`

Description `X = nctinv(P,NU,DELTA)` returns the inverse of the noncentral T cdf with `NU` degrees of freedom and noncentrality parameter, `DELTA`, for the probabilities, `P`.

The size of `X` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Example

```
x = nctinv([.1 .2],10,1)

x =

   –0.2914    0.1618
```

References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition,* John Wiley and Sons, 1993. p. 147–148.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 201–219.

See Also `icdf`, `nctcdf`, `nctpdf`, `nctrnd`, `nctstat`

nctpdf

Purpose Noncentral T probability density function (pdf).

Syntax

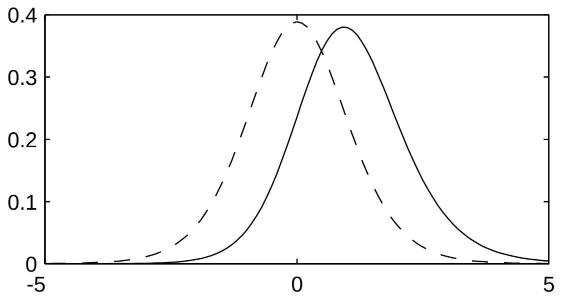
```
Y = nctpdf(X,V,DELTA)
```

Description `Y = nctpdf(X,V,DELTA)` returns the noncentral T pdf with `V` degrees of freedom and noncentrality parameter, `DELTA`, at the values in `X`.

The size of `Y` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Example Compare the noncentral T pdf with `DELTA` = 1 to the T pdf with the same number of degrees of freedom (10).

```
x = (–5:0.1:5)';
p1 = nctpdf(x,10,1);
p = tpdf(x,10);
plot(x,p,'––',x,p1,'–')
```



References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition*, John Wiley and Sons, 1993. p. 147–148.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2*, John Wiley and Sons, 1970. pp. 201–219.

See Also `nctcdf`, `nctinv`, `nctrnd`, `nctstat`, `pdf`

Purpose Random matrices from noncentral T distribution.

Syntax

```
R = nctrnd(V,DELTA)
R = nctrnd(V,DELTA,m)
R = nctrnd(V,DELTA,m,n)
```

Description `R = nctrnd(V,DELTA)` returns a matrix of random numbers chosen from the noncentral T distribution with parameters `V` and `DELTA`. The size of `R` is the common size of `V` and `DELTA` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other parameter.

`R = nctrnd(V,DELTA,m)` returns a matrix of random numbers with parameters `V` and `DELTA`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = nctrnd(V,DELTA,m,n)` generates random numbers with parameters `V` and `DELTA`. The scalars `m` and `n` are the row and column dimensions of `R`.

Example

```
nctrnd(10,1,5,1)

ans =

    1.6576
    1.0617
    1.4491
    0.2930
    3.6297
```

References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition,* John Wiley and Sons, 1993. p. 147–148.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 201–219.

See Also `nctcdf`, `nctinv`, `nctpdf`, `nctstat`

nctstat

Purpose Mean and variance for the noncentral t distribution.

Syntax

```
[M,V] = nctstat(NU,DELTA)
```

Description `[M,V] = nctstat(NU,DELTA)` returns the mean and variance of the noncentral t pdf with `NU` degrees of freedom and noncentrality parameter, `DELTA`.

- The mean is $\frac{\delta(\nu/2)^{1/2}\Gamma((\nu-1)/2)}{\Gamma(\nu/2)}$

where $\nu > 1$.

- The variance is $\frac{\nu}{(\nu-2)}(1+\delta^2)-\frac{\nu}{2}\delta^2\left[\frac{\Gamma((\nu-1)/2)}{\Gamma(\nu/2)}\right]^2$

where $\nu > 2$.

Example

```
[m,v] = nctstat(10,1)

m =

    1.0837

v =

    1.3255
```

References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition,* John Wiley and Sons, 1993. p. 147–148.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 201–219.

See Also `nctcdf`, `nctinv`, `nctpdf`, `nctrnd`

Purpose Noncentral chi-square cumulative distribution function (cdf).

Syntax

```
P = ncx2cdf(X,V,DELTA)
```

Description `ncx2cdf(X,V,DELTA)` returns the noncentral chi-square cdf with `V` degrees of freedom and positive noncentrality parameter, `DELTA`, at the values in `X`.

The size of `P` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

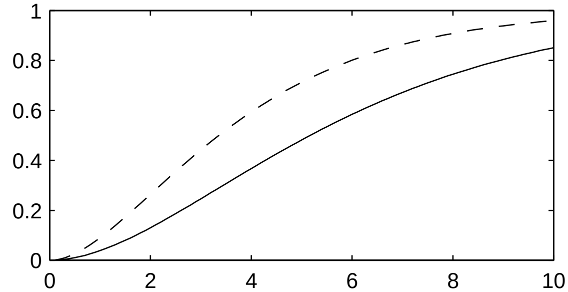
Some texts refer to this distribution as the generalized Rayleigh, Rayleigh-Rice, or Rice distribution.

The noncentral chi-square cdf is:

$$F(x|\nu,\delta) = \sum_{j=0}^{\infty}\left(\frac{\left(\frac{1}{2}\delta\right)^j}{j!}e^{-\frac{\delta}{2}}\right)Pr[\chi^2_{\nu+2j} \le x]$$

Example

```
x = (0:0.1:10)';
p1 = ncx2cdf(x,4,2);
p = chi2cdf(x,4);
plot(x,p,'--',x,p1,'-')
```



References

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 130–148.

See Also `cdf`, `ncx2inv`, `ncx2pdf`, `ncx2rnd`, `ncx2stat`

ncx2inv

Purpose Inverse of the noncentral chi-square cdf.

Syntax `X = ncx2inv(P,V,DELTA)`

Description `X = ncx2inv(P,V,DELTA)` returns the inverse of the noncentral chi-square cdf with parameters `V` and `DELTA`, at the probabilities in `P`.

The size of `X` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Algorithm `ncx2inv` uses Newton's method to converge to the solution.

Example

```
ncx2inv([0.01 0.05 0.1],4,2)

ans =

    0.4858    1.1498    1.7066
```

References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition*, John Wiley and Sons, 1993. p. 50–52.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2*, John Wiley and Sons, 1970. pp. 130–148.

See Also `ncx2cdf`, `ncx2pdf`, `ncx2rnd`, `ncx2stat`

Purpose

Noncentral chi-square probability density function (pdf).

Syntax

```
Y = ncx2pdf(X,V,DELTA)
```

Description

`Y = ncx2pdf(X,V,DELTA)` returns the noncentral chi-square pdf with `v` degrees of freedom and positive noncentrality parameter, `DELTA`, at the values in `X`.

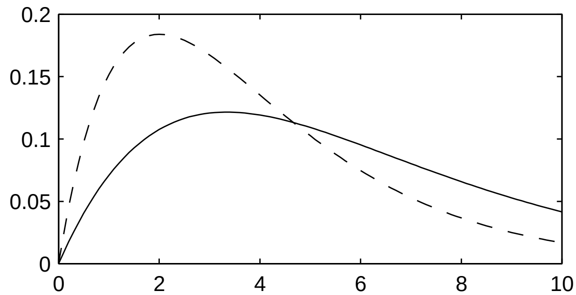
The size of `Y` is the common size of the input arguments. A scalar input functions as a constant matrix of the same size as the other inputs.

Some texts refer to this distribution as the generalized Rayleigh, Rayleigh-Rice, or Rice distribution.

Example

As the noncentrality parameter, δ, increases, the distribution flattens as in the plot.

```
x = (0:0.1:10)';
p1 = ncx2pdf(x,4,2);
p = chi2pdf(x,4);
plot(x,p,'--',x,p1,'-')
```



References

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 130–148.

See Also

`ncx2cdf`, `ncx2inv`, `ncx2rnd`, `ncx2stat`

Purpose Random matrices from the noncentral chi-square distribution.

Syntax

```
R = ncx2rnd(V,DELTA)
R = ncx2rnd(V,DELTA,m)
R = ncx2rnd(V,DELTA,m,n)
```

Description `R = ncx2rnd(V,DELTA)` returns a matrix of random numbers chosen from the non-central chisquare distribution with parameters `V` and `DELTA`. The size of `R` is the common size of `V` and `DELTA` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other parameter.

`R = ncx2rnd(V,DELTA,m)` returns a matrix of random numbers with parameters `V` and `DELTA`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = ncx2rnd(V,DELTA,m,n)` generates random numbers with parameters `V` and `DELTA`. The scalars `m` and `n` are the row and column dimensions of `R`.

Example

```
ncx2rnd(4,2,6,3)

ans =

    6.8552    5.9650   11.2961
    5.2631    4.2640    5.9495
    9.1939    6.7162    3.8315
   10.3100    4.4828    7.1653
    2.1142    1.9826    4.6400
    3.8852    5.3999    0.9282
```

References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition,* John Wiley and Sons, 1993. p. 50–52.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 130–148.

See Also `ncx2cdf`, `ncx2inv`, `ncx2pdf`, `ncx2stat`

Purpose Mean and variance for the noncentral chi-square distribution.

Syntax

```
[M,V] = ncx2stat(NU,DELTA)
```

Description `[M,V] = ncx2stat(NU,DELTA)` returns the mean and variance of the noncentral chi-square pdf with `NU` degrees of freedom and noncentrality parameter, `DELTA`.

For the noncentral chi-square distribution:

- The mean is $\nu + \delta$.
- The variance is $2(\nu + 2\delta)$.

Example

```
[m,v] = ncx2stat(4,2)

m =

     6

v =

    16
```

References

Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition*, John Wiley and Sons, 1993. p. 50–52.

Johnson, N., and S. Kotz, *Distributions in Statistics: Continuous Univariate Distributions-2,* John Wiley and Sons, 1970. pp. 130–148.

See Also `ncx2cdf`, `ncx2inv`, `ncx2pdf`, `ncx2rnd`

nlinfit

Purpose Nonlinear least-squares data fitting by the Gauss-Newton method.

Syntax

```
[beta,r,J] = nlinfit(X,y,'model',beta0)
```

Description

`beta = nlinfit(X,y,'model',beta0)` returns the coefficients of the nonlinear function described in `'model'`.

`'model'` is a user-supplied function having the form: $\hat{y} = f(\beta, X)$. It returns the predicted values of y given initial parameter estimates, β, and the independent variable, X.

The matrix, `X`, has one column per independent variable. The response, `y`, is a column vector with the same number of rows as `X`.

`[beta,r,J] = nlinfit(X,y,'model',beta0)` returns the fitted coefficients, `beta`, the residuals, `r`, and the Jacobian, `J`, for use with `nlintool` to produce error estimates on predictions.

Example

```
load reaction
betafit = nlinfit(reactants,rate,'hougen',beta)

betafit =
    1.2526
    0.0628
    0.0400
    0.1124
    1.1914
```

See Also `nlintool`

Purpose Fits a nonlinear equation to data and displays an interactive graph.

Syntax

```
nlintool(x,y,'model',beta0)
nlintool(x,y,'model',beta0,alpha)
nlintool(x,y,'model',beta0,alpha,'xname','yname')
```

Description `nlintool(x,y,'model',beta0)` is a prediction plot that provides a nonlinear curve fit to *(x,y)* data. It plots a 95% global confidence interval for predictions as two red curves. `beta0` is a vector containing initial guesses for the parameters.

`nlintool(x,y,'model',beta0,alpha)` plots a 100(1 – `alpha`) percent confidence interval for predictions.

`nlintool` displays a "vector" of plots, one for each column of the matrix of inputs, `x`. The response variable, `y`, is a column vector that matches the number of rows in `x`.

The default value for `alpha` is 0.05, which produces 95% confidence intervals.

`nlintool(x,y,'model',beta0,alpha,'xname','yname')` labels the plot using the string matrix, `'xname'` for the *X* variables and the string `'yname'` for the *Y* variable.

You can drag the dotted white reference line and watch the predicted values update simultaneously. Alternatively, you can get a specific prediction by typing the value for *X* into an editable text field. Use the pop-up menu labeled **Export** to move specified variables to the base workspace.

Example See the section "Nonlinear Regression Models" in Chapter 1.

See Also `nlinfit`, `rstool`

Purpose Confidence intervals on estimates of parameters in nonlinear models.

Syntax

```
ci = nlparci(beta,r,J)
```

Description `nlparci(beta,r,J)` returns the 95% confidence interval `ci` on the nonlinear least squares parameter estimates `beta`, given the residuals, `r`, and the Jacobian matrix ,`J`, at the solution. The confidence interval calculation is valid for systems where the number of rows of `J` exceeds the length of `beta`.

`nlparci` uses the outputs of `nlinfit` for its inputs.

Example Continuing the example from `nlinfit`:

```
load reaction
[beta,resids,J] = nlinfit(reactants,rate,'hougen',beta);
ci = nlparci(beta,resids,J)

ci =

   –1.0798    3.3445
   –0.0524    0.1689
   –0.0437    0.1145
   –0.0891    0.2941
   –1.1719    3.7321
```

See Also `nlinfit`, `nlintool`, `nlpredci`

Purpose

Confidence intervals on predictions of nonlinear models.

Syntax

```
ypred = nlpredci('model',inputs,beta,r,J)
[ypred,delta] = nlpredci('model',inputs,beta,r,J)
```

Description

`ypred = nlpredci('model',inputs,beta,r,J)` returns the predicted responses,`ypred`, given the fitted parameters, `beta`, residuals, `r`, and the Jacobian matrix, `J`. `inputs` is a matrix of values of the independent variables in the nonlinear function.

`[ypred,delta] = nlpredci('model',inputs,beta,r,J)` also returns 95% confidence intervals, `delta`, on the nonlinear least squares predictions, `pred`. The confidence interval calculation is valid for systems where the length of `r` exceeds the length of `beta` and `J` is of full column rank.

`nlpredci` uses the outputs of `nlinfit` for its inputs.

Example

Continuing the example from `nlinfit`:

```
load reaction
[beta,resids,J]=nlinfit(reactants,rate,'hougen',beta);
ci = nlpredci('hougen',reactants,beta,resids,J)

ci =

    8.2937
    3.8584
    4.7950
   –0.0725
    2.5687
   14.2227
    2.4393
    3.9360
   12.9440
    8.2670
   –0.1437
   11.3484
    3.3145
```

See Also

`nlinfit`, `nlintool`, `nlparci`

normcdf

Purpose

Normal cumulative distribution function (cdf).

Syntax

```
P = normcdf(X,MU,SIGMA)
```

Description

`normcdf(X,MU,SIGMA)` computes the normal cdf with parameters `MU` and `SIGMA` at the values in `X`. The arguments `X`, `MU` and `SIGMA` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameter `SIGMA` must be positive.

The normal cdf is:

$$p = F(x|\mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}}\int_{-\infty}^{x} e^{\frac{-(t-\mu)^2}{2\sigma^2}}\, dt$$

The result, p, is the probability that a single observation from a normal distribution with parameters μ and σ will fall in the interval ($-\infty$ x].

The *standard normal* distribution has $\mu = 0$ and $\sigma = 1$.

Examples

What is the probability that an observation from a standard normal distribution will fall on the interval [–1 1]?

```
p = normcdf([–1 1]);
p(2) – p(1)

ans =

    0.6827
```

More generally, about 68% of the observations from a normal distribution fall within one standard deviation,σ, of the mean, μ.

Purpose Parameter estimates and confidence intervals for normal data.

Syntax

```
[muhat,sigmahat,muci,sigmaci] = normfit(X)
[muhat,sigmahat,muci,sigmaci] = normfit(X,alpha)
```

Description `[muhat,sigmahat,muci,sigmaci] = normfit(X)` returns estimates, `muhat` and `sigmahat`, of the parameters, μ and σ, of the normal distribution given the matrix of data, `X`. `muci` and `sigmaci` are 95% confidence intervals. `muci` and `sigmaci` have two rows and as many columns as the data matrix, `X`. The top row is the lower bound of the confidence interval and the bottom row is the upper bound.

`[muhat,sigmahat,muci,sigmaci] = normfit(X,alpha)` gives estimates and 100(1–alpha) percent confidence intervals. For example, `alpha` = 0.01 gives 99% confidence intervals.

Example In this example the data is a two-column random normal matrix. Both columns have $\mu = 10$ and $\sigma = 2$. Note that the confidence intervals below contain the "true values."

```
r = normrnd(10,2,100,2);
[mu,sigma,muci,sigmaci] = normfit(r)

mu =
   10.1455   10.0527

sigma =
    1.9072    2.1256

muci =
    9.7652    9.6288
   10.5258   10.4766

sigmaci =
    1.6745    1.8663
    2.2155    2.4693
```

See Also `betafit`, `binofit`, `expfit`, `gamfit`, `poissfit`, `unifit`, `weibfit`

norminv

Purpose

Inverse of the normal cumulative distribution function (cdf).

Syntax

```
X = norminv(P,MU,SIGMA)
```

Description

`norminv(P,MU,SIGMA)` computes the inverse of the normal cdf with parameters `MU` and `SIGMA` at the values in `P`. The arguments `P`, `MU`, and `SIGMA` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameter `SIGMA` must be positive and `P` must lie on [0 1].

We define the normal inverse function in terms of the normal cdf.

$$x = F^{-1}(p|\mu,\sigma) = \{x{:}F(x|\mu,\sigma) = p\}$$

$$where \quad p = F(x|\mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}}\int_{-\infty}^{x} e^{\frac{-(t-\mu)^2}{2\sigma^2}}\,dt$$

The result, x, is the solution of the integral equation above with the parameters μ and σ where you supply the desired probability, p.

Examples

Find an interval that contains 95% of the values from a standard normal distribution.

```
x = norminv([0.025 0.975],0,1)

x =

   –1.9600    1.9600
```

Note the interval `x` is not the only such interval, but it is the shortest.

```
xl = norminv([0.01 0.96],0,1)

xl =

   –2.3263    1.7507
```

The interval `xl` also contains 95% of the probability, but it is longer than `x`.

Purpose Normal probability density function (pdf).

Syntax

```
Y = normpdf(X,MU,SIGMA)
```

Description `normpdf(X,MU,SIGMA)` computes the normal pdf with parameters `mu` and `SIGMA` at the values in `X`. The arguments `X`, `MU` and `SIGMA` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameter `SIGMA` must be positive.

The normal pdf is:

$$y = f(x|\mu, \sigma) = \frac{1}{\sigma\sqrt{2\pi}} e^{\frac{-(x-\mu)^2}{2\sigma^2}}$$

The *likelihood function* is the pdf viewed as a function of the parameters. Maximum likelihood estimators (MLEs) are the values of the parameters that maximize the likelihood function for a fixed value of `x`.

The *standard normal* distribution has $\mu = 0$ and $\sigma = 1$.

If x is standard normal, then $x\sigma + \mu$ is also normal with mean μ and standard deviation σ. Conversely, if y is normal with mean μ and standard deviation σ, then $x = (y - \mu)/\sigma$ is standard normal.

Examples

```
mu = [0:0.1:2];
[y i] = max(normpdf(1.5,mu,1));
MLE = mu(i)

MLE =

    1.5000
```

normplot

Purpose Normal probability plot for graphical normality testing.

Syntax

```
normplot(X)
h = normplot(X)
```

Description `normplot(X)` displays a normal probability plot of the data in `X`. For matrix `X`, `normplot` displays a line for each column of `X`.

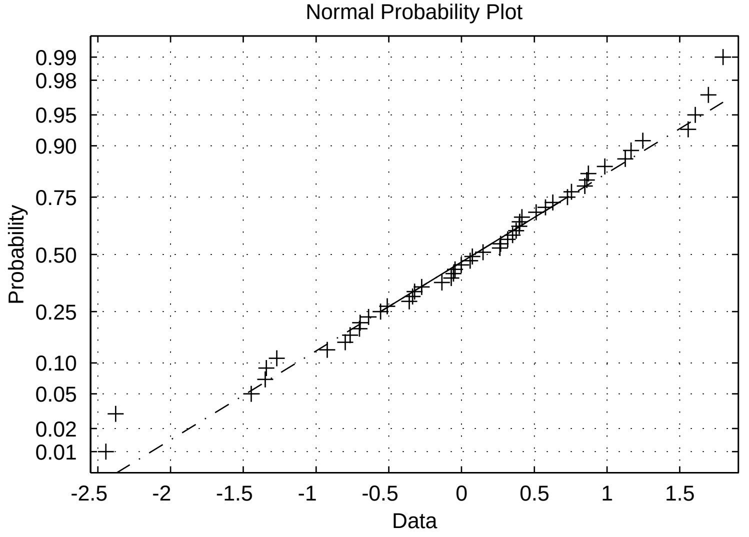
The plot has the sample data displayed with the plot symbol '+'. Superimposed on the plot is a line joining the first and third quartiles of each column of `x`. (A robust linear fit of the sample order statistics.) This line is extrapolated out to the ends of the sample to help evaluate the linearity of the data.

If the data does come from a normal distribution, the plot will appear linear. Other probability density functions will introduce curvature in the plot.

`h = normplot(X)` returns a handle to the plotted lines.

Examples Generate a normal sample and a normal probability plot of the data.

```
x = normrnd(0,1,50,1);
h = normplot(x);
```



The plot is linear, indicating that you can model the sample by a normal distribution.

Purpose

Random numbers from the normal distribution.

Syntax

```
R = normrnd(MU,SIGMA)
R = normrnd(MU,SIGMA,m)
R = normrnd(MU,SIGMA,m,n)
```

Description

`R = normrnd(MU,SIGMA)` generates normal random numbers with mean, `MU`, and standard deviation, `SIGMA` . The size of `R` is the common size of `MU` and `SIGMA` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other parameter.

`R = normrnd(MU,SIGMA,m)` generates normal random numbers with parameters `MU` and `SIGMA`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = normrnd(MU,SIGMA,m,n)` generates normal random numbers with parameters `MU` and `SIGMA`. The scalars `m` and `n` are the row and column dimensions of `R`.

Examples

```
n1 = normrnd(1:6,1./(1:6))

n1 =

    2.1650    2.3134    3.0250    4.0879    4.8607    6.2827

n2 = normrnd(0,1,[1 5])

n2 =

    0.0591    1.7971    0.2641    0.8717   -1.4462

n3 = normrnd([1 2 3;4 5 6],0.1,2,3)

n3 =

    0.9299    1.9361    2.9640
    4.1246    5.0577    5.9864
```

normspec

Purpose

Plot normal density between specification limits.

Syntax

```
p = normspec(specs,mu,sigma)
[p,h] = normspec(specs,mu,sigma)
```

Description

`p = normspec(specs,mu,sigma)` plots the normal density between a lower and upper limit defined by the two elements of the vector, `specs`. `mu` and `sigma` are the parameters of the plotted normal distribution.

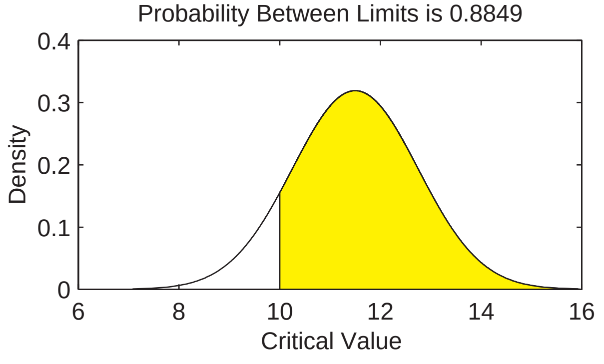
`[p,h] = normspec(specs,mu,sigma)` returns the probability, `p`, of a sample falling between the lower and upper limits. `h` is a handle to the line objects.

If `specs(1)` is `–Inf`, there is no lower limit, and similarly if `specs(2) = Inf`, there is no upper limit.

Example

Suppose a cereal manufacturer produces 10 ounce boxes of corn flakes. Variability in the process of filling each box with flakes causes a 1.25 ounce standard deviation in the true weight of the cereal in each box. The average box of cereal has 11.5 ounces of flakes. What percentage of boxes will have less than 10 ounces?

```
normspec([10 Inf],11.5,1.25)
```



See Also

`capaplot`, `disttool`, `histfit`, `normpdf`

Purpose Mean and variance for the normal distribution.

Syntax

```
[M,V] = normstat(MU,SIGMA)
```

Description For the normal distribution:

- The mean is μ.
- The variance is σ^2.

Examples

```
n = 1:5;
[m,v] = normstat(n'∗n,n'*n)
[m,v] = normstat(n'*n,n'*n)

m =

     1     2     3     4     5
     2     4     6     8    10
     3     6     9    12    15
     4     8    12    16    20
     5    10    15    20    25

v =

     1     4     9    16    25
     4    16    36    64   100
     9    36    81   144   225
    16    64   144   256   400
    25   100   225   400   625
```

pareto

Purpose

Pareto charts for Statistical Process Control.

Syntax

```
pareto(y)
pareto(y,'names')
h = pareto(...)
```

Description

`pareto(y,names)` displays a Pareto chart where the values in the vector `y` are drawn as bars in descending order. Each bar is labeled with the associated value in the string matrix `names`. `pareto(y)` labels each bar with the index of the corresponding element in `y`.

The line above the bars shows the cumulative percentage.

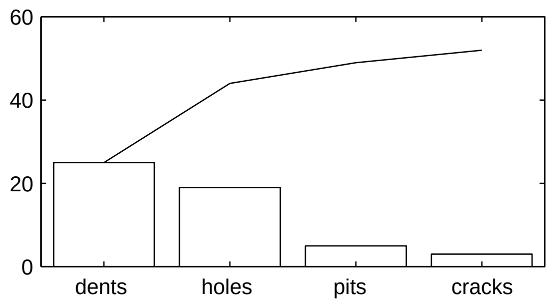
`pareto(y,'names')` labels each bar with the row of the string matrix, `'names'`, that corresponds to the plotted element of `y`.

`h = pareto(...)` returns a combination of patch and line handles.

Example

Create a Pareto chart from data measuring the number of manufactured parts rejected for various types of defects.

```
defects = ['pits  ';'cracks';'holes ';'dents '];
quantity = [5 3 19 25];
pareto(quantity,defects)
```



See Also

`bar`, `capaplot`, `ewmaplot`, `hist`, `histfit`, `schart`, `xbarplot`

Purpose Principal Components Analysis (PCA) using the covariance matrix.

Syntax

```
pc = pcacov(X)
[pc,latent,explained] = pcacov(X)
```

Description `[pc,latent,explained] = pcacov(X)` takes the covariance matrix `X` and returns the principal components in `pc`, the eigenvalues of the covariance matrix of `X` in `latent`, and the percentage of the total variance in the observations explained by each eigenvector in `explained`.

Example

```
load hald
covx = cov(ingredients);
[pc,variances,explained] = pcacov(covx)

pc =

    0.0678   –0.6460    0.5673   –0.5062
    0.6785   –0.0200   –0.5440   –0.4933
   –0.0290    0.7553    0.4036   –0.5156
   –0.7309   –0.1085   –0.4684   –0.4844

variances =

  517.7969
   67.4964
   12.4054
    0.2372

explained =

   86.5974
   11.2882
    2.0747
    0.0397
```

References

Jackson, J. E., *A User's Guide to Principal Components*, John Wiley and Sons, Inc. 1991. pp. 1–25.

See Also `barttest`, `pcares`, `princomp`

Purpose

Residuals from a Principal Components Analysis.

Syntax

```
residuals = pcares(X,ndim)
```

Description

`pcares(X,ndim)` returns the `residuals` obtained by retaining `ndim` principal components of `X`. Note that `ndim` is a scalar and must be less than the number of columns in `X`. Use the data matrix, *not* the covariance matrix, with this function.

Example

This example shows the drop in the residuals from the first row of the Hald data as the number of component dimensions increase from one to three.

```
load hald
r1 = pcares(ingredients,1);
r2 = pcares(ingredients,2);
r3 = pcares(ingredients,3);
r11 = r1(1,:)

r11 =

    2.0350    2.8304   –6.8378    3.0879

r21 = r2(1,:)

r21 =

   –2.4037    2.6930   –1.6482    2.3425

r31 = r3(1,:)

r31 =

    0.2008    0.1957    0.2045    0.1921
```

Reference

Jackson, J. E., *A User's Guide to Principal Components*, John Wiley and Sons, Inc. 1991. pp. 1–25.

See Also

`barttest`, `pcacov`, `princomp`

Purpose Probability density function (pdf) for a specified distribution.

Syntax

```
Y = pdf('name',X,A1,A2,A3)
```

Description `pdf('`*`name`*`',X,A1,A2,A3)` returns a matrix of densities. `'`*`name`*`'` is a string containing the name of the distribution. `X` is a matrix of values, and `A1`, `A2`, and `A3` are matrices of distribution parameters. Depending on the distribution, some of the parameters may not be necessary.

The arguments `X`, `A1`, `A2`, and `A3` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

`pdf` is a utility routine allowing access to all the pdfs in the Statistics Toolbox using the name of the distribution as a parameter.

Examples

```
p = pdf('Normal',–2:2,0,1)

p =

    0.0540    0.2420    0.3989    0.2420    0.0540


p = pdf('Poisson',0:4,1:5)

p =

    0.3679    0.2707    0.2240    0.1954    0.1755
```

Purpose Pairwise distance between observations.

Syntax

```
Y = pdist(X)
Y = pdist(X,'metric')
Y = pdist(X,'minkowski',p)
```

Description `Y = pdist(X)` computes the Euclidean distance between pairs of objects in the data matrix `X`. `X` is an m by n matrix, treated as m vectors of size n. For a dataset made up of m objects, there are $(m-1) \cdot m/2$ pairs.

The output, `Y`, is a vector of length $(m-1) \cdot m/2$, containing the distance information. The distances are arranged in the order (1,2), (1,3),..., (1,m), (2,3),..., (2,m), ..., ...,(m-1, m). `Y` is also commonly known as a similarity matrix or dissimilarity matrix.

To save space and computation time, `Y` is formatted as a vector. However, you can convert this vector into a square matrix using the `squareform` function so that element *(i,j)* in the matrix corresponds to the distance between objects *i* and *j* in the original dataset.

`Y = pdist(X,'metric')` computes the distance between objects in the data matrix, `X`, using the method specified by `'metric'`. `'metric'` can be any of the following character strings that identify ways to compute the distance.

String	Meaning
`'Euclid'`	Euclidean distance (default)
`'SEuclid'`	Standardized Euclidean distance
`'Mahal'`	Mahalanobis distance
`'CityBlock'`	City Block metric
`'Minkowski'`	Minkowski metric

`Y = pdist(X,'minkowski', p)` computes the distance between objects in the data matrix, `X`, using the Minkowski metric. `p` is the exponent used in the Minkowski computation which, by default, is 2.

Mathematical Definitions of Methods . Given an m-by-n data matrix X, which is treated as m (1-by-n) row vectors $x_1, x_2, \ldots, x_m$, the various distances between the vector x_r and x_s are defined as follows:

- Euclidean distance:

  $$d_{rs}^2 = (x_r - x_s)(x_r - x_s)'$$

- Standardized Euclidean distance:

  $$d_{rs}^2 = (x_r - x_s)D^{-1}(x_r - x_s)'$$

  where D is the diagonal matrix with diagonal elements given by v_j^2 , which denotes the variance of the variable X_j over the m objects.

- Mahalanobis distance:

  $$d_{rs}^2 = (x_r - x_s)'V^{-1}(x_r - x_s)$$

  where V is the sample covariance matrix.

- City Block metric:

  $$d_{rs} = \sum_{j=1}^{n} \left| x_{rj} - x_{sj} \right|$$

- Minkowski metric:

  $$d_{rs} = \left\{ \sum_{j=1}^{n} \left| x_{rj} - x_{sj} \right|^p \right\}^{1/p}$$

  Notice that when $p = 1$, it is the City Block case, and when $p = 2$, it is the Euclidean case.

Examples

```
X = [1 2; 1 3; 2 2; 3 1]
X =
     1     2
     1     3
     2     2
     3     1

Y = pdist(X,'mahal')

Y =
    2.3452    2.0000    2.3452    1.2247    2.4495    1.2247

Y = pdist(X)

Y =
    1.0000    1.0000    2.2361    1.4142    2.8284    1.4142

squareform(Y)
ans =
         0    1.0000    1.0000    2.2361
    1.0000         0    1.4142    2.8284
    1.0000    1.4142         0    1.4142
    2.2361    2.8284    1.4142         0
```

See Also

cluster, clusterdata, cophenet, dendrogram, inconsistent, linkage, squareform

Purpose All permutations.

Syntax

```
P = perms(v)
```

Description `P = perms(v)`, where v is a row vector of length `n`, creates a matrix whose rows consist of all possible permutations of the `n` elements of `v`. The matrix, `P`, contains `n!` rows and `n` columns.

`perms` is only practical when `n` is less than 8 or 9.

Example

```
perms([2 4 6])

ans =

     6     4     2
     4     6     2
     6     2     4
     2     6     4
     4     2     6
     2     4     6
```

poisscdf

Purpose

Poisson cumulative distribution function (cdf).

Syntax

```
P = poisscdf(X,LAMBDA)
```

Description

`poisscdf(X,LAMBDA)` computes the Poisson cdf with parameter settings `LAMBDA` at the values in `X`. The arguments `X` and `LAMBDA` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument. The parameter, `LAMBDA`, is positive.

The Poisson cdf is:

$$p = F(x|\lambda) = e^{-\lambda} \sum_{i=0}^{floor(x)} \frac{\lambda^i}{i!}$$

Examples

For example, consider a Quality Assurance department that performs random tests of individual hard disks. Their policy is to shut down the manufacturing process if an inspector finds more than four bad sectors on a disk. What is the probability of shutting down the process if the mean number of bad sectors (λ) is two?

```
probability = 1 – poisscdf(4,2)

probability =

    0.0527
```

About 5% of the time, a normally functioning manufacturing process will produce more than four flaws on a hard disk.

Suppose the average number of flaws (λ) increases to four. What is the probability of finding fewer than five flaws on a hard drive?

```
probability = poisscdf(4,4)

probability =

    0.6288
```

This means that this faulty manufacturing process continues to operate after this first inspection almost 63% of the time.

Purpose Parameter estimates and confidence intervals for Poisson data.

Syntax

```
lambdahat = poissfit(X)
[lambdahat,lambdaci] = poissfit(X)
[lambdahat,lambdaci] = poissfit(X,alpha)
```

Description `poissfit(X)` returns the maximum likelihood estimate (MLE) of the parameter of the Poisson distribution, λ, given the data `X`.

`[lambdahat,lambdaci] = poissfit(X)` also gives 95% confidence intervals in `lamdaci`.

`[lambdahat,lambdaci] = poissfit(X,alpha)` gives 100(1–alpha) percent confidence intervals. For example `alpha` = 0.001 yields 99.9% confidence intervals.

The sample average is the MLE of λ.

$$\hat{\lambda} = \frac{1}{n}\sum_{i=1}^{n} x_i$$

Example

```
r = poissrnd(5,10,2);
[l,lci] = poissfit(r)

l =

    7.4000    6.3000

lci =

    5.8000    4.8000
    9.1000    7.9000
```

See Also `betafit`, `binofit`, `expfit`, `gamfit`, `poissfit`, `unifit`, `weibfit`

poissinv

Purpose Inverse of the Poisson cumulative distribution function (cdf).

Syntax

```
X = poissinv(P,LAMBDA)
```

Description `poissinv(P,LAMBDA)` returns the smallest value, `X`, such that the Poisson cdf evaluated at `X` equals or exceeds `P`.

Examples If the average number of defects (λ) is two, what is the 95th percentile of the number of defects?

```
poissinv(0.95,2)

ans =

     5
```

What is the median number of defects?

```
median_defects = poissinv(0.50,2)

median_defects =

     2
```

Purpose Poisson probability density function (pdf).

Syntax

```
Y = poisspdf(X,LAMBDA)
```

Description `poisspdf(X,LAMBDA)` computes the Poisson pdf with parameter settings `LAMBDA` at the values in `X`. The arguments `X` and `LAMBDA` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument.

The parameter, λ, must be positive.

The Poisson pdf is:

$$y = f(x|\lambda) = \frac{\lambda^x}{x!}e^{-\lambda}I_{(0, 1, \ldots)}(x)$$

x can be any non-negative integer. The density function is zero unless x is an integer.

Examples A computer hard disk manufacturer has observed that flaws occur randomly in the manufacturing process at the average rate of two flaws in a 4 Gb hard disk and has found this rate to be acceptable. What is the probability that a disk will be manufactured with no defects?

In this problem, $\lambda = 2$ and x = 0.

```
p = poisspdf(0,2)

p =

    0.1353
```

poissrnd

Purpose Random numbers from the Poisson distribution.

Syntax

```
R = poissrnd(LAMBDA)
R = poissrnd(LAMBDA,m)
R = poissrnd(LAMBDA,m,n)
```

Description `R = poissrnd(LAMBDA)` generates Poisson random numbers with mean `LAMBDA`. The size of `R` is the size of `LAMBDA`.

`R = poissrnd(LAMBDA,m)` generates Poisson random numbers with mean `LAMBDA`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = poissrnd(LAMBDA,m,n)` generates Poisson random numbers with mean `LAMBDA`. The scalars `m` and `n` are the row and column dimensions of `R`.

Examples Generate a random sample of 10 pseudo-observations from a Poisson distribution with $\lambda = 2$:

```
lambda = 2;
random_sample1 = poissrnd(lambda,1,10)

random_sample1 =

     1     0     1     2     1     3     4     2     0     0

random_sample2 = poissrnd(lambda,[1 10])

random_sample2 =

     1     1     1     5     0     3     2     2     3     4

random_sample3 = poissrnd(lambda(ones(1,10)))

random_sample3 =

     3     2     1     1     0     0     4     0     2     0
```

Purpose Mean and variance for the Poisson distribution.

Syntax

```
M = poisstat(LAMBDA)
[M,V] = poisstat(LAMBDA)
```

Description `M = poisstat(LAMBDA)` returns the mean of the Poisson distribution with parameter, `LAMBDA`. `M` and `LAMBDA` match each other in size.

`[M,V] = poisstat(LAMBDA)` also returns the variance of the Poisson distribution.

For the Poisson distribution:

- the mean is λ.
- the variance is λ.

Examples Find the mean and variance for the Poisson distribution with $\lambda = 2$:

```
[m,v] = poisstat([1 2; 3 4])

m =

     1     2
     3     4

v =

     1     2
     3     4
```

polyconf

Purpose Polynomial evaluation and confidence interval estimation.

Syntax

```
[Y,DELTA] = polyconf(p,X,S)
[Y,DELTA] = polyconf(p,X,S,alpha)
```

Description `[Y,DELTA] = polyconf(p,X,S)` uses the optional output, `S`, generated by polyfit to give 95% confidence intervals `Y +/– DELTA`. This assumes the errors in the data input to `polyfit` are independent normal with constant variance.

`[Y,DELTA] = polyconf(p,X,S,alpha)` gives 100(1–`alpha`)% confidence intervals. For example, `alpha` = 0.1 yields 90% intervals.

If `p` is a vector whose elements are the coefficients of a polynomial in descending powers, such as those output from `polyfit`, then `polyconf(p,X)` is the value of the polynomial evaluated at `X`. If `X` is a matrix or vector, the polynomial is evaluated at each of the elements.

Examples This example gives predictions and 90% confidence intervals for computing time for LU factorizations of square matrices with 100 to 200 columns.

```
n = [100 100:20:200];
for i = n
A = rand(i,i);
tic
B = lu(A);
     t(ceil((i–80)/20)) = toc;
end

[p,S] = polyfit(n(2:7),t,3);
[time,delta_t] = polyconf(p,n(2:7),S,0.1)

time =

    0.0829    0.1476    0.2277    0.3375    0.4912    0.7032

delta_t =

    0.0064    0.0057    0.0055    0.0055    0.0057    0.0064
```

Purpose Polynomial curve fitting.

Syntax

```
[p,S] = polyfit(x,y,n)
```

Description

`p = polyfit(x,y,n)` finds the coefficients of a polynomial `p(x)` of degree `n` that fits the data, `p(x(i))` to `y(i)`, in a least-squares sense. The result `p` is a row vector of length `n+1` containing the polynomial coefficients in descending powers.

$$p(x) = p_1x^n + p_2x^{n-1} + \dots p_nx + p_{n+1}$$

`[p,S] = polyfit(x,y,n)` returns polynomial coefficients `p`, and matrix, `S` for use with `polyval` to produce error estimates on predictions. If the errors in the data, `y`, are independent normal with constant variance, `polyval` will produce error bounds which contain at least 50% of the predictions.

You may omit `S` if you are not going to pass it to `polyval` or `polyconf` for calculating error estimates.

Example

```
[p,S] = polyfit(1:10,[1:10] + normrnd(0,1,1,10),1)

p =

    1.0300    0.4561

S =

  –19.6214   –2.8031
         0   –1.4639
    8.0000         0
    2.3180         0
```

See Also

`polyval`, `polytool`, `polyconf`

`polyfit` is a function in MATLAB.

polytool

Purpose

Interactive plot for prediction of fitted polynomials.

Syntax

```
polytool(x,y)
polytool(x,y,n)
polytool(x,y,n,alpha)
```

Description

`polytool(x,y)` fits a line to the column vectors, `x` and `y`, and displays an interactive plot of the result. This plot is graphic user interface for exploring the effects of changing the polynomial degree of the fit. The plot shows the fitted curve and 95% global confidence intervals on a new predicted value for the curve. Text with current predicted value of *y* and its uncertainty appears left of the *y*-axis.

`polytool(x,y,n)` initially fits a polynomial of order, `n`.

`polytool(x,y,n,alpha)` plots 100(1–`alpha`)% confidence intervals on the predicted values.

`polytool` fits by least-squares using the regression model,

$$y_i = \beta_0 + \beta_1 x_i + \beta_2 x_i^2 + \ldots + \beta_n x_i^n + \varepsilon_i$$

$$\varepsilon_i \sim N(0, \sigma^2) \quad \forall i$$

$$Cov(\varepsilon_i, \varepsilon_j) = 0 \quad \forall i, j$$

Evaluate the function by typing a value in the *x*-axis edit box or dragging the vertical reference line on the plot. The shape of the pointer changes from an arrow to a cross hair when you are over the vertical line to indicate that the line is draggable. The predicted value of *y* will update as you drag the reference line.

The argument, `n`, controls the degree of the polynomial fit. To change the degree of the polynomial, choose from the pop-up menu at the top of the figure.

When you are done, press the **Close** button.

Purpose

Polynomial evaluation.

Syntax

```
Y = polyval(p,X)
[Y,DELTA] = polyval(p,X,S)
```

Description

`Y = polyval(p,X)` returns the predicted value of a polynomial given its coefficients, `p`, at the values in `X`.

`[Y,DELTA] = polyval(p,X,S)` uses the optional output, `S`, generated by `polyfit` to generate error estimates, `Y` +/– `DELTA`. If the errors in the data input to `polyfit` are independent normal with constant variance, `Y` +/– `DELTA` contains at least 50% of the predictions.

If `p` is a vector whose elements are the coefficients of a polynomial in descending powers, then `polyval(p,X)` is the value of the polynomial evaluated at `X`. If `X` is a matrix or vector, the polynomial is evaluated at each of the elements.

Examples

Simulate the function $y = x$, adding normal random errors with a standard deviation of 0.1. Then use `polyfit` to estimate the polynomial coefficients. Note that tredicted `Y` values are within `DELTA` of the integer, `X`, in every case.

```
[p,S] = polyfit(1:10,(1:10) + normrnd(0,0.1,1,10),1);
X = magic(3);
[Y,D] = polyval(p,X,S)

Y =

    8.0696    1.0486    6.0636
    3.0546    5.0606    7.0666
    4.0576    9.0726    2.0516

D =

    0.0889    0.0951    0.0861
    0.0889    0.0861    0.0870
    0.0870    0.0916    0.0916
```

See Also

`polyfit`, `polytool`, `polyconf`

`polyval` is a function in MATLAB.

Purpose

Percentiles of a sample.

Syntax

```
Y = prctile(X,p)
```

Description

`Y = prctile(X,p)` calculates a value that is greater than `p` percent of the values in `X`. The values of `p` must lie in the interval [0 100].

For vectors, `prctile(X,p)` is the `p`th percentile of the elements in `X`. For instance, if `p` = 50 then `Y` is the median of `X`.

For matrix `X` and scalar `p`, `prctile(X,p)` is a row vector containing the `p`th percentile of each column. If `p` is a vector, the ith row of `Y` is `p(i)` of `X`.

Examples

```
x = (1:5)'*(1:5)

x =

     1     2     3     4     5
     2     4     6     8    10
     3     6     9    12    15
     4     8    12    16    20
     5    10    15    20    25

y = prctile(x,[25 50 75])

y =

    1.7500    3.5000    5.2500    7.0000    8.7500
    3.0000    6.0000    9.0000   12.0000   15.0000
    4.2500    8.5000   12.7500   17.0000   21.2500
```

Purpose

Principal Components Analysis (PCA).

Syntax

```
PC = princomp(X)
[PC,SCORE,latent,tsquare] = princomp(X)
```

Description

`[PC,SCORE,latent,tsquare] = princomp(X)` takes a data matrix `X` and returns the principal components in `PC`, the so-called Z-scores in `SCORE`, the eigenvalues of the covariance matrix of `X` in `latent`, and Hotelling's T^2 statistic for each data point in `tsquare`.

The Z-scores are the data formed by transforming the original data into the space of the principal components. The values of the vector, `latent`, are the variance of the columns of `SCORE`. Hotelling's T^2 is a measure of the multivariate distance of each observation from the center of the data set.

Example

Compute principal components for the `ingredients` data in the Hald dataset, and the variance accounted for by each component.

```
load hald;
[pc,score,latent,tsquare] = princomp(ingredients);
pc,latent

pc =

    0.0678   –0.6460    0.5673   –0.5062
    0.6785   –0.0200   –0.5440   –0.4933
   –0.0290    0.7553    0.4036   –0.5156
   –0.7309   –0.1085   –0.4684   –0.4844

latent =

  517.7969
   67.4964
   12.4054
    0.2372
```

Reference

Jackson, J. E., *A User's Guide to Principal Components*, John Wiley and Sons, Inc. 1991. pp. 1–25.

See Also

`barttest`, `pcacov`, `pcares`

qqplot

Purpose Quantile-quantile plot of two samples.

Syntax

```
qqplot(X,Y)
qqplot(X,Y,pvec)
h = qqplot(...)
```

Description `qqplot(X,Y)` displays a quantile-quantile plot of two samples. If the samples do come from the same distribution, the plot will be linear.

For matrix `X` and `Y`, `qqplot` displays a separate line for each pair of columns. The plotted quantiles are the quantiles of the smaller dataset.

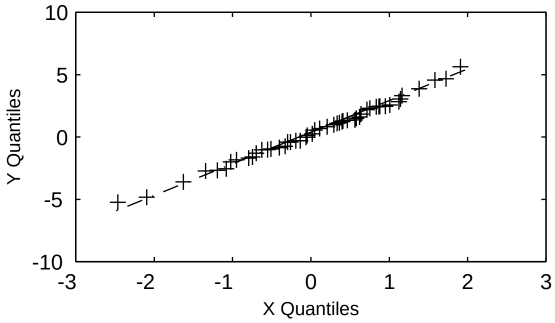
The plot has the sample data displayed with the plot symbol '+'. Superimposed on the plot is a line joining the first and third quartiles of each distribution (this is a robust linear fit of the order statistics of the two samples). This line is extrapolated out to the ends of the sample to help evaluate the linearity of the data.

Use `qqplot(X,Y,pvec)` to specify the quantiles in the vector `pvec`.

`h = qqplot(X,Y,pvec)` returns handles to the lines in `h`.

Examples Generate two normal samples with different means and standard deviations. Then make a quantile-quantile plot of the two samples.

```
x = normrnd(0,1,100,1);
y = normrnd(0.5,2,50,1);
qqplot(x,y);
```



Purpose Random numbers from a specified distribution.

Syntax `y = random('name',A1,A2,A3,m,n)`

Description `random` is a utility routine allowing you to access all the random number generators in the Statistics Toolbox using the name of the distribution as a parameter.

`y = random('name',A1,A2,A3,m,n)` returns a matrix of random numbers. `'name'` is a string containing the name of the distribution. `A1`, `A2`, and `A3` are matrices of distribution parameters. Depending on the distribution some of the parameters may not be necessary.

The arguments containing distribution parameters must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The last two parameters, `d` and `e`, are the size of the matrix, `y`. If the distribution parameters are matrices, then these parameters are optional, but they must match the size of the other matrix arguments (see second example).

Examples

```
rn = random('Normal',0,1,2,4)

rn =

    1.1650    0.0751   -0.6965    0.0591
    0.6268    0.3516    1.6961    1.7971

rp = random('Poisson',1:6,1,6)

rp =

     0     0     1     2     5     7
```

randtool

Purpose Interactive random number generation using histograms for display.

Syntax

```
randtool
r = randtool('output')
```

Description The `randtool` command sets up a graphic user interface for exploring the effects of changing parameters and sample size on the histogram of random samples from the supported probability distributions.

The M-file calls itself recursively using the `action` and `flag` parameters. For general use call `randtool` without parameters.

To output the current set of random numbers, press the **Output** button. The results are stored in the variable `ans`. Alternatively, the command

`r = randtool('output')` places the sample of random numbers in the vector, `r`.

To sample repetitively from the same distribution, press the **Resample** button.

To change the distribution function, choose from the pop-up menu of functions at the top of the figure.

To change the parameter settings, move the sliders or type a value in the edit box under the name of the parameter. To change the limits of a parameter, type a value in the edit box at the top or bottom of the parameter slider.

To change the sample size, type a number in the **Sample Size** edit box.

When you are done, press the **Close** button.

For an extensive discussion, see “The disttool Demo” on page 1-125.

See Also `disttool`

Purpose Sample range.

Syntax

```
y = range(X)
```

Description `range(X)` returns the difference between the maximum and the minimum of a sample. For vectors, `range(x)` is the range of the elements. For matrices, `range(X)` is a row vector containing the range of each column of `X`.

The range is an easily calculated estimate of the spread of a sample. Outliers have an undue influence on this statistic, which makes it an unreliable estimator.

Example The range of a large sample of standard normal random numbers is approximately six. This is the motivation for the process capability indices C_p and C_{pk} in statistical quality control applications.

```
rv = normrnd(0,1,1000,5);
near6 = range(rv)

near6 =

    6.1451    6.4986    6.2909    5.8894    7.0002
```

See Also `std`, `iqr`, `mad`

Purpose Wilcoxon rank sum test that two populations are identical.

Syntax

```
p = ranksum(x,y,alpha)
[p,h] = ranksum(x,y,alpha)
```

Description `p = ranksum(x,y,alpha)` returns the significance probability that the populations generating two independent samples, `x` and `y`, are identical. `x` and `y` are vectors but can have different lengths; if they are unequal in length, `x` must be smaller than `y`. `alpha` is the desired level of significance and must be a scalar between zero and one.

`[p,h] = ranksum(x,y,alpha)` also returns the result of the hypothesis test, `h`. `h` is zero if the populations of `x` and `y` are not significantly different. `h` is one if the two populations are significantly different.

`p` is the probability of observing a result equally or more extreme than the one using the data (`x` and `y`) if the null hypothesis is true. If `p` is near zero, this casts doubt on this hypothesis.

Example This example tests the hypothesis of equality of means for two samples generated with `poissrnd`.

```
x = poissrnd(5,10,1);
y = poissrnd(2,20,1);
[p,h] = ranksum(x,y,0.05)

p =

    0.0028

h =

     1
```

See Also `signrank`, `signtest`, `ttest2`

Purpose Rayleigh cumulative distribution function (cdf).

Syntax

```
P = raylcdf(X,B)
```

Description `P = raylcdf(X,B)` returns the Rayleigh cumulative distribution function with parameter `B` at the values in `X`.

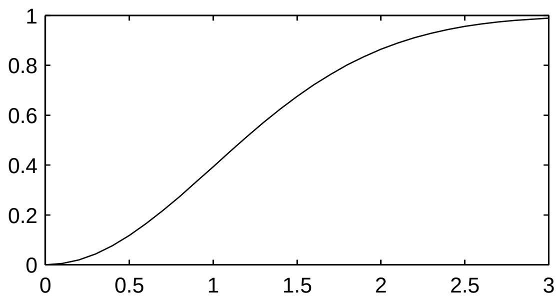
The size of `P` is the common size of `X` and `B`. A scalar input functions as a constant matrix of the same size as the other input.

The Rayleigh cdf is:

$$y = F(x|b) = \int_0^x \frac{t}{b^2} e^{\left(\frac{-t^2}{2b^2}\right)} dt$$

Example

```
x = 0:0.1:3;
p = raylcdf(x,1);
plot(x,p)
```



Reference Evans, M., N. Hastings, and B. Peacock, *Statistical Distributions, Second Edition*, Wiley 1993. pp. 134–136.

See Also `cdf`, `raylinv`, `raylpdf`, `raylrnd`, `raylstat`

raylinv

Purpose Inverse of the Rayleigh cumulative distribution function.

Syntax `X = raylinv(P,B)`

Description `X = raylinv(P,B)` returns the inverse of the Rayleigh cumulative distribution function with parameter `B` at the probabilities in `P`.

The size of `X` is the common size of `P` and `B`. A scalar input functions as a constant matrix of the same size as the other input.

Example

```
x = raylinv(0.9,1)

x =

    2.1460
```

See Also `icdf`, `raylcdf`, `raylpdf`, `raylrnd`, `raylstat`

Purpose Rayleigh probability density function.

Syntax

```
Y = raylpdf(X,B)
```

Description `Y = raylpdf(X,B)` returns the Rayleigh probability density function with parameter `B` at the values in `X`.

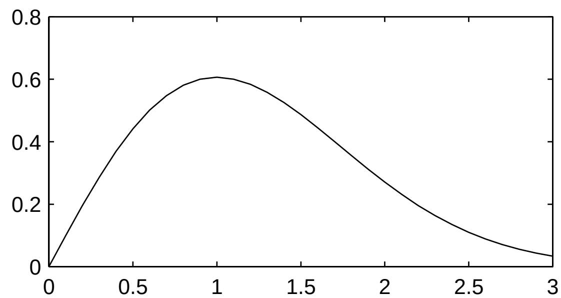
The size of `Y` is the common size of `X` and `B`. A scalar input functions as a constant matrix of the same size as the other input.

The Rayleigh pdf is:

$$y = f(x|b) = \frac{x}{b^2}e^{\left(\frac{-x^2}{2b^2}\right)}$$

Example

```
x = 0:0.1:3;
p = raylpdf(x,1);
plot(x,p)
```



See Also `raylcdf`, `raylinv`, `raylrnd`, `raylstat`

Purpose Random matrices from the Rayleigh distribution.

Syntax

```
R = raylrnd(B)
R = raylrnd(B,m)
R = raylrnd(B,m,n)
```

Description `R = raylrnd(B)` returns a matrix of random numbers chosen from the Rayleigh distribution with parameter `B`. The size of `R` is the size of `B`.

`R = raylrnd(B,m)` returns a matrix of random numbers chosen from the Rayleigh distribution with parameter `B`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = raylrnd(B,m,n)` returns a matrix of random numbers chosen from the Rayleigh distribution with parameter `B`. The scalars `m` and `n` are the row and column dimensions of `R`.

Example

```
r = raylrnd(1:5)

r =

    1.7986    0.8795    3.3473    8.9159    3.5182
```

See Also `random`, `raylcdf`, `raylinv`, `raylpdf`, `raylstat`

Purpose Mean and variance for the Rayleigh distribution.

Syntax

```
M = raylstat(B)
[M,V] = raylstat(B)
```

Description `[M,V] = raylstat(B)` returns the mean and variance of the Rayleigh distribution with parameter `B`.

For the Rayleigh distribution:

- The mean is $b\left(\frac{\pi}{2}\right)^{\frac{1}{2}}$.
- The variance is $\frac{4-\pi}{2}b^2$.

Example

```
[mn,v] = raylstat(1)

mn =

    1.2533

v =

    0.4292
```

See Also `raylcdf`, `raylinv`, `raylpdf`, `raylrnd`

Purpose Residual case order plot.

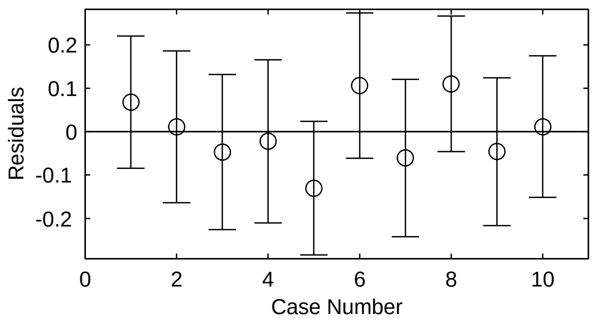
Syntax

```
rcoplot(r,rint)
```

Description `rcoplot(r,rint)` displays an errorbar plot of the confidence intervals on the residuals from a regression. The residuals appear in the plot in case order. `r` and `rint` are outputs from the `regress` function.

Example

```
X = [ones(10,1) (1:10)'];
y = X * [10;1] + normrnd(0,0.1,10,1);
[b,bint,r,rint] = regress(y,X,0.05);
rcoplot(r,rint);
```



The figure shows a plot of the residuals with error bars showing 95% confidence intervals on the residuals. All the error bars pass through the zero line, indicating that there are no outliers in the data.

See Also `regress`

Purpose

Add a polynomial curve to the current plot.

Syntax

```
h = refcurve(p)
```

Description

`refcurve` adds a graph of the polynomial, `p`, to the current axes. The function for a polynomial of degree n is:

$$y = p_1 x^n + p_2 x^{(n-1)} + \ldots + p_n x + p_{n+1}$$

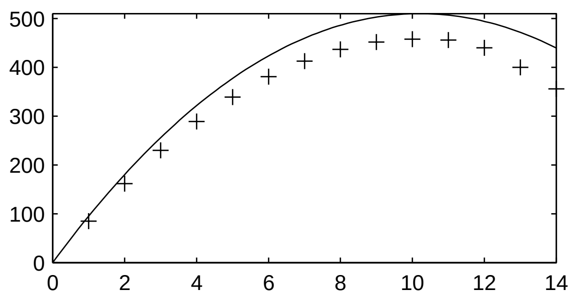
Note that p_1 goes with the highest order term.

`h = refcurve(p)` returns the handle to the curve.

Example

Plot data for the height of a rocket against time, and add a reference curve showing the theoretical height (assuming no air friction). The initial velocity of the rocket is 100 m/sec.

```
h = [85 162 230 289 339 381 413 437 452 458 456 440 400 356];
plot(h,'+')
refcurve([–4.9 100 0])
```



See Also

`polyfit`, `polyval`, `refline`

refline

Purpose Add a reference line to the current axes.

Syntax

```
refline(slope,intercept)
refline(slope)
h = refline(slope,intercept)
refline
```

Description `refline(slope,intercept)` adds a reference line with the given `slope` and `intercept` to the current axes.

`refline(slope)`, where `slope` is a two-element vector, adds the line

$$y = SLOPE(2) + SLOPE(1)x$$

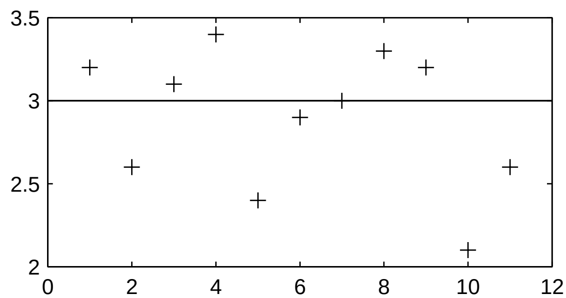
to the figure.

`h = refline(slope,intercept)` returns the handle to the line.

`refline` with no input arguments superimposes the least squares line on each line object in the current figure (except `LineStyles` `'–','– –','.–'`). This behavior is equivalent to `lsline`.

Example

```
y = [3.2 2.6 3.1 3.4 2.4 2.9 3.0 3.3 3.2 2.1 2.6]';
plot(y,'+')
refline(0,3)
```



See Also `lsline`, `polyfit`, `polyval`, `refcurve`

Purpose Multiple linear regression.

Syntax

```
b = regress(y,X)
[b,bint,r,rint,stats] = regress(y,X)
[b,bint,r,rint,stats] = regress(y,X,alpha)
```

Description `b = regress(y,X)` returns the least squares fit of `y` on `X`.

`regress` solves the linear model

$$y = X\beta + \varepsilon$$
$$\varepsilon \sim N(0, \sigma^2 I)$$

for β, where:

- y is an nx1 vector of observations,
- X is an nxp matrix of regressors,
- β is a px1 vector of parameters, and
- ε is an nx1 vector of random disturbances.

`[b,bint,r,rint,stats] = regress(y,X)` returns an estimate of β in `b`, a 95% confidence interval for β, in the p-by-2 vector `bint`. The residuals are in `r` and a 95% confidence interval for each residual, is in the n-by-2 vector `rint`. The vector, `stats`, contains the R^2 statistic along with the F and p values for the regression.

`[b,bint,r,rint,stats] = regress(y,X,alpha)` gives 100(1-`alpha`)% confidence intervals for `bint` and `rint`. For example, `alpha` = 0.2 gives 80% confidence intervals.

Examples Suppose the true model is:

$$y = 10 + x + \varepsilon$$
$$\varepsilon \sim N(0, 0.01I)$$

where I is the identity matrix.

```
X = [ones(10,1) (1:10)']
X =
     1     1
     1     2
     1     3
     1     4
     1     5
     1     6
     1     7
     1     8
     1     9
     1    10

y = X * [10;1] + normrnd(0,0.1,10,1)
y =
   11.1165
   12.0627
   13.0075
   14.0352
   14.9303
   16.1696
   17.0059
   18.1797
   19.0264
   20.0872

[b,bint] = regress(y,X,0.05)

b =
   10.0456
    1.0030

bint =
    9.9165   10.1747
    0.9822    1.0238
```

Compare `b` to `[10 1]'`. Note that `bint` includes the true model values.

Reference

Chatterjee, S. and A. S. Hadi. *Influential Observations, High Leverage Points, and Outliers in Linear Regression*. Statistical Science, 1986. pp. 379–416.

Purpose Regression diagnostics graphical user interface.

Syntax

```
regstats(responses,DATA)
regstats(responses,DATA,'model')
```

Description

`regstats(responses,DATA)` generates regression diagnostics for a linear additive model with a constant term. The dependent variable is the vector, `responses`. Values of the independent variables are in the matrix, `DATA`.

The function creates a figure with a group of checkboxes that save diagnostic statistics to the base workspace using variable names you can specify.

`regstats(responses,data,'model')` controls the order of the regression model. `'model'` can be one of these strings:

- `'interaction'` – includes constant, linear, and cross product terms.
- `'quadratic'` – interactions plus squared terms.
- `'purequadratic'` – includes constant, linear and squared terms.

The literature suggests many diagnostic statistics for evaluating multiple linear regression. `regstats` provides these diagnostics:

- Q from QR decomposition.
- R from QR decomposition.
- Regression coefficients.
- Covariance of regression coefficients.
- Fitted values of the response data.
- Residuals.
- Mean squared error.
- Leverage.
- “Hat” matrix.
- Delete-1 variance.
- Delete-1 coefficients.
- Standardized residuals.
- Studentized residuals.
- Change in regression coefficients.

- Change in fitted values.
- Scaled change in fitted values.
- Change in covariance.
- Cook's distance.

For more detail press the **Help** button in the `regstats` window. This displays a hypertext help that gives formulae and interpretations for each of these regression diagnostics.

Algorithm

The usual regression model is: $y = X\beta + \varepsilon$
where:

- y is an n by 1 vector of responses.
- X is an n by p matrix of predictors.
- β is an p by 1 vector of parameters.
- ε is an n by 1 vector of random disturbances.

Let `X = Q*R` where `Q` and `R` come from a QR Decomposition of `X`. `Q` is orthogonal and `R` is triangular. Both of these matrices are useful for calculating many regression diagnostics (Goodall 1993).

The standard textbook equation for the least squares estimator of β is:

$$\beta = b = (X'X)^{-1}X'y$$

However, this definition has poor numeric properties. Particularly dubious is the computation of $(X'X)^{-1}$, which is both expensive and imprecise.

Numerically stable MATLAB code for β is: `b = R\(Q'*y);`

Reference

Goodall, C. R. (1993). *Computation using the QR decomposition*. Handbook in Statistics, Volume 9. Statistical Computing (C. R. Rao, ed.). Amsterdam, NL Elsevier/North-Holland.

See Also

`leverage`, `stepwise`, `regress`

Purpose

Parameter estimates for ridge regression.

Syntax

```
b = ridge(y,X,k)
```

Description

`b = ridge(y,X,k)` returns the ridge regression coefficients, `b`.

Given the linear model $y = X\beta + \varepsilon$
where:

- X is an n by p matrix.
- y is the n by 1 vector of observations.
- k is a scalar constant (the ridge parameter).

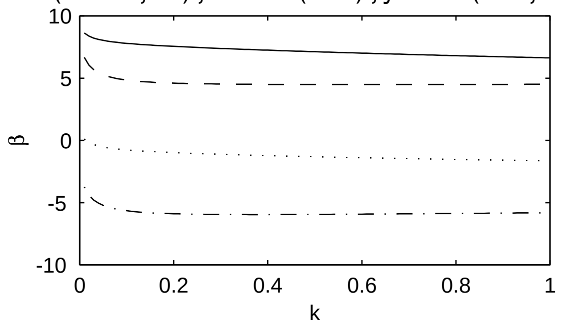
The ridge estimator of β is: $b = (X'X + kI)^{-1}X'y$.

When `k` = 0, `b` is the least squares estimator. For increasing `k`, the bias of `b` increases, but the variance of `b` falls. For poorly conditioned `X`, the drop in the variance more than compensates for the bias.

Example

This example shows how the coefficients change as the value of `k` increases, using data from the `hald` dataset.

```
load hald;
b = zeros(4,100);
kvec = 0.01:0.01:1;
count = 0;
for k = 0.01:0.01:1
count = count + 1;
b(:,count) = ridge(heat,ingredients,k);
end
plot(kvec',b'),xlabel('k'),ylabel('b','FontName','Symbol')
```



See Also `regress`, `stepwise`

Purpose

D-optimal design of experiments – row exchange algorithm.

Syntax

```
settings = rowexch(nfactors,nruns)
[settings,X] = rowexch(nfactors,nruns)
[settings,X] = rowexch(nfactors,nruns,'model')
```

Description

`settings = rowexch(nfactors,nruns)` generates the factor settings matrix, `settings`, for a D-Optimal design using a linear additive model with a constant term. `settings` has `nruns` rows and `nfactors` columns.

`[settings,X] = rowexch(nfactors,nruns)` also generates the associated design matrix, `X`.

`[settings,X] = rowexch(nfactors,nruns,'model')` produces a design for fitting a specified regression model. The input, `'model'`, can be one of these strings:

- `'interaction'` – includes constant, linear, and cross product terms.
- `'quadratic'` – interactions plus squared terms.
- `'purequadratic'` – includes constant, linear and squared terms.

Example

This example illustrates that the D-optimal design for three factors in eight runs, using an interactions model, is a two level full-factorial design.

```
s = rowexch(3,8,'interaction')

s =

    –1    –1     1
     1    –1    –1
     1    –1     1
    –1    –1    –1
    –1     1     1
     1     1     1
    –1     1    –1
     1     1    –1
```

See Also

`cordexch`, `daugment`, `dcovary`, `fullfact`, `ff2n`, `hadamard`

rsmdemo

Purpose Demo of design of experiments and surface fitting.

Syntax `rsmdemo`

Description `rsmdemo` creates a GUI that simulates a chemical reaction. To start, you have a budget of 13 test reactions. Try to find out how changes in each reactant affect the reaction rate. Determine the reactant settings that maximize the reaction rate. Estimate the run-to-run variability of the reaction. Now run a designed experiment using the model pop-up. Compare your previous results with the output from response surface modeling or nonlinear modeling of the reaction. The GUI has the following elements:

- A **Run** button to perform one reactor run at the current settings.
- An **Export** button to export the X and y data to the base workspace.
- Three sliders with associated data entry boxes to control the partial pressures of the chemical reactants: Hydrogen, n-Pentane, and Isopentane.
- A text box to report the reaction rate.
- A text box to keep track of the number of test reactions you have left.

Example See “The rsmdemo Demo” on page 1-131.

See Also `rstool`, `nlintool`, `cordexch`

Purpose

Interactive fitting and visualization of a response surface.

Syntax

```
rstool(x,y)
rstool(x,y,'model')
rstool(x,y,'model',alpha,'xname','yname')
```

Description

rstool(x,y) displays an interactive prediction plot with 95% global confidence intervales. This plot results from a multiple regression of *(X,y)* data using a linear additive model.

`rstool(x,y,'model')` allows control over the initial regression model. `'model'` can be one of the following strings:

- `'interaction'` – includes constant, linear, and cross product terms.
- `'quadratic'` – interactions plus squared terms.
- `'purequadratic'` – includes constant, linear and squared terms.

`rstool(x,y,'model',alpha)` plots 100(1 – `alpha`)% global confidence interval for predictions as two red curves. For example, `alpha` = 0.01 gives 99% confidence intervals.

`rstool` displays a "vector" of plots, one for each column of the matrix of inputs, `x`. The response variable, `y`, is a column vector that matches the number of rows in `x`.

`rstool(x,y,'model',alpha,'xname','yname')` labels the graph using the string matrix `'xname'` for the labels to the *x*-axes and the string, `'yname'`, to label the *y*-axis common to all the plots.

Drag the dotted white reference line and watch the predicted values update simultaneously. Alternatively, you can get a specific prediction by typing the value of *x* into an editable text field. Use the pop-up menu labeled **Model** to interactively change the model. Use the pop-up menu labeled **Export** to move specified variables to the base workspace.

Example

See "Quadratic Response Surface Models" on page 1-73.

See Also

`nlintool`

Purpose Chart of standard deviation for Statistical Process Control.

Syntax

```
schart(DATA,conf)
schart(DATA,conf,specs)
schart(DATA,conf,specs)
[outliers,h] = schart(DATA,conf,specs)
```

Description `schart(data)` displays an S chart of the grouped responses in `DATA`. The rows of `DATA` contain replicate observations taken at a given time. The rows must be in time order. The upper and lower control limits are a 99% confidence interval on a new observation from the process. So, roughly 99% of the plotted points should fall between the control limits.

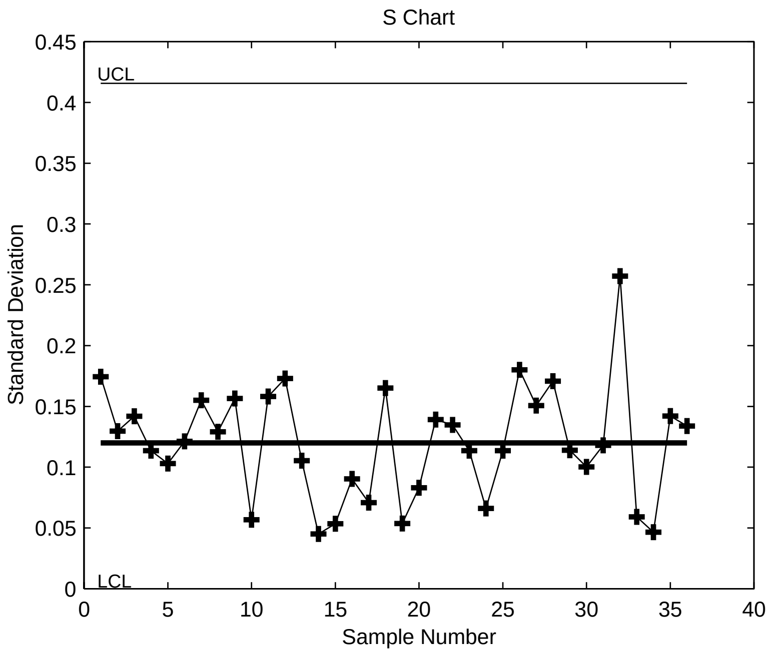
`schart(DATA,conf)` allows control of the the confidence level of the upper and lower plotted confidence limits. For example, `conf` = 0.95 plots 95% confidence intervals.

`schart(DATA,conf,specs)` plots the specification limits in the two element vector, `specs`.

`[outliers,h] = schart(data,conf,specs)` returns `outliers`, a vector of indices to the rows where the mean of `DATA` is out of control, and `h`, a vector of handles to the plotted lines.

Example This example plots an S chart of measurements on newly machined parts, taken at one hour intervals for 36 hours. Each row of the `runout` matrix contains the measurements for 4 parts chosen at random. The values indicate, in thousandths of an inch, the amount the part radius differs from the target radius.

```
load parts
schart(runout)
```



Reference

Montgomery, D., *Introduction to Statistical Quality Control,* John Wiley and Sons 1991. p. 235.

See Also

`capaplot`, `ewmaplot`, `histfit`, `xbarplot`

signrank

Purpose Wilcoxon signed rank test of equality of medians.

Syntax

```
p = signrank(x,y,alpha)
[p,h] = signrank(x,y,alpha)
```

Description `p = signrank(x,y,alpha)` returns the significance probability that the medians of two matched samples, `x` and `y`, are equal. `x` and `y` must be vectors of equal length. `alpha` is the desired level of significance, and must be a scalar between zero and one.

`[p,h] = signrank(x,y,alpha)` also returns the result of the hypothesis test, `h`. `h` is zero if the difference in medians of `x` and `y` is not significantly different from zero. `h` is one if the two medians are significantly different.

`p` is the probability of observing a result equally or more extreme than the one using the data (`x` and `y`) if the null hypothesis is true. `p` is calculated using the rank values for the differences between corresponding elements in `x` and `y`. If `p` is near zero, this casts doubt on this hypothesis.

Example This example tests the hypothesis of equality of means for two samples generated with `normrnd`. The samples have the same theoretical mean but different standard deviations.

```
x = normrnd(0,1,20,1);
y = normrnd(0,2,20,1);
[p,h] = signrank(x,y,0.05)

p =

    0.2568

h =

     0
```

See Also `ranksum`, `signtest`, `ttest`

Purpose

Sign test for paired samples.

Syntax

```
p = signtest(x,y,alpha)
[p,h] = signtest(x,y,alpha)
```

Description

`p = signtest(x,y,alpha)` returns the significance probability that the medians of two matched samples, `x` and `y`, are equal. `x` and `y` must be vectors of equal length. `y` may also be a scalar; in this case, `signtest` computes the probability that the median of `x` is different from the constant, `y`. `alpha` is the desired level of significance and must be a scalar between zero and one.

`[p,h] = signtest(x,y,alpha)` also returns the result of the hypothesis test, `h`. `h` is zero if the difference in medians of `x` and `y` is not significantly different from zero. `h` is one if the two medians are significantly different.

`p` is the probability of observing a result equally or more extreme than the one using the data (`x` and `y`) if the null hypothesis is true. `p` is calculated using the signs (plus or minus) of the differences between corresponding elements in `x` and `y`. If `p` is near zero, this casts doubt on this hypothesis.

Example

This example tests the hypothesis of equality of means for two samples generated with `normrnd`. The samples have the same theoretical mean but different standard deviations.

```
x = normrnd(0,1,20,1);
y = normrnd(0,2,20,1);
[p,h] = signtest(x,y,0.05)

p =

    0.8238

h =

     0
```

See Also

`ranksum`, `signrank`, `ttest`

skewness

Purpose Sample skewness.

Syntax

```
y = skewness(X)
```

Description `skewness(X)` returns the sample skewness of `X`. For vectors, `skewness(x)` is the skewness of the elements of `x`. For matrices, `skewness(X)` is a row vector containing the sample skewness of each column.

Skewness is a measure of the asymmetry of the data around the sample mean. If skewness is negative, the data are spread out more to the left of the mean than to the right. If skewness is positive, the data are spread out more to the right. The skewness of the normal distribution (or any perfectly symmetric distribution) is zero.

The skewness of a distribution is defined as:

$$y = \frac{E(x-\mu)^3}{\sigma^3}$$

where $E(x)$ is the expected value of x.

Example

```
X = randn([5 4])

X =

    1.1650    1.6961   –1.4462   –0.3600
    0.6268    0.0591   –0.7012   –0.1356
    0.0751    1.7971    1.2460   –1.3493
    0.3516    0.2641   –0.6390   –1.2704
   –0.6965    0.8717    0.5774    0.9846

y = skewness(X)

y =

   –0.2933    0.0482    0.2735    0.4641
```

See Also `kurtosis`, `mean`, `moment`, `std`, `var`

Purpose

Reformat the output of `pdist` into a square matrix.

Syntax

```
S = squareform(Y)
```

Description

`S = squareform(Y)` reformats the distance information returned by `pdist` from a vector into a square matrix. In this format, $S(i,j)$ denotes the distance between the i and j observations in the original data.

See Also

See `pdist`.

Purpose

Standard deviation of a sample.

Syntax

```
y = std(X)
```

Description

`std(X)` computes the sample standard deviation of the data in `X`. For vectors, `std(x)` is the standard deviation of the elements in `x`. For matrices, `std(X)` is a row vector containing the standard deviation of each column of `X`.

`std(X)` normalizes by $n-1$ where n is the sequence length. For normally distributed data, the square of the standard deviation is the minimum variance unbiased estimator of σ^2 (the second parameter).

The standard deviation is

$$s = \left(\frac{1}{n-1} \sum_{i=1}^{n} (x_i - \bar{x})^2 \right)^{\frac{1}{2}}$$

where the sample average is $\bar{x} = \frac{1}{n} \sum x_i$.

Examples

In each column, the expected value of `y` is one.

```
x = normrnd(0,1,100,6);
y = std(x)

y =

    0.9536    1.0628    1.0860    0.9927    0.9605    1.0254

y = std(–1:2:1)

y =

    1.4142
```

See Also

`cov`, `var`

`std` is a function in MATLAB.

Purpose

Interactive environment for stepwise regression.

Syntax

```
stepwise(X,y)
stepwise(X,y,inmodel)
stepwise(X,y,inmodel,alpha)
```

Description

`stepwise(X,y)` fits a regression model of `y` on the columns of `X`. It displays three figure windows for interactively controlling the stepwise addition and removal of model terms.

`stepwise(X,y,inmodel)` allows control of the terms in the original regression model. The values of vector, `inmodel`, are the indices of the columns of the matrix, `X`, to include in the initial model.

`stepwise(X,y,inmodel,alpha)` allows control of the length confidence intervals on the fitted coefficients. `alpha` is the significance for testing each term in the model. By default, `alpha` = $1 - (1 - 0.025)^{(1/p)}$ where p is the number of columns in `X`. This translates to plotted 95% simultaneous confidence intervals (Bonferroni) for all the coefficients.

The least squares coefficient is plotted with a green filled circle. A coefficient is not significantly different from zero if its confidence interval crosses the white zero line. Significant model terms are plotted using solid lines. Terms not significantly different from zero are plotted with dotted lines.

Click on the confidence interval lines to toggle the state of the model coefficients. If the confidence interval line is green the term is in the model. If the the confidence interval line is red the term is not in the model.

Use the pop-up menu, **Export**, to move variables to the base workspace.

Example

See "Stepwise Regression" on page 1-75.

Reference

Draper, N. and H. Smith, *Applied Regression Analysis, Second Edition*, John Wiley and Sons, Inc. 1981 pp. 307–312.

See Also

`regstats`, `regress`, `rstool`

surfht

Purpose Interactive contour plot.

Syntax

```
surfht(Z)
surfht(x,y,Z)
```

Description `surfht(Z)` is an interactive contour plot of the matrix `Z` treating the values in `Z` as height above the plane. The *x*-values are the column indices of `Z` while the *y*-values are the row indices of `Z`.

`surfht(x,y,Z)`, where `x` and `y` are vectors specify the *x* and *y*-axes on the contour plot. The length of `x` must match the number of columns in `Z`, and the length of `y` must match the number of rows in `Z`.

There are vertical and horizontal reference lines on the plot whose intersection defines the current *x*-value and *y*-value. You can drag these dotted white reference lines and watch the interpolated *z*-value (at the top of the plot) update simultaneously. Alternatively, you can get a specific interpolated *z*-value by typing the *x*-value and *y*-value into editable text fields on the *x*-axis and *y*-axis respectively.

Purpose Frequency table.

Syntax

```
table = tabulate(x)
tabulate(x)
```

Description `table = tabulate(x)` takes a vector of positive integers, `x`, and returns a matrix, `table`.

The first column of `table` contains the values of `x`. The second contains the number of instances of this value. The last column contains the percentage of each value.

`tabulate` with no output arguments displays a formatted table in the command window.

Example

```
tabulate([1 2 4 4 3 4])

  Value    Count    Percent
      1        1     16.67%
      2        1     16.67%
      3        1     16.67%
      4        3     50.00%
```

See Also `pareto`

tblread

Purpose

Read tabular data from the file system.

Syntax

```
[data,varnames,casenames] = tblread
[data,varnames,casenames] = tblread('filename')
[data,varnames,casenames] = tblread('filename','delimiter')
```

Description

`[data,varnames,casenames] = tblread` displays the **File Open** dialog box for interactive selection of the tabular data file. The file format has variable names in the first row, case names in the first column and data starting in the (2,2) position.

`[data,varnames,casenames] = tblread(filename)` allows command line specification of the name of a file in the current directory, or the complete pathname of any file.

`[data,varnames,casenames] = tblread(filename,'delimiter')` allows specification of the field `'delimiter'` in the file. Accepted values are `'tab'`, `'space'`, or `'comma'`.

`tblread` returns the data read in three values.

Return Value	Description
`data`	Numeric matrix with a value for each variable-case pair.
`varnames`	String matrix containing the variable names in the first row.
`casenames`	String matrix containing the names of each case in the first column.

Example

```
[data,varnames,casenames] = tblread('sat.dat')

data =

   470   530
   520   480

varnames =

Male
Female

casenames =

Verbal
Quantitative
```

See Also

`caseread`, `tblwrite`

tblwrite

Purpose Writes tabular data to the file system.

Syntax

```
tblwrite(data,'varnames','casenames')
tblwrite(data,'varnames','casenames','filename')
```

Description `tblwrite(data,'varnames','casenames')` displays the File Open dialog box for interactive specification of the tabular data output file. The file format has variable names in the first row, case names in the first column and `data` starting in the (2,2) position.

`'varnames'` is a string matrix containing the variable names. `'casenames'` is a string matrix containing the names of each case in the first column. `data` is a numeric matrix with a value for each variable-case pair.

`tblwrite(data,'varnames','casenames','filename')` allows command line specification of a file in the current directory, or the complete pathname of any file in the string, `'filename'`.

Example Continuing the example from `tblread`:

```
tblwrite(data,varnames,casenames,'sattest.dat')
type sattest.dat

               Male    Female
Verbal         470     530
Quantitative   520     480
```

See Also `casewrite`, `tblread`

Purpose

Student's t cumulative distribution function (cdf).

Syntax

```
P = tcdf(X,V)
```

Description

`tcdf(X,V)` computes Student's t cdf with `V` degrees of freedom at the values in `X`. The arguments `X` and `V` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument.

The parameter, `V`, is a positive integer.

The t cdf is:

$$p = F(x|\nu) = \int_{-\infty}^{x} \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{t^2}{\nu}\right)^{\frac{\nu+1}{2}}} dt$$

The result, p, is the probability that a single observation from the t distribution with ν degrees of freedom will fall in the interval $(-\infty\ x]$.

Examples

Suppose 10 samples of Guinness beer have a mean alcohol content of 5.5% by volume and the standard deviation of these samples is 0.5%. What is the probability that the true alcohol content of Guinness beer is less than 5%?

```
t = (5.0 – 5.5) / 0.5;
probability = tcdf(t,10 – 1)

probability =

    0.1717
```

tinv

Purpose

Inverse of the Student's t cumulative distribution function (cdf).

Syntax

```
X = tinv(P,V)
```

Description

`tinv(P,V)` computes the inverse of Student's t cdf with parameter `V` for the probabilities in `P`. The arguments `P` and `V` must be the same size except that a scalar argument functions as a constant matrix of the size of the other argument.

The degrees of freedom, `V`, must be a positive integer and `P` must lie in the interval [0 1].

The t inverse function in terms of the t cdf is

$$x = F^{-1}(p|\nu) = \{x: F(x|\nu) = p\}$$

where

$$p = F(x|\nu) = \int_{-\infty}^{x} \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{t^2}{\nu}\right)^{\frac{\nu+1}{2}}} dt$$

The result, x, is the solution of the integral equation of the t cdf with parameter ν where you supply the desired probability p.

Examples

What is the 99th percentile of the t distribution for one to six degrees of freedom?

```
percentile = tinv(0.99,1:6)

percentile =

   31.8205    6.9646    4.5407    3.7469    3.3649    3.1427
```

Purpose Student's t probability density function (pdf).

Syntax

```
Y = tpdf(X,V)
```

Description `tpdf(X,V)` computes Student's t pdf with parameter `V` at the values in `X`. The arguments `X` and `V` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument.

The degrees of freedom, `V`, must be a positive integer.

Student's t pdf is:

$$y = f(x|\nu) = \frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)} \frac{1}{\sqrt{\nu\pi}} \frac{1}{\left(1+\frac{x^2}{\nu}\right)^{\frac{\nu+1}{2}}}$$

Examples The mode of the t distribution is at $x = 0$. This example shows that the value of the function at the mode is an increasing function of the degrees of freedom.

```
tpdf(0,1:6)

ans =

    0.3183    0.3536    0.3676    0.3750    0.3796    0.3827
```

The t distribution converges to the standard normal distribution as the degrees of freedom approaches infinity. How good is the approximation for v = 30?

```
difference = tpdf(–2.5:2.5,30) – normpdf(–2.5:2.5)

difference =

    0.0035   –0.0006   –0.0042   –0.0042   –0.0006    0.0035
```

trimmean

Purpose Mean of a sample of data excluding extreme values.

Syntax

```
m = trimmean(X,percent)
```

Description `trimmean(X,percent)` calculates the mean of a sample `X` excluding the highest and lowest `percent/2` of the observations. The trimmed mean is a robust estimate of the location of a sample. If there are outliers in the data, the trimmed mean is a more representative estimate of the center of the body of the data. If the data is all from the same probability distribution, then the trimmed mean is less efficient than the sample average as an estimator of the location of the data.

Examples This example shows a Monte Carlo simulation of the relative efficiency of the 10% trimmed mean to the sample average for normal data.

```
x = normrnd(0,1,100,100);
m = mean(x);
trim = trimmean(x,10);
sm = std(m);
strim = std(trim);
efficiency = (sm/strim).^2
efficiency =

    0.9702
```

See Also `mean`, `median`, `geomean`, `harmmean`

Purpose

Random numbers from Student's t distribution.

Syntax

```
R = trnd(V)
R = trnd(V,m)
R = trnd(V,m,n)
```

Description

`R = trnd(V)` generates random numbers from Student's t distribution with `V` degrees of freedom. The size of `R` is the size of `V`.

`R = trnd(V,m)` generates random numbers from Student's t distribution with `V` degrees of freedom. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = trnd(V,m,n)` generates random numbers from Student's t distribution with `V` degrees of freedom. The scalars `m` and `n` are the row and column dimensions of `R`.

Examples

```
noisy = trnd(ones(1,6))

noisy =

   19.7250    0.3488    0.2843    0.4034    0.4816   –2.4190

numbers = trnd(1:6,[1 6])

numbers =

   –1.9500   –0.9611   –0.9038    0.0754    0.9820    1.0115

numbers = trnd(3,2,6)

numbers =

   –0.3177   –0.0812   –0.6627    0.1905   –1.5585   –0.0433
    0.2536    0.5502    0.8646    0.8060   –0.5216    0.0891
```

tstat

Purpose

Mean and variance for the Student's t distribution.

Syntax

```
[M,V] = tstat(NU)
```

Description

For the Student's t distribution with parameter, ν:

- The mean is zero for values of ν greater than 1. If ν is one, the mean does not exist.
- The variance, for values of ν greater than 2, is $\frac{\nu}{\nu - 2}$.

Examples

The mean and variance for 1 to 30 degrees of freedom.

```
[m,v] = tstat(reshape(1:30,6,5))

m =

   NaN     0     0     0     0
     0     0     0     0     0
     0     0     0     0     0
     0     0     0     0     0
     0     0     0     0     0
     0     0     0     0     0

v =

       NaN    1.4000    1.1818    1.1176    1.0870
       NaN    1.3333    1.1667    1.1111    1.0833
    3.0000    1.2857    1.1538    1.1053    1.0800
    2.0000    1.2500    1.1429    1.1000    1.0769
    1.6667    1.2222    1.1333    1.0952    1.0741
    1.5000    1.2000    1.1250    1.0909    1.0714
```

Note that the variance does not exist for one and two degrees of freedom.

Purpose Hypothesis testing for a single sample mean.

Syntax

```
h = ttest(x,m)
h = ttest(x,m,alpha)
[h,sig,ci] = ttest(x,m,alpha,tail)
```

Description

`ttest(x,m)` performs a t-test at significance level 0.05 to determine whether a sample from a normal distribution (in x) could have mean `m` when the standard deviation is unknown.

`h = ttest(x,m,alpha)` gives control of the significance level, `alpha`. For example if `alpha` = 0.01, and the result, `h`, is 1 you can reject the null hypothesis at the significance level 0.01. If `h` =0, you cannot reject the null hypothesis at the `alpha` level of significance.

`[h,sig,ci] = ttest(x,m,alpha,tail)` allows specification of one or two-tailed tests. `tail` is a flag that specifies one of three alternative hypotheses:

- `tail` = 0 (default) specifies the alternative, $x \neq \mu$.
- `tail` = 1 specifies the alternative, $x > \mu$.
- `tail` = –1 specifies the alternative, $x < \mu$.

`sig` is the p-value associated with the T-statistic.

$$T = \frac{\bar{x} - \mu}{s}$$

`sig` is the probability that the observed value of T could be as large or larger *by chance* under the null hypothesis that the mean of *x* is equal to μ.

`ci` is a 1–`alpha` confidence interval for the true mean.

Example

This example generates 100 normal random numbers with theoretical mean zero and standard deviation one. The observed mean and standard deviation are different from their theoretical values, of course. We test the hypothesis that there is no true difference.

Normal random number generator test.

```
x = normrnd(0,1,1,100);
[h,sig,ci] = ttest(x,0)
h =

     0

sig =

    0.4474

ci =

   –0.1165    0.2620
```

The result, `h` = 0, means that we cannot reject the null hypothesis. The significance level is 0.4474, which means that by chance we would have observed values of T more extreme than the one in this example in 45 of 100 similar experiments. A 95% confidence interval on the mean is [–0.1165 0.2620], which includes the theoretical (and hypothesized) mean of zero.

Purpose Hypothesis testing for the difference in means of two samples.

Syntax

```
[h,significance,ci] = ttest2(x,y)
[h,significance,ci] = ttest2(x,y,alpha)
[h,significance,ci] = ttest2(x,y,alpha,tail)
```

Description

`h = ttest2(x,y)` performs a t-test to determine whether two samples from a normal distribution (in `x` and `y`) could have the same mean when the standard deviations are unknown but assumed equal.

`h`, the result, is 1 if you can reject the null hypothesis at the 0.05 significance level `alpha` and 0 otherwise.

`significance` is the p-value associated with the T-statistic.

$$T = \frac{x - y}{s}$$

`significance` is the probability that the observed value of T could be as large or larger *by chance* under the null hypothesis that the mean of x is equal to the mean of y.

`ci` is a 95% confidence interval for the true difference in means.

`[h,significance,ci] = ttest2(x,y,alpha)` gives control of the significance level, `alpha`. For example if `alpha` = 0.01, and the result, `h`, is 1, you can reject the null hypothesis at the `significance` level 0.01. `ci` in this case is a 100(1–`alpha`)% confidence interval for the true difference in means.

`ttest2(x,y,alpha,tail)` allows specification of one or two-tailed tests. `tail` is a flag that specifies one of three alternative hypotheses:

- `tail` = 0 (default) specifies the alternative, $\mu_x \neq \mu_y$.
- `tail` = 1 specifies the alternative, $\mu_x > \mu_y$.
- `tail` = –1 specifies the alternative, $\mu_x < \mu_y$.

Examples

This example generates 100 normal random numbers with theoretical mean zero and standard deviation one. We then generate 100 more normal random numbers with theoretical mean one half and standard deviation one. The observed means and standard deviations are different from their theoretical values, of course. We test the hypothesis that there is no true difference between the two means. Notice that the true difference is only one half of the standard deviation of the individual observations, so we are trying to detect a signal that is only one half the size of the inherent noise in the process.

```
x = normrnd(0,1,100,1);
y = normrnd(0.5,1,100,1);
[h,significance,ci] = ttest2(x,y)

h =

     1

significance =

    0.0017

ci =

   –0.7352   –0.1720
```

The result, `h` = 1, means that we can reject the null hypothesis. The `significance` is 0.0017, which means that by chance we would have observed values of t more extreme than the one in this example in only 17 of 10,000 similar experiments! A 95% confidence interval on the mean is [–0.7352 –0.1720], which includes the theoretical (and hypothesized) difference of –0.5.

Purpose Discrete uniform cumulative distribution (cdf) function.

Syntax

```
P = unidcdf(X,N)
```

Description `unidcdf(X,N)` computes the discrete uniform cdf with parameter settings `N` at the values in `X`. The arguments `X` and `N` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument.

The maximum observable value, `N`, is a positive integer.

The discrete uniform cdf is:

$$p = F(x|N) = \frac{floor(x)}{N} I_{(1, \ldots, N)}(x)$$

The result, p, is the probability that a single observation from the discrete uniform distribution with maximum, N, will be a positive integer less than or equal to x. The values, x, do not need to be integers.

Examples What is the probability of drawing a number 20 or less from a hat with the numbers from 1 to 50 inside?

```
probability = unidcdf(20,50)

probability =

    0.4000
```

unidinv

Purpose Inverse of the discrete uniform cumulative distribution function.

Syntax

```
X = unidinv(P,N)
```

Description `unidinv(P,N)` returns the smallest integer `X` such that the discrete uniform cdf evaluated at `X` is equal to or exceeds `P`. You can think of `P` as the probability of drawing a number as large as `X` out of a hat with the numbers `1` through `N` inside.

The argument `P` must lie on the interval [0 1] and `N` must be a positive integer. Each element of `X` is a positive integer.

Examples

```
x = unidinv(0.7,20)

x =

    14

y = unidinv(0.7 + eps,20)

y =

    15
```

A small change in the first parameter produces a large jump in output. The cdf and its inverse are both step functions. The example shows what happens at a step.

Purpose

Discrete uniform probability density function (pdf).

Syntax

```
Y = unidpdf(X,N)
```

Description

`unidpdf(X,N)` computes the discrete uniform pdf with parameter settings, `N`, at the values in `X`. The arguments `X` and `N` must be the same size except that a scalar argument functions as a constant matrix of the same size of the other argument.

The parameter `N` must be a positive integer.

The discrete uniform pdf is:

$$y = f(x|N) = \frac{1}{N} I_{(1, \ldots, N)}(x)$$

You can think of y as the probability of observing any one number between 1 and n.

Examples

For fixed `n`, the uniform discrete pdf is a constant.

```
y = unidpdf(1:6,10)

y =

    0.1000    0.1000    0.1000    0.1000    0.1000    0.1000
```

Now fix `x` , and vary `n`.

```
likelihood = unidpdf(5,4:9)

likelihood =

         0    0.2000    0.1667    0.1429    0.1250    0.1111
```

unidrnd

Purpose Random numbers from the discrete uniform distribution.

Syntax

```
R = unidrnd(N)
R = unidrnd(N,mm)
R = unidrnd(N,mm,nn)
```

Description The discrete uniform distribution arises from experiments equivalent to drawing a number from one to `N` out of a hat.

`R = unidrnd(N)` generates discrete uniform random numbers with maximum, `N`. The size of `R` is the size of `N`.

`R = unidrnd(N,mm)` generates discrete uniform random numbers with maximum, `N`. `mm` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = unidrnd(N,mm,nn)` generates discrete uniform random numbers with maximum, `N`. The scalars `mm` and `nn` are the row and column dimensions of `R`.

The parameter, `N`, must have positive integer elements.

Examples In the Massachusetts lottery a player chooses a four digit number. Generate random numbers for Monday through Saturday.

```
numbers = unidrnd(10000,1,6) – 1

numbers =

       2189        470       6788       6792       9346
```

Purpose Mean and variance for the discrete uniform distribution.

Syntax

```
[M,V] = unidstat(N)
```

Description For the discrete uniform distribution:

- The mean is $\frac{N+1}{2}$.
- The variance is $\frac{N^2-1}{12}$.

Examples

```
[m,v] = unidstat(1:6)

m =

    1.0000    1.5000    2.0000    2.5000    3.0000    3.5000

v =

         0    0.2500    0.6667    1.2500    2.0000    2.9167
```

unifcdf

Purpose

Continuous uniform cumulative distribution function (cdf).

Syntax

```
P = unifcdf(X,A,B)
```

Description

`unifcdf(X,A,B)` computes the uniform cdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A` and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

`A` and `B` are the minimum and maximum values respectively.

The uniform cdf is:

$$p = F(x|a, b) = \frac{x-a}{b-a} I_{[a, b]}(x)$$

The standard uniform distribution has `A` = 0 and `B` = 1.

Examples

What is the probability that an observation from a standard uniform distribution will be less than 0.75?

```
probability = unifcdf(0.75)

probability =

    0.7500
```

What is the probability that an observation from a uniform distribution with `a` = –1 and `b` = 1 will be less than 0.75?

```
probability = unifcdf(0.75,–1,1)

probability =

    0.8750
```

Purpose Inverse continuous uniform cumulative distribution function (cdf).

Syntax

```
X = unifinv(P,A,B)
```

Description `unifinv(P,A,B)` computes the inverse of the uniform cdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A`, and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

`A` and `B` are the minimum and maximum values respectively.

The inverse of the uniform cdf is:

$$x = F^{-1}(p|a,b) = a + p(a-b)I_{[0,1]}(p)$$

The standard uniform distribution has `A` = 0 and `B` = 1.

Examples What is the median of the standard uniform distribution?

```
median_value = unifinv(0.5)

median_value =

    0.5000
```

What is the 99th percentile of the uniform distribution between –1 and 1?

```
percentile = unifinv(0.99,–1,1)

percentile =

    0.9800
```

unifit

Purpose

Parameter estimates for uniformly distributed data.

Syntax

```
[ahat,bhat] = unifit(X)
[ahat,bhat,ACI,BCI] = unifit(X)
[ahat,bhat,ACI,BCI] = unifit(X,alpha)
```

Description

`[ahat,bhat] = unifit(X)` returns the maximum likelihood estimates (MLEs) of the parameters of the uniform distribution given the data in `X`.

`[ahat,bhat,ACI,BCI] = unifit(X)` also returns 95% confidence intervals, `ACI` and `BCI`, which are matrices with two rows. The first row contains the lower bound of the interval for each column of the matrix, `X`. The second row contains the upper bound of the interval.

`[ahat,bhat,ACI,BCI] = unifit(X,alpha)` allows control of the confidence level `alpha`. For example, if `alpha` is 0.01 then `ACI` and `BCI` are 99% confidence intervals.

Example

```
r = unifrnd(10,12,100,2);
[ahat,bhat,aci,bci] = unifit(r)

ahat =

   10.0154   10.0060

bhat =

   11.9989   11.9743

aci =

    9.9551    9.9461
   10.0154   10.0060

bci =

   11.9989   11.9743
   12.0592   12.0341
```

See Also

`betafit`, `binofit`, `expfit`, `gamfit`, `normfit`, `poissfit`, `weibfit`

Purpose Continuous uniform probability density function (pdf).

Syntax

```
Y = unifpdf(X,A,B)
```

Description `unifpdf(X,A,B)` computes the continuous uniform pdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A`, and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameter `B` must be greater than `A`.

The continuous uniform distribution pdf is:

$$y = f(x|a, b) = \frac{1}{b-a} I_{[a, b]}(x)$$

The standard uniform distribution has `A` = 0 and `B` = 1.

Examples For fixed `a` and `b`, the uniform pdf is constant.

```
x = 0.1:0.1:0.6;
y = unifpdf(x)

y =

     1     1     1     1     1     1
```

What if `x` is not between `a` and `b`?

```
y = unifpdf(-1,0,1)

y =

     0
```

unifrnd

Purpose Random numbers from the continuous uniform distribution.

Syntax

```
R = unifrnd(A,B)
R = unifrnd(A,B,m)
R = unifrnd(A,B,m,n)
```

Description `R = unifrnd(A,B)` generates uniform random numbers with parameters `A` and `B`. The size of `R` is the common size of `A` and `B` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other parameter.

`R = unifrnd(A,B,m)` generates uniform random numbers with parameters `A` and `B`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = unifrnd(A,B,m,n)` generates uniform random numbers with parameters `A` and `B`. The scalars `m` and `n` are the row and column dimensions of `R`.

Examples

```
random = unifrnd(0,1:6)

random =

    0.2190    0.0941    2.0366    2.7172    4.6735    2.3010

random = unifrnd(0,1:6,[1 6])

random =

    0.5194    1.6619    0.1037    0.2138    2.6485    4.0269

random = unifrnd(0,1,2,3)

random =

    0.0077    0.0668    0.6868
    0.3834    0.4175    0.5890
```

Purpose Mean and variance for the continuous uniform distribution.

Syntax

```
[M,V] = unifstat(A,B)
```

Description For the continuous uniform distribution:

- The mean is $\frac{a+b}{2}$.
- The variance is $\frac{(b-a)^2}{12}$.

Examples

```
a = 1:6;
b = 2.*a;
[m,v] = unifstat(a,b)

m =

    1.5000    3.0000    4.5000    6.0000    7.5000    9.0000

v =

    0.0833    0.3333    0.7500    1.3333    2.0833    3.0000
```

var

Purpose Variance of a sample.

Syntax

```
y = var(X)
y = var(X,1)
y = var(X,w)
```

Description `var(X)` computes the variance of the data in `X`. For vectors, `var(x)` is the variance of the elements in `x`. For matrices, `var(X)` is a row vector containing the variance of each column of `X`.

`var(x)` normalizes by n–1 where n is the sequence length. For normally distributed data, this makes `var(x)` the minimum variance unbiased estimator MVUE of σ^2(the second parameter) .

`var(x,1)` normalizes by n and yields the second moment of the sample data about its mean (moment of inertia).

`var(X,w)` computes the variance using the vector of weights, `w`. The number of elements in `w` must equal the number of rows in the matrix, `X`. For vector `x`, `w` and `x` must match in length. Each element of `w` must be positive.

`var` supports both common definitions of variance. Let SS be the sum of the squared deviations of the elements of a vector `x`, from their mean. Then, `var(x)` = $SS/(n\text{-}1)$ the MVUE, and `var(x,1)` = SS/n the maximum likelihood estimator (MLE) of σ^2.

Examples

```
x = [-1 1];
w = [1 3];
v1 = var(x)

v1 =

     2

v2 = var(x,1)

v2 =

     1

v3 = var(x,w)

v3 =

    0.7500
```

See Also

cov, std

weibcdf

Purpose Weibull cumulative distribution function (cdf).

Syntax

```
P = weibcdf(X,A,B)
```

Description `weibcdf(X,A,B)` computes the Weibull cdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A`, and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

Parameters `A` and `B` are positive.

The Weibull cdf is:

$$p = F(x|a, b) = \int_0^x abt^{b-1}e^{-at^b}dt = 1 - e^{-ax^b}I_{(0,\infty)}(x)$$

Examples What is the probability that a value from a Weibull distribution with parameters `a` = 0.15 and `b` = 0.24 is less than 500?

```
probability = weibcdf(500,0.15,0.24)

probability =

    0.4865
```

How sensitive is this result to small changes in the parameters?

```
[A,B] = meshgrid(0.1:0.05:0.2,0.2:0.05:0.3);
probability = weibcdf(500,A,B)

probability =

    0.2929    0.4054    0.5000
    0.3768    0.5080    0.6116
    0.4754    0.6201    0.7248
```

Purpose Parameter estimates and confidence intervals for Weibull data.

Syntax

```
phat = weibfit(x)
[phat,pci] = weibfit(x)
[phat,pci] = weibfit(x,alpha)
```

Description `phat = weibfit(x)` returns the maximum likelihood estimates, `phat`, of the parameters of the Weibull distribution given the data in the vector, `x`. `phat` is a two-element row vector. `phat(1)` estimates the Weibull parameter, a, and `phat(2)` estimates b in the pdf:

$$y = f(x|a, b) = abx^{b-1}e^{-ax^b}I_{(0,\infty)}(x)$$

`[phat,pci] = weibfit(x)` also returns 95% confidence intervals in a matrix, `pci`, with 2 rows. The first row contains the lower bound of the confidence interval. The second row contains the upper bound. The columns of `pci` correspond to the columns of `phat`.

`[phat,pci] = weibfit(x,alpha)` allows control over the confidence interval returned (100(1–alpha)%).

Example

```
r = weibrnd(0.5,0.8,100,1);
[phat,pci] = weibfit(r)

phat =

    0.4746    0.7832

pci =

    0.3851    0.6367
    0.5641    0.9298
```

See Also `betafit`, `binofit`, `expfit`, `gamfit`, `normfit`, `poissfit`, `unifit`

weibinv

Purpose Inverse of the Weibull cumulative distribution function.

Syntax

```
X = weibinv(P,A,B)
```

Description `weibinv(P,A,B)` computes the inverse of the Weibull cdf with parameters `A` and `B` for the probabilities in `P`. The arguments `P`, `A` and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

The parameters `A` and `B` must be positive.

The inverse of the Weibull cdf is:

$$x = F^{-1}(p|a, b) = \left[\frac{1}{a}\ln\left(\frac{1}{1-p}\right)\right]^{\frac{1}{b}} I_{[0, 1]}(p)$$

Examples A batch of light bulbs have lifetimes (in hours) distributed Weibull with parameters `a` = 0.15 and `b` = 0.24. What is the median lifetime of the bulbs?

```
life = weibinv(0.5,0.15,0.24)

life =

  588.4721
```

What is the 90th percentile?

```
life = weibinv(0.9,0.15,0.24)

life =

   8.7536e+04
```

Purpose Weibull negative log-likelihood function.

Syntax

```
logL = weiblike(params,data)
[logL,info] = weiblike(params,data)
```

Description `logL = weiblike(params,data)` returns the Weibull log-likelihood with parameters `params(1)` = a and `params(2)` = b given the `data`, x_i.

`[logL,info] = weiblike(params,data)` adds Fisher's information matrix, `info`. The diagonal elements of `INFO` are the asymptotic variances of their respective parameters.

The Weibull negative log-likelihood is:

$$-\log L = -\log \prod_{i=1} f(a, b|x_i) = -\sum_{i=1}^{n} \log f(a, b|x_i)$$

`weiblike` is a utility function for maximum likelihood estimation.

Example Continuing the example for `weibfit`:

```
r = weibrnd(0.5,0.8,100,1);
[logL,info] = weiblike([0.4746 0.7832],r)

logL =

  203.8216

info =

    0.0021    0.0022
    0.0022    0.0056
```

Reference

Patel, J. K., C. H. Kapadia, and D. B. Owen, *Handbook of Statistical Distributions*, Marcel-Dekker, 1976.

See Also `betalike`, `gamlike`, `mle`, `weibfit`

weibpdf

Purpose Weibull probability density function (pdf).

Syntax

```
Y = weibpdf(X,A,B)
```

Description `weibpdf(X,A,B)` computes the Weibull pdf with parameters `A` and `B` at the values in `X`. The arguments `X`, `A` and `B` must all be the same size except that scalar arguments function as constant matrices of the common size of the other arguments.

Parameters `A` and `B` are positive.

The Weibull pdf is:

$$y = f(x|a, b) = abx^{b-1}e^{-ax^b}I_{(0,\infty)}(x)$$

Some references refer to the Weibull distribution with a single parameter. This corresponds to `weibpdf` with `A` =1.

Examples The exponential distribution is a special case of the Weibull distribution.

```
lambda = 1:6;
y = weibpdf(0.1:0.1:0.6,lambda,1)

y =

    0.9048    1.3406    1.2197    0.8076    0.4104    0.1639

y1 = exppdf(0.1:0.1:0.6,1./lambda)

y1 =

    0.9048    1.3406    1.2197    0.8076    0.4104    0.1639
```

Reference

Devroye, L., *Non-Uniform Random Variate Generation*. Springer-Verlag. New York, 1986.

Purpose

Weibull probability plot.

Syntax

```
weibplot(X)
h = weibplot(X)
```

Description

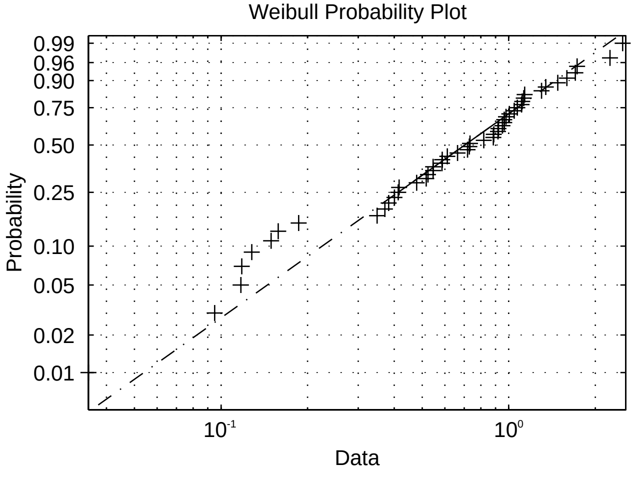
`weibplot(X)` displays a Weibull probability plot of the data in `X`. If `X` is a matrix, `weibplot` displays a plot for each column.

`h = weibplot(X)` returns handles to the plotted lines.

The purpose of a Weibull probability plot is to graphically assess whether the data in `X` could come from a Weibull distribution. If the data are Weibull the plot will be linear. Other distribution types may introduce curvature in the plot.

Example

```
r = weibrnd(1.2,1.5,50,1);
weibplot(r)
```



See Also

`normplot`

weibrnd

Purpose

Random numbers from the Weibull distribution.

Syntax

```
R = weibrnd(A,B)
R = weibrnd(A,B,m)
R = weibrnd(A,B,m,n)
```

Description

`R = weibrnd(A,B)` generates Weibull random numbers with parameters `A` and `B`. The size of `R` is the common size of `A` and `B` if both are matrices. If either parameter is a scalar, the size of `R` is the size of the other parameter.

`R = weibrnd(A,B,m)` generates Weibull random numbers with parameters `A` and `B`. `m` is a 1-by-2 vector that contains the row and column dimensions of `R`.

`R = weibrnd(A,B,m,n)` generates Weibull random numbers with parameters `A` and `B`. The scalars `m` and `n` are the row and column dimensions of `R`.

Devroye refers to the Weibull distribution with a single parameter; this is `weibrnd` with `A` = 1.

Examples

```
n1 = weibrnd(0.5:0.5:2,0.5:0.5:2)

n1 =

    0.0093    1.5189    0.8308    0.7541

n2 = weibrnd(1/2,1/2,[1 6])

n2 =

   29.7822    0.9359    2.1477   12.6402    0.0050    0.0121
```

Reference

Devroye, L., *Non-Uniform Random Variate Generation*. Springer-Verlag. New York, 1986.

Purpose Mean and variance for the Weibull distribution.

Syntax

```
[M,V] = weibstat(A,B)
```

Description For the Weibull distribution:

- The mean is:

$$a^{-\frac{1}{b}}\Gamma(1+b^{-1})$$

- The variance is:

$$a^{-\frac{2}{b}}\left[\Gamma(1+2b^{-1})-\Gamma^2(1+b^{-1})\right]$$

Examples

```
[m,v] = weibstat(1:4,1:4)

m =

    1.0000    0.6267    0.6192    0.6409

v =

    1.0000    0.1073    0.0506    0.0323

weibstat(0.5,0.7)

ans =

    3.4073
```

x2fx

Purpose Transform a factor settings matrix to a design matrix.

Syntax

```
D = x2fx(X)
D = x2fx(X,'model')
```

Description `D = x2fx(X)` transforms a matrix of system inputs, `X`, to a design matrix for a linear additive model with a constant term.

`D = x2fx(X,'model')` allows control of the order of the regression model. `'model'` can be one of these strings:

- `'interaction'` – includes constant, linear, and cross product terms.
- `'quadratic'` – interactions plus squared terms.
- `'purequadratic'` – includes constant, linear and squared terms.

Alternatively, the argument, `model`, can be a matrix of terms. In this case each row of `model` represents one term. The value in a column is the exponent to raise the same column in `X` for that term. This allows for models with polynomial terms of arbitrary order.

`x2fx` is a utility function for `rstool`, `regstats` and `cordexch`.

Example

```
x = [1 2 3;4 5 6]'; model = 'quadratic';
D = x2fx(x,model)

D =

     1     1     4     4     1    16
     1     2     5    10     4    25
     1     3     6    18     9    36
```

Let x_1 be the first column of `x` and x_2 be the second. Then, the first column of `D` is for the constant term. The second column is x_1 . The 3rd column is x_2. The 4th is x_1x_2. The fifth is x_1^2 and the last is x_2^2.

See Also `rstool`, `cordexch`, `rowexch`, `regstats`

Purpose X-bar chart for Statistical Process Control.

Syntax

```
xbarplot(DATA)
xbarplot(DATA,conf)
xbarplot(DATA,conf,specs)
[outlier,h] = xbarplot(...)
```

Description `xbarplot(DATA)` displays an x-bar chart of the grouped responses in `DATA`. The rows of `DATA` contain replicate observations taken at a given time. The rows must be in time order. The upper and lower control limits are a 99% confidence interval on a new observation from the process. So, roughly 99% of the plotted points should fall between the control limits.

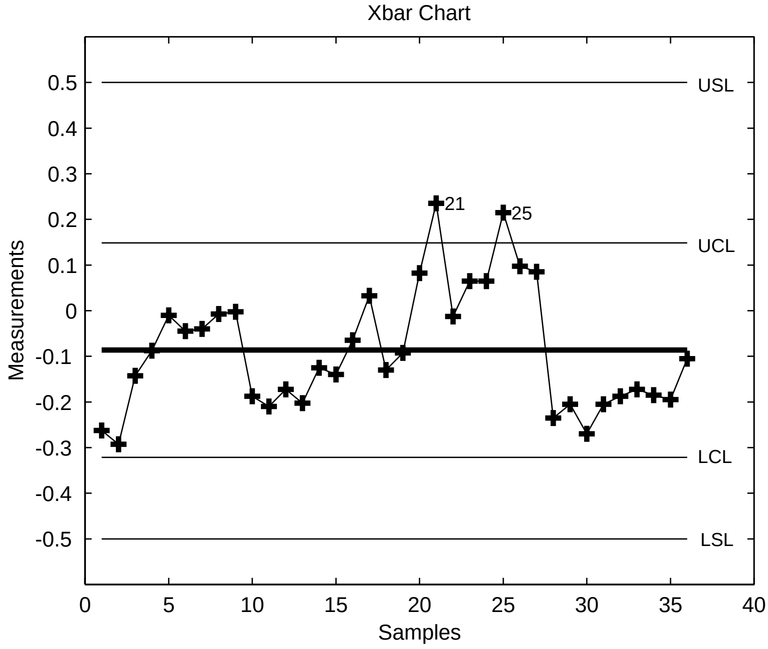
`xbarplot(DATA,conf)` allows control of the the confidence level of the upper and lower plotted confidence limits. For example, conf = 0.95 plots 95% confidence intervals.

`xbarplot(DATA,conf,specs)` plots the specification limits in the two element vector, `specs`.

`[outlier,h] = xbarplot(DATA,conf,specs)` returns `outlier`, a vector of indices to the rows where the mean of `DATA` is out of control, and `h`, a vector of handles to the plotted lines.

Example Plot an x-bar chart of measurements on newly machined parts, taken at one hour intervals for 36 hours. Each row of the `runout` matrix contains the measurements for four parts chosen at random. The values indicate, in thousandths of an inch, the amount the part radius differs from the target radius.

```
load parts
xbarplot(runout,0.999,[−0.5 0.5])
```



See Also

`capaplot`, `histfit`, `ewmaplot`, `schart`

Purpose Standardized Z score.

Syntax

```
Z = zscore(D)
```

Description `Z = zscore(D)` returns the deviation of each column of `D` from its mean, normalized by its standard deviation. This is known as the Z score of `D`.

For column vector `V`, `Z` score is `Z = (V-mean(V))./std(V)`

Purpose Hypothesis testing for the mean of one sample with known variance.

Syntax

```
h = ztest(x,m,sigma)
h = ztest(x,m,sigma,alpha)
[h,sig,ci] = ztest(x,m,sigma,alpha,tail)
```

Description `ztest(x,m,sigma)` performs a Z test at significance level 0.05 to determine whether a sample from a normal distribution (in `x`) could have mean `m` and standard deviation, `sigma`.

`h = ztest(x,m,sigma,alpha)` gives control of the significance level, `alpha`. For example if `alpha` = 0.01, and the result, `h`, is 1 you can reject the null hypothesis at the significance level 0.01. If `h` = 0, you cannot reject the null hypothesis at the `alpha` level of significance.

`[h,sig,ci] = ztest(x,m,sigma,alpha,tail)` allows specification of one or two-tailed tests. `tail` is a flag that specifies one of three alternative hypotheses:

- `tail` = 0 (default) specifies the alternative, $x \neq \mu$.
- `tail` = 1 specifies the alternative, $x > \mu$.
- `tail` = –1 specifies the alternative, $x < \mu$.

`sig` is the p-value associated with the Z statistic. $z = \frac{x - \mu}{\sigma}$

`sig` is the probability that the observed value of Z could be as large or larger *by chance* under the null hypothesis that the mean of x is equal to μ.

`ci` is a 1–`alpha` confidence interval for the true mean.

Example This example generates 100 normal random numbers with theoretical mean zero and standard deviation one. The observed mean and standard deviation are different from their theoretical values, of course. We test the hypothesis that there is no true difference.

```
x = normrnd(0,1,100,1);
m = mean(x)
m =

    0.0727

[h,sig,ci] = ztest(x,0,1)

h =

     0

sig =

    0.4669

ci =

   –0.1232    0.2687
```

The result, h = 0, means that we cannot reject the null hypothesis. The significance level is 0.4669, which means that by chance we would have observed values of Z more extreme than the one in this example in 47 of 100 similar experiments. A 95% confidence interval on the mean is [–0.1232 0.2687], which includes the theoretical (and hypothesized) mean of zero.

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